Genetic parameter estimations of three traits used to evaluate South American leaf blight (SALB) in rubber tree

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ABSTRACT

Attack severity, sporulation intensity and stromata density are three symptoms of South American Leaf Blight caused by *Microcyclus ulei* (P. Henn.) v. Arx. evaluated in the field on one to three year-old rubber tree [*Hevea brasiliensis* (Willd. ex Adr. de Juss.) Muell.-Arg.]. This genetic study under epidemiologic conditions of the Michelin plantation, Itiquira, State of Mato Grosso - Brazil, used the data from two experimental fields made of 198 clones from 22 progenies. The results indicate that small-scale clone trial is an more adapted apparatus than the seedlings selection trial for achieving the best appreciation of individual values. Moreover, this paper shows high correlations among the three parameters and gives genetic prediction values. The interest for an evaluation of the three parameters is discussed. Finally, a selection with a calculated index shows that a selection under genetic values retains the same clones as a selection under phenotypic values.

KEY WORDS: South American leaf blight, rubber tree, selection, resistance, heritability.

INTRODUCTION

Breeding programs of rubber tree [*Hevea brasiliensis* (Willd. ex Adr. de Juss.) Muell.-Arg.] for resistance to South American Leaf Blight were implemented in tropical America mainly in Brazil by Ford Plantations, the U.S. Departament of Agriculture and the Instituto Agronômico do Norte (Rands and Polhamus, 1955; Townsend, 1960); in Africa by the Firestone Plantations Company in Liberia (Bos and Mc Indoe, 1965) and in Asia, mainly by Malaysia and Sri Lanka (Brookson, 1956, Subramanian, 1969). From these works, Amazonian clones were evaluated and the best wild clones were crossed to introduce resistant characters in productive but susceptible Asiatic clones. Nowadays, some clones planted in large areas in South and Central America result from backcross breeding schemes involving resistant genitors. Nevertheless, few clones were recommended for planting in areas affected by SALB because of the instability of their resistance and because their rubber production potential was much lower than that of the Asiatic clones.

Retrospectively, among the reasons which could explain so few distributed clones from this program, we can list several factors:

· the absence of knowledge about the parasite's diversity;

· the relatively recent concept of polygenic resistance / oligogenic resistance;

· a global appreciation of the disease;

· the dearth of study regarding progenies (seeing that many of the group arose from individual selections on legitimate seeds, while others came from illegitimate seeds).

The success rate of artificial pollination is generally low and strictly dependent on the parent clone (Clément-Demange et al., 1997; Hamzah et al., 2002). This situation makes cross aptitude exploration of different groups difficult and encourages prejudicial crosses to maintain genetically diverse material. In practice, a great number of families are studied through small progenies (familial selection) then the best families are raised on a large scale to supply the elite individuals for cloning.

The progenies are submitted to three stages of selection. The first stage necessarily starts by the assessment of a population of individual genotypes structured in families (generally full-sib progenies) in which every descendant is represented by a single tree, without any replication. This situation presents theoretical disadvantages: genotypes are not evaluated under the normal form of variety diffusion (clone of

graft); in the absence of replications, it is difficult to get a precise evaluation of the genetic value of genotypes. For these reasons, the first trial, named seedlings selection trial (SST), is limited in surface (high density of planting) and in duration (precocious assessment). A family selection is performed at this stage of the breeding scheme. The SST then becomes a conservatory for the resultant genetic material.

The second step of selection takes place in small-scale clone trial (SSCT). Every genotype is represented here under graft clone, by four plots of 4 to 6 trees. The bud wood necessary for multiplication is obtained in the SST. After eight years of evaluation, competition phenomena between trees of neighbouring plots force an end to experimentation.

This strategy, employing a family selection in SST and a family structure in the SSCT, answers to a double finality: the genetic parameter study and a clonal selection. If the aim is only the clonal selection and if criteria of selection are validated, it can be considered an individual and family combined selection in the SSCT.

The aim of the present work is to estimate in cloned full-sib families, genetic parameters of three traits used to score resistance to South American Leaf Blight. The consequences for the breeding program are discussed.

MATERIAL AND METHODS

Genetic Material

The full-sib (FS) families were created in 1993 and 1994 using Asiatic clones (Wickham, W) and SALB resistant clones (Wickham Amazonian, WAm) . Only one FS family, PB5/51 x PR107, represented a cross between two W clones.

Before a pre selection in SST, the genotypes were grafted on illegitimate rootstock stumps of the clone GT1.

The SSCT number 2 and number 3 were grown at the Michelin Plantation, Itiquira, Mato Grosso State, Brasil. Eleven FS families were tested in each of these two trials, with respectively eight and ten progenies per family in trial n°2 and trial n°3 (table 1).

Field designs and measurements

The trials were made of four replications. In trial n°2, each progeny was present in 2, 3 or 4 replications with six trees per plot (unbalanced statistical desgin). In trial n°3, each progeny was present in each block with six trees per plot.

The observed parameters were :

· The attack intensity. It was scored on a scale of 0 to 4, on old leaves, considering the percentage of infected area of the leaf . 0, < 1% ; 1, 1-5% ; 2, 6-15% ; 3, 16-30% et 4, >30% (Chee, 1976)

· The sporulation intensity. It was scored on a scale of 1 to 6 on C leaf stage (chlorophylian leaflets in vertical position). 1, chlorotic lesion; 2, necrotic lesion; 3, partial sporulation around the lesion on the lower face of the leaf; 4, partial sporulation on the lower face of the lesion; 5, abundant sporulation on the lower face of the lesion; 6, abundant sporulation on the lower face and the superior face of the lesion.

· The stromata density considered on old leaves, with four levels. 0, absence of stromata; 1, less than ten stromata per leaflet; 2, between ten and thirty stromata per leaflet ; 3, more than thirty stromata per leaflet.

The evaluations were implemented monthly during the epidemic period from January to May between 1998 and 2001. These three parameters were annotated 15 times for SSCT n°2 and 10 times for SSCT n°3 during the observation periods. In order to get strong selection criteria, only maximal values for the three parameters were considered.

The data which were analyzed represented the average by plot of the maximal note observed on each tree. The data were adjusted to the block effect.

Data processing

Multivariate Variance Analyses (MANOVA)

Analyses of variance were carried out by using DIOGENE, an evolution of OPEP genetic and plant breeding software (Baradat and Labbé, 1995a), which includes automatic resampling by Jackknife and Bootstrap. We used the following statistical model:

$$Yijk = m + Fi + Gij + Eijk$$

where : Yijk is the observed value of j *th* clones in the i *th* family, m is the general mean, Fi is the random effect of the i*th* family (i =1, 2,… 11), Gij is the random effect of j*th* genotype of the i *th* family (j = 1, 2,… .8 or 10) and Eijk is the random effect of the k*th* repetition corresponding to the plot (k = 1, 2, 3, 4).

Table 1. Rubber tree families and clones issues on the small scale clone trials n°2 and 3.

Trial 2		
Crosses	Family issue	Clone issues
PR 255 x RO 38	1	37-38-44-45-49-50-90-91-94-95
PR 255 x IAN 873	2	35-47-76-79-80-81-82-83-100-106
PR 255 x FX 25	3	19-26-27-56-101-103-107-108-111-112
PR 255 x IRCA 519	4	4-5-9-57-59-60-67-68-71-75
XX 701 x RO 38	5	39-40-41-51-52-53-55-70-72-73
XX 701 x IAN 873	6	8-16-32-42-46-77-84-104-109-110
XX 701 x FX 25	7	7-11-12-15-17-20-36-48-78-102
XX 701 x IRCA 519	8	6-13-21-43-54-61-69-96-97-113
GT 1 x IAN 873	9	10-25-28-31-33-34-63-64-74-93
GT 1 x IRCA 519	10	18-23-24-29-30-85-89-98-99-105
PB 5/51 x PR 107	11	14-22-58-62-65-66-86-87-88-92
Trial 3		
Crosses	Family issue	Clone issues
PB 260 x RO38	1	11-12-13-14-16-17-18-19
PB 260 x IAN 873	2	6-22-23-28-29-33-36-43
PB 260 x FX 25	3	66-67-69-70-71-72-73-74
PB 260 x FX 3864	4	24-25-30-31-34-38-39-79
PR 255 x FX 3864	5	7-9-37-64-84-85-86-89
PR 255 x IRCA 519	6	49-50-53-54-55-63-65-68
PR 255 x IRCA 621	7	4-8-20-21-26-32-45-47
XX 701 x FX 3864	8	5-15-27-41-75-82-83-90
XX 701 x IRCA 621	9	10-51-57-61-62-77-81-87
GT 1 x FX 3864	10	35-42-52-58-60-76-78-80
GT 1 x IRCA 621	11	40-44-46-48-56-59-88-91

The corresponding variances of random effects are respectively: σ_f^2 = variance due to differences among the families, σ_g^2 = variance due to differences among genotypes and σ_e^2 = variance due to interaction of genotypes and replications.

Genetic parameters

The Coefficients of Genetic Prediction (*CGPs*) were estimated, assuming the absence of family x block interaction. The concept of CGP is a generalization of heritability when two traits are considered. After Nei's (1960) definition of 'co-heritability', Baradat (1976) gave this name to the standardized regression of genetic (or genotypic) value of one trait on the phenotypic value on another trait (the values are expressed into phenotypic standard deviations). This genetic parameter was promoted by Van Buijtenen (1992) as a practical way to compare the efficiencies of direct versus indirect selection.

Considering a q x q matrix of *CGPs* concerning q traits, the ratio of diagonal *CGP* of trait x*l* (heritability of this trait) on an off-diagonal *CGP* directly gives the relative efficiency of direct selection of trait x*l* using x*l'* as a predictor.

The *CGPs* were computed at three levels : genotype (*CGPg*), family (*CGPf*) and a combination between the genotype and the family information (*CGP*).

$$C\hat{G}P_g^{(l,l')} = \frac{\hat{\mathrm{cov}}_g^{(l,l')}}{\sqrt{\hat{\sigma}_g^{2(l)} + \hat{\sigma}_e^{2(l)}}\sqrt{\hat{\sigma}_g^{2(l')} + \hat{\sigma}_e^{2(l')}}}$$

$$C\hat{G}P_f^{(l,l')} = \frac{\hat{\mathrm{cov}}_f^{(l,l')}}{\sqrt{\hat{\sigma}_f^{2(l)} + \hat{\sigma}_g^{2(l)} + \hat{\sigma}_e^{2(l)}}\sqrt{\hat{\sigma}_f^{2(l')} + \hat{\sigma}_g^{2(l')} + \hat{\sigma}_e^{2(l')}}}$$

$$C\hat{G}P^{(l,l')} = \frac{\hat{\mathrm{cov}}_g^{(l,l')} + \hat{\mathrm{cov}}_f^{(l,l')}}{\sqrt{\hat{\sigma}_f^{2(l)} + \hat{\sigma}_g^{2(l)} + \hat{\sigma}_e^{2(l)}}\sqrt{\hat{\sigma}_f^{2(l')} + \hat{\sigma}_g^{2(l')} + \hat{\sigma}_e^{2(l')}}}$$

By stating : *l*=*l'*, one can find the formulae of heritability which are redefined as the CGP of a trait with itself : the covariance of the numerator becomes

the corresponding variance of the trait *l*.

To determine the degree of association between character pairs, Pearson's phenotypic (*P*), genetic (*G*) and environmental (*E*) correlation coefficients ($\rho^{(l,l')}$) were calculated by the following equations :

$$\rho_P^{(l,l')} = \frac{\hat{\text{cov}}_P^{(l,l')}}{\hat{\sigma}_P^{l}\hat{\sigma}_P^{l'}} \quad ; \quad \rho_G^{(l,l')} = \frac{\hat{\text{cov}}_G^{(l,l')}}{\hat{\sigma}_G^{l}\hat{\sigma}_G^{l'}} \quad ;$$

$$\rho_E^{(l,l')} = \frac{\hat{\text{cov}}_E^{(l,l')}}{\hat{\sigma}_E^{l}\hat{\sigma}_E^{l'}}$$

Significance and confidence intervals for these genetic parameters have been assessed using a Bootstrap procedure (Shao and Tu, 1995).

Selection indices

Best Linear Predictor - BLP -selection indices for culling the best genotypes on the basis of a linear combination of C predicted traits, were computed, following the general model :

$$I = \sum_{l=1}^{C} b_l \hat{g}_i(x_l)$$

where $\hat{g}_i(x_l)$ is the predicted average genetic value of the genotype *i* for trait *xl* and *bl* is the relative weight associated to this trait.

A first series of indices used only one predicted (target) character, which was its own predictor, or associated with the three other traits used as predictors, with weights 0, to improve index accuracy. These indices gave the maximum genetics gain, which could be reached for each target trait using or not using additional information on other genetically correlated traits. Lastly, we computed the three traits, trying different relative weights corresponding to the confidence we have in each trait to characterize the resistance (AT, 1; SP, 3; ST, 2). The expected genetic gains for every index computation were computed as described by Baradat et al. (1995b) in a general synthesis about allocation of predictor and target traits in a selection index.

The index on phenotypic values is calculated for each clone with values adjusted in block effect as follows:

Index clone = -[(Xat - Aat) + (3 x (Xsp - Asp)) + (2 x (Xst - Ast))]

With X : clone average ; A : overall average.

RESULTS

Distribution of the variance between the family-effect and the clone-effect

In the trial SSCT n°2, the part of the variance explained by the family represents between 54 and 72% according to the character associated to the disease (Table 2).

The part of the variance explained by the clone represents between 28% and 46%. The situation is inverse in the case of the trial SSCT n°3: the percentage of the variance associated to the clone appears stronger than the one associated to the family.

The following reasons can be delineated:

- In the SSCT n°2, the control family, PB 5/51 x PR 107, resulting from a cross between two susceptible parents, was included in the analysis, thus increasing the overall variance. The precision for evaluating the resistance of individual genotypes during the first selection stage (SST) was rather poor, having small number of annotations, difficulties of symptom appreciation, and introduction in the selection index of several other criteria (precocious production, growth) which interferred substantially with the final intensity of the selection for resistance. These facts resulted in an intra-family variability superior to inter-family variability.

Phenotypic, genetic and environmental correlations

All the correlations between the three parameters describing the SALB were highly significant (Table 3). The genetic correlations both at the family level and genotype level were superior to phenotypic correlations.

Coefficients of genetic prediction (heritability)

Table 2. Percentage of the inter-family variance on the total genetic variance (family variance + clone variance) for the SALB attack severity (at), sporulation intensity (sp) and stromata density (st) observed in two trials composed each one with eleven rubber tree families of 10 or 8 cloned full-sibs.

Trials	at	sp	st
N° 2	54.6	60.7	72.0
N° 3	36.6	21.2	37.8

The coefficients of genetic prediction taking in account the variance between families and between clones gave values around 0.7 for the three studied traits (Table 4). It can be observed that the heritability, taking into account the variance between families for the character intensity of sporulation, is superior when we use information provided by the variable intensity of attack jointly (case of the SSCT 3) or stromata density (case of the SSCT2 and 3).

This underlines the fact that the variable intensity of sporulation is more difficult to appreciate in the field than the two other variables. The intensity of sporulation is transient; it is bound to environmental conditions and its visual annotation may be altered by the rainfall washing over the lesions.

Genetic gains

The estimated genetic gains are presented in the Table 5. Stromata density appears as the variable on which the major progress could be achieved.

The gains are relatively stable and did not depend either on the predictor character which was chosen, or on the weighting of the character. This fact is related to high correlations between these three characters. Thus, we verify that if the observations were made only on the stromata density (predictor st = 1), the gains would be the same that if the three parameters would be considered (predictors at = 0, sp = 0, st =1). Considering this result, the utility of achieving a selection based on these three parameters should be questioned.

Genetic and phenotypic selections

The table 6 shows that the same head group is obtained with a selection on the genetic indexes or phenotypic values (with the exception of clones whose indexes could not be calculated by Diogène software because of missing data).

This head group is constituted, in the SSCT 2, of the clones n°39, 41, 55, 70, 72, 73 of the XX 701 x Fx 3899 cross; n°44 of PR 255 x Fx 3899 cross; n°46 of the XX 701 x IAN 873 cross; n° 47 of the PR 255 x IAN 873 cross and n° 74 of the GT 1 x IAN 873 cross.

In the SSCT 3, the head group is constituted of the clones n°6, 22, 36, of the PB 260 x IAN 873 cross; n°14, 18 of the PB 260 x Fx 3899 cross; n°38 of the PB 260 x Fx 3864 cross; n°54 of the PR 255 x IRCA 519 cross; n°57 of the XX 701 x IRCAS 621 cross and n°83, 90 of the XX 701 x Fx 3864 cross.

Table 3. Phenotipic, genetic and intra-clonal (residual) correlation for the SALB attack severity (at), sporulation intensity (sp) and stromata density (st) observed in two trials composed each one with eleven rubber tree families of 10 or 8 cloned full-sibs.

Trial 2	Phenotypic		Genetic				Residual	
			Family		Genotype			
	at	sp	at	sp	at	sp	at	sp
Sp	0.749		0.993		0.904		0.326	
E. Stand.	0.044		0.021		0.052		0.078	
Signif. (%)*	*0.000*		*0.000*		*0.000*		*0.006*	
St	0.741	0.733	0.953	0.982	0.762	0.841	0.379	0.167
E. Stand.	0.040	0.037	0.025	0.020	0.050	0.062	0.068	0.084
Signif. (%)	*0.000*	*0.000*	*0.000*	*0.000*	*0.000*	*0.000*	*0.000*	*4.372*

Trial 3	Phenotypic		Genetic				Residual	
			Family		Genotype			
	at	sp	at	sp	at	sp	at	sp
Sp	0.797		1.000		0.930		0.424	
E. Stand.	0.017		0.115		0.025		0.063	
Signif. (%)*	*0.000*		*0.000*		*0.000*		*0.000*	
St	0.865	0.708	0.975	1.000	0.923	0.834	0.567	0.259
E. Stand.	0.014	0.028	0.019	0.149	0.022	0.043	0.047	0.061
Signif. (%)	*0.000*	*0.000*	*0.000*	*0.000*	*0.000*	*0.000*	*0.000*	*0.006*

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DISCUSSION

This South American Leaf Blight breeding program aiming to obtain clones with durable resistance to *Microcyclus ulei*, is based on detailed observations of the development of the parasite. For that, three criteria are evaluated in the field that take in account different phases of the development of the parasite: the intensity of sporulation concerning the vegetative form of dissemination, the density of stromata concerning the sexual form of the parasite and the intensity of leaf attack or level of leaf distortion which is a consequence of the two first criteria.

The genetic analysis implemented on 22 progenies underlines that the variance bound to the family is strongly influenced by the type of progenies. In experimentation regrouping the WxW and WxWam families (as in the SSCT 2), the progeny variance represents 60% of the total variance whereas for an experiment with only Wam clones (case of the SSCT 3), the progeny variance for the three criteria oscillates around 30% of the genetic variance.

Table 4. Heritability (Coefficients of Genetic Prediction, *CGPs*) of the variables SALB attacks severity (at), sporulation intensity (sp), and stromata density (st) observed in two trials composed each one with eleven rubber tree families of 10 or 8 cloned full-sibs.

Trial 2	$\hat{CGP}_g$			$\hat{CGP}_f$			$\hat{CGP}$		
	at	sp	st	at	sp	st	at	sp	st
At	0.489			0.371			0.679		
E. Stand.	0.047			0.048			0.029		
Sp	0.422	0.444		0.386	0.407		0.643	0.671	
E. Stand.	0.047	0.048		0.044	0.046		0.030	0.029	
St	0.407	0.427	0.582	0.449	0.485	0.599	0.653	0.693	0.832
E. Stand.	0.044	0.049	0.040	0.040	0.037	0.035	0.029	0.029	0.017

Trial 3	$\hat{CGP}_g$			$\hat{CGP}_f$			$\hat{CGP}$		
	at	sp	st	at	sp	st	at	sp	st
At	0.714			0.289			0.796		
E. Stand.	0.028			0.054			0.017		
Sp	0.615	0.613		0.206	0.141		0.687	0.667	
E. Stand.	0.034	0.035		0.049	0.050		0.024	0.028	
St	0.655	0.548	0.706	0.287	0.215	0.300	0.749	0.640	0.794
E. Stand.	0.032	0.041	0.027	0.050	0.046	0.050	0.019	0.030	0.017

Table 5. Expected genetic gain for each trait (at, SALB attacks severity; sp, SALB sporulation intensity, st, SALB stromata density) with a selection rate of 5% and different relative weight for these three traits

Trial 2 Target traits	Predictor traits						
	at = 1 - -	- sp = 1 -	- - st = 1	at = 1 sp = 0 st = 0	at = 0 sp = 1 st = 0	at = 0 sp = 0 st = 1	at = 1 sp = 3 st = 2
At	41	-	-	46	41	37	42
Sp	-	38	-	38	43	36	42
St	-	-	92	76	79	94	87

Trial 3 Target traits	Predictor traits						
	at = 1 - -	- sp = 1 -	- - st = 1	at = 1 sp = 0 st = 0	at = 0 sp = 1 st = 0	at = 0 sp = 0 st = 1	at = 1 sp = 3 st = 2
At	39	-	-	36	32	33	35
Sp	-	26	-	25	28	21	27
St	-	-	64	57	47	62	57

A target trait is predicted by itself ou by itself and the two other traits as additional preditors.

We need to make clear that the tested material comes from a previous selection in a seedling experimentation (SST). In this first phase, no family has been rejected. In every family, eight or ten individual trees were selected to be used as mother trees.

With the aim of doing a selection for SALB resistance, it appears of great importance to eliminate, as a first step, the worst classified families at the end of the seedling selection trial. For example, the PB 5/51 x PR 107 family should have been eliminated at this step of the selection. However, the SST is not sufficient to allow a choice on the individual genotypic values: more than 70% of the individual variance in SSCT is made of genetic variance, in spite of a pre selection in SST. The SSCT permits a better selection of individual genotypes.

The criteria, intensity of attack, intensity of sporulation and density of stromata, are highly related. Broad sense heritabilities taking in account clone and family variances and phenotypic variance are high: 0.796 for the intensity of attack, 0.667 for the intensity of sporulation and 0.794 for the density of stromata in trials made of Wam individuals (SSCT3). This result indicates that the phenotypic value is close to genetic value. Several restrictions contribute to reduce the intra-clonal variance of the three traits. Firstly, the disease is evaluated only during the epidemic season from December to April. Secondly, even though various levels of disease intensity could be observed simultaneously on one individual tree, only the maximal symptom values were scored. Thirdly, between all the scores obtained by one tree during several campaigns, only the maximal score was retained for statistical analysis.

Coefficients of genetic prediction show that the variables "intensity of attack" and "density of stromata" are better scored by themselves. On the other hand, the variable "intensity of sporulation" is better predicted while using the variables "density of stromata" (for an evaluation at the family level) and "intensity of attack" (for an evaluation at the level of the clone and the family). These indicators favor a selection that would be done solely on substantial criteria easily available in the field, such as the density of stromata and the intensity of attack. However, it seems difficult not to assess the sporulation intensity for various reasons. This criterion is a quantitative

Table 6. Selection index using the three traits (at, SALB attacks severity; sp, SALB sporulation intensity; st, SALB stromata density) with the different relative weight for at = 1, sp = 3, st = 2 and comparison with a phenotypic selection. The asterisk identify the 10 best *Hevea* clones (expected or observed index).

Trial 2

Issue	Exp.	Ob.	Issue	Exp.	Ob.	Issue	Exp.	Ob.	Issue	Exp.	Ob.	Issue	Exp.	Ob.	Issue	Exp.	Ob.	Issue	Exp.	Ob.
4	-0.95	-3.78	20	0.07	0.93	36	0.20	-0.01	52	0.55	2.56	68	-1.04	-4.61	84	0.83	3.23	100	1.02	4.43
5	0.19	-0.32	21	0.43	0.93	37	0.42	1.53	53	0.90	4.13	69	0.17	0.68	85	-1.11	-4.53	101	-0.76	-3.45
6	-0.33	-0.57	22	-1.64	-5.90	38	0.12	0.63	54	-0.26	0.30	**70**	**2.42***	**9.65***	86	-1.22	-6.12	102	-1.55	-3.50
7	0.07	-1.93	23	-1.34	-5.69	**39**	**1.33***	**5.11***	**55**	**2.03***	**9.21***	71	-0.24	-0.00	87	-2.13	-7.83	103	-1.50	-5.21
8	-0.63	-2.98	24	-1.16	-6.83	40	0.88	3.65	56	-0.74	-2.63	**72**	**1.41***	**5.86***	88	-1.48	-2.93	104	0.72	2.16
9	-0.65	-4.56	25	0.46	2.68	**41**	**1.75***	**5.51***	57	-1.13	-4.34	**73**	**2.85***	**12.5***	89	-1.06	-4.41	105	-0.08	-2.51
10	0.99	3.9	26	-0.23	-1.69	42	0.70	2.72	58	-1.49	-6.20	**74**	**1.35***	**5.29***	90	0.72	2.08	106	0.96	4.13
11	-0.05	-0.12	27	-1.23	-4.83	43	-0.06	-1.23	59	-1.11	-2.58	75		-3.12	91	-0.52	-2.68	107	-0.38	-2.65
12	0.39	2.32	28	0.92	4.27	**44**	**2.55***	**9.27***	60	0.56	2.23	76	0.31	1.71	92		-9.04	108	0.00	3.07
13	0.31	0.71	29	0.23	0.99	45		1.98	61	0.83	2.80	77	1.03	4.68	93	-0.59	-2.90	109	-0.11	1.35
14	-1.33	-6.00	30	-0.79	-2.20	**46**	**1.57***	**6.92***	62	-1.23	-5.06	78	-0.30	-1.56	94	0.56	1.91	110		**6.27***
15	0.62	1.56	31	0.49	3.23	**47**	**1.47***	4.23	63	-0.47	-1.13	79	-0.12	-1.56	95	0.14	0.82	111	-0.17	-3.26
16	0.99	3.84	32	0.26	1.26	48	0.06	0.18	64	0.70	4.41	80		-1.71	96	0.78	3.71	112	-1.87	-8.07
17	0.27	0.52	33	1.28	2.15	49	-0.41	1.10	65	-1.99	-7.57	81	0.15	0.71	97	0.97	4.15	113	0.17	2.45
18	-1.07	-4.90	34	1.02	5.59	50	1.57	6.43	66	-1.33	-5.44	82	0.48	2.66	98		3.32			
19	-1.33	-5.07	35	-0.85	-3.66	51	0.37	0.38	67	0.21	1.07	83	0.56	2.23	99	-1.64	-7.48			

Trial 3

Issue	Exp.	Ob.	Issue	Exp.	Ob.	Issue	Exp.	Ob.	Issue	Exp.	Ob.	Issue	Exp.	Ob.	Issue	Exp.	Ob.	Issue	Exp.	Ob.
4	0.79	0.58	17	1.02	3.46	30	-0.89	-3.56	43	0.65	1.42	56	-1.59	-4.66	69	-1.33	-4.71	82	1.07	3.36
5	0.00	-0.60	**18**	**1.79***	**5.73***	31	0.50	2.21	44	-0.69	-2.82	**57**	**1.20***	**3.64***	70	-1.62	-4.41	**83**	**1.22***	**3.71***
6	**1.24***	**4.00***	19	1.14	3.26	32	-1.09	-3.81	45	-0.68	-2.96	58	0.45	0.88	71	-0.54	-2.27	84	-0.12	-0.12
7	1.03	2.88	20	-2.11	-6.37	33	0.59	2.00	46	-0.84	-4.21	59	0.73	1.71	72	-0.51	-2.50	85	-0.21	0.07
8	0.57	0.23	21	-2.01	-6.41	34	-0.76	-1.67	47	-1.02	-3.79	60	0.68	1.19	73	-0.67	-2.18	86	0.23	0.93
9	-0.61	-2.08	**22**	**1.62***	**5.06***	35	1.06	1.51	48	-0.20	-0.03	61	0.91	2.65	74	-1.05	-4.32	87	0.23	0.51
10	0.86	1.95	23	-1.99	-5.85	**36**	**1.46***	**5.28***	49	-0.93	-1.74	62	0.47	2.39	75	0.69	2.58	88	-0.49	-1.55
11	-1.32	-4.35	24	-1.80	-5.78	37	-1.34	-3.27	50	-0.40	-1.45	63	0.91	2.39	76	-1.61	-5.41	89	-0.15	-0.42
12	0.98	3.29	25	-0.05	-0.55	**38**	**1.19***	**3.82***	51	1.04	3.12	64	0.08	2.29	77	-0.58	-0.81	**90**	**1.30***	**3.79***
13	0.98	3.07	26	0.03	0.23	39	-1.42	-3.81	52	-0.10	0.34	65	-1.48	-4.83	78	0.39	0.91	91	0.49	2.31
14	**1.94***	**5.95***	27		**5.33***	40	0.48	1.48	53	0.42	0.91	66	-1.31	-3.55	79	-0.56	-1.70			
15	1.07	3.18	28	0.70	2.51	41	-0.44	-1.91	**54**	**1.47***	3.20	67	0.24	0.17	80	0.69	1.72			
16	-0.40	-0.92	29	0.75	2.18	42	-1.11	0.07	55	-1.30	-3.53	68	-0.11	-0.46	81	0.14	-0.12			

character whose phenotypic value can be estimated as soon as 7 days after the beginning of the infection. It can be distinguished into six symptom classes, reproducible in controlled conditions and characteristics of the host parasite interaction. Finally, it is, for the moment, our only criterion of reference to distinguish between a partial resistance (partial sporulation), and a total resistance (absence of sporulation).

For a better appreciation of this criterion to this step of the selection, observing samples of leaves using a binocular is recommended. Otherwise, the intensity of sporulation, a parameter which was originally evaluated in controlled inoculation conditions, could be made the object of an assessment in a later phase of the selection using inoculation tests with polyvirulent isolates of *Microcyclus ulei*.

In addition to this methodological work, this breeding program was oriented toward varietal creation. Of the 198 clones evaluated for their SALB resistance, 20 have been retained using an index calculated on the genetic value. Because of the strong heritability of the traits, a selection based on phenotypic index would retain the same clones as a selection based on a genetic index.

In this step of the selection, the appreciation of the selection clones' value must continue, firstly, by assessing the resistance of these clones in the multi-local trials and by artificial inoculations with polyvirulent isolates of *Microcyclus ulei*, and secondly by assessing their potential for latex production.

Nevertheless, we think that these three traits will not be sufficient to warrant the durability of SALB resistance, even if the clones used as progenitors in crosses programs were observed a long time in multi-locale trials. Therefore, since 1992, a research program on molecular markers of resistance was initiated. One progeny was studied and gave the first physical markers of resistance (Lespinasse et al., 2000). Today, more sources of resistance are investigated for the adjustment of a marker assisted selection (MAS).

RESUMO

Estimação de parâmetros genéticos de três caracteres usados para avaliar mal-das-folhas em seringueira

A severidade de ataque, a intensidade de esporulação e a densidade dos estromas são três sintómas da Mal-das-folhas da seringueira [*Hevea brasiliensis* (Willd. ex. Adr. de Juss.) Müell.-Arg.] causados pelo *Microcyclus ulei* P. Henn. Arx., avaliados no campo sobre árvores de um até três anos. Esse estudo genético dentro das condições epidemiológicas da plantação E. Michelin, Itiquira, Estado do Mato Grosso - Brasil, usa os dados de dois campos de experimentação constituidos de 198 clones provenientes de 22 famílias. Os resultados mostram que o ensaio de clone em pequena escala é um dispositivo mais adaptado que o campo de avaliação de seedlings para ter uma melhor avaliação do valor dos indivíduos. Além disso, esse trabalho mostra altas correlações entre os três sintomas e fornece valores genéticos calculados. O interesse para uma avalição dos três sintomas é discutido. Por fim, uma seleção com índices calculados mostra que a seleção sobre os valores genético retém os mesmos clones que a seleção sobre o fenotipo.

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