PLANT BREEDING

Estimation of genetic parameters and selection gains for sweet potato using Bayesian inference with *a priori* information

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ABSTRACT. The selection of superior sweet potato genotypes using Bayesian inference is an important strategy for genetic improvement. Sweet potatoes are of social and economic importance, being the material for ethanol production. The estimation of variance components and genetic parameters using Bayesian inference is more accurate than that using the frequently used statistical methodologies. This is because the former allows for using *a priori* knowledge from previous research. Therefore, the present study estimated genetic parameters and selection gains, predicted genetic values, and selected sweet potato genotypes using a Bayesian approach with *a priori* information. Root shape, soil insect resistance, and root and shoot productivity of 24 sweet potato genotypes were measured. Heritability, genotypic variation coefficient, residual variation coefficient, relative variation index, and selection gains direct, indirect and simultaneous were estimated, and the data were analyzed using Bayesian inference. Data from 11 experiments were used to obtain *a priori* information. Bayesian inference was a useful tool for decision-making, and significant genetic gains could be achieved with the selection of the evaluated genotypes. Root shape, soil insect resistance, commercial root productivity, and total root productivity showed higher heritability values. Clones UFVJM06, UFVJM40, UFVJM54, UFVJM09, and CAMBRAIA can be used as parents in future breeding programs.

Keywords: *Ipomoea batatas* (L.) Lam; genetical enhancement; bayes' theorem; biometry; experimental statistics.

Introduction

Genetic improvement increases crop productivity and quality, ensuring food security. The selection of superior genotypes is the first step in establishing a breeding program for sweet potatoes (*Ipomoea batatas* (L.) Lam.). Variance components must be estimated to select superior genotypes, predict genetic values (Oliveira, Santana, Oliveira, & Santos, 2014), and estimate selection gains. Several studies have already been conducted using the frequentist approach (Kalkmann, Peixoto, & Nóbrega, 2013; Borges, Ferreira, Soares, Santos, & Santos, 2010), however, a Bayesian approach is more advantageous for such estimations (Azevedo et al., 2017).

Bayesian inference is based on *a posteriori* distribution obtained from *a priori* information and likelihood function according to the Bayes' theorem (Oliveira, Malhado, Barbosa, Martins Filho, & Carneiro, 2015). The advantage of this is the use of *a priori* information, which results from the researcher's experience and /or experimental data. A more accurate and robust evaluation is possible with the use of this information (Klauenberg, Wübbeler, Mickan, Harris, & Elster, 2015).

Furthermore, the obtained asymmetric credibility intervals for variance components, genetic parameters, and breeding values are a peculiarity of Bayesian inference, which make this approach notably informative (Mathew et al., 2012) and facilitate hypothesis testing. According to Apiolaza, Chauhan, and Walker (2011), asymmetric credibility intervals obtained based on posterior distribution make the conclusions more realistic than symmetric credibility intervals of frequentist statistics. Additionally, Bayesian inference allows for the evaluation of unbalanced experiments and study of highly complex statistical models (Bink et al., 2007). Consequently, this approach is increasingly being used by breeders for the analysis of both molecular and phenotypic data (Azevedo et al., 2017).

The interest of public institutions in the genetic improvement of sweet potatoes has increased. This is due to the rusticity, drought tolerance, and adaptability of this crop to different types of soil and climate (Andrade Júnior et al., 2012). These characteristics make the culture of great importance for family farming. In addition, sweet potatoes can be used for ethanol production (Martins, Peluzio, Coimbra, & Oliveira Junior, 2012) and as animal feed (Valadares, Andrade Júnior, Pereira, Fialho, & Ferreira, 2019). However, private companies do not work with genetic improvement of this crop because it has a lower commercial value compared to others culture.

To this end, the present study estimated genetic parameters and selection gains, predicted genetic values, and selected sweet potato genotypes using a Bayesian approach with *a priori* information.

Material and methods

Twenty-four sweet potato clones (UFVJM25, Brazlândia Roxa - BZROXA, UFVJM07, BELGARD, UFVJM28, CAMBRAIA, ARRUBA, UFVJM05, UFVJM44, UFVJM40, UFVJM01, UFVJM15, Cariru Vermelha - CARIRUVERM, UFVJM09, UFVJM31, Tomba Carro 1 - TCARRO01, PRINCESA, UFVJM37, UFVJM41, UFVJM06, UFVJM56, UFVJM29, UFVJM54, and UFVJM21) were evaluated at the Institute of Agricultural Sciences (ICA) - Federal University of Minas Gerais (UFMG), Campus of Montes Claros, Minas Gerais State, Brazil (16°40′58.16″ S and 43°50′20.15″ W). These clones were selected in previous experiments carried out at Federal University of Jequitinhonha and Mucuri Valleys (UFVJM).

For the production of seedlings, 20 cm fragments of the branches were obtained. For rooting, these branches were kept in polyethylene pots (5 liters) with commercial substrate for 15 days. Subsequently, the seedlings were planted in the field. A randomized block design with four replications was used, each plot had 10 plants. The plots consisted of comprised 2.4 m long planting rows, with 1 m spacing between rows and 0.3 m spacing between plants (Azevedo, Andrade Júnior, Fernandes, Pedrosa, & Oliveira, 2015). During the initial 15 days, the seedlings were irrigated daily to ensure high survival. Subsequently, the seedlings were irrigated twice a week.

The experiment was performed using the Haplic Cambisol soil. Fertilization was performed based on the chemical analysis of soil and recommendations for the crop (Filgueira, 2008). Specifically, 180 kg ha^{-1} phosphorus and 30 kg ha^{-1} nitrogen were applied. Potassium fertilization was not necessary according to its level detected in soil chemical analysis.

Harvesting was performed at 165 days after planting. The shoots were cut close to the ground using pruning shears. Roots were manually harvested using hoes. After harvesting, the shoots and roots were weighed and separated to obtain the following variables: productivity of the fresh mass of branches (PFMB), total root productivity (TRP), commercial root productivity (CRP), average weight of commercial roots (AWCR), root shape (RS), and resistance to soil insects (RSI).

PFMB was calculated as the total weight of branches per plot, expressed in tons per hectare. TRP was estimated as the total weight of roots per plot, expressed in tons per hectare. For obtaining CRP, roots weighing 0.1-0.8 kg and without cracks, deformation, greening, insect damage, or veins were considered marketable, and the results were expressed in tons per hectare (Andrade Júnior, Elsayed, Azevedo, Santos, & Ferreira, 2018). The AWCR was obtained by the ratio between CRP and the number of commercial roots, expressed in grams.

RS was determined according to the following scale: grade 1, fusiform roots (excellent); grade 2, near fusiform roots (good); grade 3, irregular but not fusiform roots (acceptable); grade 4, highly irregular roots (bad); and grade 5, deformed roots (very bad) (Azevedo, Maluf, Silveira, & Freitas, 2002). RSI was determined according to the following scale: grade 1, roots free of insect damage; grade 2, roots with little but observable damage; grade 3, root with obviously visible damage; grade 4, roots with damage covering most of the surface; and grade 5, roots with damage covering the entire surface (Azevedo et al., 2002).

RS and RSI were determined by three trained evaluators. As these are qualitative ordinal variables, the average of scores assigned to each plot by the three evaluators was obtained. According to Pimentel-Gomes (2009), data obtained by averaging the measurements from three or more evaluations for qualitative ordinal variables can be analyzed statistically using the same techniques as that used for quantitative variables.

For statistical analysis, the following model was considered:

$$y = Xr + Bcov + Zg + e$$

where y is the vector of data, r is the vector of the repetition effects plus the general average, g is the vector of the genetic effects, and e is the vector of errors. The coefficient *cov* refers to the regression coefficient associated with the covariate (number of plants per plot). Capital letters represent the incidence matrix for each effect.

Assuming $e|\sigma_e^2 \sim N(0, I\sigma_e^2)$, the distribution of the observed data (likelihood function) can be given as follows:

$$y\,|r, cov, g, \sigma_g^2, \sigma_e^2 \sim N(Xr + Bcov + Zg, I\sigma_e^2)$$

where I is an identity matrix and σ_g^2 and σ_e^2 are the components of variance associated with the genotypic and residual effects, respectively.

The *a priori* distribution for the location parameters (systematic and random effects) of the model can be given as follows:

$$r\,|\,\mu_r, I_r, \sigma_r^2 \sim N\,(\mu_r, I_r\,\sigma_r^2)$$

$$cov\,|\mu_{cov}, I_{cov}, \sigma_{cov}^2 \sim N\,(\mu_{cov}, I_{cov}\,\sigma_{cov}^2)$$

$$g\,|\,I_g\,\sigma_g^2 \sim N\,(0, I_g\,\sigma_g^2)$$

where μ_r and σ_r^2 are the known parameters (hyperparameters) of the multivariate normal distribution associated with the block effect, with the covariance matrix given as $I_r\sigma_r^2$ (I_r is the identity matrix), and μ_{cov} and σ_{cov}^2 are the hyperparameters of the multivariate normal distribution associated with the covariate effect, with the covariance matrix given as $I_{cov}\sigma_{cov}^2$ (I_{cov} is the identity matrix). For the variance components σ_g^2 and σ_e^2, the following inverted-scaled chi-square distributions were assumed *a priori*:

$$\sigma_g^2\,|\,V_g, S_g \sim V_g S_g \chi_g^{-2}$$

$$\sigma_e^2\,|\,V_e, S_e \sim V_e S_e \chi_e^{-2}$$

A priori distributions for the variance components (σ_g^2 and σ_e^2) were used to reparametrize the original-scaled inverted chi-square (Scale χ^{-2}) distribution, because the rjags package does not work directly with this distribution. This distribution is a special case of the inverse gamma distribution (*inv gamma*). Thus, assuming that $\sigma^2 \sim Scale\ \chi^{-2}$ (v,S), where S is equal to $v\sigma^{2*}$ and σ^{2*} is the most probable *a priori* value of σ^2, the equivalent distribution is $\sigma^2 \sim inv\ Gamma(v/2, S/2)$, which allows using $\bar{\tau} = 1/\sigma^2 \sim gamma(v/2, S/2)$ (Silva, Viana, Faria, & Resende, 2013).

To use *a priori* information, data from 11 experiments on genotypes in the germplasm bank of UFVJM were considered (Table 1). The inverse of the average value of a given variance component ($\bar{\tau} = 1/\bar{\sigma}^2$) and its respective variance ($S_{\bar{\tau}}^2$) were calculated from a set of values reported in these studies and equalized to the expectation and variance of the distribution $gamma(\alpha, \beta)$: $\bar{\tau} = \alpha/\beta$, and $S_{\bar{\tau}}^2 = \alpha/\beta^2$. Thus, $\alpha = \bar{\tau}/S_{\bar{\tau}}^2$ and $\beta = \bar{\tau}^2/S_{\bar{\tau}}^2$, resulting in $\bar{\tau} = 1/\sigma^2 \sim gamma(\alpha, \beta)$, which is an informative priori whose expected value and variance are coincident consistent with the observed mean and variance, respectively, of the data set containing the reported values. Similar methodology has been applied in previous studies (Silva et al., 2013; Teodoro, Nascimento, Torres, Barroso, & Sagrilo, 2015; Euzebio et al., 2018). μ_r and μ_{cov} were hyperparameters of multivariate normal distribution, with a mean of 100 and standard deviation of 0.00001. σ_r^2 and σ_{cov}^2 were used as the inverse of variance components, defined as $\bar{\tau} = 1/\sigma^2 \sim gamma(0.001, 0.001)$.

According to the Bayes' theorem, the joint posteriori distribution of all unknown parameters (r, cov, g, σ_g^2 and σ_e^2) is proportional to the product of likelihood function with *a priori* distribution. Thus, the general equation for this theorem is as follows:

$$P\,(r, cov, g, \sigma_g^2\,\sigma_e^2\,|\,y)\,\alpha\,P(y\,|\,r, cov, g, \sigma_g^2, \sigma_e^2)x\,P\,(r\,|\,u_r, I_r, \sigma_r^2)\,x\,P(cov\,|\,u_{cov}, I_{cov}\,\sigma_{cov}^2)\,x\,P(g\,|\,u_g, I\sigma_g^2)x\,P(\sigma_g^2\,|\,V_g S_g)xP(\sigma_e^2\,|\,V_e S_e)$$

Using the respective probability density of the *a priori* distribution, the equation for the joint *a posteriori* distribution is as follows:

$$P\,(r, cov, g, \sigma_g^2, \sigma_e^2\,|\,y)\,\alpha\,(\sigma_e^2)^{-\frac{N}{2}}\,exp\left\{-\frac{[y-(Xr+Bcov+Zg+e)]^t[y-(Xr+Bcov+Zg+e)]}{2\sigma_e^2}\right\}x(\sigma_r^2)^{-\frac{n_r}{2}}$$

$$exp\left[-\frac{(r-u_r)^t(r-u_r)}{2\sigma_r^2}\right]x(\sigma_{cov}^2)^{-\frac{1}{2}}\,exp\left[-\frac{(cov-u_{cov})^t(cov-u_{cov})}{2\sigma_{cov}^2}\right]x(\sigma_g^2)^{-\frac{n_r}{2}}\,exp\left(-\frac{g^t g}{2\sigma_g^2}\right)x\,(\sigma_g^2)^{-\frac{V_g+1}{2}}\,exp\left(-\frac{V_g S_g}{2\sigma_g^2}\right)x$$

$$(\sigma_e^2)^{-\frac{V_e+1}{2}}\,exp\left(-\frac{V_e S_e}{2\sigma_e^2}\right)$$

Table 1. Year of execution, number of genotypes, number of repetitions, and locations of 11 experiments on sweet potato genotypes from the germplasm bank of the Federal University of Jequitinhonha and Mucuri Valleys.

Experiments	Year	N° genotypes	N° repetitions	Locations
1	2005	12	4	Diamantina, MG
2	2005	12	4	Diamantina, MG
3	2007	6	3	Diamantina, MG
4	2007/08	65	3	Diamantina, MG
5	2009	12	4	Diamantina, MG
6	2009	8	3	Diamantina, MG
7	2009	15	4	Diamantina, MG
8	2009	8	3	Diamantina, MG
9	2010/11	15	4	Couto Magalhães de Minas, MG
10	2013	72	4	Diamantina, MG
11	2015/16	10	5	Diamantina, MG

Statistical inference was based on the posterior marginal distribution $P(.|y)$ for each parameter. The necessary integrals to obtain these distributions are intractable, implying the use of numerical evaluation by specialized algorithms, such as the Markov chain Monte Carlo (MCMC) algorithm (Silva et al., 2013). These algorithms generate random samples from the posterior marginal distribution, that is, indirectly from the full conditional posterior distributions (f.c.p.d.), which are the posterior distributions for a given parameter conditional on the data and the remaining parameters. In general, when $\theta = [\theta_1, \theta_2..., \theta_p]$ is the full set of p parameters, the f.c.p.d. for a particular parameter θ_k is denoted by $P(\theta_k|\theta_1, ..., \theta_{k-1}, \theta_{k+1}, ..., \theta_p, y)$ Once these f.c.p.d.s are characterized as the known families of probability distributions to present closed forms, the Gibbs sampler algorithm can be used (Silva et al., 2013).

All analyses were performed using R. For MCMC analysis, 100,000 iterations were performed. We set the burn-in to 10,000 iterations and thinned every 15 iterations using the rjags package (Plummer, 2019). Based on the posterior distribution of variance components, the following values were estimated: heritability, genotypic variation coefficient, residual variation coefficient, and relative variation index. In addition, direct, indirect, and simultaneous selection gains were estimated using the method described by Mulamba and Mock (1978), with a selection intensity of 30%. For each parameter, the mean, mode, median, credibility interval (95%), and Geweke convergence were estimated using the BOA package (Smith, 2007).

Results

For most variables evaluated, the *a posteriori* and *a priori* distributions of genetic variance were similar. However, the *a priori* and *a posteriori* distributions of RSI and RS were different (Figure 1). Similarly, the *a priori* and *a posteriori* distributions for residual variance were different, with higher estimates for the latter distribution (Figure 2). The estimated residual variance coefficient was high for all evaluated variables (Table 2).

The p-values estimated using Geweke convergence test were greater than 0.05 for all variables, indicating convergence in the iterative process. Values close to the mean, median, and mode of the posterior distribution of the obtained parameters were calculated (Table 2). The values indicated that the distributions were approximately symmetric.

The highest heritability values were found for RS, RSI, and CRP, but the credibility intervals for these and other traits were comparable. CRP, RSI, and TRP showed higher genotypic variance coefficients, but their credibility intervals were comparable to those of the remaining traits (Table 2).

The posterior distribution of residual variance coefficient ranged from 17.34 to 47.94 for CRP. CRP showed a higher residual variance coefficient than AWCR, RS, and RSI (Table 2). Mean, mode, and median of the posterior distribution of relative variance coefficient were greater than 1 for RS alone; for IR, the value of 1.00 fell within the credibility interval (Table 2).

CRP, RSI, TRP, and PFMB showed the greatest direct selection gains, with estimates of 32%, |-24%|, 22%, and 21%, respectively (Table 3). The remaining characteristics showed lower selection gains, although no value was below 15% (Figure 3).
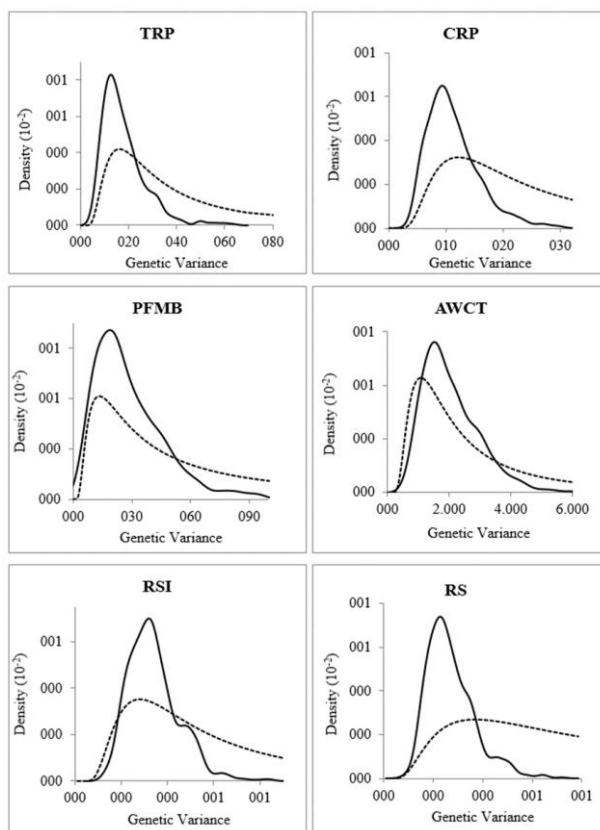
Figure 1. *A priori* (---) and *a posteriori* (–) distributions of genetic variance in total root productivity (TRP), commercial root productivity (CRP), productivity of the fresh mass of branches (PFMB), average weight of commercial roots (AWCR), resistance to soil insects (RSI), and root shape (RS) in the tested sweet potato clones.
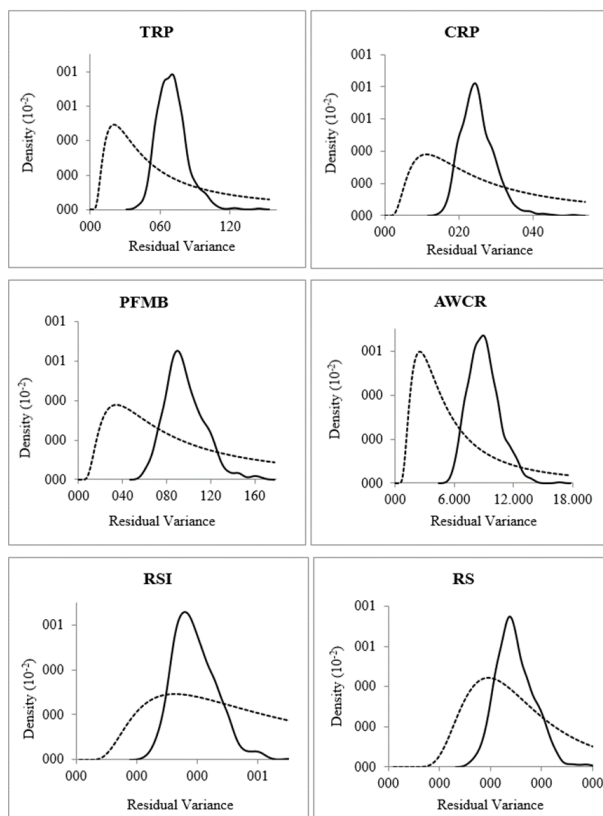

Figure 2. *A priori* (---) and *a posteriori* (–) distributions of residual variance in total root productivity (TRP), commercial root productivity (CRP), productivity of the fresh mass of branches (PFMB), average weight of commercial roots (AWCR), resistance to soil insects (RSI), and root shape (RS) evaluated in sweet potato clones.

Table 2. Mean (Me), median (Md), mode (Mo), credibility intervals of posterior densities (HPD), and p-value of Geweke convergence for the estimates of heritability, genotypic variance coefficient (%), residual variance coefficient (%), and relative variance coefficient the in tested sweet potato clones.

Variables	Descriptive Analysis			HPD (95%)		p-valor (Geweke)
	Me	Md	Mo	low	upper	
Heritability						
TRP	0.20	0.18	0.15	0.06	0.36	0.93
CRP	0.30	0.30	0.29	0.15	0.48	0.81
PFMB	0.22	0.20	0.16	0.05	0.44	0.69
AWCR	0.19	0.17	0.13	0.07	0.34	0.23
RS	0.51	0.51	0.54	0.33	0.68	0.63
RSI	0.46	0.45	0.41	0.29	0.63	0.85
Genotypic variance coefficient (%)						
TRP	21.26	20.41	17.71	11.99	30.54	0.94
CRP	31.60	30.82	30.20	21.18	44.44	0.33
PFMB	18.99	18.06	17.00	8.11	29.62	0.71
AWCR	14.87	14.41	13.20	9.02	21.24	0.28
RS	18.33	17.95	17.42	13.04	25.04	0.45
RSI	22.90	22.68	22.74	16.76	29.96	0.34
Residual variance coefficient (%)						
TRP	43.16	43.05	41.52	36.36	51.18	0.91
CRP	47.92	47.60	47.94	39.78	55.87	0.14
PFMB	36.05	35.65	35.57	29.62	42.21	0.91
AWCR	31.58	31.50	30.14	26.92	37.50	0.92
RS	17.83	17.70	17.34	15.57	20.58	0.78
RSI	24.85	24.61	23.18	20.57	28.91	0.06
Relative variance coefficient						
TRP	0.50	0.48	0.42	0.26	0.74	0.94
CRP	0.66	0.65	0.64	0.42	0.96	0.78
PFMB	0.54	0.50	0.43	0.23	0.90	0.72
AWCR	0.48	0.46	0.39	0.27	0.73	0.24
RS	1.03	1.01	1.08	0.69	1.44	0.50
RSI	0.93	0.91	0.83	0.61	1.26	0.84

Note: Total root productivity = TRP, commercial root productivity = CRP, productivity of the fresh mass of branches = PFMB, average weight of commercial roots = AWCR, resistance to soil insects = RSI, and root shape = RS.

Table 3. Direct (main diagonal), indirect (outside the diagonal), and simultaneous (MM, Mulamba & Mock, 1978) selection gains for the tested sweet potato clones.

Variable	Selection criteria						
	TRP	CRP	PFMB	AWCR	RS	RSI	MM
TRP	21.91	17.41	6.33	2.85	0.37	-4.02	7.36
CRP	8.67	32.34	4.07	-4.62	-0.68	-6.24	9.63
PFMB	6.77	6.00	20.57	8.78	0.97	6.59	12.04
AWCR	-3.70	1.84	-9.56	-15.81	-1.49	-3.12	-5.29
RS	-2.59	-7.62	-1.98	-3.38	-16.62	-15.24	-7.98
RSI	3.45	1.59	-3.27	-4.3	-11.58	-24.12	-9.82

Note: Total root productivity = TRP, commercial root productivity = CRP, productivity of the fresh mass of branches = PFMB, average weight of commercial roots = AWCR, resistance to soil insects = RSI, and root shape = RS.

In the selection of TRP, favorable indirect gains were observed (Table 3) for all variables, except AWCR and RSI. In the selection of CRP, indirect unfavorable effects were observed for AWCR and RSI. In the selection of PFMB, indirect favorable effects were observed for all variables. In the selection for AWCR, RS, and RSI, indirect unfavorable effects were observed for CRP (Table 3). In simultaneous selection (MM), favorable gains were observed for all variables (Table 3).

The credibility intervals for genetic variance in TRP and PFMB overlapped (Figure 4). UFVJM40 and BELGARD showed the highest and lowest CRP, respectively. UFVJM28 and BELGARD showed the highest and lowest AWCR, respectively (Figure 4).

BELGARD, CAMBRAIA, UFVJM40, and UFVJM06 showed significantly lower RSI than UFVJM28. UFVJM06, UFVJM40, CAMBRAIA, and BELGARD showed significantly lower RS than UFVJM28 (Figure 4).
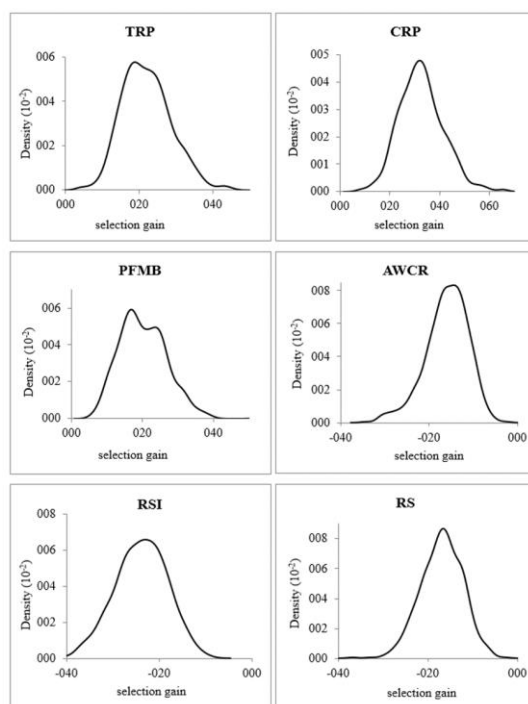
Figure 3. *A posteriori* distribution for the estimated selection gain (%) in total root productivity (TRP), commercial root productivity (CRP), productivity of the fresh mass of branches (PFMB), average weight of commercial roots (AWCR), resistance to soil insects (RSI), and root shape (RS) in the tested sweet potato clones.
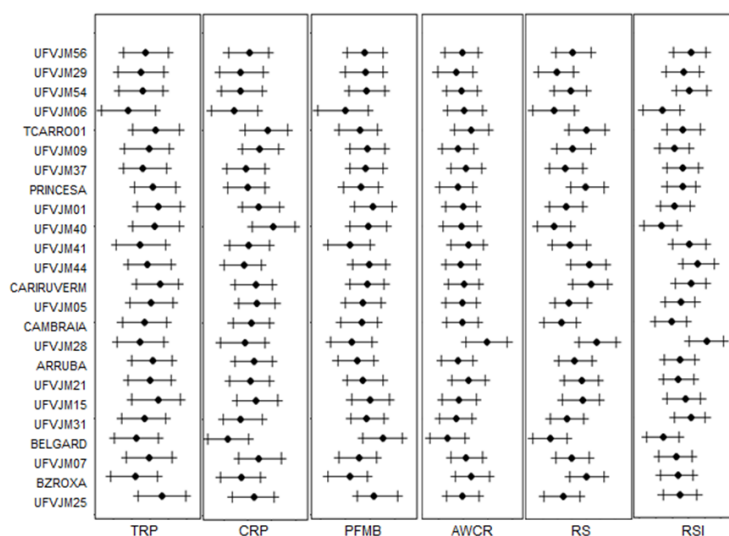

Figure 4. Representation of the mode of genetic parameters within credibility intervals obtained based on the posterior distribution (95%) of total root productivity (TRP), commercial root productivity (CRP), productivity of the fresh mass of branches (PFMB), average weight of commercial roots (AWCR), resistance to soil insects (RSI), and root shape (RS) in the tested sweet potato clones.

Discussion

The possibility of estimating the posterior distribution of parameters is one of the greatest advantages of Bayesian inference (Torres et al., 2018). This approach can be used in plant breeding, allowing us to obtain credibility intervals, which are important for understanding the genetic nature of variables of interest (Silva et al., 2013). For these variables, we can estimate genetic parameters, such as heritability, and variance components, such as genotypic, residual, and relative variance coefficients (Waldmann & Ericsson, 2006).

The proximity between *a priori* and *a posteriori* distributions of genetic variance for most variables in this study indicates that genetic variability was maintained relative to the previous experiments. Values of the *a posteriori* distribution of residual variance were the highest for AWCR, TRP, CRP, RS, and RSI. These characteristics are influenced by soil type. In sandy soils, as in the case of previous experiments, the lateral

growth of roots is greater and fewer deformed roots are formed. Sandy soil also facilitates sweet potato harvest with less physical damage and greater yield (Silva, Lopes, & Magalhães, 2008). The present experiment was performed in Haplic Cambisol soil, which has a clayey texture, rendering the root harvest difficult. In terms of RSI, clayey soils are more conducive to the development of sweet potato borer (*Euscepes postfasci*), one of the major pests of the crop (Kuriwada, Kumano, Shiromoto, Haraguchi, & Kohama, 2012), as the insects can use cracks in the soil to reach the roots. Sweet potato borer infestation leads to substantial productivity losses. This does not occur in sandy soils, in which no cracks are formed with tuber development, and the insects cannot access the roots (Menezes, 2002).

The credibility intervals for variance components and genetic parameters make Bayesian inference more informative (Mathew, Léon, & Sillanpää, 2015) because this approach does not require derivation of complex estimators and various assumptions, as does the frequentist approach, to obtain credibility intervals. In this study, Geweke test demonstrated the reliability of results for all parameters, proving the convergence of the iterative process.

Heritability estimates showed great potential for selection. Previous studies have shown heritability values close to those found in this work (Borges et al., 2010). The high estimates of residual variance coefficients (above 20%) for most variables can be justified by difficulties encountered during crop harvest, resulting in incomplete root harvest (Azevedo et al., 2015). In studies of crops with underground structures, environmental control is difficult, which results in variance coefficients above 30% (Cavalcante et al., 2006). This susceptibility of root parameters to environmental factors has been observed in several studies of sweet potatoes (Andrade Júnior et al., 2009, Moreira, Queiroga, Sousa Júnior, & Santos, 2011).

The estimated genetic and relative variance coefficients were promising for all characteristics evaluated, specifically RS and RSI. These parameters measure the degree of genetic determination of a trait and also indicate genotypes with high genetic variability (Azevedo et al., 2015). Relative variance coefficient and heritability indicate the reliability of phenotypic values representing the genotypic values. This increases the discriminatory power and expected selection gains (Ivoglo et al., 2008). The mode of relative variance coefficient was greater than 1 for RS, and the value of 1 fell within the credibility interval for IR. These results indicate favorable experimental conditions for the selection of RS and IR. Therefore, Bayesian inference in indeed advantageous for estimating parameters and their reliability, helping decision-making in breeding programs. For TRP, CRP, AWCR, and PFMB, relative variance coefficients were smaller than 1, indicating that environmental variation exceeds the genetic variation for these traits (Alves, Peixoto, Vieira, & Boiteux, 2006).

CRP and RSI are fundamental to commercialization. Selection gains greater than 20% were estimated for these characteristics, in addition to PMVR. Azevedo et al. (2015) observed values of 68% for CRP; however, the authors considered the selection index to be 20%, while we considered it to be 30% in the present study. Lower indices of selection provide higher gains; however, this greatly restricts genetic variability, which is not reflected at the beginning of genetic improvement programs. Azevedo et al. (2015) observed a selection gain of -4.90% for RSI. This estimate is much lower (in module) than our estimate (24%).

Simultaneous selection maximizes the probability of success in improvement, providing balanced gains for all characteristics (Cruz, Regazzi, & Carneiro, 2012). With indirect selection, favorable gains were observed for all variables with selection for PFMB. This information is important for breeding program aimed at the increasing the yield of shoots as animal feed.

The UFVJM40 genotype, with higher CRP and lower RSI and RS, was superior to others. UFVJM06 and CAMBRAIA also exhibited lower RSI and RS. BELGARD showed lower RS, RSI, and AWCR, resulting in lower CRP, which is not desirable. The worst results were observed for UFVJM28, with higher RSI, RS, and AWCR.

Conclusion

It is possible to take the advantage of *a priori* knowledge obtained in previous experiments through Bayesian inference, which may serve as an efficient tool assisting with decision-making in sweet potato genetic improvement programs. The variables CRP, RS, and RSI showed higher heritability, and substantial gains can be achieved with the selection of the genotypes with these traits. Simultaneous selection is an important strategy to maximize selection gains for all characteristics in sweet potato. UFVJM40, UFVJM06, UFVJM09, and CAMBRAIA are superior to others and can be used as parents in future breeding programs.

Acknowledgements

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