

Genotype-environment interaction and the number of test sites for the genetic improvement of rubber trees (*Hevea*) in São Paulo State, Brazil

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Abstract

The present study quantifies the possible genotype-environment interactions and determines the ideal number of test sites for rubber trees [*Hevea brasiliensis* (Willd ex A. de Juss.) Muell Arg] in the plateau region of São Paulo State. The study was based on the genetic correlation among progenies at three different sites and on estimates of genetic gains with indirect selection of rubber trees. Twenty-two half-sib progenies were planted at the Jaú, Pindorama and Votuporanga experimental stations using random blocks with five replications and 10 plants per plot. At three years of age, the plants were evaluated for their total number of latex ring vessels (NR), rubber production (RP), bark thickness (BT) and girth (SG). There was significant genetic variability in the characters RP, SG and BT, mainly among progenies from Pindorama and Votuporanga. The effects of genotype-site interactions were significant for RP and SG. The finding of significant interactions was not a complicating factor because of the large genetic correlation detected. These results indicate that the use of two sites is more profitable when the gains in efficiency of selection are greater than 10%. Thus, Pindorama and Votuporanga will satisfactorily attend the studied region.

INTRODUCTION

The rubber tree [*Hevea brasiliensis* (Willd ex A. de Juss.) Muell Arg] is a valuable market species because the rubber that it produces is widely used in industry. The main cultivation sites in Brazil, known as "escape areas", are located in areas free of South American leaf blight, caused by *Microcyclus ulei* (P. Henn.) v. Arx. The plateau region of the State of São Paulo is the most important rubber-producing area in the country (Boock *et al.*, 1995).

Genotype x environment interactions in perennial species have received considerable attention recently through the use of progeny tests set up in different locations. Depending on whether they are controlled or not such interactions can lead to gains or losses in breeding programs (Zobel and Talbert, 1984).

The assessment of genotype x environment interaction is important in plant breeding since, depending on the degree of plant adaptation, the expression of a new element of the phenotypic trait may occur. This element arises from the interaction between a given genotype and an environmental condition (Vencovsky and Barriga, 1992). If the interaction exists, the best genotype in one environment may not be the best in another (Cruz and Regazzi, 1994). This interaction influences the gain obtained in selection and hinders the recommendation of

cultivars with a wide ability to adapt. The effects of the genotype x environment interaction in the rubber tree have been recognized and widely used in Malaysia (Tan, 1995), Sri Lanka (Jayasekera, 1983; Jayasekera *et al.* 1977, 1984 a,b), Indonesia (Daslin *et al.*, 1986), Nigeria (Onokpise *et al.*, 1986), India (Menattoor *et al.*, 1991) and, more recently, in Brazil (Gonçalves *et al.*, 1990, 1991, 1998 a,b,c).

One of the main practical uses for genotype x environment interaction studies is the determination of an adequate number of experimental locations. The choice of the number of locations needed to evaluate the genotypes depends on the magnitude of this interaction (Resende, 1998). Generally, the practical relevance of the interaction has been inferred by considering the relative magnitude of the genotype x environment interaction in relation to the genetic variance obtained from the joint analysis of variance in several environments, and from the genetic correlation among materials in the environments studied (Ramalho *et al.*, 1993; Resende, 1998).

The present study quantified the genotype x environment interaction effect for several traits, and also determined the ideal number of experimental locations based on estimates of the genetic correlation among progenies in the different locations and on estimates of the genetic gain from indirect selection.

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MATERIAL AND METHODS

Genetic material

The genetic material consisted of 22 half-sib progenies from open-pollinated seeds obtained from 22 parental clones phenotypically selected from an *H. brasiliensis* population of Asian origin. The following parental clones were selected: AVROS 49, AVROS 255, AVROS 352, AVROS 363, AVROS 1328, AVROS 1126, C 22, C 256, C290, C 297, C 318, GT 127, GT 711, PB 49, PB 86, PB 5/63, PR 107, RRIM 513, RRIM 600, Tjir 1 and Tjir 16.

Experimental sites

The progeny tests were set up at three experimental stations belonging to the Instituto Agronômico de Campinas (IAC), located in different rubber tree cultivation regions in São Paulo State:

a) Jaú experimental station: latitude 22°17'S, longitude 48°34'W, altitude 580 m. The soil is dark red latosol, alio, clay texture, deep and flat with a well-drained topography. An Aw (Köppen) climate predominates in this region, with a defined dry season, annual mean temperature of 21.6°C, average humidity of around 70% with extremes of 77% in February and 59% in August. The mean annual rainfall is around 1,344 mm.

b) Pindorama experimental station: latitude 21°13'S, longitude 48°56'W, altitude 560 m, with red-yellow podzolic soil TB eutrophic, medium texture, deep, abrupt and well drained (Lepsch and Valadares, 1976). The climate is tropical, with a wet summer and a dry winter period. Mean monthly temperatures vary from 16.6 to 28.9°C, and annual mean rainfall is 1,390.3 mm. The period from October to April usually has favorable precipitation for growth and production. Precipitation deficiencies and low temperatures occur from May to September.

c) Votuporanga experimental station: latitude 20°25'S, longitude 49°50'W, altitude 450 m. The soil is podzolic sandy phase type and the climate, tropical, with a hot wet summer and a dry winter, with low temperatures and rainfall. Mean monthly temperatures varies from 20 to 25°C and annual mean rainfall ranges from 1,087 to 1,537 mm. The winter drought varies from four to six dry months, with an average water deficiency of 180 mm.

The seeds were collected at the IAC Experimental Center in Campinas, germinated in polyethylene bags at the three experimental stations and taken to the definitive locations with two leaf whorls.

Statistical design and measurements

The seedlings were set out in a randomized complete block design with 22 treatments, five replications and 10 plants per plot spaced at 1.5 x 1.5 m in single rows. The progenies were assessed when they were three years old.

Yield determination in dry rubber (RP) was done using the Hamker-Morris-Mann test (HMM) (Tan and Subramaniam, 1976), as follows: thirty tappings were done with a half-spiral alternate daily (1/2 S d/2) tapping system at a height of 20 cm from the ground. The yield was recorded by cup coagulation. The "coagula" were air dried for two months until they gave a constant weight. The results were expressed in grams per tapping.

Virgin bark samples were removed from the trunk as plugs at 20 cm high on the opposite side of the tapping panel. Bark thickness (BT) was measured using the sample for each progeny.

The total number of latex vessel rings (NR) in longitudinal and transverse sections of the bark sample was determined. Details of the procedure are described by Gonçalves *et al.* (1996). Girth was measured using a steel measuring tape at 0.50 m from the ground.

Biostatistical analysis

Joint analysis of variance

The mathematical model used considered locations and genotypes as random effects and was equivalent to the following equation described by Cruz and Regazzi (1994):

$$Y_{ijk} = \mu + G_i + A_j + GA_{ij} + B/A_{jk} + \varepsilon_{ijk}$$

where Y_{ijk} = observed value of the i th progeny of the j th environment in the k th replications, μ = general mean, G = effect of the i th genotype ($i = 1, 2, \dots, 22$), A_j : effect of the j th environment ($j = 1, 2, \dots, 3$), GA_{ij} = effects of the interaction of the i th progeny with the j th environment, B/A_{jk} = effect of the k th block within the j th environment, and ε_{ijk} = random error.

The expected mean squares (Table I) were determined using the randomized complete block design for the joint analysis based on Cruz and Regazzi (1994). The genetic correlation among the pairs of locations for each trait under study was obtained as suggested by Yamada (1962), using the following expression:

$$r_g = \frac{\sigma_g^2}{[\sigma_g^2 + \sigma_{ge}^2 - 0.5(\sigma_{g1} - \sigma_{g2})^2]}$$

where r_g = coefficient of correlation between the two locations for a certain trait, σ_{g1}^2 = genetic variance at location 1, σ_{g2}^2 = genetic variance at location 2, σ_g^2 = joint genetic variance of the joint analysis, and σ_{ge}^2 = variation of the progenies x environment interaction.

Number of experimental locations needed

The most adequate number of experimental locations was obtained from the genetic correlation estimate. This

Table I - Degrees of freedom (d.f.) and expected mean squares (EMS) of joint analyses for estimating the components of variance.

Source of variation	d.f.	MS	EMS	F
Replications/sites	a(r-1)	MS ₁	$\sigma^2 + g \sigma_b^2$	MS ₁ /MS ₅
Sites (S)	a-1	MS ₂	$\sigma^2 + r \sigma_{ga}^2 + g \sigma_b^2 + gr \sigma_a^2$	(MS ₂ /MS ₅)/(MS ₁ + MS ₄)
Progenies (P)	g-1	MS ₃	$\sigma^2 + r \sigma_{ga}^2 + ar \sigma_g^2$	MS ₃ /MS ₄
P x S	(a-1)(g-1)	MS ₄	$\sigma^2 + r \sigma_{ga}^2$	MS ₄ /MS ₅
Residual	a(r-1)(g-1)	MS ₅	σ^2	

σ_g^2 : Variance due to differences among progeny variance; σ_a^2 : variance due to differences among sites; σ_b^2 : variance among replications; σ_{ga}^2 : variance due to interaction of progenies and sites; r: number of replications within each site; a: number of sites; g: number of progenies; b: number of replications.

was calculated using the estimators obtained by Resende (1998) from F-values of the joint analysis involving the three locations for the sources of variation (genetic material and genotype x environment interaction).

$$\sigma_{ge}^2 / \sigma_g^2 = \frac{(1 - 1/F^*)}{F - 1} l$$

$$r_{gg} = \frac{\sigma_g^2}{\sigma_g^2 + \sigma_{ge}^2} = \frac{F - 1}{(F - 1) + l(1 - 1/F^*)} = \frac{F - 1}{(F - 1) + (l - l/F^*)}$$

where r_{gg} = genetic correlation between the material in the environment, l = number of environments or locations included in the joint analysis of variance, F = F obtained for the genotype effect and F^* = F obtained for the genotype x environment interaction. Once the results r_{gg} had been obtained, the values tabulated by Resende (1989) were used to determine the ideal number of experimental locations.

Heritability estimates

Narrow sense heritabilities determined on an individual basis for each site were calculated according to Resende and Higa (1994), using the following equation:

$$h_{ib}^2 = \frac{4\sigma_p^2}{\sigma_p^2 + \sigma_e^2 + \sigma_w^2}$$

where, σ_p^2 = variance due to differences among progenies = $1/4 \sigma_A^2$ (σ_A^2 = additive genetic variance); σ_e^2 = variance due to interaction of progenies and replication; σ_w^2 = variance due to differences among plants within plots.

Expected progress with selection

The expected progress with selection among half-sib progeny means for each trait, in each of the situations described below, was calculated using the expression described by Resende (1989). The following situations were considered:

a) Direct progress - Selection and progress in a single environment:

$$G_{s(i/i)} = \frac{K}{\sigma_{\bar{F}_i}} \sigma_{gi}^2$$

where K = standardized selection differential, $\sigma_{\bar{F}_i}$ = estimate of phenotypic deviation among progeny means in the i th environment, σ_{gi}^2 = estimate of the genetic variance among progenies in the i th environment.

b) Indirect progress - selection in one environment (j th) and progress in another (i th):

$$G_{s(i/j)} = \frac{K}{\sigma_{\bar{F}_j}} \sigma_{gij}^2$$

where σ_{gij}^2 = estimate of genetic covariance among progeny means in the i th and j th environments, and $\sigma_{\bar{F}_j}$ = estimate of the standard phenotypic deviation among progeny means in the j th environment.

c) Selection based on the mean of the i th, j th and k th environments and progress in individual environments:

$$G_{s(j/ijk)} = \frac{K}{3\sigma_{\bar{F}_{ijk}}} [\sigma_{gi}^2 + \sigma_{gij}^2 + \sigma_{gkj}^2]$$

where $\sigma_{\bar{F}_{ijk}}$ = estimate of the standard phenotypic deviation among progeny means in the i th, j th and k th environments obtained from the joint analysis of variance, and σ_{gkj}^2 = estimate of genetic covariance among progeny means in the k th and j th environments.

d) Selection based on the means of the i th and j th environments and progress in the i th environment.

$$G_{s(j/ij)} = \frac{K}{2\sigma_{\bar{F}_j}} [\sigma_{gi}^2 + \sigma_{gij}^2]$$

The other environment combinations were considered

in the calculations of the expected progress in each of the above items. The mean progress in the three environments was obtained using the following expressions (Resende, 1989):

a) Selection in each environment and average progress in the three locations:

$$G_{s(ij/k)} = \frac{1}{3} [G_{s(k/k)} + G_{s(i/k)} + G_{s(j/k)}]$$

$$G_{s(ij/k/j)} = \frac{1}{3} [G_{s(j/j)} + G_{s(i/j)} + G_{s(k/j)}]$$

$$G_{s(ij/k/i)} = \frac{1}{3} [G_{s(i/i)} + G_{s(j/i)} + G_{s(k/i)}]$$

b) Selection using the mean of two locations and progress in the mean of the three locations:

$$G_{s(ij/k/ij)} = \frac{1}{3} [G_{s(i/ij)} + G_{s(j/ij)} + G_{s(k/ij)}]$$

$$G_{s(ij/k/ik)} = \frac{1}{3} [G_{s(i/ik)} + G_{s(j/ik)} + G_{s(k/ik)}]$$

$$G_{s(ij/k/jk)} = \frac{1}{3} [G_{s(i/jk)} + G_{s(j/jk)} + G_{s(k/jk)}]$$

c) Selection using the mean of the three locations and the average progress in the three locations.

$$G_{s(ij/k/ijk)} = \frac{1}{3} [G_{s(i/ijk)} + G_{s(j/ijk)} + G_{s(k/ijk)}]$$

RESULTS AND DISCUSSION

Joint analysis of variance

Joint analysis of variance for all the locations

The four traits studied showed significant genetic variation among progenies based on the F-values from the joint analyses of variance (Table II). These variations indicate good prospects for selection among progenies and for continuity in the genetic breeding program.

In the joint analysis of variance for locations, the experimental coefficients of variation (CV%) showed higher values for dry rubber production and lower values for girth, bark thickness and total number of latex vessel rings. These values express intrinsic properties of the traits. The values were of low to medium magnitude for field experiments (Pimentel Gomes, 1982) and were therefore accurate in the experiments.

The effect of location, expressed by F-values in the joint analysis of variance, was significant for dry rubber production and girth, but not for the total number of latex vessel rings and bark thickness, indicating that these traits were less affected by local variation under the conditions of the present study. The effect of progeny x location interaction was significant for all the traits studied. Significant results for progeny x year interaction for this species were reported by Gonçalves *et al.* (1991) for rubber production, and by Gonçalves *et al.* (1998b) for girth. According to Vencovsky (1978), the progeny x location interaction reflects the difference in the variability among progenies and the lack of correlation among materials from different locations. Kageyama (1980) pointed out that for selection purposes, the second component of interaction would be the most important as it allows inferences about the efficiency of indirect selection, i.e., selection in one location and genetic gain in another.

Although the three experimental locations were located at similar latitudes, longitudes and altitudes in the plateau region of São Paulo State, the performance of the genotypes was very variable. This suggests that other environmental factors such as soil fertility, as well as soil type and structure may interfere with performance (Pinheiro *et al.*, 1980; Pushparajah, 1983; Huang and Zheng, 1983).

Joint analysis of variance for two locations (Pindorama and Votuporanga)

Joint analyses of variance for all the traits studied at Pindorama and Votuporanga (Table III) showed the same trend in genetic variation as the joint analyses of all the locations. Exceptions were NR (among progenies) and SG (locations and locations x progeny interaction effects), which had nonsignificant F-values, suggesting that these traits were less affected by the site conditions.

As with the joint analysis for all the traits, the experimental coefficients of variation were greater for dry rubber production and lower for girth, bark thickness and the number of latex vessel rings. The progenies x location interaction effects were also similar to that obtained by the joint analysis of all the locations, with higher and more significant values for the RP traits. However, the interactions for NR and BT were not significant. These results may reflect high affinity for the soil-climate conditions of the locations analyzed.

A high genetic correlation between the two locations was found for materials in the environments for BT, SG and RP but there was a low correlation for NR. The high correlation of the genetic material in the environments indicated that a single breeding program could satisfactorily serve both locations. This assertion is valid for RP, BT and SG, which can be better characterized using the concept of genetic correlation among locations (Vencovsky and Barriga, 1992).

Table II - Mean squares (MS) and F-values from ANOVA of the total number of vessel rings (NR), rubber production (RP), bark thickness (BT) and girth (SG) for 22 *Hevea* progenies established at three sites. São Paulo State, Brazil.

Source of variation	d.f.	Total number of vessel rings		Rubber production		Bark thickness		Girth	
		MS	F	MS	F	MS	F	MS	F
Replications/sites	12	0.0554	1.7922 ^{ns}	0.0398 ^{ns}	0.2342 ^{ns}	0.4079	0.9402 ^{ns}	10.6360	0.7395 ^{ns}
Sites (S)	2	0.0546	0.8661 ^{ns}	2.8948	14.0571 ^{**}	0.7814	1.1944 ^{ns}	1712.6714	68.8129 ^{**}
Progenies (P)	21	0.0955	3.0931 ^{**}	0.5373	3.1579 ^{**}	3.3468	7.7151 ^{**}	129.8085	9.0248 ^{**}
P x S	42	0.0309	1.5388 ^{**}	0.1701	2.9669 ^{**}	0.4338	1.9376 ^{**}	14.3835	1.5991 ^{**}
Residual (mean)	252	0.0201	-	0.0574	-	0.2239	-	8.9945	-
Mean		1.6889		0.6556		3.2586		18.6874	
Coefficient of variation %		4.6538		28.1366		9.0393		9.0761	

¹Total number of NR, RP, BT and SG are expressed in unit, g, mm, and cm, respectively. * P < 0.05, ** P < 0.01, ns = nonsignificant.

Table III - Mean squares (MS) and F-values from ANOVA of the Pindorama and Votuporanga sites for four traits of 22 three-year-old open pollinated progenies of *Hevea*. São Paulo State, Brazil.

Source of variation	d.f.	Total number of vessel rings (NR)		Rubber production (RP)		Bark thickness (BT)		Girth (SG)	
		MS	F	MS	F	MS	F	MS	F
Replications/sites	08	0.0321	0.7548 ^{ns}	0.0404	0.1889 ^{ns}	0.2437	0.9179 ^{ns}	6.5307	0.3762 ^{ns}
Sites (S)	1	0.0147	0.4902 ^{ns}	5.7445	22.8349 ^{**}	0.0880	0.6202 ^{ns}	319.2045	13.7914 ^{**}
Progenies (P)	21	0.0641	1.5047 ^{ns}	0.5666	2.6491 [*]	2.7623	10.4041 ^{**}	105.2553	6.0638 [*]
P x S	21	0.0426	1.9456 ^{**}	0.2139	3.4301 ^{**}	0.2655	1.1655 ^{ns}	17.3579	1.6931 [*]
Residual (mean)	168	0.0219	-	0.0624	-	0.2278	-	10.2520	-
Mean		1.7009		0.6639		3.3059		20.8568	
Genetic correlation		0.39		0.79		0.98		0.86	
Coefficient of variation %		5.4257		31.1570		6.9701		8.9334	

¹Total number of NR, RP, BT and SG are expressed in unit, g, mm, and cm, respectively. * P < 0.05, ** P < 0.01, ns = nonsignificant.

Joint analysis of variance for two locations (Pindorama and Jaú)

The results of the joint analysis involving Pindorama and Jaú (Table IV) showed greater genetic variability among progenies than those for Pindorama and Votuporanga. The analyses were based on significant F-values for all the traits studied, although the observed values were less expressive for RP, BT and SG. The experimental coefficients of variation had the same tendency as those obtained in the previous joint analyses, with a greater value for RP and lower values for SG, BT and NR.

As with the joint analysis for Pindorama and Votuporanga, the location effect showed less expressive or significant values for RP and SG. Less expressive and nonsignificant values were obtained for NR and BT, indicating that these traits were less affected by environmental variations at the test sites.

The effect of the progenies x location interaction gave significant F-results for all the traits as in the joint analysis of all locations, again with more expressive and

significant results for RP and BT. This finding agrees with the results obtained by Gonçalves *et al.* (1991, 1998a).

Generally, there was a tendency for greater variability in the genotype performance when compared to the results obtained for Pindorama and Votuporanga. Although the environmental conditions were not very different, other factors, mainly the soil (fertility, structure and type), may have interfered with genotype performance (Pinheiro *et al.*, 1980).

The genetic correlation obtained for Pindorama and Jaú was high for RP, BT, SG and medium for NR. The highest values, however, were smaller than those from the analysis of Pindorama and Votuporanga. As in the previous analysis, these results characterize the interaction for RP, BT and SG. This indicates that only one breeding program for these characters will attend satisfactorily the region of the involved places.

Joint analysis of variance for two locations (Votuporanga and Jaú)

The joint analyses of variance for all traits at the above

two locations (Table V) showed significant genetic variation among progenies. A small variation in magnitude among the values was obtained for NR, RP and BT, but this was greater for SG. These variations still indicated good perspectives for the selection of progenies and for continuity in the genetic breeding program at Votuporanga and Jaú. As with the previous joint analyses, the experimental coefficients of variation were higher for RP and lower for BT, SG and NR. This analysis showed the lowest coefficient of variation for the RP trait, suggesting greater accuracy in the field trails.

The location effect yielded significant values for RP and SG. Less expressive (nonsignificant) values were obtained for NR and BT, again showing that these traits were less affected by environmental variation. The effect of the progeny x location interaction was significant only for the BT trait. Values of less extent were obtained for NR, RP

and SG, showing that these traits were less affected by variation between the locations involved.

The genetic correlation was higher for SG, RP and BT and lower for NR. These results characterized small interactions for RP, BT and SG, and indicated that a single breeding program could satisfactorily serve the region covering these two locations.

Adequate number of experimental locations

Using the estimated values (Tables VI and VII) and utilizing the table of estimators presented by Resende (1998) it was possible to determine the ideal number of experimental locations as follows:

a) Total number of latex vessel rings: considering the values of $(\sigma_{ge}^2 / \sigma_g^2) = 0.501$ and $r_{gg} = 0.666$, the efficiency of selection based on the mean of two and three locations for

Table IV - Mean squares (MS) and F-values from ANOVA of the Pindorama and Jaú sites for four traits of 22 three-year-old open pollinated progenies of *Hevea*. São Paulo State, Brazil.

Source of variation	d.f.	Total number of vessel rings (NR)		Rubber production (RP)		Bark thickness (BT)		Girth (SG)	
		MS	F	MS	F	MS	F	MS	F
Replications/sites	08	0.0691	2.1540*	0.0386	0.1513 ^{ns}	0.4913	0.8583 ^{ns}	15.0415	0.8898 ^{ns}
Sites (S)	01	0.1069	1.2324 ^{ns}	1.9102	6.7533**	0.8162	0.9719 ^{ns}	1547.070	48.7166**
Progenies (P)	21	0.0852	2.6558*	0.5083	1.9938*	2.3393	4.0868**	85.7301	5.0713**
P x S	21	0.0321	1.7953*	0.2549	3.5415**	0.5724	2.6299**	16.9050	1.8268*
Residual (mean)	168	0.0179	-	0.0720	-	0.2176	-	9.2538	-
Mean		1.6870		0.7323		3.2250		17.0004	
Genetic correlation		0.66		0.75		0.73		0.86	
Coefficient of variation %		4.7485		30.8363		10.4916		10.8459	

[†]Total number of NR, RP, BT and SG are expressed in unit, g, mm, and cm, respectively. * P < 0.05, ** P < 0.01, ns = nonsignificant.

Table V - Mean squares (MS) and F-values from ANOVA of the Votuporanga and Jaú sites for four traits of 22 three-year-old open pollinated progenies of *Hevea*. São Paulo State, Brazil.

Source of variation	d.f.	Total number of vessel rings (NR)		Rubber production (RP)		Bark thickness (BT)		Girth (SG)	
		MS	F	MS	F	MS	F	MS	F
Replications/sites	08	0.0648	3.6017**	0.0461	0.9762 ^{ns}	0.4886	1.0541 ^{ns}	10.3358	1.1629 ^{ns}
Sites (S)	01	0.0423	0.0758 ^{ns}	1.0295	13.4154**	1.4402	1.7502 ^{ns}	3271.7389	170.5837**
Progenies (P)	21	0.0726	4.0361**	0.1697	4.0854**	2.0258	4.3702**	83.0150	9.3405**
P x S	21	0.0180	0.8798 ^{ns}	0.0415	1.1007 ^{ns}	0.4635	2.0490**	8.8876	1.1885 ^{ns}
Residual (mean)	168	0.0205	-	0.0377	-	0.2262	-	7.4778	-
Mean		1.6789		0.5707		3.2450		18.2050	
Genetic correlation		0.59		0.98		0.77		0.99	
Coefficient of variation %		3.5737		15.9750		9.3833		7.3235	

[†]Total number of NR, RP, BT and SG are expressed in unit, g, mm, and cm, respectively. * P < 0.05, ** P < 0.01, ns = nonsignificant.

Table VI - Estimated variance components for Pindorama ($\sigma_{g_i}^2$), Votuporanga ($\sigma_{g_j}^2$), Jaú ($\sigma_{g_k}^2$) joint analysis (σ_g^2) and progenies x sites interaction (σ_{gs}^2) for four traits used to estimate the correlations (r_{gg}) and genetic gains in São Paulo State, Brazil.

Estimated variation components	Total number of vessel rings	Rubber production	Bark thickness	Girth
$\sigma_{g_i}^2$	0.0093	0.1140	0.3009	10.9298
$\sigma_{g_j}^2$	0.0032	0.0176	0.2131	9.4871
$\sigma_{g_k}^2$	0.0069	0.0099	0.1944	5.8961
σ_g^2 (1 x 2)	0.0021	0.0353	0.2497	8.7897
σ_g^2 (1 x 3)	0.0053	0.0253	0.1767	6.8825
σ_g^2 (2 x 3)	0.0055	0.0128	0.1562	7.4127
σ_{gs}^2 (1 x 2)	0.0041	0.0303	0.0075	1.4212
σ_{gs}^2 (1 x 3)	0.0028	0.0366	0.0709	1.5302
σ_{gs}^2 (2 x 3)	0.0027	0.0008	0.0475	0.2820

σ_g^2 (1 x 2), σ_g^2 (1 x 3), σ_g^2 (2 x 3) = Genetic variance of the joint analysis for Pindorama x Votuporanga, Pindorama x Jaú and Votuporanga x Jaú, respectively. σ_{gs}^2 (1 x 2), σ_{gs}^2 (1 x 3), σ_{gs}^2 (2 x 3) = Variance of the interaction of Pindorama x Votuporanga x Jaú, respectively.

Table VII - Estimated variance components of the interaction progenies x sites relative to genetic variance (σ_{ge}^2/σ_g^2) and genetic correlation (r_{gg}) between the sites, in São Paulo State, Brazil.

Parameters	Total number of vessel rings	Rubber production	Bark thickness	Girth
σ_{ge}^2/σ_g^2	0.501	0.922	0.216	0.140
r_{gg}	0.666	0.520	0.822	0.877

Table VIII - Narrow sense heritability coefficients based on individuals within the block (h_{ib}^2) for total number of vessel rings (NR), rubber production (RP), bark thickness (BT) and girth (SG) for a population of 22 *Hevea* progenies determined at three sites in São Paulo State, Brazil.

Sites	Heritabilities			
	NR	RP	BT	SG
Pindorama	0.17	0.61	0.51	0.36
Votuporanga	0.06	0.24	0.35	0.32
Jaú	0.11	0.11	0.30	0.33

Table IX - Estimates of genetic gain in three-year-old open pollinated rubber tree progenies at the Pindorama, Votuporanga and Jaú sites in São Paulo State, Brazil.

Parameters	Expected gain (%)						
	$G_{s(ijk/i)}$	$G_{s(ijk/j)}$	$G_{s(ijk/k)}$	$G_{s(ijk/ij)}$	$G_{s(ijk/ik)}$	$G_{s(ijk/jk)}$	$G_{s(ijk/ijk)}$
Total number of vessel rings (NR)	5.06	4.16	6.06	5.96	6.46	5.79	6.54
Rubber production (RP)	42.66	38.47	30.78	45.04	44.00	34.68	45.32
Bark thickness (BT)	22.24	21.78	19.42	22.99	23.80	22.85	23.74
Girth (SG)	22.80	24.05	23.57	25.23	25.01	24.93	25.71

$G_{s(ijk/i)}$ = Selection in Pindorama and expected gain at the three sites. $G_{s(ijk/j)}$ = Selection in Votuporanga and expected gain at the three sites. $G_{s(ijk/k)}$ = Selection in Jaú, and expected gain at the three sites. $G_{s(ijk/ij)}$ = Selection based in Pindorama (*i*) and Votuporanga (*j*) means and expected gain at the three sites. $G_{s(ijk/ik)}$ = Selection based in Pindorama (*i*) and Jaú (*k*) means and expected gain at the three sites. $G_{s(ijk/jk)}$ = Selection based in Votuporanga (*j*) and Jaú (*k*) means and expected gain at the three sites. $G_{s(ijk/ijk)}$ = Selection based in Pindorama (*i*), Votuporanga (*j*) and Jaú (*k*) means and expected gain at the three sites.

selection at a single location was 10, 13 and 15%, respectively. Thus, the use of only two experimental locations was considered adequate since it would be advantageous to use a further location only if the efficiency gain were greater than 10%.

b) Rubber production: considering the values of (σ_{ge}^2/σ_g^2) = 0.922 and r_{gg} = 0.520, the efficiency of selection based on the mean of two, three and four locations in relation to selection at a single location was 14, 21 and 25%, respectively. Again, the use of only two experimental locations would be suitable.

c) Bark thickness: considering the values of (σ_{ge}^2/σ_g^2) = 0.216 and r_{gg} = 0.822, the efficiency of selection based on the mean of two and three locations, compared with selection at a single location, was 4 and 6%, respectively. Thus, the use of a single experimental location would be adequate.

d) Girth: considering the values of (σ_{ge}^2/σ_g^2) = 0.140 and r_{gg} = 0.877, the efficiency of selection based on the mean of two and three locations in relation to selection at a single location was 2 and 3%, respectively. As with the previous item, the use of only one experimental location would be adequate.

Expected progress with selection

Narrow sense heritabilities estimated for total number of vessel rings, rubber production, bark thickness and girth (Table VIII) varied among sites, showing higher values for rubber production in Pindorama, suggesting great possibilities of genetic gain for this character at this site. The predictions of expected progress with selection (Table IX) assumed a selection intensity of 10% for all the traits. The values varied considerably among traits, with greater gains for RP. These values were within the limits obtained by Paiva (1980), Vasconcellos (1982), Moreti *et al.* (1994) and Boock *et al.* (1995). The results showed a tendency for greater gains, except for NR, when the selection took place in Pindorama and Votuporanga.

Based on the mean indirect gain for RP from Pindo-

rama and Votuporanga, which was almost the same as the mean gain with selection for the three locations, the use of the three locations is not justified. This conclusion agrees with the genetic correlation of the materials according to location and may also be explained by the genetic correlation of 0.98 (Table V) between Votuporanga and Jaú, which shows that when Votuporanga was used as an experimental location, the inclusion of Jaú did not add substantial information for the breeder. The two locations have the same discrimination power for the genetic materials.

The use of only the Pindorama site should lead to a mean gain of 42.7% in the three locations. The inclusion of Votuporanga increased this gain to 45.04%, providing an additional 6% efficiency. The efficiency was lower than the mean efficiency of 10%, probably because of the heterogeneity of the genetic variances observed at these locations. Thus, the breeder must judge whether this small increment is worthwhile. Based on these results, the use of the Pindorama and Votuporanga sites is suggested for continuing the breeding program, since together they satisfactorily serve the region covered by this study.

ACKNOWLEDGMENTS

The authors are grateful to Mr. Ari de Camargo, Mr. Isaac de Jesus and Mr. Edison Bernardes de Freitas, agricultural technicians from Campinas, Votuporanga and Pindorama, respectively, for the field work; Mrs. Lígia Regina Lima Gouvêa and Mrs. Rosimeire Moreira Boschini, laboratory technicians from Rubber Tree Program of the Instituto Agrônômico de Campinas for the laboratory work. R.B.C. is the recipient of a CAPES fellowship. Research and publication supported by the Fundação de Amparo à Pesquisa do Estado de São Paulo (FAPESP).

RESUMO

O presente estudo objetivou quantificar possíveis interações de progênie x local, bem como determinar o número ideal de locais de experimentação com base em estimativas de correlação genética entre progênes nos diferentes locais e estimativa de ganhos genéticos com seleção indireta em seringueira [*Hevea brasiliensis* (Willd ex A.Dr. de Juss.) Müell. Arg.]. Vinte e duas progênes de meio-irmãos foram plantadas nas Estações Experimentais de Jaú, Pindorama e Votuporanga, todas em SP, no delineamento de blocos ao acaso, com cinco repetições e dez plantas por parcela. Aos três anos de idade foram avaliados os caracteres: número total de anéis de vasos laticíferos, produção de borracha seca, espessura da casca e perímetro do caule. Os resultados demonstraram haver variabilidade genética significativa entre progênes para os caracteres produção, perímetro do caule e espessura da casca, evidenciados em Pindorama e Votuporanga. O efeito da interação genótipo x locais significativos, especialmente para os caracteres produção de borracha e perímetro do caule, não é um fator complicador para o melhorista devido às altas correlações genéticas detectadas. Considerando ser vantajoso o uso de um local a mais apenas quando o ganho em eficiência for superior a 10%, no presente caso a utilização de dois locais de experimentação é a mais adequada. O uso dos locais Pindorama e Votuporanga atenderá satisfatoriamente a região de abrangência do estudo.

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(Received September 21, 1998)

