Adaptability and stability in rubber tree progenies under different environmental conditions

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Abstract - The aim of this work was to select progenies with high adaptability and stability from the dry rubber yield (PBS), of genotypes from a three-year-old rubber tree population, installed in three different locations (Selvíria, MS, Votuporanga, SP and Colina, SP), by the MHPRVG (Harmonic mean of the relative performance of the genetic value) method predicted by BLUP. The progenies were installed in a randomized block design with 30 treatments (progenies), three replications and 10 plants per plot, with spacing of 3.00 x 3.00 m (Selvíria, MS) and 1.50 x 1.50 m (Colina, SP and Votuporanga, SP). The PBS presented considerable genetic coefficient variability, ranging from 23.03 to 27.82% and average heritability ranging from 0.47 to 0.99, indicating the high value of the progeny tests in rubber tree breeding programs. The MHPRVG method provided a genetic gain ranging from 11 to 38% in 10 progenies to the PBS and allowed the selection of progenies with high predicted yield potential.

Adaptabilidade e estabilidade de progênies de seringueira sob diferentes condições ambientais

Resumo - O objetivo deste trabalho foi selecionar progênies com alta adaptabilidade e estabilidade a partir da produção de borracha seca (PBS), de genótipos de uma população de três anos de idade, instalada em três diferentes locais (Selvíria, MS, Votuporanga, SP e Colina, SP), pelo método MHPRVG (média harmônica da performance relativa do valor genético) predito por BLUP. As progênies foram instaladas em blocos casualizados com 30 tratamentos (progênies), três repetições e 10 plantas por parcela, num espaçamento de 3.00 x 3.00 m (Selvíria, MS) e 1.50 x 1.50 m (Colina, SP e Votuporanga, SP). A PBS apresentou um considerável coeficiente de variabilidade genética, variando de 23.03 a 27.82% e a herdabilidade média variou de 0.47 a 0.99, indicando o alto valor de um teste de progênies em programas de melhoramento genético de seringueira. O método MHPRVG proporcionou um ganho genético de 11 a 38% em 10 progênies para PBS e permitiu a seleção de progênies com alto potencial predito de produção.

Introduction

Decentralization of agricultural production is an important factor for economic growth and social development. Thus, yield of the most productive genotypes in different environments are estimated and this depends on their genotypic constitution and interaction with the environment in which they are planted. Therefore obtaining high yielding rubber tree clones [*Hevea brasiliensis* (Willd. ex Adr. de Juss.) Muell. Arg.] with adaptability and stability to several environments is essential for the development of rubber tree cropping in Brazil. According to Carbonell et al. (2007), simultaneous selection that provides these traits in the context of mixed models can be achieved by the MHPRVG (harmonic average performance relative breeding values) method.

The variance component estimation based on Residual Maximum Likelihood (REML) and the Best Linear Unbiased Prediction (BLUP) of genetic values have been adopted in the perennial and annual crop breeding (Souza et al., 2000; Paiva et al., 2002; Eagles & Moody, 2004; Missio et al., 2004, 2005; Bauer et al., 2006; Farias Neto et al., 2009; Pedrozo et al., 2009; Verardi et al., 2009; Viana et al., 2010a, 2010b).

The MHPRVG method, proposed by Resende (2004), is similar to the methodologies by Annicchiarico (1992) and Lin & Binns (1988) and allows, according to Sturion & Resende (2005), selection for three attributes mentioned simultaneously in addition to other advantages. It considers the genotype effects as random and therefore gives genotype adaptability and stability so that unbalanced data, non-orthogonal designs and variance heterogeneity can be dealt with. It also allows consideration of errors correlated within locations and adaptability and stability in selection of within-progeny individuals. Furthermore, it gives genetic values already penalized for instability and can be applied to any number of environments. Finally, it generates results in the unit itself or scale of the trait assessed, that can be interpreted directly as genetic values. The method has been used in several crops, including *Ilex paraguariensis* (Sturion & Resende, 2005), *Saccharum officinarum* (Oliveira et al., 2005; Bastos et al., 2007; Zeni Neto et al., 2008), *Eucalyptus grandis* (Pinto Junior et al., 2006), *Phaseolus vulgaris* (Carbonell et al., 2007) and in *Hevea brasiliensis* (Verardi et al., 2009). Therefore, the objective was to select progenies with high adaptability and stability from the dry rubber yield of a three-year-old rubber tree population, founded in three different environments via the MHPRVG method predicted by BLUP.

Material and methods

The seeds used to produce the saplings in the progeny tests were mostly from clones of Asiatic origin from the clone collection installed in the experimental area of the Votuporanga Regional Pole of the Paulista Agency for Agrobusiness Technology (APTA), São Paulo State, Brazil. The seeds were collected from an opened pollination clone test such as: 1-12-56-77, 64B 850, Fx (2261 and 3864), GT1, IAC (15, 301, 307, 311, 35, 40, 41 and 44), IAN 873, IRCA 111, MT 45, PB (217, 235, 252, 260, 28/59 and 330), Pind 595/89, PR 255 and 261, RO/I (35 and 110), RRIM (600, 606 and 701). The three progeny tests were set up simultaneously in the following locations: 1) the Teaching, Research and Extension Farm/ Engineering College at Ilha Solteira/UNESP, located in Selvíria, MS; 2) APTA – Votuporanga Regional Pole, SP and 3) APTA – Colina Regional Pole, SP.

The seeds were placed to germinate in polyethylene bags and the progenies transported to the definitive location with two open leaves. The progeny were installed in each location in a randomized block design, consisting of 30 treatments (progenies), three replications and linear plots of 10 plants, in 3.00 x 3.00 spacing (Selvíria, MS) and 1.50 x 1,50 m (Votuporanga, SP), in a total of 900 useful plants.

When three years old, the progenies were assessed for dry rubber yield, obtained by the Hamaker Morris-Mann (HMM) test modified for three-year-old saplings (Tan & Subramanian, 1976), using the total rubber yield from 10 incisions per plant. The tapping panel was opened 30 cm height from the soil, tapping at an 45° angle, by the S/2 d/2 2.5% Ethefon system in a total of 15 incisions. The first five samples were discarded, that corresponded to the panel adjustment phase. The 10 tapping collected were open air drought and weighed on precision scales. The S/2 nomenclature corresponds to a half spiral cut and the d/2 nomeclature expresses the between bleeding intervals, that is, one bleeding every two days and 2.5% Ethefon is the product concentration. The plants from the plot were bled randomly, and the weakest plants were excluded.

The genotype adaptability and stability was studied using the MHPRVG method that corresponds to model 51 of the Selegen software (Resende, 2002b), complete block design in several locations and several observations per plot.

Thus the statistical model used was:

y = Xb + Za + Wc + Tp + e

where y is the data vector, b is the vector of the replication effects (assumed fixed) added to the general mean, *a* is the vector of the genotypic effects (assumed random), *c* is the vector of the plot effects (random), *p* is the vector of the genotype x environment interaction effects, considered random (permanent environment within plot + non genetics additive effects) and e is the vector of the residual errors (random). The upper case letters represent the incidence matrixes for the referred effects.

Distribution and structure of means and variances

Cov (a,c') = 0; Cov (a,p') = 0; Cov (a,e') = 0;

$$y \mid b,V \sim N(Xb,V)$$
$$g \mid A,\sigma_G^2 \sim N(0,\sigma_g^2)$$
$$c \mid \sigma_c^2, \sim N(0,I\sigma_c^2)$$
$$p \mid \sigma_p^2, \sim N(0,I\sigma_p^2)$$
$$e \mid \sigma_e^2, \sim N(0,I\sigma_e^2)$$

Cov (p,c') = 0; Cov (p,e') = 0; Cov (c,e') = 0; that is:

The following genetic parameters were estimated

$$E\begin{bmatrix} y \\ g \\ c \\ p \\ e \end{bmatrix} = \begin{bmatrix} Xb \\ 0 \\ 0 \\ 0 \\ 0 \end{bmatrix}; \quad Var\begin{bmatrix} y \\ g \\ c \\ p \\ e \end{bmatrix} = \begin{bmatrix} V & ZG & WC & TP & R \\ GZ' & G & 0 & 0 & 0 \\ CW' & 0 & C & 0 & 0 \\ PT' & 0 & 0 & P & 0 \\ R & 0 & 0 & 0 & R \end{bmatrix}$$

where:

$$P = I\sigma_P^2 \; ; \; V = ZA\sigma_g^2 Z' + WI\sigma_c^2 W' + TI\sigma_p^2 T' + I\sigma_e^2$$

Mixed model equations:

$$\begin{bmatrix} X'X & X'Z & X'W & X'T \\ Z'X & Z'Z + A^{-1}\lambda_1 & Z'W & Z'T \\ W'X & W'Z & W'W + I\lambda_2 & W'T \\ T'X & T'Z & T'W & T'T + I\lambda_3 \end{bmatrix} \begin{bmatrix} \hat{b} \\ \hat{g} \\ \hat{c} \\ \hat{p} \end{bmatrix} = \begin{bmatrix} X'y \\ Z'y \\ W'y \\ T'y \end{bmatrix}$$

where:

$$\lambda_1 = \frac{1-\rho}{h^2} = \frac{\sigma_e^2}{\sigma_g^2}; \quad \lambda_2 = \frac{1-\rho}{c^2} = \frac{\sigma_e^2}{\sigma_c^2}; \quad \lambda_3 = \frac{1-\rho}{p^2} = \frac{\sigma_e^2}{\sigma_p^2};$$

$$h^2 = \frac{\sigma_g^2}{\sigma_g^2 + \sigma_c^2 + \sigma_p^2 + \sigma_e^2} = \text{Individual broad-sense heritability within block;}$$

$$\rho = \frac{\sigma_g^2 + \sigma_c^2 + \sigma_p^2}{\sigma_g^2 + \sigma_c^2 + \sigma_p^2 + \sigma_e^2} = \text{Individual repeatability within block;}$$

$$p^2 = \frac{\sigma_p^2}{\sigma_g^2 + \sigma_c^2 + \sigma_p^2 + \sigma_e^2} = \text{Coefficient of determination of environment effects within plot;}$$

$$c^2 = \frac{\sigma_c^2}{\sigma_g^2 + \sigma_c^2 + \sigma_p^2 + \sigma_e^2} = \text{Correlation due common environment plot.}$$

Iterative estimators of variance components in REML by EM algorithm:

$$\hat{\sigma}_e^2 = \left[y'y - \hat{b}'X'y - \hat{g}'Z'y - \hat{c}'W'y - \hat{p}'T'y \right] / \left[N - r(x) \right]$$

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

$$\hat{\sigma}_c^2 = \left[\hat{c}'c + \hat{\sigma}_e^2 tr C^{33} \right] / s$$

$$\hat{\sigma}_p^2 = \left[\hat{p}'\hat{p} + \hat{\sigma}_e^2 tr C^{44} \right] / q$$

where C^{22}, C^{33} and C^{44} come from:

$$C^{-1} = \begin{bmatrix} C_{11} & C_{12} & C_{13} & C_{14} \\ C_{21} & C_{22} & C_{23} & C_{24} \\ C_{31} & C_{32} & C_{33} & C_{34} \\ C_{41} & C_{42} & C_{43} & C_{44} \end{bmatrix}^{-1} = \begin{bmatrix} C^{11} & C^{12} & C^{13} & C^{14} \\ C^{21} & C^{22} & C^{23} & C^{24} \\ C^{31} & C^{32} & C^{33} & C^{34} \\ C^{41} & C^{42} & C^{43} & C^{44} \end{bmatrix}$$

from the components of variance associated to the effects by model 51:

$$\hat{h}_g^2 = \frac{\hat{\sigma}_g^2}{\hat{\sigma}_f^2}$$ = individual heritability in the broad sense, that is the total genotypic effects;

$$\hat{c}_{parc}^2 = \frac{\hat{\sigma}_c^2}{\hat{\sigma}_f^2}$$ = coefficient of determination of the plot effects;

$\hat{c}_{int}^2$ = coefficient of determination of the genotype x environment interaction effects;

$$CV_g\,(\%) = \frac{\sqrt{\hat{\sigma}_g^2}}{\mu}.100$$ = coefficient of genotypic variation;

$$CV_e\,(\%) = \frac{\sqrt{\hat{\sigma}_e^2}}{\mu}.100$$ = coefficient of residual variation;

$$\hat{c}_{int}^2 = \frac{\hat{\sigma}_{int}^2}{\hat{\sigma}_f^2}$$ = coefficient of determination of the effects of the genotype x environment interaction;

$$\hat{r}_{gloc} = \frac{\hat{\sigma}_g^2}{(\hat{\sigma}_g^2 + \hat{\sigma}_{int}^2)}$$ = genotype correlation between the performance in the several environments;

$$\hat{h}_{mg}^2 = \frac{\hat{\sigma}_g^2}{\hat{\sigma}_g^2 + \hat{\sigma}_c^2/b + \hat{\sigma}_e^2/(nb)}$$ = heritability of the genotypic mean, assuming total survival; n: number of plots; b: number of blocks;

$$\hat{r}_{\hat{g}g}^2 = \sqrt{\hat{h}_{mg}^2}$$ = genotype selection accuracy, assuming total survival;

$\hat{\sigma}_g^2$, genotypic variance; $\hat{\sigma}_c^2$, among plot environmental variance; $\hat{\sigma}_{int}^2$, variance of the genotype x environment interaction; $\hat{\sigma}_e^2$, residual variance; $\hat{\sigma}_f^2$, individual phenotypic variance; μ, general mean of the experiment.

Results and discussion

The significance of the additive genetic effects and the progeny x location interaction effects in the joint analysis involving the three locations was assessed by deviance analysis ANADEV shown in Table 1.

Table 1. Analysis of deviance (ANADEV) for dry rubber yield (g.plant^{-1}) in the three different locations analyzed at three years of age.

Effects	dry rubber yield			
	Colina, SP	Votuporanga, SP	Selvíria, MS	Conjoint
Progenies	3,29^{ns}	18,41**	60,49**	5,23*
Plot	35,86**	0,12^{ns}	0,14^{ns}	15,23**
Progenies X Locations	-	-	-	43,34**

Tabled chi-square: 3.84 (*) and 6.63 (**) for the levels of significance of 5 and 1%, respectively; ns = not significant at the level of 5% probability.

The plot effects were significant only in Colina (Table1), that means that there was heterogeneity among the blocks but this heterogeneity was not observed in Votuporanga and Selviria. The progeny effects were significant only in Votuporanga and Selviria, indicating that these two locations were more propitious for expression of the variability existing in the population. The progeny x location interaction was significant. Thus different ranking of the genotypes were observed in the different locations.

Table 2 shows the difference between the genotypic variation ($\hat{\sigma}_g^2$) among regions. Such values come from the phenotypic variation and they are standardized by the coefficient of genetic variation (CVg). Selvíria, MS, showed, in average, a higher phenotypic yield and eventually a higher $\hat{\sigma}_g^2$ than Colina and Votuporanga, SP.

Table 2. Estimates of genetic parameters for dry rubber yield (g plant^{-1}) in rubber trees, in three different regions and three years old. Individual and joint analysis of the experiments.

Genetics parameters	Dry rubber yield			
	Colina, SP	Votuporanga, SP	Selvíria, MS	Conjoint
$\hat{\sigma}^2_g$	18,4829	27,0198	574,7824	62,3587
$\hat{\sigma}^2_c$	44,5336	1,8163	9,1358	48,18734
$\hat{\sigma}^2_{int}$	-	-	-	134,7394
$\hat{\sigma}^2_e$	190,8137	155,5490	1441,1838	446,6702
$\hat{\sigma}^2_f$	253,8302	184,3851	2025,1020	691,9556
$\hat{h}^2_g$	0,1957±0,08	0,3938±0,12	0,7628±0,22	0,0901±0,022
$\hat{c}^2_{parc}$	0,1754	0,0099	0,0045	0,0696
$\hat{c}^2_{int}$	-	-	-	0,1947
$\hat{h}^2_{mg}$	0,4657	0,8235	0,9938	0,5303
$\hat{r}_{\hat{g}g}$	0,6824	0,9075	0,9969	0,7282
$\hat{r}_{gloc}$	-	-	-	0,3164
CVg%	27,8226	23,0314	25,3094	17,8836
CVe%	89,3958	34,4411	26,5650	21,8227
μ	15,4521	22,5693	94,7264	44,1563

$\hat{\sigma}^2_g$: genotypic variance; $\hat{\sigma}^2_c$: among plot environmental variance; $\hat{\sigma}^2_{int}$: variance of the genotype x environment interaction; $\hat{\sigma}^2_e$: residual variance; $\hat{\sigma}^2_f$: individual phenotypic variance; $\hat{h}^2_g$ = individual heritability in the restricted sense for the individual and broad analysis in the set; $\hat{c}^2_{parc}$: coefficient of determination of the plot effects; $\hat{c}^2_{int}$: coefficient of determination of the genotype x environment interaction effects; $\hat{h}^2_{mg}$: Heritability of the genotypic mean, assuming total survival; $\hat{r}_{\hat{g}g}$: accuracy of genotype selection, assuming total survival; $\hat{r}_{gloc}$: genotypic correlation among the performances in the several environments; CVg%: genotype coefficient of variation; CVe%: coefficient of residual variation; μ: general mean.

The CVg, that expresses in percentage of the general mean the quantity of genetic variation existing, had a moderate value for rubber yield, ranging from 23.03 to 27.82%, indicating that the population could be considered appropriate for the genetic breeding program.

The CVg(%) value for PBS corroborated studies carried out in Votuporanga, SP, by Costa et al. (2000, 2008), Gonçalves et al. (1998a, 2005, 2009), Boock et al. (1995) and Moretti et al. (1994), in Jaú, SP, by Gonçalves et al. (1998b) and in Pindorama, SP, by Gonçalves et al. (2004).

The coefficient of determination of the plot effects ($\hat{c}^2_{parc}$) was low and insignificant magnitude, showing that the experimental design used was excellent because the within-block environmental homogeneity remained, except in Colina, SP, where a significant ($\hat{c}^2_{parc}$) was observed.

According to Resende (2002a) accuracy is a measure that is associated to the precision in selection, and is the main component of genetic progress that the breeder can alter to maximize the genetic gain. Accuracy ($\hat{r}_{\hat{g}g}$) or correlation among the predicted and true genetic values is considered of high magnitude starting at 0.70.

The genotypic correlation between the progeny performance in the several environments ($\hat{r}_{gloc}$) was of low magnitude (0.3164), slightly lower than that reported by Verardi et al. (2009), showing a high level of complex interaction that indicated that progeny classification by the environments would not necessarily be the same, that is, one progeny could be classified as high yielding in Selviria, MS, but might not be in Colina, SP or Votuporanga, SP.

Table 3. Adaptability of the genotypic values (PRVG), stability of genotypic values (MHVG), genotypic value adaptability and stability (MHPRVG) for the rubber yield trait (g plant⁻¹) of the 30 rubber tree progeny assessed in three locations in the State of São Paulo.

Progeny	PRVG	PRVG. μ	Progeny	MHVG	Progeny	MHPRVG	MHPRVG.μ
RRIM 600	1,46	64,47	RRIM 600	36,52	GT1	1,38	60,92
GT1	1,38	60,93	PB 28/59	34,52	PB 28/59	1,34	59,38
PB 28/59	1,35	59,61	GT1	34,46	IAC 35	1,28	56,49
IAC 35	1,30	57,48	IAC 35	34,25	RRIM 600	1,25	55,12
PB 217	1,23	54,47	IAC 301	31,64	PB 217	1,23	54,29
IAC 301	1,21	53,54	PB 217	31,18	RRIM 606	1,20	52,98
RRIM 606	1,20	53,03	RRIM 606	29,78	IAC 301	1,20	52,80
IAC 41	1,16	51,29	IRCA 111	29,22	IAC 41	1,16	51,18
IRCA 111	1,15	50,76	IAC 41	28,80	IRCA 111	1,15	50,63
PB 235	1,12	49,55	PB 235	28,46	PB 235	1,11	49,14
PR 261	1,10	48,70	RRIM 701	26,06	PR 261	1,08	47,83
PR 255	1,08	47,74	PR 255	25,94	PR 255	1,07	47,43
RRIM 701	1,07	47,04	64B 850	25,93	RRIM 701	1,06	46,98
64B 850	1,04	45,90	IAC 15	25,58	64B 850	1,03	45,54
PB 260	1,03	45,31	PR 261	25,27	IAC 15	1,02	45,21
IAC 15	1,03	45,28	PB 260	25,10	PB 260	1,02	45,07
IAN 873	1,00	44,00	PB 252	23,94	IAN 873	0,99	43,59
PB 252	0,98	43,24	IAN 873	23,55	PB 252	0,98	43,17
IAC 307	0,93	41,19	IAC 44	22,97	IAC 44	0,92	40,79
IAC 44	0,92	40,83	IAC 307	22,58	IAC 40	0,91	40,21
IAC 40	0,92	40,69	IAC 40	21,84	IAC 307	0,90	39,59
FX 2261	0,89	39,18	IAC 311	21,79	IAC 311	0,88	38,78
IAC 311	0,88	38,86	PIND 595/89	20,37	FX 2261	0,85	37,56
PB 330	0,86	37,95	PB 330	19,96	PB 330	0,85	37,45
PIND 595/89	0,80	35,31	FX 2261	19,56	PIND 595/89	0,75	33,08
1-12-56-77	0,69	30,37	1-12-56-77	14,93	1-12-56-77	0,66	29,05
ROI 110	0,64	28,19	ROI 110	13,91	ROI 110	0,61	27,08
FX 3864	0,57	25,32	ROI 35	13,84	FX 3864	0,56	24,88
ROI 35	0,56	24,65	FX 3864	13,19	ROI 35	0,54	24,05
MT 45	0,45	19,81	MT 45	9,92	MT 45	0,43	19,09

MHVG = harmonic mean of the predicted genetic values; PRVG = performance relative to the genetic values; MHPRVG = Harmonic mean of the relative performance of the genetic value; μ = general mean.

According to Table 3, the most productive progeny by the MHPRVG criterion were 38% superior compared to the general mean of the three environments. Verardi et al. (2009) reported values of 19% in the most productive progenies. The MHPRVG x general mean value is the mean genotypic value of the progenies in the locations assessed already penalized for instability and capitalized by adaptability (Carbonell et al., 2007). By the MHPRVG criterion, the three best progenies produced between 28 and 38% more compared to the mean of the environments in which they were planted, that showed good adaptability or response capacity to improvement in the environment and a constant yield in the three locations. The ten best progeny were derived from clones GT 1, PB 28/59, IAC 35, RRIM 600, PB 217, RRIM 606, IAC 31, IAC 41, IRCA 111 and PB 235.

Conclusions

1. The most productive, stable and adaptable progenies to the regions tested where GT1, PB 28/59, IAC 35, RRIM 600, PB 217, RRIM 606, IAC 31, IAC 41, IRCA 111 and PB 235 via MHPRVG.

2. The heritabilities of the genotypic mean presented moderate to high magnitudes, allowing selection accuracy in a range of 68.24 to 99.69%.

3. Among the progenies evaluated in all locations, the three best ones produced between 28, 34 and 38% (GT1, PB 28/59, IAC 35, respectively) more, compared to the mean of the environments tested.

Acknowledgements

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