Individual multivariate REML/BLUP in the presence of genotype x environment interaction in rubber tree (*Hevea*) breeding

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ABSTRACT

The present study was carried out to estimate genetic parameters and additive genetic values by the individual REML/BLUP procedure for rubber tree [*Hevea brasiliensis* (Willd. ex Adr. de Juss.) Muell.-Arg.] selection in the presence of genotype x environment interaction. Twenty-two half-sib progenies were planted in Experimental Stations at Jaú, Pindorama and Votuporanga in São Paulo State, Brazil, in a randomized complete block design with five replicates and 10 plants per plot, and assessed for dry rubber yield at three years of age. The results for yield showed the presence of genetic variability among progenies with higher values for Pindorama, especially for additive genetic and phenotypic variance estimates, characterizing the location as a favorable environment for the expression of the population genetic variability. The high correlation among progenies observed between the Votuporanga and Jaú environments confirmed that a single breeding program can satisfactorily attend both regions. The genetic gains estimated by the multivariate and univariate BLUP methods showed superiority (5% to 21%) for the individual multivariate BLUP procedure, reflecting the great efficacy and flexibility of the method for predicting genetic values and gains in the presence of genotype x environment interaction. The use of information from the three locations combined leads to the maximization of the genetic gain with the selection.

KEY WORDS: *Hevea brasiliensis*, progeny, heritability, selection, correlation.

INTRODUCTION

The rubber tree [*Hevea brasiliensis* (Willd. ex Adr. de Juss.) Muell.-Arg.] is an important commercial species and has been subjected to breeding for increased latex yield, especially in areas free (escape areas) of South American Leaf Bligh. The species is considered a preferentially cross-pollinating, diploid, perennial species, with a long breeding cycle. Usually, three selection stages are involved and 25 to 30 years are required until the final choice of clones for large scale planting can be made. This long breeding process has led to considerable investment in studies of genetics parameters to maximize the selection progress.

Plantings were established in different environments in São Paulo state to assess the species adaptability to different areas. Quantification of the genotype x environment interaction is important for effective selection of the best genotypes to continue in the breeding program.

Several reports on genotype x environment interaction for the species are available: Tan (1995) (Malaysia); Jayasekera (1983), Jayasekera and Karunsekara (1984) (Sri Lanka), Daslin et al. (1986) (Indonesia), Onokpise et al. (1986) (Nigeria), Meenattor et al. (1991)(India), Gonçalves et al. (1990, 1991, 1998a, 1998b) and Costa et al. (2000a) (Brazil).

In these reports, interaction was studied using traditional methods based on the analysis of variance (estimation method named least squares), considering progeny mean values. It is necessary, however, to assess candidates for selection at the individual level by the predicted additive genetic values, using methods compatible with the unbalanced structure of the genetic assessment experiments.

Accurate prediction of genetic values of individual candidates for selection is an essential part of forest breeding programs (Resende et al., 1999). The random variable prediction procedure, also known as BLUP (best line unbiased prediction) or mixed

linear models methodology, was formally presented by Henderson (1973, 1975), and is an optimum prediction procedure of genetic values (Henderson, 1984; Gianola and Hammond, 1990; Robinson 1991; Searle et al., 1992). The REML (restricted maximum likelihood) method (Patterson and Thompson, 1971) is also an optimum procedure for estimating variance components, especially for unbalanced data. The individual BLUP (the animal model) was developed by Quaas and Pollak (1980) for application in animal breeding and is the most recommended procedure for forest breeding, as it allows prediction of genetic values of individual trees (Resende and Fernandes, 1999).

The mixed model methodology was applied mainly on family means in unbalanced data situations (death during time) (White and Hodge, 1989; Resende et al., 1993; Resende et al., 1996a, 1996b; Resende and Oliveira, 1997; Bueno Filho, 1997) to assess individual candidates for selection, leading to the maximization of the genetic gain. In this context, Resende and Dias (2000) emphasized that selection of individuals for seed propagation should be based on the predicted additive genetic values of several candidates in the locations.

In Brazil, in unbalanced data situations, the selection of individuals has been carried out using the multi-effect index method presented by Resende and Higa (1994a), which has proved superior to other forms of joint selection (Bueno Filho, 1992; Resende and Higa 1994b; Pires et al., 1996; Costa et al., 1999, 2000b). The used index is an optimum selection procedure for unbalanced data situations, as it considers all the random effects of the statistical model associated to the randomized complete block design with several plants per plot (Resende and Fernandes, 1999). The individual BLUP procedure using variance components estimated by least squares was used by Costa et al. (1999) while variance components estimated by REML were used by Kalil Filho et al. (2000), specifically for the rubber tree.

The present study was carried out to estimate genetic parameters and additive genetic values by the REML/individual BLUP procedure for rubber tree selection in the presence of genotype x environment interaction.

MATERIAL AND METHODS

Progeny tests were installed in three experimental stations of the Instituto Agronômico (IAC) at Campinas in São Paulo State, Brazil placed in different rubber tree cultivation regions. The characteristics of these three places are now described:

The Jaú Experimental Station: located at latitude 22°17′S, longitude 48°34′W and altitude of 580m. The soil is dark red latosols type, clay texture, deep, with well-drained flat topography. The Aw climate (Köpen) predominates in this region with a defined dry season, average annual temperature of 21.6°C, average moisture of around 70% with extremes of 77% in February and 59% in August. The average annual rainfall is around 1,344 mm.

The Pindorama Experimental Station: located at latitude 21°13′S, longitude 48°56′W and 560 m of altitude. The soil is Red-yellow TB eutrophic podzolized soil, medium texture, deep, abrupt and well drained (Lepesch and Valadares, 1976). The climate is continental tropical, with predominance of a wet summer and a dry winter period with lower temperatures. The average annual temperature and rainfall are 16.6°C and 1,390.3 mm, respectively. Generally, from October to April a favorable water balance for growth and yield occur. Water deficits and low temperatures occur from May to September.

The Votuporanga Experimental Station: located at latitude 20°25′S, longitude 49°59′W and altitude of 450 m. The soil is sandy phase podzolized type and the climate is continental tropical with predominance of a wet summer and a dry winter period with lower temperatures. The average annual temperature and annual rainfall are 22.3°C and 1,420 mm, respectively.

The genetic material was compounded by open pollinated progenies (individuals within progeny considered as half-sibs) with the reference population as tester. The individuals used as parents were taken randomly from the base or reference population.

Seeds were collected at the Experimental Station at Campinas, sowed in polyethylene bags in the three experimental stations and transported to the definitive planting location when showing two developed flush of leaves.

Ten seedlings were space planted at 1.5m within single-row plots. Between-plot spacing was also 1.5 m. The experimental design was a randomized complete block with 22 treatments and five replicates.

Progenies were assessed at three years of age for dry rubber yield, obtained by the Hamaker-Morris-Mann (HMM) test modified for three-year-old seedlings (Tan and Subramanian, 1976) using the dry rubber yield mean from 30 tappings per seedling. The tapping panel was opened 20 cm above ground, using the 1/2S d/3 system. The 1/2S nomenclature corresponds to the half spiral system and the d/3 nomenclature expresses the three-day interval between tappings.

Mixed Linear Model

The mixed linear model (additive univariate model) used in the present study for the individual analysis of each experiment followed the methodology of Resende and Fernandes (1999) and Resende and Dias (2000):

y = Xb + Za + Wc + e, where:

y, b, a, c and e are data vectors of block effects (fixed), additive genetic effects (random), plot effects (random) and random errors, respectively. X, Z e W are incidence matrixes for b, a e c, respectively.

Distributions and structures of means and variances

$y|b, V \sim N(Xb, \ V)$

$a|A, \ \sigma_A^2 \sim N(0, \ A \ \sigma_a^2)$

$c|\sigma_c^2 \sim N(0, \ I \ \sigma_c^2)$

$e|\sigma_e^2 \sim N(0, \ I \ \sigma_e^2)$

$Cov \ (a, \ c') = 0; \quad Cov \ (a, \ e') = 0; \quad Cov \ (c, \ e') = 0$

that is,

$$E\begin{bmatrix} y \\ a \\ c \\ e \end{bmatrix} = \begin{bmatrix} Xb \\ 0 \\ 0 \\ 0 \end{bmatrix} \quad and \quad Var \begin{bmatrix} y \\ a \\ c \\ e \end{bmatrix} = \begin{bmatrix} V & ZG & WC & R \\ GZ' & G & 0 & 0 \\ CW' & 0 & C & 0 \\ R & 0 & 0 & R \end{bmatrix}, \text{ where:}$$

$G = A \ \sigma_A^2$

$R = I \ \sigma_c^2$

$C = I \ \sigma_e^2$

$V = ZA \ \sigma_a^2 Z' + WI \ \sigma_c^2 W' + I \ \sigma_e^2 = ZGZ' + WCW' + R.$

Mixed model equations

$$\begin{bmatrix} X'X & X'Z & X'W \\ Z'X & Z'Z + A^{-1}\lambda_1 & Z'W \\ W'X & W'Z & W'W + I\lambda_2 \end{bmatrix} \begin{bmatrix} \hat{b} \\ \hat{a} \\ \hat{c} \end{bmatrix} = \begin{bmatrix} X'y \\ Z'y \\ W'y \end{bmatrix}, \text{ where:}$$

$$\lambda_1 = \frac{\sigma_e^2}{\sigma_a^2} = \frac{1 - h^2 - c^2}{h^2}; \qquad \lambda_2 = \frac{\sigma_e^2}{\sigma_a^2} = \frac{1 - h^2 - c^2}{c^2}$$

$$h^2 = \frac{\sigma_a^2}{\sigma_a^2 + \sigma_c^2 + \sigma_e^2} = \text{ individual narrow sense}$$

habitability in the block;

$$c^2 = \sigma_c^2 / (\sigma_a^2 + \sigma_c^2 + \sigma_e^2) = \text{ correlation due to}$$

common environment in the plot;

σ_a^2 = additive genetic variance;

σ_c^2 = among plot variance;

σ_e^2 = residual variance (within plot environmental + non- additive genetic variance);

A = matrix of additive genetic correlation among individuals under assessment.

The solutions of the mixed model equations should be obtained using iterative methods for solving linear equation systems, such as the Gauss Seidel. A direct solution by inversion of the matrix of coefficients is impossible in practice.

For the balanced case, solutions obtained for **â** from the mixed model equations is equivalent to the predictions obtained by the multi-effect index (Resende & Higa, 1994a), given by:

$I = b_1(Y_{ijK} - \overline{Y}_{ij.}) + b_2(\overline{Y}_{i..} - \overline{Y}_{...}) + b_3(\overline{Y}_{ij.} - \overline{Y}_{i..} - \overline{Y}_{.j.} + \overline{Y}_{...})$, where:

$$b_1 = \frac{(1 - \rho_g) \ \sigma_a^2}{\sigma_{dp}^2}; \qquad b_2 = \frac{\frac{[1 + (nb - 1) \ \rho_g]}{nb} \sigma_a^2}{\sigma_f^2 + \sigma_c^2 / b + \sigma_{dp}^2 / nb}; \qquad b_3 = \frac{\frac{(1 - \rho_g)}{n} \sigma_a^2}{\sigma_{dp}^2 / n + \sigma_c^2}$$

ρ_g = intraclass additive genetic correlation ($\rho_g = 0.25$ for half-sib families);

$\sigma_f^2, \ \sigma_c^2 \ and \ \sigma_{dp}^2$ = variance among families, among and within plots, respectively.

$Y_{ijk}, \ \overline{Y}_{ij.}, \ \overline{Y}_{i..}, \ \overline{Y}_{.j.} \ and \ \overline{Y}_{...}$ = individual phenotypic value, plot mean, progeny mean, block mean and general mean, respectively.

REML estimates of the variance components via EM algorithm

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

$\hat{\sigma}_a^2 = [\hat{a}' A^{-1} \ \hat{a} + \hat{\sigma}_e^2 \ tr \ (A^{-1} \ C^{22})] / q$

$$\hat{\sigma}_c^2 = [\hat{c}'c + \hat{\sigma}_e^2 \; tr \; C^{33}]/s, \qquad \text{where:}$$

C^{22} e C^{33} comes from:

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

C = matrix of the coefficients of the mixed model equation;

tr = matrix trace operator;

r(x) = X matrix rank;

N, q, s = total data number, individual and plot number, respectively.

Column sequence in the data file for analysis by the DFREML software (Meyer, 1991): Individual, Father, Mother, Block, Plot, Variable 1 .... Variable n.

In this case, only a single file that works simultaneously as structural pedigree and data file is needed. The DFPREP and then DFUNI sub-programs should be run.

The methodology described below was used for the multivariate analysis involving the three locations.

Mixed linear model (multivariate multi-experiment model)

Y = Xb + Za + Wc + e, where:

$$\begin{bmatrix} y_1 \\ y_2 \\ \vdots \\ y_\ell \end{bmatrix} = \begin{bmatrix} X_1 & \cdots & 0 \\ 0 & X_2 & \cdots & 0 \\ \vdots & \vdots & \ddots & \vdots \\ 0 & 0 & \cdots & X_\ell \end{bmatrix} \begin{bmatrix} b_1 \\ b_2 \\ \vdots \\ b_\ell \end{bmatrix} + \begin{bmatrix} Z_1 & \cdots & 0 \\ 0 & Z_2 & \cdots & 0 \\ \vdots & \vdots & \ddots & \vdots \\ 0 & 0 & \cdots & Z_\ell \end{bmatrix} \begin{bmatrix} a_1 \\ a_2 \\ \vdots \\ a_\ell \end{bmatrix} + \begin{bmatrix} W_1 & \cdots & 0 \\ 0 & W_2 & \cdots & 0 \\ \vdots & \vdots & \ddots & \vdots \\ 0 & 0 & \cdots & W_\ell \end{bmatrix} \begin{bmatrix} c_1 \\ c_2 \\ \vdots \\ c_\ell \end{bmatrix} + \begin{bmatrix} e_1 \\ e_2 \\ \vdots \\ e_\ell \end{bmatrix}$$

This multivariate model treats the same trait in different locations as different traits (Resende et al., 1999).

Distributions and structures of means and variances

$$E \begin{bmatrix} y_1 \\ y_2 \\ a_1 \\ a_2 \\ c_1 \\ c_2 \\ e_1 \\ e_2 \end{bmatrix} = \begin{bmatrix} X_1 b_1 \\ X_2 b_2 \\ 0 \\ 0 \\ 0 \\ 0 \\ 0 \\ 0 \end{bmatrix}; \quad Var \begin{bmatrix} a_1 \\ a_2 \\ c_1 \\ c_2 \\ e_1 \\ e_2 \end{bmatrix} = \begin{bmatrix} A\sigma_{a_1}^2 & A\sigma_{a_{12}} & 0 & 0 & 0 & 0 \\ A\sigma_{a_{12}} & A\sigma_{a_2}^2 & 0 & 0 & 0 & 0 \\ 0 & 0 & I\sigma_{c_1}^2 & 0 & 0 & 0 \\ 0 & 0 & 0 & I\sigma_{c_2}^2 & 0 & 0 \\ 0 & 0 & 0 & 0 & I\sigma_{e_1}^2 & 0 \\ 0 & 0 & 0 & 0 & 0 & I\sigma_{e_2}^2 \end{bmatrix}$$

$$Var(y_1) = V_1 = Z_1 A \; \sigma_{a_1}^2 \; Z'_1 + W_1 I \; \sigma_{c_1}^2 \; W'_1 + I \; \sigma_{e_1}^2$$

$$Var(y_2) = V_2 = Z_2 A \; \sigma_{a_2}^2 \; Z'_2 + W_2 I \; \sigma_{c_2}^2 \; W'_2 + I \; \sigma_{e_2}^2$$

For the case involving three experiments,

$$Var \begin{bmatrix} a_1 \\ a_2 \\ a_3 \\ c_1 \\ c \\ c_3 \\ e_1 \\ e_2 \\ e_3 \end{bmatrix} = \begin{bmatrix} A\sigma_{a_1}^2 & A\sigma_{a_{12}} & A\sigma_{a_{13}} & 0 & 0 & 0 & 0 & 0 & 0 \\ A\sigma_{a_{12}} & A\sigma_{a_2}^2 & A\sigma_{a_{23}} & 0 & 0 & 0 & 0 & 0 & 0 \\ A\sigma_{a_{13}} & A\sigma_{a_{23}} & A\sigma_{a_3}^2 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & I\sigma_{c_1}^2 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & I\sigma_{c_2}^2 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & I\sigma_{c_3}^2 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & I\sigma_{e_1}^2 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & I\sigma_{e_2}^2 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & I\sigma_{e_3}^2 \end{bmatrix}$$

, where:

$\sigma_{a_1}^2$, $\sigma_{a_2}^2$ e $\sigma_{a_3}^2$ = additive genetic variances at the locations (or experiments) 1, 2 e 3, respectively;

$\sigma_{a_{12}}$, $\sigma_{a_{13}}$ e $\sigma_{a_{23}}$ = additive genetic covariance involving the 1-2, 1-3 and 2-3 combinations of locations, respectively, or additive genetic variances free from genotype x environment interactions;

$\sigma_{c_1}^2$, $\sigma_{c_2}^2$ e $\sigma_{c_3}^2$ = among plot variances, at locations 1, 2 and 3, respectively;

$\sigma_{e_1}^2$, $\sigma_{e_2}^2$ e $\sigma_{e_3}^2$ = residual variances, at locations 1, 2 and 3, respectively.

Mixed model equations

$$\begin{bmatrix} X'R^{-1}X & X'R^{-1}Z & X'R^{-1}W \\ Z'R^{-1}X & Z'R^{-1}Z+G^{-1} & Z'R^{-1}W \\ W'R^{-1}X & W'R^{-1}Z & W'R^{-1}W+C^{-1} \end{bmatrix} \begin{bmatrix} \hat{b} \\ \hat{a} \\ \hat{c} \end{bmatrix} = \begin{bmatrix} X'R^{-1}y \\ Z'R^{-1}y \\ W'R^{-1}y \end{bmatrix}$$

, where,

$$X = \begin{bmatrix} X_1 & 0 & 0 \\ 0 & X_2 & 0 \\ 0 & 0 & X_3 \end{bmatrix}; \quad Z = \begin{bmatrix} Z_1 & 0 & 0 \\ 0 & Z_2 & 0 \\ 0 & 0 & Z_3 \end{bmatrix}; \quad W = \begin{bmatrix} W_1 & 0 & 0 \\ 0 & W_2 & 0 \\ 0 & 0 & W_3 \end{bmatrix}$$

$$R^{-1} = R_0^{-1} \otimes I; \quad G^{-1} = G_0^{-1} \otimes A^{-1}; \quad C^{-1} = C_0^{-1} \otimes I$$

$$R_O = \begin{bmatrix} \sigma_{e_1}^2 & 0 & 0 \\ 0 & \sigma_{e_2}^2 & 0 \\ 0 & 0 & \sigma_{e_3}^2 \end{bmatrix}; \quad G_O = \begin{bmatrix} \sigma_{a_1}^2 & \sigma_{a_{12}} & \sigma_{a_{13}} \\ \sigma_{a_{12}} & \sigma_{a_2}^2 & \sigma_{a_{23}} \\ \sigma_{a_{13}} & \sigma_{a_{23}} & \sigma_{a_3}^2 \end{bmatrix}; \quad C_O = \begin{bmatrix} \sigma_{c_1}^2 & 0 & 0 \\ 0 & \sigma_{c_2}^2 & 0 \\ 0 & 0 & \sigma_{c_3}^2 \end{bmatrix}$$

, where:

The variance components are associated with the parameters h^2, c^2 e r_a, in the following manner:

$$\sigma_{a_i}^2 = h_i^2 \, \sigma_{F_i}^2; \quad \sigma_{c_i}^2 = c_i^2 \, \sigma_{F_i}^2; \quad \sigma_{e_i}^2 = (1 - h_i^2 - c_i^2) \, \sigma_{F_i}^2; \quad \sigma_{a_{ij}} = \rho_{a_{ij}} \, \sigma_{a_i} \, \sigma_{a_j}$$

, where:

$$\rho_{a_{ij}} = \frac{\sigma_{a_{ij}}^2}{\sigma_{a_i}^2 \, \sigma_{a_j}^2} = \text{ genetic correlation among the}$$

performance at the ith and jth locations;

σ_F^2 = individual level phenotypic variance at the ith location.

REML variance component estimators

Due to the model complexity and to the high number of variance components to be estimated, the DF algorithm is recommended:

Column sequence in the data file for analysis by DFREML software: Experiment; Individual; Father; Mother; Block; Plot; Variable 1 . . . . Variable n.

In this case, two files are needed: a data file, according to the structure presented above and another with the pedigree formed by the Individual, Father and Mother columns. The DFPREP and then the DXMUX subprograms should be run.

RESULTS AND DISCUSSION

Table 1 shows the estimates of the components of the additive genetic variance, among plot genetic variance, residual variance and phenotypic variance, and their respective deviates, for rubber yield in grams in the three locations studied.

The estimates varied widely among locations, and the most expressive values, especially for additive genetic and phenotypic variances, were obtained by the Pindorama Experimental Station. These results characterized the location as an environment suitable for the expression of the population genetic variability. This finding was confirmed by Costa et al. (2000b) using a coefficient of genetic variation that was larger in Pindorama than in Votuporanga and Jaú experimental stations. Similarly, the results are in line with those reported by Moreti et al. (1994) for the same trait and locations.

It is important to emphasize that although the three trial places were located at a Plateau in the state of São Paulo , with latitudes, longitudes, altitudes and close precipitations, the performance of the genotypes was variable. This suggests that other factors such as fertility, structures and soil type can be interfering in the high yield performance of the Pindorama station ,allowing for a larger genetic expression for the character rubber yield. The similarity among the performances of the Votuporanga and Jaú experimental stations produced the most expressive value genetic correlation, when compared to those of the Pindorama station.

Table 2 shows estimates for genotype x location interaction variances, percentages of genetic variances and genetic correlation among pairs of locations for rubber yield in grams. The estimate for the Votuporanga x Jaú interaction variance was lower than the estimates for the Votuporanga x Pindorama and Pindorama x Jaú variances. The high correlation of progenies found between the Votuporanga and Jaú environments confirmed that a single breeding program could satisfactorily attend both regions, using components of variances estimated by least squares (Costa et al., 2000b).

Table 1. Estimates and respective deviations of the additive genetic variance (σ_A^2), variance among plots (σ_c^2), residual variance (σ_e^2) and phenotypic variance (σ_f^2) components for rubber yield (in grams) in the three locations and for pairs of locations.

Locations	Estimates			
	σ_A^2	σ_e^2	σ_c^2	σ_f^2
Votuporanga	0.0360±0.0192	0.0011±0.0045	0.2003±0.0183	0.2375±0.0116
Pindorama	0.3511±0.1342	0.0324±0.0163	0,3333±0.1047	0.7168±0.0440
Jaú	0.0917±0.0481	0.0287±0.0115	0,2392±0.0399	0.3596±0.0207
Votup x Pind	0.0857±0.0399	-	-	0.0857±0.0399
Votup x jaú	0.0557±0.0242	-	-	0.0557±0.0242
Pind x Jaú	0.1047±0.0608	-	-	0.1047±0.0608

Table 3 shows rubber yield genetic gain estimates for the nine best parents from each location, using individual multivariate BLUP/REML in the three locations, and the univariate BLUP in each location separately.

Results varied among locations, and the largest values were obtained in Pindorama followed by Jaú and Votuporanga stations. The referred estimates are rigorously in line with their respective heritability estimates, emphasizing the large value obtained by the Pindorama station when compared to Jaú and Votuporanga stations. These results corroborate those of Gonçalves et al. (1983), Moreti et al. (1994), Boock et al. (1995) and, more recently, Costa et al. (2000a, 2000b) for the same species.

Results indicated a superiority (5% against 21%) of the multivariate over the univariate procedure regarding the genetic gains obtained by both multivariate and univariate BLUP methods.

These findings reflect the great efficacy and flexibility of the procedure for predicting genetic values and gains in the presence of genotype x environment interaction. The use of data from the three locations in the procedure leads to the maximization of genetic gain from selection. The simultaneous use of a large amount of data from different locations, also generates more reliable estimates (Resende and Dias, 2000).

The BLUP procedure assumes that the variance components (G and R matrixes) are known, and that the properties of the predictors are only warranted under these conditions (Henderson, 1984). Thus, in practice, variance components should be estimated

Table 2. Rubber yield (in grams) estimates of the variances of the genotype x location (σ^2_{ge}) interaction and their percentages $\left[\sigma^2_{ge}(\%)\right]$ in relation to the genetic variances free from biases caused by the interaction variance and by the genetic correlation (r_{gg}) among the pairs of locations.

Parameters	Pairs of Locations[1]		
	Votup x Pind	Votup x Jaú	Pind x Jaú
σ^2_{ge}	0.0214	0.0006	0.0659
$\sigma^2_{ge}(\%)$	0.25	0.01	0.63
r_{gg}	0.7626±0.2096	0.9704±0.2355	0.5839±0.2480

[1] $\sigma^2_{ge}(\%)$ = ratio between the genotype x location interaction variance and the additive variance free from biases caused by the intection variance or by the additive covariance from one location with another.

Table 3. Estimates of the rubber yield genetic gains in rubber tree populations, for the nine best genotypes in each location, according to two methods: Individual multivariate BLUP/REML involving the three locations and univariate BLUP considering each location separately.

Methods [1]	Locations		
	Votuporanga	Pindorama	Jaú
BLUP (multivariado)	0.1685 (1.1959) [2]	0.5017 (1.0516) [2]	0.2468 (1.2122)
BLUP (univariado)	0.1409	0.4771	0.2036
h^2	0.1414	0.4900	0.2435
c^2	0.004	0.045	0.082

[1] h^2 = narrow sense heritability and c^2 = correlation due to plot common environment; [2] Multivariate BLUP/REML method genetic gain efficiency in relation to BLUP (univariate).

in the most reliable way to substitute the parametric values adequately (Resende et al. 1999). In this case, the standard method for estimation of variance component in mixed linear models is the restricted maximum likelihood (REML) procedure described by Searle et al. (1992).

The relevance of the REML flexibility associated to the mixed models methodology (BLUP) is emphasized by Resende and Dias (2000). The method allows for the development of national genetic assessment models, where individuals belonging to different breeding programs can be compared. This leads to the construction of a single rank for each environment containing all the individuals under assessment in the country, even those not directly assessed in that specific environment.

ACKNOWLEGMENTS

RESUMO

Procedimento REML/BLUP individual na presença de interação genótipo x ambiente no melhoramento da seringueira (*Hevea*)

O presente estudo objetivou estimar parâmetros genéticos e valores genéticos aditivos através do procedimento REML/BLUP individual para a seleção em presença de interação genótipo x ambiente em seringueira [*Hevea brasiliensis* (Willd ex Adr. de Juss.) Muell.-Arg.]. Vinte e duas progênies de meio-irmãos foram plantadas nas Estações Experimentais de Jaú, Pindorama e Votuporanga, todas no Estado de São Paulo, no delineamento de blocos ao acaso, com cinco repetições e dez plantas por parcela. Aos três anos de idade as progênies foram avaliadas quanto ao caráter produção de borracha seca. Os resultados demonstraram haver variabilidade genética entre progênies para o caráter, com valores mais expressivos em Pindorama, especialmente para a variância genética aditiva e variância fenotípica, bem como caracterizam o referido local como um ambiente propício para a expressão da variabilidade genética

existente na população. A alta correlação dos materiais genéticos entre os ambientes de Votuporanga e Jaú, reafirma que um único programa de melhoramento genético poderá atender satisfatoriamente esta região de abrangência do estudo. Os ganhos genéticos obtidos através dos dois métodos utilizados (BLUP multivariado e BLUP univariado) revelaram superioridade (5% a 21%) para o procedimento BLUP individual multivariado, refletindo a grande eficácia e flexibilidade do procedimento para predição de valores e ganhos genéticos em presença da interação genótipo x ambiente. A utilização de informações referentes aos três locais, usados conjuntamente no procedimento, conduz à maximização do genético com a seleção.

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