COMPONENTS OF VARIANCE AND INTERACTION BETWEEN GENOTYPE AND ENVIRONMENT FOR ANNUAL GIRTH INCREMENT IN RUBBER TREE[1]

PAULO DE SOUZA GONÇALVES[2], PAULO BOLLER GALLO[3], IVO SEGNINI JUNIOR[4], ALTINO ALDO ORTOLANI[5], AFONSO PEDRO BRIOSCHI[6], MARCOS GUIMARÃES LANDELL[7] and SÉRGIO RICARDO DE SOUZA[8]

ABSTRACT - To determine the nature and extent of genetical and environmental control of vigour through annual girth increment in rubber trees [*Hevea brasiliensis* (Willd. ex Adr. de Juss.) Müell. Arg.], seven clones were studied in a replicated trial in São Paulo State at four different locations. The clones represented a range of imported germoplasm while the locations were selected to represent a range of rubber growing areas. Trees were studied for annual girth increment over five years before the initiation of tapping for latex. The results of the analyses show a consistent decrease in genetic component over the five years from 10 per cent to 0.5 per cent with a corresponding increase in the effect of environment (19.0 per cent to 93.0 per cent). The genotype x environment effects from combined analysis were significant for three factor analysis of variance. Genetic correlations between locations for annual girth increment revealed a consistent positive and significant correlation between Mococa and Matão in the fifth year (r_g= 0.7128), Ribeirão Preto and Matão in the fifth year (r_g=0.7113) and Ribeirão Preto and Presidente Prudente in the fourth year (r_g=0.9367). The implications of these findings in selection of rubber for annual girth increment trait are discussed.

Index terms: *Hevea brasiliensis*, clones, genetic correlations.

COMPONENTES DE VARIÂNCIA E INTERAÇÃO ENTRE GENÓTIPO E AMBIENTE NO INCREMENTO ANUAL DO CAULE EM SERINGUEIRA

RESUMO - Com o objetivo de determinar a natureza da grandeza e controle genético e ambiental do vigor através do incremento anual do caule em seringueira [*Hevea brasiliensis* (Willd. ex Adr. de Juss.) Müell. Arg.], sete clones foram estudados em quatro diferentes locais do Estado de São Paulo. Os clones em estudo, na sua maioria, são de origem asiática, e os locais selecionados representam as diferentes regiões da heveicultura do Estado. O incremento anual da circunferência das árvores de cada local foi obtido por um período de cinco anos antes do início da sangria para obtenção do látex. Os resultados das análises mostraram uma redução consistente no componente genético, no período de cinco anos, de 10,0 a 0,5 por cento, com um aumento correspondente no efeito do ambiente de 19,0 a 93,0 por cento. Os efeitos de genótipo x ambiente da análise de variância agrupada foram significantes para análise de variância de três fatores (genótipos x locais x anos). Correlações genéticas entre locais para o incremento anual do caule mostraram valores positivos entre Mococa e Matão no quinto ano (r_g = 0,7128), Ribeirão Preto e Matão no quinto ano (r_g = 0,7113), e Ribeirão Preto e Presidente Prudente no quarto ano (r_g = 0,9367). Discutem-se as implicações destes resultados em relação à seleção de clones com base no incremento anual do caule.

Termos para indexação: *Hevea brasiliensis*, clones, correlações genéticas.

INTRODUCTION

Rubber [*Hevea brasiliensis* (Willd. ex Adr. de Juss.) Muell. Arg.] is an important plantation crop in São Paulo state among other crops like oranges, coffee etc. The total extent of cultivated rubber has been estimated to be about 40 thousand hectares distributed among 2.5 thousand producers. In the last decade, the number of trees almost quadrupled allowing yield estimations of nine thousand t/year, 40% of the total Brazilian yield (Putz, 1993), but insignificant compared to world natural rubber production.

Rubber trees are grown for their latex from which rubber is coagulated and processed and hence it is the dry rubber yield which determines the level of output. Girth is an economically important character and is considered to be a measure of vigour. It determines the age at which a clone could be explored and is therefore important in shortening the uneconomic, immature period. In Brazil it has been standard practice to open buddings when they reach a minimum girth of 45 cm at 1.20 m above the bud union. Furthermore, large trunks have more timber value.

It has been frequently reported that the performance of *Hevea* genotypes is quite variable for several quantitative traits under varying environmental conditions (Tan, 1980). Factors such as physical and chemical properties of the soil, temperature and rainfall affect several components of the life cycle of *Hevea* genotypes (Pushparajah, 1980). Therefore, taking into account genotype x environment interaction, more than one environment is recommended for the identification of outstanding genotypes with high performance over a wide range of environments. Knowledge of the magnitude of genotype-environment interactions may be helpful in delimiting spatial areas of adaptation.

Genotypic (G), environmental (E) and genotype x environment interaction (G x E) are the three main components of variability in any population. The relative magnitudes of these not only determine the response to selection but also the method of selection in any breeding programme. Thus, a knowledge of these components of variation is of great value to the breeders. Several workers have emphasized the importance of evaluating the materials under more

than one environment to obtain information on the relative magnitude of components of variance. An illustration of such use is provided by Homer & Frey (1957).

No extensive studies have been made on genotype x environment interaction in *Hevea*. Preliminary studies have been conducted in Sri Lanka by Jayasekera et al. (1977) and Jayasekera & Karunasekera (1984). Only recently Jayasekera et al. (1994) reported results of the analysis of girth collected over a 15-year period, and yield data collected during the first five years of tapping have shown how relative contributions of genetic, environment and genotype x site interaction components change over time. In Brazil, studies were carried out by Gonçalves et al. (1990) and Gonçalves et al. (1992) aiming to assess the annual environmental influence on genetic variation in five years of yielding. Components of variance were estimated from these analyses in an attempt to quantify genotype x environment interactions.

The objective of the present paper was to determine the nature and extent of genetic and environmental control of vigour through annual increment of girth, collected over a five-year period from four trials in different locations of São Paulo State in Brazil.

MATERIAL AND METHODS

The genetic material originally consisted of seven *Hevea* clones which are listed in Table 1. They were chosen to represent good clones available at the time of establishing this experiment. Some clones such as PR 261, PR 255, GT 1, RRIM 600 and IAN 873 are recommended clones, whereas others had been used as parents in rubber breeding programmes in the State of São Paulo. One clone, PB 217, had to be removed from the analysis of data because it was found to be of very poor growth and low survival. One and a half-year old rootstock seedlings raised in nurseries were used to bud graft clonal materials. Bud grafting was made in December, 1989. The successful bud grafts were uprooted and planted in polyethylene bags. After the first emission of flush leaves the experiments were placed in the field.

Plants were spaced at 7.00 m between rows and 3.00 m within the row. The experimental plots were fertilized with NPK mixture applied according to recomendations of the Instituto Agronômico (Cardoso, 1989). Missing plants

were replaced with spares during the first two years after planting to maintain the plantation density, but were not scored.

The experiments were conducted at four different locations chosen to represent different rubber planting districts. Part of the experiments were located on private farms and part at Experimental Stations of the Instituto Agronômico. The land at these locations was previously used for natural rubber production. They are representative of the most important non-traditional area, of continental climate, of rubber production in Brazil (Table 2).

The experimental design was a randomized complete block with three replications. In all locations except Matão, thirty plants were used in each plot. In Matão, a large plot

TABLE 1. List of rubber clones, parentage and places of origin.

Clone[1]	Parentage	Origin
GT 1	Primary clone	Indonesia
PR 261	Tjir 1 x PR 107	Indonesia
PR 255	Tjir 1 x PR 107	Indonesia
IAN 873	PB 86 x FA 1717	Brazil
RRIM 701	44/553 x RRIM 501	Malaysia
PB 235	PB 5/51 x PB S.78	Malaysia
RRIM 600[2]	Tjir 1 x PB 86	Malaysia

[1] GT: Godang Tapen; RRIM: Rubber Research Institute of Malaysia; IAN: Instituto Agronômico do Norte; PR: Proefstation voor Rubber; PB: Prang Besar; Tjir: Tjirandji; FA: Ford Acre.
[2] Control clone.

size of forty plants was used, because of the facilities. A plot consisted of five rows of six or eight plants.

Vigour in terms of girth (annual) increment was obtained by difference of annual measurement from the data of planting. In the first year diameter was recorded, because plants were too small to measure girth, and converted to girth assuming that the stem was cylindrical. At this age, girth was determined by measuring the diameter of the plants at 0.50 m and 1.20 m above ground level by a slide calipers. The five annual measurements were taken at 1.20 m above the highest point of the bud union respectively.

All the analyses were performed on annual girth increment measurements data from the first five years of growth. First, a two factor analysis of variance (Table 3) was carried out on the data collected from increment of each year, and analysed separately. These clones and years were the main source of variation. For all genotype locations combined the statistical model used was:

$$Y_{ijk} = \mu + G_i + P_j + (GP)_{ij} + R_{k(j)} + E_{ijk} \text{ where,}$$

Y_{ijk} is the observation on the ith genotype (clone) in the jth location in kth replication;
μ is the general mean;
G_i is the fixed effect of the ith genotype;
P_j is the effects of the jth location;
$(GP)_{ij}$ is the interaction of the ith genotype with jth location;
$R_{k(j)}$ is the effect of kth randomized block within the jth location;
E_{ijk} is the experimental error associated within the ijkth observation.

TABLE 2. Details of experimental locations and planting dates.

Remark	Locations			
	Mococa	Ribeirão Preto	Matão	Presidente Prudente
Year of planting	1989	1989	1989	1989
Planting material	Budded stumps	Budded stumps	Budded stumps	Budded stumps
Spacing (m)	7.00 x 3.00	7.00 x 3.00	7.00 x 3.00	7.00 x 3.00
Planting density	5 rows x 6 trees	5 rows x 6 trees	5 rows x 8 trees	5 rows x 6 trees
	30 trees/plot	30 trees/plot	40 trees/plot	30 trees/plot
Design of experiment	RBD[1]	RBD	RBD	RBD
Numbers of replications	3	3	4	3
Total area (ha)	2	2	3	2
Elevation (m) (mean sea level)	665	621	551	467
Annual rainfall (mm) (mean anual)	1500	1534	1480	1257
Soil type[2]	Red yellow latosol	"Terra roxa estruturada"	Podzolized soil of Lins	Podzolized soil of Lins
Terrain	Flat to undulating	Flat to undulating	Flat	Flat

[1] Randomized block design.
[2] In accordance with Brasil (1960).

TABLE 3. Degree of freedom (D.F.), mean square (M.S.) and expected mean square (E.M.S.) for two-factor analysis of variance.

Source of variations	D.F.	M.S.	F	E. M. S.
Repetition/locations	p(r-1)	M_1	M_1/M_5	$\sigma_E^2 + g\,\sigma_R^2$
Locations (P)	p-1	M_2	M_2/M_1	$\sigma_E^2 + g\,\sigma_R^2 + rgV_P^2$
Genotypes (G)	g-1	M_3	M_3/M_5	$\sigma_E^2 + rpV_G$
G x P	(g-1)(p-1)	M_4	M_4/M_5	$\sigma_E^2 + rV_{GP}$
Residual (mean)	p(g-1)(r-1)	M_5	·	σ_E^2

A three-factor analyses of variance (Table 4) was also performed on data collected from all places and years. The model underlying the analysis may be written as:

$Y_{ijkl}=\mu + G_i + P_l + T_k + (GP)_{ij} + (GY)_{ik} + (GY)_{ik} +$
$+ (PY)_{jkl}\,(GPY)_{ijk} + E_{ijklv}$ where,

Y_{ijkl} is the lth observation on the ith clone in the jth place in the kth year. The first four terms on the left hand side are the mean and the main effects of genotypes (clones), locations and time (year); the next three terms are the first order interactions, then the second order interaction and finally the micro-environmental deviation within locations and years. It is usually assumed, perhaps gratuitously, that genotypes (clones), and places can all be regarded as fixed effects and years random effects, so that the model is a mixed effects model. The analysis of variance is shown algebraically in Table 4, on the assumption that genotypes have been tested in p locations for y years with r replications.

Genetic correlations between locations (Burdon, 1977) were calculated, characterizing environments within the year. This is based on the concept of considering performance in each environment as a distinct trait (Falconer, 1981).

Genotypic, phenotypic and environmental components of variance and covariance for each location within each year were estimated from algebraic manipulation of the mean square manipulation of the Table 5 (Vencovsky & Barriga, 1992).

The genotypic (r_{gij}) correlations were worked out as follows:

$r_{gij}=\mathrm{cov}_{gij}\ \sqrt{\sigma_{gi}^2 . \sigma_{gj}^2}$ where,

cov_{gij} = genotypic covariance of annual girth increment for location i and j respectively;

s_{gi}^2 = genotypic variance for annual girth increment for location i;
s_{gj}^2 = genotypic variance for annual girth increment for location j.

The significance of these correlations was tested using the table showed by Fisher & Yates (1981) for simple correlation for 5.0 and 1.0 percent of probability.

RESULTS AND DISCUSSION

Means of final girth and standard deviation for *Hevea* clones measured in each location are shown in Table 6. Circunference means were generally higher for Matão for all studied genotypes. Clone RRIM 600, the most planted genotype in the state, had it best performance at Matão and Presidente Prudente. Although the genotypes, including the control clone RRIM 600, had their best performance at Matão (Table 6), the significant location effect as well as a significant genotype x location interaction from two factor analyses (Table 7), is a reflection of the changes in genotype ranking from one location to another.

Opposed to genotypes, genotype x locations interaction effects for annual girth increment changed the clonal rankings across the four locations (Table 6). For example, only genotype GT 1 ranked among the top four genotypes in all four locations. Genotype RRIM 701, on the other hand, was among the best three genotypes at Mococa, Ribeirão Preto

TABLE 4. Scheme of pooled analysis of variance degree of freedom (D.F.), mean square (M.S.) and expected mean square (E.M.S.) for three factor analyses of variance.

Source of variations	D.F.	M.S.	F	E.M.S.
Replication (P/Y)	py (r-1)	M_1	M_1/M_9	$\sigma_E^2 + g\,\sigma_R^2$
Locations (P)	p-1	M_2	M_2/M_4	$\sigma_E^2 + g\,\sigma_R^2 + \frac{p}{p-1}\,rg\sigma_{PY}^2 + ryg\,V_P$
Years (Y)	y-1	M_3	M_3/M_1	$\sigma_E^2 + g\,\sigma_R^2 + rpg\,V_Y$
P x Y	(p-1)(y-1)	M_4	M_4/M_1	$\sigma_E^2 + g\,\sigma_R^2 + \frac{p}{p-1}\,rg\,\sigma_{PY}^2$
Genotypes (G)	(g-1)	M_5	M_5/M_7	$\sigma_E^2 + \frac{g}{g-1}\,rp\,\sigma_{GY}^2 + rpy\,V_G$
G x P	(g-1)(p-1)	M_6	M_6/M_8	$\sigma_E^2 + \frac{g}{g-1}\cdot\frac{p}{p-1}\,r\sigma_{GPY}^2 + ryV_{GP}$
GxY	(g-1)(y-1)	M_7	M_7/M_9	$\sigma_E^2 + \frac{g}{g-1}\,rp\,\sigma_{GY}^2$
G x P x Y	(g-1)(p-1)(y-1)	M_8	M_8/M_9	$\sigma_E^2 + \frac{g}{g-1}\cdot\frac{p}{p-1}\,r\,\sigma_{GPY}^2$
Residual (mean)	(r-1)(g-1) yp	M_9		σ_E^2

TABLE 5. Scheme of analysis of variance, degree of freedom (D.F.), expected mean square (E.M.S.) and expected mean covariance product (E. M.C.P.) used for estimating components of variance and covariance values for annual girth increment.

Source of variations	D.F.	E.M.S.[1]	E. M.C.P.[2]
Replications	r-1	-	-
Clones (genotypes)	c-1	$\sigma_e^2 + r\,\sigma_g^2$	$Cov_{eij} + r\,Cov_{gij}$
Error	(r-1)(c-1)	σ_e^2	Cov_{eij}

[1] σ_g^2: variance due to differences among clones; σ_e^2: variance due to interaction between clones and replications; r: number of replications;
[2] Cov_{gij}: covariance due to locations i and j; Cov_{eij}: covariance due to interaction of clones and replications of i and j locations.

and Matão, but had the second worst genotype girth increment performance in Presidente Prudente. Similarly, clone RRIM 600 had one of the two best annual girth increments at Presidente Prudente, but the worst at Ribeirão Preto. An ideal clone would be one which had high performance over a broad range of locations (Eberhart & Russell, 1966). In spite of absence of significance among genotypes (Table 8),

clone GT 1 was the best among the seven genotypes in three of the four locations (Table 6). It is possible that it will be an ideal clone in the future, if its latex production is as good as the vigour reported here.

Variability among locations for annual girth increment can be attributed to differences in soil type, rainfall distribution, temperature extremes and management of experimental field across the four locations. Matão, which recorded the best performance for all the seven genotypes, including RRIM 600 (Table 6), has better drainage and a more regular annual rainfall distribution than the other three locations. Although rainfall is highest at Ribeirão Preto, most of the rains are concentrated within a few months. A more even rainfall distribution is usually observed for Matão and Mococa which gives to these two locations and similar environments a much longer growing season. It was expected to have comparatively high performance at Ribeirão Preto such as was obtained at Mococa. However, Ribeirão Preto actually had the least mean performance for growth.

The significant components of the tree-factor analysis of variance are tabulated in Table 8. A general feature of such analysis is the absence of genotype x location interaction, and the presence of the second order genotype x location x year interaction.

To remove the year effect from the analysis and also to study genotypic, environmental (locations) and their interaction effects in more detail, a two-factor analyses of variance (Table 7) was carried out for each year separately. Absence of significance among genotypes was observed over the years. Al-though genotypes x locations interaction was not statistically significative from the third year, selec-tion of one or more genotypes in different locations is not possible, considering the inexistence of sig-nificative differences among genotypes in individual years.

TABLE 6. Mean of annual girth increment in centimeters of seven genotypes (clones) within each location and for all locations pooled.

Genotypes	Locations				Pooled mean
	Mococa	Ribeirão Preto	Matão	P. Prudente	
GT 1	5.2566	4.7453	7.5300	6.2406	5.9431
	$(26.28 \pm 3.05)^1$	(23.73 ± 3.04)	(37.65 ± 0.55)	(31.20 ± 0.72)	(29.71 ± 1.84)
IAN 873	5.6940	4.3533	6.2867	6.1473	5.6203
	(28.46 ± 2.88)	(21.77 ± 2.19)	(31.43 ± 1.65)	(30.74 ± 1.05)	(28.10 ± 1.94)
PR 261	5.2067	4.5627	6.5440	6.0153	5.5822
	(26.03 ± 3.22)	(22.81 ± 2.71)	(32.72 ± 0.97)	(30.08 ± 2.51)	(27.91 ± 2.35)
PB 235	5.8267	4.4027	6.2167	6.0000	5.6115
	(29.13 ± 2.98)	(22.01 ± 2.99)	(31.08 ± 1.91)	(30.00 ± 1.28)	(28.05 ± 2.29)
RRIM 701	5.9880	4.5573	7.2887	5.9713	5.9513
	(29.94 ± 2.66)	(22.78 ± 3.84)	(36.44 ± 1.64)	(29.85 ± 1.88)	(29.75 ± 2.50)
PR 255	4.4513	4.4600	6.9960	5.8046	5.4280
	(22.2 ± 3.01)	(22.30 ± 2.27)	(34.98 ± 1.83)	(29.02 ± 0.22)	(27.14 ± 1.88)
RRIM 600[2]	4.8760	4.0100	6.8093	6.1720	5.4668
	(24.38 ± 2.89)	(20.05 ± 2.99)	(34.05 ± 1.58)	(30.86 ± 1.57)	(28.08 ± 2.26)

[1] Figures in bracket are the final girth mean of the fifth year of the clones in each location.
[2] Control clone.

TABLE 7. Analysis of variance annual girth increment for girth in centimeters for all four locations.

Source of variation	D.F.	Mean square for annual girth increments[1]				
		1	2	3	4	5
Replications/locations	8	0.11519 ns	0.39873 ns	0.96600*	0.45669 ns	4.90445 ns
Locations	3	162.98487**	11.51764**	84.68769**	25.78899**	40.55326**
Genotypes (clones)	6	0.92498 ns	0.48717 ns	1.78385 ns	2.69597 ns	2.82594 ns
Genotype x locations	18	1.60468**	0.75323*	0.91426 ns	3.16348 ns	2.79872 ns
Residual	48	0.13087	0.39200	0.39324	2.61969	2.70447
Mean (cm)		5.21643	2.84524	5.02202	7.69333	7.51107
Coef. of variation (%)		7.36	21.72	12.60	20.12	23.55

[1] 1: total 12 months growth data of planting; 2: data of growth obtained from the difference of 24 and 12 months and so on respectively.
* $p < 0.05$.
** $p < 0.01$.
ns Non-significant.

TABLE 8. Degrees of freedom (D.F.), mean squares (M.S.), estimates of variance components (σ^2) and degree of significance (P), for three factor analyses of variance of annual girth increment.

Source of variations	D.F.	M.S.	σ^2	P
Replications (P/Y)	40	1.36821	0.01717	ns
Locations (P)	3	107.43335	0.5039	ns
Years (Y)	4	337.83824	4.02168	**
P x Y	12	54.52477	1.9467	**
Genotypes (G)	6	2.66140	0.0158	ns
G x P	18	2.22678	0.0333	ns
G x Y	24	1.48913	0.0172	ns
G x P x Y	72	1.72690	0.1025	**
Residual	240	1.24805	1.24805	-

** P < 0.01.
ns Non-significant.

TABLE 9. Estimates of environmental (σ_E^2), genotype x location interaction (V_{GP}^2) and genotypic (V_G^2) variances annual girth increment.

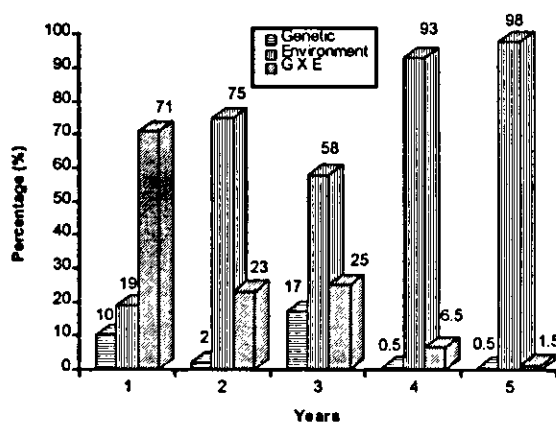| Year	σ_E^2	V_{GP}^2	V_G^2
1	0.13087	0.49127	0.06617
2	0.39200	0.12040	0.0079
3	0.39324	0.17367	0.11588
4	2.61967	0.18126	0.00635
5	2.70447	0.03142	0.01012

Genotypic, environmental (locations) and genotype x locations interaction variance components for each year were estimated from the two-factor analyses and are presented in Table 9. The percentage contributions of these components to the total variation were also estimated and are presented for each year in Fig 1. In the first year, the genetic component of annual girth increment was only 10.0 per cent and was the smallest component when compared with the other two components: locations (19.0 per cent) and genotype x locations (71.0 per cent). But it can be seen from Fig. 1 that over the years the genetic component gradually decreases at the expense of the environment (locations) components and stabilizes at around 0.5 per cent in the fourth year. The environmental locations component which contributed 19.0 per cent to total variation in the first year contributed 98.0 per cent in the fifth year after planting. These values show some difficulty in the selection of one or more genotypes in each location, without enlargement of the sample of genotypes.

The genotype x location interaction component decreased from 71.0 percent in the first year to 1.5 per cent in the fifth year. This decrease is not consistent, as was found in the genetic component and there are fluctuations in the years. By about the fourth year, the contribution of genotype x locations interaction became stabilized at between 93.0 and 98.0

FIG. 1. Change of genetic (G) environment (E) and genotype place interaction (G x E) components over years of annual girth increment.

per cent, which means, however, that this interaction can be stabilized over the years. It is important to emphasize that the genotypic value is, by the definition of Bulmer (1980), an average value over a range of conditions and therefore depends on the condition under which the genotype has been tested.

Genotypic correlations between locations, for annual girth increment (Table 10), revealed a consistent positive and significant correlation between Mococa and Ribeirão Preto in the third year

P. DE S. GONÇALVES et al.

TABLE 10. Genotypic correlations between locations within each annual girth increment.

Year	Location pair[1]					
	1 vs. 2	1 vs. 3	1 vs. 4	2 vs. 3	2 vs. 4	3 vs. 4
I	-0.3883 ns	0.3308 ns	-0.6474*	-0.5085 ns	0.1739 ns	-0.4305 ns
II	-0.5462 *	-0.3173 ns	0.0832 ns	-0.4871 ns	0.2566 ns	-0.1852 ns
III	0.7128 **	-0.2036 ns	-0.2405 ns	0.2405 ns	0.2621 ns	0.0584 ns
IV	0.4192 ns	-0.3346 ns	0.2521 ns	0.3977 ns	0.9367 **	-0.4231 ns
V	-0.0126 ns	-0.2234 ns	0.4109 ns	0.7113 **	0.2334 ns	0.1289 ns

[1] 1: Mococa; 2: Ribeirão Preto; 3: Matão; 4: Presidente Prudente.
* $p < 0.05$.
** $p < 0.01$.
ns Non-significant.

($r_g = 0.7128$), between Ribeirão Preto and Matão in the fifth year ($r_g = 0.7113$), and between Ribeirão Preto and Presidente Prudente in the fourth year ($r_g = 0.9367$). Negative correlations were obtained for several location pairs. For example, Mococa was negatively correlated with Presidente Prudente in the first year ($r_g = -0.6474$), and with Ribeirão Preto in the second year ($r_g = -0.5462$). Ribeirão Preto was negatively correlated with Matão in the first ($r_g = -0.5085$) and second year ($r_g = -0.4871$).

The other genotypic correlations, although positive, were very low and nonsignificant. These results would indicate that independent of the year, all locations are in different breeding zones. Thus, clonal selections can not make in one location for planting in another location. However, unless a relatively stable clone with average performance over all locations is obtained, selections made in any location will not do well in an environmentally similar location. As only five years of girth increment data have been analysed, it is premature to comment on the optimum stage for early prediction.

CONCLUSIONS

1. The presence of genotype x location interaction in the first and second years and absence of this type of interaction from the third year on suggest the inexistence of genotypes adapted to different localities over the years.

2. Analysis for annual girth increment shows a consistent decrease in genetic component over five years from 10.0 per cent to 0.5 per cent with a corresponding increase in the effect of environment (19.0 per cent to 93.0 per cent).

ACKNOWLEDGMENTS

REFERENCES

BRASIL. Ministério da Agricultura. Centro Nacional de Ensino e Pesquisas Agronômicas. Comissão de Solos. **Levantamento de reconhecimento dos solos do Estado de São Paulo.** Rio de Janeiro, 1960. 634p. (Boletim, 12).

BULMER, M.G. **The mathematical theory of quantitative genetics.** New York: Oxford University Press, 1980. 254p.

BURDON, R.D. Genetic correlations for studying genotype environment interaction in forest tree breeding. **Silvae Genetic,** v.26, p.168-175, 1977.

CARDOSO, M. **Instruções para a cultura da seringueira.** Campinas: Instituto Agronômico de Campinas, 1989. 50p. (Boletim, 196).

EBERHART, S.A.; RUSSELL, W.A. Stability parameters for comparing varieties. **Crop Science,** v.6, p.36-40, 1966.

FALCONER, D.S. **An introduction to quantitative genetics.** 2.ed. London: Longman, 1981. 340p.

FISHER, R.A.; YATES, F. **Statistical tables for biological agricultural and medical research.** 3.ed. Edinburgh: Olivier & Boyd, 1981. 150p.

GONÇALVES, P. de S.; CARDOSO, M.; COLOMBO, C.A.; ORTOLANI, A.A.; MARTINS, A.L.M.; SANTOS, I.C.I. dos. Variabilidade genética da produção anual da seringueira: estimativas de parâmetros genéticos e estudo da interação genótipo x ambiente. **Bragantia,** Campinas, v.48, n.2, p.306--320, 1990.

GONÇALVES, P. de S.; CARDOSO, M.; SANTOS, I.C.I. dos; MARTINS, A.L.M.; ORTOLANI, A.A.; COLOMBO, C.A. Selection of Hevea mother trees adapted to unpredictable annual climatic variability. **Brazilian Journal of Genetics,** v.15, n.1, p.137--147, 1992.

HORNER, T.W.; FREY, K.J. Methods for, determining natural areas for oat varietal recomendations. **Agronomy Journal,** v.49, p.313-315, 1957.

JAYASEKERA, N.E.M.; KARUNASEKERA, K.B. Effect of environment on clonal performance with respect to early vigour and yield of *Hevea brasiliensis.* In: PHYSIOLOGY AND BREEDING MEETING, Montpelier. **Proceedings...** Montpelier, France: IRRDB, 1984. p.330-340.

JAYASEKERA, N.E.M.; KARUNASEKERA, K.B.; KEARSEY, M.J. Genetics of production traits in *Hevea brasiliensis* (rubber). I. Changes in genetical control with age. **Heredity,** v.73, p.650-656, 1994.

JAYASEKERA, N.E.M.; SAMARANAYAKE, P.; KARUNASEKERA, K.B. Initial studies on the nature of genotype-environment interactions in some *Hevea* clones. **Journal of Rubber Research Institute of Sri Lanka,** v.54, p.33-42, 1977.

PUSHPARAJAH, E. Differential reaction of clones to soils and nutrient status. In: HEVEA COURSES LECTURE NOTES. Kuala Lumpur: Rubber Research Institute of Malaysia, 1980. p.9-13.

PUTZ, P. Editorial. **Informativo APABOR,** v.1, n.7, p.2, 1993.

TAN, H. Biometrical Genetics in Hevea buding. In: HEVEA BREEDING COURSES LECTURE NOTES. Kuala Lumpur: Rubber Research Institute of Malaysia, 1980. p.16-22.

VENCOVSKY, R.; BARRIGA, P. **Genética biométrica no fitomelhoramento.** Ribeirão Preto: Sociedade Brasileira de Genética, 1992. 496p.