GENETICS OF ANTHRACNOSE PANEL CANKER DISEASE RESISTANCE AND ITS RELATIONSHIP WITH YIELD AND GROWTH CHARACTERS IN HALF-SIB PROGENIES OF RUBBER TREE *(Hevea brasiliensis)*

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ABSTRACT

Rubber tree [*Hevea brasiliensis* (Willd. ex Adr. de Juss.) Muell-Arg] anthracnose panel canker disease resistance, caused by *Colletotrichum gloeosporioides* (Penz.) Sacc., and growth and yield characters were assessed at three years old in the nursery, in 18 half-sib progenies. There were highly significant (P < 0.01) genetic differences among progenies for most characters. The genetic component of variance accounted for 3.37, 6.07, 12.74, 12.13, 19.82 and 3.58% of the phenotypic variance for anthracnose-infected area, anthracnose lesion stripe length, yield, girth, virgin bark thickness and total number of latex vessel rings, respectively. Narrow-sense heritability estimates for the above characters were 13.45, 24.30, 50.97, 48.52, 79.30 and 14.30%, respectively. No significant genetic correlations were found among anthracnose panel canker resistance, yield and growth characters. The frequency distribution of anthracnose-infected area and anthracnose lesion stripe length suggests polygenic control. Selecting the best three progenies out of 18 progenies would result in a genetic gain of 12.87 and 24.24% for infected area and lesion stripe length, respectively. The best five selected individuals out of 50 individuals within each progeny would result in a genetic gain of 9.47 and 24.62%, with a total gain of 22.34 and 48.87% for these two characters, respectively.

INTRODUCTION

The rubber tree [*Hevea brasiliensis* (Willd. ex Adr. de Juss.) Muell-Arg] is a tree crop with a long generative and testing cycle. Usually one generative cycle takes four to five years (excluding seven to 10 years of evaluation for parental performance) and about 20 to 30 years for one testing cycle from the time of cross pollination. Thus, one of the most desirable innovations in tree breeding is a technique for predicting the breeding value of material at the juvenile stage (Varghese, 1992).

The rubber tree breeding program of the Instituto Agronômico (IAC) started as early as 1965, but attention to the genetics of this crop only began in the late 1980s when the breeders encountered difficulties in yield improvement. Attempts have been made with varying degrees of success to predict major economic characters such as yield and vigor of the crop (Moreti *et al.*, 1994; Boock *et al.*, 1995; Gonçalves *et al.*, 1996). No emphasis, however, was given to the genetic aspects of panel disease resistance at that time. Only recently, when anthracnose panel canker disease, caused by *Colletotrichum gloeosporioides*

(Penz.) Sacc., was detected in tapping panels of clone RRIM 600 by Silveira *et al.* (1992), were genetic studies initiated. This disease has since assumed epidemic proportions in many rubber plantations in São Paulo State (Brazil) (Trindade and Furtado, 1997).

The present study was done to analyze the nature of variation of anthracnose panel canker resistance, growth and yield characters and to estimate heritability genetic gains. Attempts have also been made to determine the relationship of anthracnose panel canker resistance to other quantitative characters.

MATERIAL AND METHODS

The material for this experiment consisted of seeds from 18 half-sib progenies randomly selected from a population base from 100 Asiatic clones. They were sown in autumn of 1991 in individual polyethylene bags (12 cm x 18 cm x 18 cm) filled with a mixture of 70% humus and 30% sand. The seedlings remained in these pots during the first six months of the growing season. They were planted out at the Pindorama Experimental Station (21°13'S, 48°56'W) in a randomized complete block design with five replications and 10 seedlings per plot. Space between rows and between trees within rows was 1.5 m. This region has a humid tropical climate with a mean yearly temperature of 21°C and a red yellow podzolic type soil (Lepsch and Valadares, 1976).

Inoculation

Five sources of *Colletotrichum gloesporioides* inoculum from different origins in São Paulo State rubber

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tree plantations were mixed and cultured in potato-dextrose agar (PDA).

The three-year-old rubber tree seedlings were artificially inoculated with the mixed fungus inoculum after seven-day culture during the period from March 20 to 30, 1994. The method of assessing progeny susceptibility to anthracnose panel canker has recently been developed by Silveira *et al.* (1992). This method involves removal of a bark disc (5 mm in diameter) at a height of 1 m from the ground and replacing it with an agar disc of the same size containing mycelia and conidia of the mixed fungus cultured on PDA, and then covered with a polyethylene strip.

Measurements

The size of the lesion was determined five weeks after inoculation by paring away the bark. The length and breadth of the lesion were measured.

Yield determination was made using the principle of the Hamker-Morris-Mann test (HMM) (Tan and Subramaniam, 1976), as follows: 30 tappings were made with a half-spiral, alternate daily (1/2S d/3) tapping system at a height of 20 cm from the ground. Yield recording was done by cup coagulation. The "coagula" were air-dried for a two-month period, until they gave a constant weight. The results of each tree performance were expressed in grams per tapping.

Virgin bark samples were removed from the trunk as plugs at 20 cm height on the opposite side of the tapping panel. Bark thickness was measured for each progeny.

The total number of latex vessel rings in longitudinal and transversal sections of the bark sample was determined. Complete details of the procedure were described by Gonçalves *et al.* (1995). Girth was measured with a steel measuring tape at 0.50 m height from the ground.

Biostatistical analysis

Analyses were performed using version 1.0 of the computer program SELEGEN (Resende and Oliveira, 1997). Least square solutions, including expected mean squares and expected mean covariance products, were obtained (Table I). The linear model for the analysis was:

$$Y_{ijk} = \mu + p_i + b_j + e_{ij} + d_{ijk}$$

where Y_{ijk} = observed value of the k_{th} ortet of the i_{th} repetition; μ = overall mean; p_i = effect of the i_{th} progeny (i = 1, 2 ...p, p = 18); b_j = effect of the j_{th} repetition (j = 1, 2...b, b = 5); e_{ij} = interaction between i_{th} progeny and j_{th} repetition; d_{ijk} = effect among plants within the plots due to the t_k individual of the i_{th} progeny in the j_{th} repetition.

Variance and covariance components were calculated through "Expected Mean Square" components given on the right side of the ANOVA table. Duncan's test was applied to determine which entries were different from each other.

Heritability and gain estimates

Heritabilities on an individual basis (h_i^2), within plot (h_w^2), and among progeny means ($h_{\bar{x}}^2$) were worked out for all the characters using the formula suggested by Vencovsky and Barriga (1992), as follows:

$$h_i^2 = 4\sigma_p^2/(\sigma_w^2 + \sigma_e^2 + \sigma_g^2)$$

$$h_w^2 = 3\sigma_p^2/\sigma_w^2, \text{ and}$$

$$h_{\bar{x}}^2 = \sigma_p^2/(\sigma_w^2/nr) + (\sigma_e^2/r) + \sigma_g^2$$

where σ_p^2 = phenotypic variance; σ_e^2 = variance due to interaction of progenies and replication; σ_g^2 = variance due to differences among progenies; h_w^2 = variance due to dif-

Table I - Degrees of freedom (d.f.), expected mean square (EMS) and expected mean covariance product (EMCP) for estimating components of variance, covariance and heritabilities in an open-pollinated progeny test of rubber tree (*Hevea brasiliensis*).

Source of variation	d.f.	EMS[1]	EMCP[2]
Replications	r - 1	-	-
Progenies	g - 1	$(1/k)\,\sigma_w^2 + \sigma_{rg}^2 + r\sigma_g^2$	$(1/k)\,\text{Cov}_{w(xy)} + \text{Cov}_{rg(xy)} + r\text{Cov}_{g(xy)}$
Progenies x replications	(r - 1) (g - 1)	$(1/k)\,\sigma_w^2 + \sigma_{rg}^2$	$(1/k)\,\text{Cov}_{w(xy)} + \text{Cov}_{rg(xy)}$
Within plot	N - rg	σ_w^2	$\text{Cov}_{w(xy)}$

[1]σ_w^2 = Variance due to differences among plants within plots. σ_{rg}^2 = Variance due to interaction of progenies and replications. σ_g^2 = Variance due to differences among progenies $^{1/4}\sigma_A^2$ (σ_A^2 = aditive genetic variance). r = Number of replications. k = Harmonic mean of plants per plot. N = Total number of individuals in the trial. g = Number of progenies. [2]$\text{Cov}_{w(xy)}$ = covariance among trees within plots of *x* and *y* characters. $\text{Cov}_{rg(xy)}$ = covariance due to interaction of progenies and replications of *x* and *y* characters. $\text{Cov}_{g(xy)}$ = covariance due to progenies for characters *x* and *y*.

ferences among plants within plots; n and r = number of progenies and number of replication.

Genetic gain from selection among progeny (G_g) and within progeny (G_w) levels was also computed using Vencovsky and Barriga's (1992) formula:

$$G_g = k_i \, (1/4) \, \sigma_A^2 \, / \sqrt{\sigma_g^2 + (\sigma_e^2/r) + (\sigma_w^2/rn)}$$

$$G_w = k_2 \, (3/4) \, \sigma_A^2 / \sqrt{\sigma_w^2}$$

where k_1 and k_2 are the intensity of selection. There was a selection intensity of 17 and 20% among and within progenies, respectively.

The genetic gains expressed as a percent of the mean obtained from among and within half-sib progenies ($G_{g\%}$) were estimated using the formula:

$$G_{g\%} = \frac{G_g}{\bar{x}} \cdot 100 \text{ or } G_{w\%} = \frac{G_w}{\bar{x}} \cdot 100$$

where $\bar{x}$ is the general mean.

Genetic coefficients of variation were estimated by the formula suggested by Vencovsky (1987) by dividing the square root of genotypic variance by the population mean and multiplying by 100.

Correlation coefficients

To determine the degree of association between the anthracnose panel canker disease resistance, genotypic ($r_{g(xy)}$) and phenotypic ($r_{F(xy)}$) correlations were worked out according to Kempthorne (1966) as follows:

$$rg_{(xy)} = \text{Cov}_{g(xy)} / \sqrt{\sigma_{gx}^2 \cdot \sigma_{gy}^2}$$

$$rp_{(xy)} = \text{Cov}_{p(xy)} / \sqrt{\sigma_{px}^2 \cdot \sigma_{py}^2}$$

where $\text{Cov}_{g(xy)}$ and $\text{Cov}_{p(xy)}$ = the genotypic and phenotypic covariances for traits x and y, respectively; σ_{gx}^2 and σ_{px}^2 =

genotypic and phenotypic variances for trait x; σ_{gy}^2 and σ_{py}^2= genotypic and phenotypic variances for trait y.

The significance of these correlations was tested using the table in Fisher (1941), for simple correlations for 5 and 1% probability. The genotypic and phenotypic correlations were tested with the degrees of freedom of the error.

RESULTS AND DISCUSSION

Genetic variation

Highly significant differences ($P < 0.01$) were observed among open-pollinated progenies for all characters (Table II). This suggests that differences were attributable to genetic causes and that selection within the rubber tree population included in this test is possible.

The progenies were ranked and distributed into homogeneous groups using Duncan's test (Table III). The most infected progeny was PB 86, while the most resistant progeny was P/9. Considering lesion strip length, progeny B 3363 was the most susceptible and Fx 3899 was the most resistant. There was an increase in resistance of 260 and 380% depending on the type of evaluation. Anthracnose-infected area and lesion strip length were distributed into six different groups. The last group encompassed the five most resistant progenies (Table III).

Yield averaged 10.03 g/tapping/plant. The lowest yielding progeny was P/9, while the highest yielding progeny was PB 5/63, i.e., 692% more productive. The progenies were distributed into eight groups (Table III).

Girth taken at 50 cm from the ground averaged 24.87 cm. The slowest growing progeny P/9 averaged 10.56 cm, and the fastest growing progeny PB 5/63 averaged 22.78 cm, a 216% difference. Girth was distributed into five homogeneous groups (Table III). The first group contained the six best progenies.

Bark thickness averaged 3.655 mm. The progeny with the thickest bark was PB 5/63, with 4.054 mm, while

Table II - Results of ANOVA (mean squares) for anthracnose panel canker disease resistance, yield, girth, bark thickness and number of latex vessel rings for open pollinated progenies of rubber tree (*Hevea brasiliensis*).

Source of variation	Degrees of freedom	Anthracnose panel disease resistance		Yield (g/plant/tapping)	Girth (cm)	Virgin bark thickness (mm)	Number of latex vessel rings
		Infected area (cm²)	Lesion strip length (cm)				
Replications	4	0.2612	7.7959	140.5543	10.5581	0.1381	0.2889
Progenies	17	0.2812*	38.2147*	117.4913**	12.1492**	1.8841**	0.3495*
Progenies x replications	68	0.1414	17.6057	19.2339	3.0816	0.2125	0.1816
Within plot	610	0.7598	54.1013	125.9011	11.1760	1.3259	0.8322
General mean		1.2920	8.6711	10.0266	24.8740	3.6547	2.5601
Coef. of variation %		29.11	48.39	43.74	7.06	12.6120	16.6475

* = $P < 0.05$; **$P < 0.01$.

Table III - Distribution of rubber tree (*Hevea brasiliensis*) progenies into homogeneous groups for several characters according to Duncan's test (P < 0.05).

Anthracnose panel canker disease				Yield		Girth		Bark thickness		Number of latex vessels	
Infected area		Lesion strip length									
Progenies	Mean (cm²)	Progenies	Mean (cm)	Progenies	Mean (g)	Progenies	Mean (cm)	Progenies	Mean (mm)	Progenies	Mean (unity)
PB 86	1.5	B 3363	14.7	PB 5/63	15.366	PB 5/63	22.8	PB 5/63	4.054	Fx 25	3.02
Fx 652	1.4	Fx 25	12.5	PB 86	13.112	GT 711	21.8	IAN 2324	4.008	Fx 652	2.96
IAN 2324	1.4	IAC 2	11.2	B 3363	10.940	Tjir 1	21.1	B 3363	3.964	B 3363	2.56
PB 5/63	1.4	PB 5/63	10.1	C 256	10.704	B 3363	20.5	Fx 25	3.772	C 256	2.54
Fx 25	1.4	C 256	9.8	GT 711	10.562	LCB 510	20.2	AVROS 1328	3.714	PB 5/63	2.52
GT 711	1.3	Fx 652	9.7	RRIM 600	9.852	IAC 2	19.5	GT 711	3.626	RRIM 600	2.44
C 256	1.3	IAN 2324	8.7	RRIM 513	9.302	PB 86	19.4	LCB 510	3.588	PB 86	2.44
Tjir 1	1.8	Tjir 1	7.9	Fx 25	7.476	Fx 652	19.2	RRIM 513	3.496	LCB 510	2.39
RRIM 513	1.2	PB 86	7.3	AVROS 363	7.294	C 256	19.1	Tjir 1	3.468	AVROS 363	2.36
AVROS 1328	1.2	AVROS 1328	6.8	Fx 3899	6.828	IAN 2324	18.9	C 256	3.464	IAC 2	2.34
B 3363	1.2	Fx 2784	6.3	IAC 2	6.298	Fx 2784	18.4	Fx 652	3.358	IAN 2324	2.32
AVROS 363	1.1	AVROS 363	5.6	IAN 2324	6.106	RRIM 600	18.4	PB 86	3.350	Tjir 1	2.30
IAC 2	1.1	RRIM 513	5.1	Fx 652	5.934	RRIM 513	18.0	AVROS 363	3.338	GT 711	2.16
Fx 3899	0.9	GT 711	5.0	Tjir 1	5.198	Fx 25	17.9	IAC 2	3.210	RRIM 513	2.14
LCB 510	0.9	LCB 510	4.9	LCB 510	4.148	AVROS 363	17.1	Fx 3899	3.120	Fx 2784	2.13
RRIM 600	0.8	RRIM 600	4.5	AVROS 1328	3.780	AVROS 1328	16.7	Fx 2784	3.004	AVROS 1328	2.08
Fx 2784	0.8	P/9	3.8	Fx 2784	3.476	Fx 3899	16.4	RRIM 600	2.776	Fx 3899	1.98
P/9	0.6	Fx 3899	3.7	P/9	2.220	P/9	10.6	P/9	2.101	P/9	1.04

the thinnest bark was found in P/9, with 2.101 mm, i.e., 192% variation in bark thickness.

The progeny distribution among many homogeneous groups suggests a polygenic mode of inheritance for all the characters. The results demonstrate that considerable genetic variation exists at the progeny level for the most economically important characters. This high genetic diversity could be used in an operational program or as the base for future breeding activities.

Variance components

Genetic component estimates of variance accounted for 3.37, 6.07, 12.74, 12.13, 19.82 and 3.58% of the phenotypic variance for anthracnose-infected area, anthracnose

lesion strip length, yield, girth, virgin bark thickness and number of latex vessel rings, respectively (Table IV). It is evident that the estimates of progeny genetic variance for anthracnose-infected area were substantially smaller than those for anthracnose lesion strip length. In addition, the estimates of progeny genetic variance for the two anthracnose characters were substantially smaller than those for yield and growth characters with the exception of number of latex vessels.

Heritabilities

Heritability among progeny means ($h_{\bar{x}}^2$) for anthracnose-infected area and anthracnose lesion stripe length was around 50% (Table V). These data agree with Tan

Table IV - Components of variance (σ^2) for six characters of 18 open-pollinated progenies of rubber tree (*Hevea brasiliensis*).

Characters	σ_w^2	σ_e^2	σ_g^2	σ_p^2	σ_A^2
Anthracnose panel canker (infected area)	0.7598	0.0370	0.0280	0.8315	0.1120
Anthracnose panel canker (lesion strip length)	54.1013	10.1730	4.1218	67.8511	16.4872
Yield	125.9011	1.9369	19.615	154.2295	78.4600
Girth	11.1760	1.5461	1.8135	14.9510	7.2541
Virgin bark thickness	1.3259	0.0303	0.3343	1.6864	1.3373
Number of latex vessel rings	0.8322	0.0673	0.0336	0.9390	0.1344

σ_w^2 = Variance due to differences among plants within plots. σ_e^2 = Variance due to interaction of progenies and replications. σ_g^2 = Variance due to differences among progenies $^{1/4}$ σ_A^2 (σ_A^2 = additive genetic variance). σ_p^2 = Phenotypic variance.

Table V - Genotypic coefficient of variation (CV_g) and heritabilities on an individual basis (h_i^2), within progeny plot (h_w^2) and among progeny means ($h_{\bar{x}}^2$) for six different characters in 18 open-pollinated progenies of rubber tree *(Hevea brasiliensis)*.

Characters	CV_g %	Heritabilities		
		h_i^2	h_w^2	$h_{\bar{x}}^2$
Anthracnose panel canker (infected area)	12.95	0.1345	0.1104	0.5382
Anthracnose panel canker (lesion strip length)	23.41	0.2430	0.2286	0.5838
Yield	44.21	0.5097	0.4683	0.9052
Girth	5.41	0.4852	0.4868	0.8079
Virgin bark thickness	15.82	0.7930	0.7565	0.9604
Number of latex vessel rings	7.16	0.1430	0.1210	0.5198

and Tan's (1996) results. They reported broad sense heritabilities of 28.9% up to 57.7% for anthracnose leaf disease, indicating that both panel and leaf anthracnose disease had moderately high heritability estimates (Table V). It implies that there is a large genetic variability for anthracnose resistance character in the population studied.

Heritabilities for other characters such as yield and virgin bark thickness were relatively high, i.e., 50.97 and 79.30% on an individual basis, 46.83 and 75.65% within progeny and 90.52 and 96.04% among progeny, respectively. These highly significant heritability estimates coupled with the large amount of variation observed within the rubber tree population suggest that an effort to increase both yield and girth growth through progeny selection would be rewarding.

Expected genetic gains

Expected genetic gains are shown in Table VI. If the best five progenies were selected and planted on sites similar to that used in the experiment trial, a genetic gain among progenies in anthracnose-infected area and lesion strip length rate of about 12.87 and 24.24%, respectively,

could be achieved. When only the five best progenies (i.e., five progenies out of 18 progenies) were selected, for yield with a selection intensity of 0.17 the gain in yield at age three was 12.39 g, which is 57.35% greater than the overall progeny means. Even smaller increases than these would result in appreciable improvement if the planting is large enough.

On the other hand, if the best two individuals were selected within progenies, asexually multiplied and planted at the same site, the genetic gains for anthracnose-infected area and lesion stripe length would be about 9.46 and 24.62%, respectively. For yield, girth and virgin bark thickness the gains would be 66.55, 8.31 and 30.27%, respectively. Considering combined selection among and within progenies the total genetic gains would be 22.34 and 48.87% for anthracnose-infected area and lesion stripe length, and 123.56% for yielding, respectively.

Gains in anthracnose panel canker disease appear to be possible in the rubber tree. Improvement, however, requires either that selection be done in a plantation which has been heavily exposed to the fungus or that progeny tests of selected trees be conducted in areas where the fungus is prevalent. The association of the two types of selection would probably contribute to greater gains.

Correlations

Phenotypic correlations between anthracnose-infected area and other characters like yield and girth were generally significant (Table VII). Progenies with high yield and vigor often exhibited a high anthracnose susceptibility.

The influence of anthracnose panel canker disease resistance on latex yield and vigor is not evident in the field. Data from observations that selected high yielding and/or vigorous genotypes have varying degrees of disease resistance. An inverse genetic association between disease resistance and the important economic characters is not evident.

Table VI - Expected gains from selection and percentage of the mean among (G_g) and within (G_w) progenies selection and total (G_{tot}) for six different characters in 18 open-pollinated progenies of rubber tree *(Hevea brasiliensis)*.

Characters	*From selection*			*In percent of the mean*		
	G_g	G_w	G_{tot}	G_g	G_w	G_{tot}
Anthracnose panel canker (infected area)	0.1663	0.1223	0.2886	12.8712	9.4657	22.3369
Anthracnose panel canker (lesion stripe length)	2.1022	2.1351	4.2373	24.2437	24.623	48.8668
Yield	5.7161	6.6728	12.3889	57.0095	66.5511	123.5606
Girth	1.6404	2.0668	3.707	6.5948	8.3091	14.9031
Virgin bark thickness	0.7679	1.1062	1.8741	21.5417	30.2677	51.2789
Number of latex vessel rings	0.1791	0.1402	0.3193	6.9959	5.4764	12.4724

G_{tot} = Total genetic gain $(G_g + G_w)$.

Table VII - Estimates of genotypic (r_g) and phenotypic (r_p) correlation coefficients, based on individual trees among anthracnose panel canker disease yield and growth characters of 18 open-pollinated progenies of rubber tree *(Hevea brasiliensis)*.

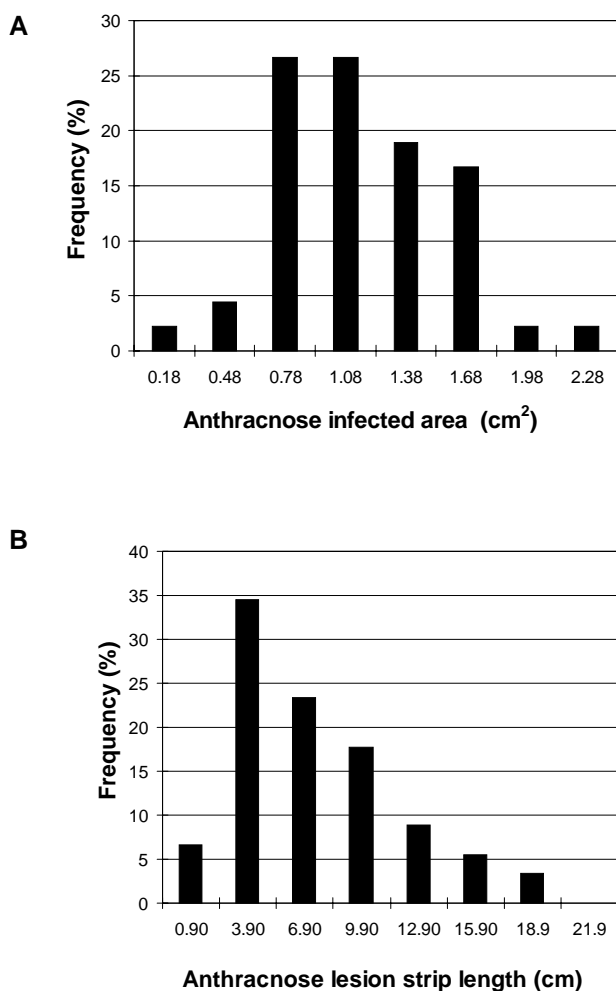| Characters		Lesion stripe length	Yield	Girth	Virgin bark thickness	Total number of latex vessel rings
Anthracnose panel canker	r_g	0.3233	0.2932	0.4218	0.4674*	0.2932
(infected area)	r_p	0.6028**	0.6546**	0.7603**	0.5521*	0.6667**
Anthracnose panel canker	r_g	-	0.1606	0.1552	0.3417	0.5916**
(lesion stripe length)	r_p	-	0.2306	0.3120	0.5467*	1.1582
Yield	r_g		-	0.6661**	0.5286*	0.3697
	r_p		-	0.7603**	0.5521*	0.5324*
Girth	r_g			-	0.6397**	0.3680
	r_p			-	0.7416**	0.7498**
Virgin bark	r_g				-	0.4026
thickness	r_p				-	0.6156**

* = P < 0.05; ** = P < 0.01.

Figure 1 - Frequency distribution in the tested rubber tree population evaluated for anthracnose panel canker disease resistance for infected area and lesion strip length.

There were fairly large phenotypic and genetic correlations among yield, total number of latex vessel rings, girth, and virgin bark thickness. Significant positive correlations among these characters imply genetic gain in all of these characters even if selection is undertaken on only one character.

Type of distribution

The frequency histograms for anthracnose-infected area (Figure 1A) and anthracnose lesion strip length (Figure 1B) have a fairly normal distribution. These variation patterns indicate quantitative characters that are polygenically controlled.

Basically, two broad categories of genetic variations can be recognized, namely major gene and polygenic inheritance. While there are several ways to differentiate various forms of genetic mechanisms (Simmonds, 1982), one of the criteria is to monitor the distribution or variation pattern of a specific character in a given population. A character which shows continuous variation is often referred to as a likely candidate for polygenic inheritance. Similar observations concerned the degree of resistance to anthracnose leaf disease in the field, nursery or laboratory. Wastie (1973) demonstrated a continuous form of variation, implying polygenic inheritance.

Breeding strategy

Based on the results of this experiment it is possible to develop a program for rubber tree improvement. According to Zobel and Talbert (1984), the "progeny plus within-family selection" method is the predominant form of selection used in most advanced generation tree improvement programs. This method consists of selecting the best

progenies along with the best individuals within those progenies. Consequently, this method will be adopted for improving anthracnose panel canker disease resistance, yield and girth. Since there is no significant genetic correlation among the three characters, indirect selection is not applicable in this instance. For this purpose "tandem selection" will be employed, e.g., the anthracnose panel canker disease resistance will be improved first. When a desired resistance level has been obtained, breeding efforts will be concentrated on yield and growth characters. However, if the intention is to improve anthracnose panel canker disease resistance and yield simultaneously, then an "independent culling" method would be recommended.

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RESUMO

Estudos genéticos da relação da resistência da antracnose do painel, caracteres da produção e vigor da seringueira [*Hevea brasiliensis* (Willd. ex. Adr. de Juss.) Muell-Arg] foram conduzidos em 18 progenies de meios-irmãos na Estação Experimental de Pindorama, Estado de São Paulo. Os resultados obtidos mostraram diferenças genéticas significativas entre progenies para a maioria dos caracteres estudados. Os componentes genéticos da variância contribuíram com 3,37% da variância fenotípica para área infectada, 6,07% para comprimento de estrias, ambos causados pela anthracnose, 12,74% para produção, 12,13% para perímetro do caule, 19,82% para espessura de casca virgem e 3,58% para número total de vasos laticíferos. As herdabilidades no sentido restrito para os caracteres acima foram: 13,45%, 24,30%, 50,97%, 48,52%, 79,30% e 14,30%, respectivamente. Correlações significativas não foram encontradas entre anthracnose do painel e caracteres da produção e perímetro do caule. A distribuição de freqüência de anthracnose sugere que o caráter é poligênico. A seleção das três melhores progenies resultaria em um ganho genético para anthracnose de 12,87% e 24,24% para área infectada e comprimento das estrias, respectivamente. A seleção dos cinco melhores indivíduos dentre os 50 indivíduos de cada progênie, para ambos os caracteres, resultaria em ganho genético de 9,47% e 24,62% com ganho total de 22,34% e 48,87%, respectivamente.

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