Brazilian Journal of Genetics, 18, 4, 605-609 (1995)
(Revista Brasileira de Genética)

Broad sense heritability values and possible genetic gains in clonal selections of *Hevea*

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ABSTRACT

Estimates of heritability of nine biometrical characters were computed using data from a replicated mature clonal trial involving 11 clones of rubber tree [*Hevea brasiliensis* (Wildd. ex Adr. de Juss.) Müell. Arg.] grown in Tabapuã, State of São Paulo, Brazil. The characters were: average yield over four years (MY), girth at opening (GO), girth after four years of tapping (GC), girth increment over four years of tapping (GI), virgin bark thickness (BT), total number of latex vessel rings (LV), overall density of latex vessels per ring per five millimeters of bark (DV), average diameter of latex vessels (DL) and average distance between consecutive latex vessel rings (AD). Total genetic variance (Vg), environmental variance (Ve), estimates of heritability (h^2) on a single and replicated plot basis, and the expected gain (Gs) from selection, assuming the top 27.3% of the population, were computed. Broad sense heritability estimates (h^2) were obtained for all characters and there was considerable genetic variation among clones for MY and GI, as indicated by large values of h^2 obtained for these traits. Heritability estimates for GO, GC and BT were moderately high. The expected gain in percent of the mean for MY was 29.3%, whereas estimates for GI, BT and LV were 30.55%, 13.73% and 11.00%, respectively.

INTRODUCTION

Yield (latex production) is the most important economic character of the rubber tree [*Hevea brasiliensis* (Willd. ex Adr. de Juss.) Müell. Arg.]. Characters such as bark thickness, girth, stem form, brown bast and resistance to diseases are of secondary interest.

Hevea breeding consists of alternating cycles of seedlings and clonal selections. Selection and budgrafting of seedling progenies from the sexual cycle provide the next generation of clones for commercial planting and also serve as parents for the next breeding phase. Knowledge of the heritability of variables such as yield, its components and other plant characters is useful in designing an efficient breeding program for any crop, especially in *Hevea* that has long breeding (10-15 years) and selection (25-30 years) cycles imposed by its perennial nature. Heritability values calculated from clonal tests can be used to forecast genetic gain in clonal propagation (Wright, 1976). The reliability of such estimates depends greatly on minimizing the environmental differences between and within clones.

The aim of this study was to provide further estimates of broad sense heritability of yield, growth, bark thickness and some characters of the laticiferous system held in the bark. This parameter was used to estimate genetic gains for different characters which could be applied to future rubber breeding programs.

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MATERIAL AND METHODS

The data were collected from a clone trial established in Água Milagrosa plantation, Tabapuã, State of São Paulo, Brazil (21°11'25" latitude South). The climate is considered to be humid tropical with a mean yearly temperature of 21°C. The trial consisted of eleven clones, tested in randomized blocks with six replications and five trees row plots spaced 7.0 m apart, with plants spaced 3.0 m apart.

The traits studied were average yield over four years (MY), girth at opening (GO), girth after four years of tapping (GC), girth increment over four years (GI), virgin bark thickness (BT), number of latex vessel rings (LV), overall density of latex vessels per ring per five millimeters of bark (DV), average diameter of latex vessels (DL), and average distance between consecutive latex vessel rings (AD).

At maturity (six years after planting) the trees were opened for tapping. Clonal yields were collected for four years on a single plot basis. Yields were obtained as described by Gonçalves *et al.* (1990) where cup coagula were collected once a month and left to dry in the field under shade. The annual yields were expressed in grams per tree per tapping by dividing the total plot yield by the number of cup coagula in a year and the number of trees per plot. Stem girth was measured with a steel tape at a height of 1.20 m from the ground.

BT was obtained from samples taken at 1.20 m height, after four years of yielding. LV was determined by examining the radial longitudinal section of these same bark samples. DL was observed in the transverse section of the bark samples. DV was determined per five square millimeters of the laticiferous tissue of bark and AD was determined based on all rings.

Genetic and other components of variance for each trait were estimated from algebraic manipulation of the mean squares expectations of the ANOVA.

Heritabilities on single and replicated plot basis were estimated according to Vencovsky and Barriga (1992) as follows:

$$H^2_m = \frac{Vg}{Vg + Ve} \quad \text{and} \quad H^2_p = \frac{Vg}{Vg + \frac{Ve}{r}}$$

where: H^2_m = heritabilities on a single plot basis;
H^2_p = heritabilities on a replicated plot basis;
Vg = genetic variance among clones;
Ve = environmental variance among plots and
r = number of replications.

The coefficients of genetic variation were estimated based on the variances (CVg% = 100 (Vg/x). In a similar way the coefficient of phenotypic (CV_F%) and environmental variation (CVe%) were estimated, where x represents the general mean for each trait.

The expected gain from selection (Gs) was calculated on the clonal mean and plot mean basis, assuming the selection of the top 27.3% of the population from the following relationship:

$$Gs = i\ Vg/V_F$$

where: i = selection intensity and
V_F = phenotypic variance.

The 27.3% of selection intensity was utilized for all traits studied. Because the size of the clone population was less than 50, Fisher and Yates (1971) correction was used for obtaining the selection intensity calculation.

The expected gain in percent of the mean was calculated as:

$$Gs\% = (Gs/x) \cdot 100,$$

where x represents the general mean of each trait.

The genetic parameters and the value of the "θ" index (θ = CVg/CVe) were estimated following Vencovsky (1987) and are presented in Table III.

RESULTS AND DISCUSSION

The mean squares for the various characters studied are summarized in Table I. Differences between clones were significant for all characters studied. The best clones exceeded the clones with lowest values in yield by 156% and in girth at opening by 49%. The maximum and minimum clonal values for LV and DL varied by 51% and 33%, respectively.

The mean and standard deviation of the characters for each clone are shown in Table II. The overall means, the ranges, standard deviations and coefficients of variation are shown in Table III. There was a wide range of variability for some characters among the clones. MY appeared to be the most variable character, and had the highest coefficient of variation. The second highest coefficient of variation was found for GI, with a mean that ranged between 2.63% and 5.78%. The CVs found in Table III suggest that besides average yield over four years, GI of the nine-year old clones have higher variations than LV at this age. G and BT were also highly variable among clones studied.

Table I - Mean squares of analysis of variance for average yield over four years (MY), girth at opening (GO), girth after four years of tapping (GC), girth increment over four years of tapping (GI), virgin bark thickness (BT), total number of latex vessel rings (LV), overall of latex vessels per ring per five millimeters of bark (DV), average diameter of latex vessels (DL) and average distance between consecutive latex vessel rings (AD) from 11 clones of *Hevea*.

Source	d.f.[1]	Mean squares								
		MY	GO	GC	GI	BT	LV	DV	DL	AD
Blocks	5	55.57ns	22.70ns	43.96ns	0.88ns	0.35ns	0.09ns	4.65ns	14.59*	902.96ns
Clones	10	583.44**	155.35**	350.65**	6.99**	4.69**	0.93**	11.69*	23.87**	2904.86**
Error	50	44.28	19.39	32.14	0.57	0.50	0.13	4.62	4.60	938.19

[1]d.f. = degrees of freedom.
* = $P < 0.05$; ** = $P < 0.01$; ns = not significant.

Table II - Means and standard deviations for average yield over four years (MY), girth at opening (GO), girth after four years of tapping (GC), girth increment over four years of tapping (GI), virgin bark thickness (BT), total number of latex vessel rings (LV), overall density of latex vessels per ring per five millimeters of bark (DV), average diameter of latex vessels (DL), and average distance between consecutive latex vessel rings (AD), from 11 clones of *Hevea*.

Clones	MY	GO	GC	GI	BT	LV	DV	DL	AD
AVROS	37.65 ± 6.54	41.25 ± 2.81	50.04 ± 2.98	2.93 ± 0.97	6.73 ± 0.79	3.60 ± 0.47	49.44 ± 2.84	24.25 ± 2.40	154.58 ± 30.98
RRIM 600	27.59 ± 5.80	41.63 ± 4.75	50.17 ± 7.08	2.84 ± 0.79	5.88 ± 0.87	3.37 ± 0.32	48.12 ± 1.82	27.02 ± 3.29	146.11 ± 34.06
PB 235	60.09 ± 12.18	50.61 ± 3.93	63.58 ± 3.66	4.32 ± 0.88	7.41 ± 0.34	3.94 ± 0.41	49.47 ± 1.25	25.73 ± 1.64	123.68 ± 27.58
GT 1	23.49 ± 4.18	44.63 ± 1.35	54.42 ± 3.25	3.26 ± 0.87	6.24 ± 0.37	3.43 ± 0.31	50.23 ± 2.48	25.53 ± 2.05	139.39 ± 21.19
PB 217	33.59 ± 5.04	34.32 ± 9.32	42.81 ± 12.42	2.83 ± 1.07	4.39 ± 1.11	2.68 ± 0.62	45.72 ± 2.67	21.67 ± 3.29	182.64 ± 49.99
RRIM 701	38.64 ± 3.09	45.13 ± 3.69	53.71 ± 5.27	2.86 ± 0.54	6.64 ± 0.63	3.66 ± 0.40	50.75 ± 1.80	26.08 ± 2.65	154.52 ± 27.65
IAN 873	34.57 ± 3.56	48.53 ± 4.53	65.86 ± 4.83	5.78 ± 0.35	6.16 ± 0.60	3.52 ± 0.09	48.47 ± 2.76	25.89 ± 1.24	144.72 ± 20.99
TAB 821	33.13 ± 6.77	45.38 ± 2.86	60.25 ± 4.41	4.96 ± 1.11	7.16 ± 0.58	3.66 ± 0.25	48.78 ± 1.77	26.38 ± 1.55	137.04 ± 8.33
IAC 15	28.58 ± 4.22	51.12 ± 2.94	65.15 ± 4.07	4.68 ± 0.41	7.70 ± 0.59	4.04 ± 0.12	50.13 ± 2.10	28.39 ± 1.85	133.88 ± 18.35
TAB 804	40.80 ± 11.52	47.68 ± 2.46	57.11 ± 2.66	3.14 ± 0.53	6.40 ± 0.27	3.24 ± 0.18	48.64 ± 1.18	28.76 ± 2.48	136.47 ± 11.44
IAC 222	27.61 ± 3.44	39.23 ± 5.00	47.13 ± 5.81	2.63 ± 0.46	6.57 ± 0.99	3.12 ± 0.29	50.12 ± 2.19	24.35 ± 2.23	171.92 ± 10.19

Table III - Means ($\bar{X}$), range, standard deviations (S.D.) and coefficient of variation (CV%) of average yield over four years (MY), girth at opening (GO), girth after four years of tapping (GC), girth increment over four years of tapping (GI), virgin bark thickness (BT), total number of latex vessel rings (LV), overall density of latex vessels per ring per five millimeters of bark (DV), average diameter of latex vessels (DL), and average distance between consecutive latex vessel rings (AD), from 11 clones of *Hevea*.

Characters	$\bar{X}$	Range	S.D.	CV%
MY	35.06	23.49 - 60.09	9.86	29.11
GO	44.50	34.32 - 51.12	5.09	11.43
GC	55.47	42.81 - 65.86	7.64	13.78
GI	3.66	2.63 - 5.78	1.08	28.36
BT	6.48	4.39 - 7.70	0.88	13.63
LV	3.48	2.68 - 4.04	0.38	10.94
DV	49.08	45.72 - 50.75	1.39	2.84
DL	25.82	21.67 - 28.76	1.97	7.65
AD	147.72	123.68 - 182.64	17.29	11.70

The estimates of values of genetic (Vg) and environmental (Ve) variances, broad sense heritabilities (h^2) and expected genetic gains (Gs) for the traits under study are shown in Table IV. There is evidence that the clonal populations under study have considerable genetic variation for MY, GO and GC, DV, DL and AD, as indicated by the significant estimates of genetic variance (Vg) obtained. Differences among clones include all genetic sources of variation and some non-genetic sources of variation, such as effects due to vegetative propagation.

Broad sense heritabilities, both at the single plot and replicated basis (Table IV), and genetic coefficients of variation (Table V) were high for MY and GI, indicating a very favorable condition for selection for these traits. Therefore, broad sense heritability estimates from clonal tests set upper limits to the ratio of genotypic variance. These are easy estimates and useful in measuring the genetic determination of a character, especially in clonal propagation. However

Table IV - Mean (X), genetic variance (Vg), environmental variance (Ve), heritability (h^2) (single plot and replicated basis), expected gain (Gs) from selection on single plot and replicated basis and expected gain in percent of average yield over four years (MY), girth at opening (GO), girth after four years of tapping (GC), girth increment over four years of tapping (GI), virgin bark thickness (BT), total number of latex vessel rings (LV), overall density of latex vessels per ring per five millimeters of bark (DV), average diameter of latex vessels (DL) and average distance between consecutive latex vessel rings (AD) from 11 clones of *Hevea*.

Characters	Vg	Ve	Heritability (h^2)		Expected gain (S) from selection on		Expected gain in percent of the mean
			Single plot basis	Replicated basis	Single plot basis	Replicated basis	
MY	89.8607	44.2818	0.6699	0.9241	8.7440	10.2699	29.2856
GO	22.6584	19.3958	0.5388	0.8751	3.9377	5.0185	11.2771
GC	53.0850	32.1384	0.6229	0.9083	6.4806	7.8259	14.1070
GI	1.0701	0.5676	0.6534	0.9188	0.9424	1.1175	30.5515
BT	0.6981	0.5031	0.5812	0.8928	0.7178	0.8897	13.7298
LV	0.1330	0.1295	0.5067	0.8603	0.2925	0.3812	10.9876
DV	1.1789	4.6174	0.2034	0.6050	0.5518	0.9518	1.9393
DL	3.2111	4.5993	0.4111	0.8073	1.2949	1.8145	7.0144
AD	327.7791	938.1877	0.2589	0.6770	10.3823	16.7887	11.2209

Table V - Genetic coefficient of variation (CVg), phenotypic coefficient of variation (CVp), environmental coefficient of variation (CVe) and index of variation (θ) of average yield over four years (MY), girth at opening (GO), girth after four years of tapping (GC), girth increment over four years of tapping (GI), virgin bark thickness (BT), total number of latex vessel rings (LV), overall number of latex vessels per ring per five millimeters of bark (DV), average diameter of latex vessels (DL), and average distance between consecutive latex vessel rings (AD) from 11 clones of *Hevea*.

Characters	CVg (%)	CVp (%)	CVe (%)	θ
MY	28.0315	28.1196	18.9757	1.4245
GO	10.6963	11.4338	9.8963	1.0808
GC	13.1336	13.7803	10.2191	1.2852
GI	28.2816	29.5052	20.5974	1.3731
BT	12.8931	13.6450	10.9452	1.1780
LV	10.5114	11.3328	10.3737	1.0133
DV	2.2122	2.8441	4.3782	0.5053
DL	6.9271	7.7096	8.2903	0.8356
AD	12.1004	14.7061	20.4717	0.5911

caution is needed in application of the values especially because of the impossibility of distinguishing additive from non-additive genetic effects, and when working with half sibs.

The lower values of broad sense heritabilities and genetic coefficients of variation for BT, GO and GC and the characters of the laticiferous system (number, density, diameter and distance) indicated that attainment of genetic gain for these traits tends to be slower than for MY and GI.

The MY data did not agree with Tan's (1979) results who reported broad sense heritabilities of 0.27-0.34 for average yield over five years, using a single pair mating design (SPM) outlined by Kearsey (1965). However, values of 0.60 reported by Nga and Subramaniam (1974) and Simmonds (1969) are in agreement. It is possible that the observed relatively low broad sense heritabilities for yield found by Tan (1979) indicate a reduction in the genotypic variation in base population. Though heritabilities are specific to the population from which they are derived, our estimate 0.70, higher than that of Tan (1979), 0.34, may indicate that our clonal stock has a larger genetic base.

Considering the high expected gain that can be achieved by mass selection on a single plot level, based on yield GI, GO and GC, and the low gains expected from selection based on the characters of the laticiferous system, it appears appropriate to place emphasis on selection for higher yield and vigor during the initial phase of a breeding program. Selection for the characters of the laticiferous system requires considerable sampling, which increases the cost.

The expected genetic gains in percent of the mean in this study were computed on a replicated plot basis. Since heritabilities were used in the calculations, the estimates reflect genetic gains that would be realized by direct utilization of the subset of the three clones selected, and not those from growing seedlings from the recombinant population from these clones. As expected, a sizeable genetic gain of almost 30% was estimated for total yield. The traits indirectly affected were BT, LV and AD. DV and DL remained unchanged.

The majority "θ" indices estimated had values higher than 1.00 (Table V). According to Vencovsky (1987), in experiments with maize (*Zea mays* L.) "θ" values equal to or superior than 1.00 indicate genetic conditions favorable to rapid genetic advance.

ACKNOWLEDGMENTS

The authors are grateful to Mr. Edson Bernardes de Freitas, agricultural technician from Pindorama Experimental Station for field work, Miss Rosilei Felismino da Silva for the typist work, Mrs. Rosimeiry Moreira Boschini and Mrs. Ligia Regina Lima Gouvea for laboratory work. This work was supported by FAPESP. Publication supported by FAPESP.

RESUMO

Estimativas de herdabilidade para nove caracteres biométricos, foram calculadas a partir de um experimento de avaliação instalado no município de Tabapuã, envolvendo 11 clones de seringueira [*Hevea brasiliensis* (Willd. ex. Adr. de Juss.) Müell. Arg.]. Os caracteres estudados foram: média de produção de quatro anos (MY), circunferência do caule na abertura do painel (GO), circunferência do caule no quarto ano de sangria (GC), incremento da circunferência de quatro anos de sangria (GI), espessura de casca virgem (BT), número total de anéis de vasos laticíferos (LV), densidade dos vasos em 5 mm do anel (DV), diâmetro dos vasos laticíferos dos anéis (DL) e distância média entre os consecutivos anéis de vasos laticíferos (AD). Foram computadas a variância genética total (Vg), variância ambiental (Ve), estimativa de herdabilidade (h^2) ao nível de médias e ao nível de parcelas e o progresso esperado com pressão de seleção de 27,30% na população. Herdabilidades no sentido amplo foram obtidas para esses caracteres, apresentando valores moderadamente altos. Houve considerável variação genética entre os diferentes clones para MY e GI conforme indicado pelos altos valores de h^2, obtidos para esses caracteres. Os resultados mostraram para os caracteres estudados que estes apresentaram altas diferenças significativas entre os clones. A percentagem de ganho esperado ao nível de médias para MY foi 29.28%, ao passo que para GI, BT e LV foram 30.55%, 13.73% e 10.99%, respectivamente.

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(Received April 30, 1993)