GENETIC VARIABILITY FOR GIRTH GROWTH AND RUBBER YIELD IN *Hevea brasiliensis*

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ABSTRACT: Basic knowledge of genetic characteristics of populations is necessary to conduct effective breeding and selection. The objective of this paper is describing the genetic variation of rubber yield and the correlation with other traits, and estimating the genetic parameters for girth growth and total number of latex vessels. Sixty seven clones of *Hevea brasiliensis* (Willd. ex Adr. de Juss.) Muell.-Arg. were tested at five sites during 10 years. Characters girth growth at panel opening and rubber yield, showed broad sense heritability on plot mean level, from 0.32 to 0.66 and 0.59 to 0.92, respectively. Predicted genetic gains equal to 0.73 cm and 0.79 g increase respectively on girth and yield in the opening panel and mature phases seems realistic, even with moderate selection intensities. Genetic correlations with rubber yield, bark thickness and total number of latex vessels were very large, and almost no genotype-environment interaction was present for girth growth. High genotype-environment interaction was present for rubber yield with genetic and phenotypic correlations across the sites, ranging from 0.64 to 0.92 (genetic) and 0.63 to 0.89 (phenotypic). Total number of latex vessels rings had a high heritability, ranging from 20.0% to 64.0% in the sites E and B, respectively.
Key words: rubber tree, heritability, genetic correlations, genotype-environment interaction

VARIABILIDADE GENÉTICA PARA CRESCIMENTO DO CAULE E PRODUÇÃO DE BORRACHA EM *Hevea brasiliensis*

RESUMO: O conhecimento básico das características presentes nas populações de plantas é essencial para a condução dos trabalhos de seleção e melhoramento. Neste trabalho, objetivou-se descrever a variação genética da produção de borracha e correlaciná-las com outras características, assim como estimar os parâmetros genéticos para perímetro do caule e o número de anéis de vasos laticíferos. Um total de 67 clones de seringueira [*Hevea brasiliensis* (Willd. ex Adr. Juss.) Muell.-Arg.] foram avaliados em cinco locais durante 10 anos. Os caracteres perímetro do caule na abertura do painel e produção de borracha mostraram herdabilidades no sentido amplo ao nível de média de parcela entre 0,32 a 0,66 e 0,59 a 0,92, respectivamente. Ganhos genéticos preditos de 0,73 cm e 0,79g de incremento de perímetro na fase juvenil parecem viáveis mesmo com uma intensidade de seleção moderada. Correlações genéticas entre produção de borracha, espessura de casca e número total de vasos laticíferos foram muito altas, e praticamente não houve interação genótipo-ambiente para perímetro do caule. Alta interação genótipo-ambiente foi detectada para produção de borracha, com correlações genéticas e fenotípicas por locais variando entre 0,64 e 0,92 (genéticas) e 0,63 e 0,89 (fenotípicas). O caráter total de anéis de vasos laticíferos apresentou alta herdabilidade, variando de 20% até 63% nos locais E e B, respectivamente.
Palavras-chave: seringueira, herdabilidade, correlação genética, interação genótipo-ambiente

INTRODUCTION

To improve the productivity of rubber plantations, *Hevea* breeding programs exploit genetically variable populations to obtain superior trees. A basic knowledge of the genetic characteristics of plant populations is necessary to conduct effective breeding and selection. Quantitative information is required about the size of genetic variances, the type of gene action, and the heritability and genetic correlations for economically important traits. This enables the outcome of selection to be predicted, particularly genetic gains. It also helps determining difficulties in selection and the strategies to overcome such problems. In a broader context, it broadens knowledge of the genetics and breeding behavior of the species involved.

The Instituto Agronômico (IAC) conducts a Brazilian *Hevea* breeding program, with emphasis on

improvement and selection of vigour and quality traits, such as latex vessels rings. The objective of this paper is describing the genetic variation of rubber yield, and its correlation with other traits. Genetic parameters for girth and total number of latex vessels of 67 clones, 13 years after establishment in the field, were also studied.

MATERIAL AND METHODS

Plant material and experimental locations

Thirty one Brazilian, 10 Indonesian, and 26 Malaysian *Hevea brasiliensis* genotypes (clones) were used in this study. The Brazilian clones Fx, IAC, and IAN were developed by the Fordland breeding program, Instituto Agronômico (IAC), and former "Instituto Agronômico do Norte (IAN)", now Embrapa Ocidental. The Indonesian clones comprised GT, PR, and AVROS, from Gondang Tapen, Proefstation voor Rubber, and Algemene Verening Rubber Planters Oostkust Sumatra experimental stations, respectively. The Malaysian cultivars consisted of RRIM and PB, from Rubber Research Institute of Malaysia, and Prang Besar private rubber plantation respectively. Among the 67 clones, PB 235, GT 1, RRIM 600 and IAN 873 are recommended production clones, whereas RRIM 701, PR 255, PR 261, IAN 873, PB 216, and RO 38, are used as parents in local rubber breeding programs. The rubber clones were grafted over established GT 1 rootstocks at the nursery. One year-old rootstocks seedlings raised in nurseries were used to budgraft clonal materials. The successful budgrafts were uprooted and planted in polyethylene bags. After the first flush of leaves developed, plants were established in the field.

The clones were grown for ten years in five contrasting test environments (A, B, C, D and E) in the plateau region of São Paulo State, ecological conditions summarized as:

• Jaú (A): 22º17'S, 48º34'W; altitude 580 m; mean annual temperature 21.6ºC; mean annual rainfall 1,344 mm; Kandiudox soil, with good nutrient status and physical structure.

• Mococa (B): 21º18'S, 47º01'W; altitude 665 m; mean annual temperature 24ºC; mean annual rainfall 1,500 mm; Eutrustok soil, with good nutrient status and physical structure.

• Ribeirão Preto (C): 22º11'S, 47º48'W; altitude 467 m; mean annual temperature 29ºC; mean annual rainfall 1,530 mm; Kandiudox soil, with good nutient status but poor physical structure.

• Votuporanga (D): 20º25'S, 49º50'W; altitude 450 m; mean temperature during growing season 32ºC; mean annual rainfall 1,480 mm; Paleudalf soil, with average nutrient status and poor physical structure.

• Matão (E): 21º18'S, 48º40'W; altitude 551 m; mean annual temperature 25ºC; mean annual rainfall 1,480 mm; Paleudox soil type, with average nutrient status and very good physical structure.

These locations represent the most important continental climate, non-traditional rubber production areas in Brazil. Experimental design at each test location was randomized complete blocks (n = 3), with ten plants per one-row plot in all locations. Trees were spaced 8.00 m between and 2.50 m within rows (500 trees ha^{-1}).

Measurements

At the end of the seventh year, girth, bark thickness and total latex vessel rings at panel opening for tapping and rubber yield of each tree were measured. Girth measurements were recorded at 1.20 m from the highest point of the bud union. For annual latex production, attempts were made to record five annual yields after panel opening. The latex extracted from the tapping panel followed a half-spiral, four-daily tapping system (seven tappings per month), 11 months per year. After tapping, latex was collected in plastic cups provided for each recording tree. Once the latex flow was stopped, rubber was coagulated in the cup by adding 2% acetic acid solution and stirring. The coagulated rubber was pressed into a cylinder, hang-dried for 30 days, and their weighed for calculation of the dry rubber content.

Statistical analyses within sites

The following linear model was used to analyze the data within sites: $Y_{ij} = \mu + b_j + c_i + \varepsilon_{ij}$, where Y_{ij} = performance of the ramet of ith clone within j^{th} block; μ = overall mean, b_j = random effect of the jth block; c_i = random effect of the ith clone, $E(c_i) = 0$ and *Var* $(c_i) = \sigma_c^2$, ε_{ij} = random error, equal to the interaction between the ith clone and j^{th} block, $E(\varepsilon_{ij}) = 0$ and *Var* $(\varepsilon_{ij}) = \sigma_e^2$. The analysis of variance was performed using procedures of the software "Selegen", version 1.0 (Resende & Oliveira, 1997) to estimate covariances. Tests for normal distribution of single tree data, clone means data and residuals were made using the "Genes" software, Windows version, 2001 (Cruz, 2001).

A few missing measurements in the trials were due to low development of the trees girth, mainly explained by the lack of compatibility between rootstocks and scions. Broad sense heritabilities on plot and clone mean levels were calculated. Following Cotterill

(1987), a distinction was made between different heritabilities depending on the purpose. The calculated broad sense heritability on plot mean level is, in this case, used to calculate genetic gains by mass selection on sites similar to the trials, where the block effects can not be taken into account. The broad sense heritability on a clonal mean basis is appropriate for predicting genetic gains from selection among the clones in the trials. In this case, the effect of blocks can be accounted for prior to selection.

The plot mean broad sense heritability h_p^2 was therefore calculated as: $h_p^2 = \sigma_c^2 / (\sigma_c^2 + \sigma_b^2 + \sigma_e^2)$, where σ_c^2 = genetic variance or covariance components between clones, σ_b^2 is the block variance, and σ_e^2 the error variance components. The broad sense heritability on clone mean level h_m^2 was calculated as: $h_m^2 = \sigma_c^2 / (\sigma_c^2 + \sigma_e^2 / b)$, where b is the harmonic mean of ramets per clone in the trial. Approximate standard deviations of heritabilities were found using the delta technique (Bulmer, 1980). The genetic correlations r_g between trait x and y within sites were calculated according to Falconer (1989) as: $r_g = Cov_{c_{xy}} / (\sqrt{\sigma_{cx}^2 \sigma_{cy}^2})$.

The genetic covariance $Cov_{c_{xy}}$ was obtained by using mean cross products from the "Genes" procedure. Approximate standard deviations of the genetic correlations within sites were calculated according to Falconer (1989). The phenotypic correlations r_p between trait x and y were calculated as the Pearson correlation using the procedures of the "Sanest" computer program (Zonta & Machado, 1992), since the phenotypic correlations in this case included all elements of covariances/variances: the genetic, the block and the error covariance/variance. So, according to Falconer (1989):

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where $Cov_{c_{xy}}$ is genetic covariance between trait x and y; $Cov_{b_{xy}}$ is block covariance between trait x and y; $Cov_{e_{xy}}$ is the error covariance between trait x and y; σ_c^2 and σ_b^2 are clone and block variances. σ_e^2 subscripts refer to traits x or y.

Statistical analyses across sites

The linear model for the analysis of variance across sites had the following composition: $Y_{ijk} = \mu + e_i + b_{j(i)} + c_k + ce_{ik} + \varepsilon_{ijk}$, where Y_{ijk} is the performance of the ramet of the kth clone in j^{th} block within i^{th} site; μ is the overall mean; e_i is the fixed effect of ith site; $b_{j(i)}$ is the fixed effect of jth block within i^{th} sites; c_k is the random effect of kth clone with $E(c_k) = 0$ and $Var(c_k) = \sigma_c^2$; ce_{ik} is the random effect of interaction between i^{th} site and k^{th} clone, with $E(ce_{ik})$ 0 and $Var(ce_{ik}) = \sigma_{ce}^2$; and ε_{ijk} is the random error due to clone by block interaction within the ith site with $E(\varepsilon_{ijk}) = 0$ and $Var(\varepsilon_{ijk}) = \sigma_e^2$.

To be valid, the test of genotype-environment interaction in the model requires: 1) homogeneous clonal variances across the different sites to avoid a generation of genotype-environment interaction due to scale effects; 2) homogeneous residual variance among environments; and 3) normal distribution of the residuals (Burdon, 1977). These conditions for the model were fulfilled, testing the genotype-environment interaction concerning number of latex vessels between the four trials. However, some transformation of data from trial D, was necessary in the analyses between trial A-D, B-D and C-D. The transformations implied a reduction of the values by a factor equal to the ratio of variance of residuals from the two sites in the analyses, to assure homogenous residual variances across sites. In those cases, it was later necessary to use logarithmic values to get normal distributions of the residuals.

Genetic correlations r_g across sites for all traits were calculated using type B covariances (Burdon, 1977), and the genetic variances of the traits within sites, considering the same trait measured on different sites as different traits. Therefore, the genetic correlation across sites according to the definition in Falconer (1989) was: $r_g = Cov_{g_{xy}} / (\sqrt{\sigma_{g_x}^2 \sigma_{g_y}^2})$.

Correlations across sites for total number of latex vessels were therefore considered as intra class correlations on basis of the variance components in the model used for the analyses across sites. The intra class correlations r_g is alternatively calculated as: $r_g = \sigma_c^2 / (\sigma_c^2 + \sigma_{ce}^{2'})$, where r_g is the correlation across sites; σ_c^2 is clone variance across two sites; $\sigma_{ce}^{2'}$ is clone-environment interaction, adjusted for site differences in variance, estimated as: $\sigma_{ce}^{2'} = \sigma_{ce}^2 - (\sqrt{\sigma_{cx}^2} - \sqrt{\sigma_{cy}^2})^2 / 2$, where σ_{cx}^2 = genetic or clone variance on site x, and σ_{cy}^2 = genetic or clone variance on site y. Eisen (1994) found this method to give biased estimates in case of unbalanced data, unless genetic variances and residual variances on different sites are equal to each other. Even though data were not fully balanced, given that genetic variances and that residual variances on at least three of the sites (A, B and C) were similar, the formula described by Fernando et al. (1984) was considered appropriate to estimate the genetic correlations, calculated as:

$$y = \begin{bmatrix} y_1 \\ y_2 \end{bmatrix} = \begin{bmatrix} l_1 \ \mu_1 \\ l_2 \ \mu_2 \end{bmatrix} + \begin{bmatrix} Z_1 \\ Z_2 \end{bmatrix} u_G + \begin{bmatrix} Z_1 & 0 \\ 0 & Z_2 \end{bmatrix} u_I + e$$

where y_i is the $n_j \times 1$ vector of data for trait i, i -= 1, 2 and n_j is the number of observations for trait i; μ_i is the expected value of trait i and l_j is an $n_j \times 1$ vector of ones; u_G is a vector of average genetic-group effects

of environments; u_I is a vector of genotype x environment interaction effects; and e_i is a vector of residual effects.

Differences between clone means on one site and clone means on another site were calculated to investigate differences between clones, concerning sensitivity to changes in the environment. The differences were found after adjustments due to differences in variances between two sites, x and y. This was done by multiplying the clone mean on one of the sites with regression coefficients b_{yx}. The difference between a clone mean on site x and y, dif_{xy} was e.g. found as: $dif_{xy} = (b_{yx}\overline{m}_x) - \overline{m}_y$, where b_{yx} is regression coefficient to adjust for differences in variances between clone means on two sites x and y, in this case used to make means on site x comparable to means on site y; $\overline{m}_x$ is clone mean on site x, and $\overline{m}_y$ is clone mean on site y.

The regression coefficient b can be found as: $b_{yx} = Cov_{xy}/V_x = (r\sqrt{V_x}\sqrt{V_y})/V_x$, where Cov_{xy} is covariance between clone mean on site x and site y, assuming zero genotype-environment interaction; r is the clonal mean correlations across sites, equal to 1 since the genotype-environment interaction is assumed to be zero; V_x is the clone mean variance on site x; and V_y is the clone mean variance on site y.

Differences were calculated considering one site that was both independent and dependent in relation to another site. An analysis of variance of the numeric differences between clone means on different sites was then carried out to examine if some clones, in general, react more sensitively to environmental changes than others.

RESULTS AND DISCUSSION

Girth at panel opening

Differences between clones were highly significant in A and B trials, and individual broad sense heritabilities were about 0.55 in trials A and B, and lower ($h_i^2 = 0.47$) in trial C, which probably can be attributed to a sampling error due to missing trees in the trial, and variable growth conditions within the replication (Table 1). The phenotypic standard deviations were between 2.4 and 3.8 cm, and the average of girth at panel opening in the trials was about 42.9 cm. Compared to other traits, heritabilities were quite low but absolute values of the phenotypic standard deviations

Table 1 - Variance components and broad sense heritabilities on the different sites. Furthermore predict gains (G) by phenotypic selections with selection intensity i= 1.352 and by selection among the clones in the trial, using the clonal mean heritability and with a selection intensity of i= 0.821. Data from sixty seven 10 years old clones of *Hevea*, tested at five locations in São Paulo State, Brazil.

Traits[1]	Sites[2]	Variance components[3]				CV%	$\overline{x}$	Heritabilities[4]			Phenotypic selection		Selection in trial	
		σ_b^2	σ_c^2	σ_e^2	σ_p^2			h_p^2	s.e.	$h_{\overline{x}}^2$	G	G%	G	G%
Go	A	0.1695	3.1096**	2.78882	6.0673	3.9086	45.1161	0.5125	0.16	0.7699	0.6929	1.53	0.9710	2.16
	B	0.0768	8.3424**	5.8644	14.2836	7.5969	38.0195	0.5840	0.09	0.8101	0.7895	2.08	0.5725	1.51
	C	0.3763	1.1790ns	5.6887	6.9440	3.0705	35.3633	0.4697	0.10	0.3834	0.5294	1.50	0.8434	2.38
	D	-	6.2977ns	13.5096	19.8073	5.2276	48.0052	0.3179	0.08	0.5831	0.4298	0.09	0.2888	0.60
	E	0.8493	7.0146ns	2.7712	10.6357	5.5025	48.1567	0.6595	0.09	0.8866	0.8916	1.85	0.9655	2.00
Yr	A	0.2198	92.8353**	7.4995	100.5546	18.0751	53.3061	0.9232	0.04	0.9738	0.2482	0.465	0.8179	1.53
	B	-	18.0633**	11.3164	29.3797	18.6175	22.8286	0.6148	0.04	0.8272	0.8312	3.64	0.8001	3.50
	C	0.4423	18.6988**	2.5188	21.6609	14.9008	29.0200	0.8632	0.05	0.9570	1.1670	4.02	0.7580	2.61
	D	-	133.1347**	16.2864	149.4211	29.0448	39.7261	0.5910	0.03	0.9608	1.2046	3.03	0.7893	1.99
Bt	A	-	0.1001**	0.0396	0.1397	5.5398	5.7105	0.7165	0.04	0.8834	0.9687	16.96	0.8058	14.11
	B	-	0.1117**	0.0333	0.2250	5.8980	4.2319	0.6787	0.03	0.3950	1.0528	24.87	0.8100	19.14
	E	0.0003	0.1876**	0.0261	0.2140	7.9069	5.5852	0.8766	0.04	0.9535	1.1852	21.86	0.8165	14.60
Lv	A	-	0.5572**	0.3201	0.8713	5.5719	13.3248	0.6326	0.03	0.8378	0.8553	6.42	0.8025	6.02
	B	0.0577	0.3444**	0.1397	0.5418	7.6517	7.6700	0.6356	0.04	0.8809	0.8593	11.20	0.8061	10.51
	D	-	0.4010ns	1.1527	1.5537	4.9361	12.8280	0.2580	0.05	0.5106	0.3488	2.72	0.7362	5.74
	E	-	0.2390ns	1.1956	1.4946	3.7069	14.7514	0.2000	0.06	0.4286	0.2704	1.83	0.6689	4.53

[1]Go = girth at panel opening, Yr = rubber yield, Bt = bark thickness, Lv = total number of latex vessel rings. [2]Jaú (A), Mococa (B), Ribeirão Preto (C), Votuporanga (D) and Matão (E). [3] σ_b^2 = block variance; σ_c^2 = genetic variance between clones; σ_e^2 = error variance; σ_p^2 = phenotypic variance. [4] h_p^2 = broad sense heritability on plot mean level; $h_{\overline{x}}^2$ = broad sense heritability based on clone means. **$P < 0.01$; ns = not significant.

were high. A moderate selection intensity $i = 0.82$ equal to a selection of the 43% best clones will give a predicted genetic gain about 0.66 cm while a mass selection outside the trials will give a predicted gain about 0.73 cm with a selection intensity $i = 1.35$, equal to a selected proportion about 14%. The mean girth of about 43 cm on panel opening in the trials agrees with former findings by Gonçalves et al. (1998).

Investigations of immature rubber tree in Amazon registered individual broad sense heritabilities of about $h_i^2 = 0.57$ (Gonçalves et al., 1983). Heritabilities found in this investigation seem small compared to that. More precise measurements e.g. on adult trees, would probably have led to smaller residual variances and hence higher broad sense heritabilities. The phenotypic standard deviations were similar to those reported by Gottardi et al. (1995) for girth at panel opening.

Rubber yield, bark thickness and total number of latex vessels rings

Clonal differences in rubber yield and bark thickness were highly significant on all sites (Table 1), with moderate to high individual broad sense heritabilities, ranging from 0.59 to 0.92 for rubber yield and from 0.68 to 0.87 for bark thickness at seven years. Predicted genetic gain for bark thickness was 2.41% for a selection intensity of 50% based on clonal means. The predicted gain from a mass selection is about 0.60 to 19.14% for a selection intensity of 14% ($i = 1.35$). The heritabilities on clone mean levels and phenotypic standard deviations are close to those reported by Gonçalves et al. (2004) in the same and other 10 year old trials. Heritabilities for rubber yield and bark thickness on site D were lower compared to the other sites, probably as a result of very uneven growth conditions.

Total number of latex vessels rings had a moderate to low broad sense heritability on individual tree level at 0.43, and a coefficient of variance at 5.46%. Predicted gains are about 6.70% for a selection of the best 50% clones in the trials, and about 5.54% following mass selection of the 14% best individuals.

Correlations between traits within sites

Girth at panel opening showed in general very large genetic and phenotypic correlations with bark thickness (Table 2). This is in agreement with findings of Gonçalves et al. (1989) for 33 IAC clones, and Gottardi et al. (1995) for 11 clones at the fourth year of yield. Also Gonçalves (1982) found, in wild mother trees from 10 sites, pronounced differences in bark thickness between fast growing and slow growing trees in the Amazon valley basin. However, fast growing trees of *Hevea* have a tendency to maintain a higher level of positive girth correlation with bark thickness. Gonçalves

(1982) found larger standard deviations within the groups, which would suggest a strong genetic influence on bark thickness. Results from Ho (1976), who investigated 24 *Hevea* clones from different trials, showed that the fastest growing trees also had a greater bark thickness compared to the slow growing groups. However these results should be interpreted with caution given the reduced number of trees in each group. The stands were further characterized by high site indices, which might explain why the correlation with growth for the trees in the most fast growing group was apparent in the bark thickness. Moreti et al. (1994) and Boock et al. (1995) working with progenies in juvenile stage, also found that fastest growing plants tend to maintain high level of bark thickness.

Very high phenotypic and genetic correlations were found between girths at panel opening and rubber yield (Table 2). The high positive correlations found between rubber yield and number of latex vessels is in agreement with former research findings (Ho, 1976; Tan, 1987; Narayanan et al., 1973; Gonçalves et al., 1989; Kalil Filho, 1982; Licy & Premakumari, 1988). Moderate to high positive phenotypic and genetic correlations between bark thickness and total number of latex vessels were also found in the trials (Table 2). Similar results have been found by Gonçalves et al. (1998) in four trials.

Effects of sites and genotype-site interaction

Girth at panel opening - Although differences of girth at panel opening between the sites were small, they were statistically different, except between trial A and B (Table 3). Very high genetic correlations across sites showed that girth at panel opening has very little genotype-environment interaction (Table 4). However, all hypothesis of genotype-environment interactions equal to zero between different environments were rejected in the analysis of variance across sites. The analysis of variance of the differences between clone means on different sites revealed significant differences among clones concerning sensitivity to changes in the environment (Table 5).

Rubber yield - Significant differences between the sites were present Site A had the highest rubber yield and site B the poorest rubber yield. Genotypic and phenotypic correlations for rubber yield across sites (Table 4) are very high, ranging from 0.63 to 0.89 (phenotypic) and from 0.64 to 0.92 (genotypic), agreeing with previous estimates by Gonçalves et al. (1998). The analysis of variance between clone means of rubber yield on different sites showed that some clones, in general, were more sensitive to changes in the environments (Table 5).

Table 2 - Phenotypic (r_p) and genotypic (r_g) correlations within Jaú (A), Mococa (B), Ribeirão Preto (C), Votuporanga (D) e Matão (E) sites among girth at panel opening (Go), rubber yield (Yr), bark thickness (Bt) and number latex vessel rings (Lv) of sixty seven 10 years old clones of *Hevea*, tested at five locations in São Paulo State, Brazil.

Site/traits	Correlation Type	Traits		
		Girth at panel opening (Go)	Rubber yield (Yr)	Bark thickness (Bt)
A - Indiana				
Rubber yield (Yr)	r_p	0.5847**		
	r_g	0.6277**		
Bark thickness (Bt)	r_p	0.7929**	-0.1333ns	
	r_g	0.6968**	-0.1547ns	
Latex vessel rings (Lv)	r_p	-0.3527ns	0.7615**	0.7458**
	r_g	-0.2662ns	0.6493**	0.7593**
B - Mococa				
Rubber yield (Yr)	r_p	0.6510**		
	r_g	0.6673**		
Bark thickness (Bt)	r_p	0.6461**	0.2688ns	
	r_g	0.7039**	0.1708ns	
Latex vessel rings (Lv)	r_p	-0.2042ns	0.8007**	0.6792**
	r_g	-0.1421ns	0.9238**	0.9721**
C - Ribeirão Preto				
Rubber yield (Yr)	r_p	0.7235**		
	r_g	0.6328**		
Bark thickness (Bt)	r_p	0.6154**	0.0666ns	
	r_g	0.6521**	0.1062ns	
Latex vessel rings (Lv)	r_p	0.0233ns	0.8972**	0.9075**
	r_g	0.1251ns	0.6321**	0.8253**
D - Votuporanga				
Rubber yield (Yr)	r_p	0.7436**		
	r_g	0.6520**		
Bark thickness (Bt)	r_p	0.7781**	0.3841ns	
	r_g	0.8625**	0.2351ns	
Latex vessel rings (Lv)	r_p	-0.2619ns	0.5944**	0.5913**
	r_g	0.2615ns	0.8738**	0.8215**
E - Matão				
Bark thickness (Bt)	r_p	0.7563**	-	
	r_g	0.8124**	-	
Latex vessel rings (Lv)	r_p	0.0865ns	-	0.5537**
	r_g	0.1415ns	-	0.5771**

*$P < 0.05$; ** $P < 0.01$; ns = not significant.

Correlations between different traits across sites

Genetic correlations between different traits across sites, using the B covariances between clone means as described by Burdon (1977) were in general smaller and of opposite signs compared with the correlations found within sites, although differences were small (Table 6). Probably the differences ascribe to influence of sampling errors, genotype-environments interactions for the traits, and by the fact that environmental correlations are zero across sites, but negative within sites. The moderate genetic correlation between rubber yield and bark thickness in trial C almost disappear between rubber yield in trial C and bark thickness in trial A, as well as the strong correlation between girth at panel opening and rubber yield in trial C disappear between girth at panel opening in trial A

Table 3 - Results from the analysis of variance across sites concerning girth at panel opening of sixty seven 10 years old *Hevea* clones, tested at five locations in São Paulo State, Brazil.

Trials / Source	D.F.	A-B	A-C	A-D	A-E	B-C
		Mean Squares				
Blocks/sites	4	2.2044	17.1061	0.9032	0.6624	19.0974**
Sites	1	6.5447ns	100.6571**	86.5558**	14.7048**	158.7315**
Clones	66	9.5077**	21.8296**	13.6654**	25.5238**	27.2432
Clones x sites	66	4.2620ns	6.9299ns	5.2439ns	11.5837ns	9.7507ns
Residual	134	3.0170	4.2391	3.0723	5.4868	4.6240
Trials / Source	D.F.	B-D	B-E	C-D	C-E	D-E
		Mean Squares				
Blocks/sites	4	2.8945	4.7589	22.0199	15.7839	2.1762
Sites	1	1584.2429**	967.7760	740.0402**	342.6286**	75.5761**
Clones	66	19.0040**	23.3108ns	37.3913**	46.4386**	26.0787ns
Clones × sites	66	8.1397ns	22.0311**	4.7423ns	13.893ns	24.4028**
Residual	134	3.4573	5.8717	4.6793	7.0932	5.9271

$*P < 0.05$; $**P < 0.01$; ns = not significant. Sites: Jaú (A), Mococa (B), Ribeirão Preto (C), Votuporanga (D) and Matão (E).

Table 4 - Phenotypic (r_p) and genotypic (r_g) correlations across Jaú (A), Mococa (B), Ribeirão Preto (C), Votuporanga (D) and Matão (E) sites for girth at panel opening (Go), rubber yield (Yr), bark thickness (Bt) and latex vessel rings (Lv) for sixty seven 10-year old *Hevea* clones in São Paulo State, Brazil.

Traits		GoA	YrA	BtA	LvA	GoB	YrB	BtB	LvB	GoC	YrC	GoD	YrD	LvD
GoB	r_p	0.6456**	0.3489ns	-0.1999ns	0.0039ns									
	rg	0.7745**	0.3592ns	-0.2380ns	-0.0233ns									
YrB	r_p	0.5038*	0.8005**	0.1208ns	0.3159ns									
	rg	0.4791*	0.8485**	0.0740ns	0.3036ns									
BtB	r_p	-0.0448ns	0.3660ns	0.7017**	0.7519**									
	rg	-0.2644ns	0.5875**	1.1128ns	1.4148ns									
LvB	r_p	0.4465*	0.7246**	0.0148ns	0.3126ns									
	rg	0.4828*	0.7557**	0.0099ns	0.3605ns									
GoC	r_p	0.8469**	0.4226ns	-0.5041*	-0.3753ns	0.5103*	0.1700ns	-0.4132ns	0.1651ns					
	rg	0.6819**	0.7203**	-0.8256**	-0.4474*	0.5582*	0.6199**	-0.8326**	0.1646ns					
YrC	r_p	0.0425ns	0.6363**	0.3228ns	0.7606**	0.3566ns	0.7445**	0.3492ns	0.5515**					
	rg	0.0260ns	0.6429**	0.3493ns	0.8374**	0.3471ns	0.7915**	1.3920ns	0.5640**					
GoD	r_p	0.5419*	0.4610*	0.1680ns	0.1256ns	0.6212**	0.2762ns	-0.0643ns	-0.0733ns	0.6061**	0.3500ns			
	rg	0.8886**	0.5857**	0.3109ns	0.2990ns	0.5911**	0.3013ns	-0.3028ns	-0.0574ns	0.8982**	0.5401*			
YrD	r_p	0.6022**	0.8865**	0.0199ns	0.2586ns	0.4344*	0.7995**	0.3136ns	0.5004*	0.4996*	0.7416**			
	rg	0.7032**	0.9252**	0.0427ns	0.3072ns	0.5313*	0.9361**	0.5442*	0.5462**	0.8500**	0.7907**			
LvD	r_p	0.4138ns	0.5004*	0.5641**	0.3786**	-0.0863ns	0.3368ns	0.0900ns	0.1996ns	0.2513ns	0.3332ns			
	rg	0.7620**	0.6843**	0.9029**	0.7560ns	-0.2971ns	0.3721ns	0.0288*	0.3173ns	0.8397**	0.4639*			
GoE	r_p	0.7220**	0.5812**	0.0408ns	-0.2071ns	0.5516**s	0.2716ns	0.0379ns	0.2530ns	0.5361*	-0.5095*	0.6190**	0.5095*	0.7919**
	rg	0.8294**	0.6242**	0.0145ns	-0.2830ns	0.6142**	0.2449ns	0.0213ns	0.2645ns	0.7766**	-0.0773ns	0.8315**	0.5496**	1.1864ns
BtE	r_p	0.2001ns	0.0683ns	0.7631**	0.4136ns	0.0140ns	0.1923ns	0.3415**	0.3225ns	-0.1210ns	0.0495ns	0.1571ns	0.0429ns	0.6869**
	rg	0.2742ns	0.0816ns	0.8266**	0.4256ns	0.0410ns	0.2323ns	0.1446ns	0.3968ns	-0.0671ns	0.0646ns	0.2056ns	0.0354ns	1.0077ns
LvE	r_p	-0.5932**	-0.1393ns	0.7051**	0.4795*	-0.7952**	-0.2280ns	0.3671ns	-0.2281ns	-0.6858**	0.0529ns	-0.0246ns	-0.1875ns	0.4248ns
	rg	-0.9769**	-0.1375ns	0.1795ns	0.7296**	-1.1535ns	-0.2452ns	1.2474ns	-0.1144ns	-1.4191ns	0.1834ns	0.1780ns	-0.3630ns	1.5298*

$*P < 0.05$; $** P < 0.01$; ns = not significant.

Table 5 - Results of mean squares from the analyses of variance on differences between clone means on different sites for girth at panel opening and rubber yield of sixty seven 10 years old *Hevea* clones, tested at five locations in São Paulo State, Brazil.

	Girth at panel opening			
Source	D.F.	MS	F value	P > F
Clone	6	327	6.8**	0.0001
Residual	72	48	-	-
	Rubber yield			
Source	D.F.	MS	F value	P>F
Clone	6	169	2.38*	0.0001
Residual	72	71	-	-

* $P < 0.05$; ** $P < 0.01$

Table 6 - Results from the analysis of variance across sites concerning rubber yield of sixty seven 10 years old *Hevea* clones, tested at five locations in São Paulo State, Brazil.

Trials Source	D.F	A-B	A-C	A-D
		Mean Squares		
Blocks/sites	4	308.1572	77.6571	78.0524
Sites	1	3946.3499**	2318.9030**	838.8402**
Clones	66	269.9573**	154.7602*	386.7198**
Clones x sites	66	68.2242**	111.9687**	216.7319**
Residual	134	18.0214	9.1632	14.3810
Trials Source	D.F	B-C	B-D	C-D
		Mean Squares		
Blocks	4	9.5073	9.9026	6.0914
Sites	1	215.0619**	146.3128**	1203.5364**
Clones	66	171.9772**	471.9499**	352.9145**
Clones × sites	66	57.0538**	93.8039**	121.3910**
Residual	134	14.1029	19.3206	9.4026

*$P < 0.05$; ** $P < 0.01$; ns = not significant. Sites: Jaú (A), Mococa (B), Ribeirão Preto (C) and Votuporanga (D).

and rubber yield in trial C. Possibly the change in correlations across trials A and C are caused by genotype-environment interaction for bark thickness and rubber yield, which eliminates the correlations between those traits and girth at panel opening rubber yield seen within C.

Finally, measurements of girth at panel opening at one site seem to be enough, given the very high genetic correlations across sites. Considerable gains in rubber yield (above 2.0%) are possible even with moderate selection among the clones. The genetic correlations across the sites did not clearly indicate any significant advantages, using target environments. Bark thickness showed the expected positive high correlation with rubber yield and the trait must definitely be taken into consideration when selecting for rubber yield. Heritability and standard deviation for total number of latex vessels were moderate. The potential for improving the total number of latex vessels is high with moderate heritability and positively correlated with girth at panel opening and rubber yield.

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