Floresta & Ambiente

Genetic evaluation of *Hevea brasiliensis* [(Willd ex Adr. de Juss.) Müell. Arg.] for juvenile vigour using the Reml/Blup method

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Recebido em 23 de maio de 2005

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Abstract

This paper intended to estimate genetic values and parameters for plant height, diameter at the base of the plant and leaf-storey number of rubber tree [*Hevea brasiliensis* (Willd ex Adr. de Juss.) Müell. Arg.] half-sib progenies using the mixed-model methodology (Reml/Blup procedure). The rubber tree progenies were obtained from a second generation population produced from the recombination of 30 original parents, pertaining to the Instituto Agronômico de Campinas (IAC) in São Paulo state. At the age of eight months the variables were evaluated. Results demonstrated the existence of significant genetic variability among the progenies for the studied traits. The estimates of the heritability coefficient showed moderate values for both height and leaf-storey number, and low values for plant diameter at the base of the plant. There are good possibilities of genetic gain for these main traits in the context of the improvement program that was started in Mato Grosso do Sul state.

Key words: Rubber Tree, Reml/Blup method, genetic parameters.

Introduction

The rubber tree [*Hevea brasiliensis* (Willd ex Adr. de Juss.) Muell.-Arg.], a crop of major economic importance, has been subjected to genetic improvement programs aiming the increase of latex production, especially in south-eastern states "escape areas" of the South America-leaf-blight (SALB) caused by fungus *Microcyclus ulei* (P. Henn.) von Arx.

Many projects of genetic evaluation of the species aiming at the maximization of the genetic gain with selection are being carried out in Malaysia (Tan, 1995), Sri Lanka (Jayasekera, 1983), Indonesia (Daslin et al., 1986), Nigeria (Onokpise et al., 1986), India (Meenattor et al., 1991) and Brasil (Gonçalves et al., 1998 a, b, c, and Costa et al., 2000 a, b, c). Details about the genetic improvement programs in Brazil, Malaysia and south-east Asia are described by Tan et al. (1975), Simmonds (1989) and Gonçalves et al. (1995).

The accurate prediction of individual genetic values of the candidates to selection is an essential part of forest genetic improvement programs (Resende, 2002a). In this sense, the individual linear mixed model methodology (Reml/Blup) for unbalanced data, developed for the improvement of perennial plants by Resende & Fernandes (1999) and Resende (2000) has led to maximization of genetic gain with selection.

In the specific case of rubber tree progenies, which have been implanted recently in the field in an settlement area in the state of Mato Grosso do Sul, there is an expressive interest by the local community concerning the cultivation of the species. Although the State is located in an area considered as an "escape area", rubber plantations are not traditionally common in this region. Therefore, it is important to evaluate all the phases of the plant development, including the growth in nursery, which will help further comparison of the genetic material established in the field.

The present study intended to estimate genetic values and parameters for plant height, diameter do at the base of the plant and leaf-storey number of the progenies using the mixed-model methodology (Reml/Blup). These estimates provide useful information for the development of the first improvement program of the species in Mato Grosso do Sul state.

Materials and Methods

The rubber tree open pollinated progenies (assumed as half-sib) were obtained from a second generation population produced from the recombination of 30 original parents. The recombined population was established at the Votuporanga Experimental Station, SP, pertaining to the Agronomic Institute of Campinas (IAC) in the state of São Paulo, Brazil.

The seedlings were distributed into polyetilene bags at Plant Matt nursery in the Ponta Porã city, state of Mato Grosso do Sul, Brazil, under a randomised complete block design, with four replications and 10 plants per plot. Ponta Porã city is located at latitude 22^{0}32'S, longitude 55^{0}54'W and altitude 460 m above sea level. The spacing was 40 cm x 40 cm. At the age of eight months, total height (using measuring tape, data obtained in cm), diameter at the height of the base of the plants (data obtained in mm) and leaf-storey number of the progenies were recorded.

As the data were unbalanced, the traits were analysed using the linear mixed model methodology (univariated additive model) – Reml/Blup, following the procedure proposed by Resende (2002b). The linear model was:

y = Xb + Za + Wc + e, where:

y, b, a, c e e: data vector, block effects (assumed as fixed or random, providing the same results), additive genetic effects (random), plot effects (random) and random error effects, respectively.

X, Z e W: incidence matrices for b, a and c, respectively.

The estimates of the genetic parameters were obtained trough the Reml (restricted maximum likelihood) procedure through iterates in the mixed-model equations. The Reml estimates and the Blup prediction of the additive genetic values of the individuals were obtained using the computer software Selegen-Reml/Blup (Resende, 2002b).

The coefficient of genetic (CV$_g$%) and experimental (CV$_e$%) variation were estimated using the following formulas presented by Vencovsky and Barriga (1992).

where:

$$CV_g(\%) \quad \frac{\sqrt{{}^{2}_{p}}}{\bar{X}}\ 100$$

$$CV_e(\%) \quad \frac{\sqrt{\frac{{}^{2}_{c}}{n} \quad {}^{2}_{d}}}{\bar{X}}\ 100$$

σ_p^2 = genetic variance among progenies;

σ_c^2 = environmental variance among plot

σ_d^2 = phenotypic variance among plants within plots

Results and Discussion

Table 1 shows the analysis of variance for height, diameter and leaf-storey number. Significant among-family differences were detected at 0.01 level of significance by the F test. This variability was an essential condition for establishing a genetic breeding program and it could be effectively exploited to increase height and diameter associated with rubber production future.

For all traits studied the coefficients of environmental variation among plots showed low magnitudes, revealing environmental homogeneity within blocks and good experimental precision. The experimental coefficient of variation varied from 15.10% to 19.04%

for the three traits. These values are regarded as intermediate according to Garcia (1989).

The coefficient of genetic variation, which expresses the amount of genetic variation existent as percentage of the general mean, showed moderate values (11.51; 5.46 and 12.19) for height, diameter and leaf-storey number, respectively. These results reveal that the population is suitable for breeding programs. In other words, genetic gain from selection is expected in the population after the application of adequate selection procedures.

Table 1. Mean squares from ANOVA, of the experimental coefficient of variation ($CV_e\%$) and genetic coefficient of variation ($CV_g\%$) for height, diameter and leaf-storey number in 30 eight months open pollinated progenies of Hevea, in Ponta Porã City, Mato Grosso do Sul state.

Source of variation[1]	Mean squares		
	Height	Diameter	Leaf-storey number
Replicates	25.28	1.09	0.44
Progenies	200.65**	1.55**	1.33**
Residual	61.04	0.89	0.79
General Mean	**51.73**	**5.38**	**4.69**
CV_e (%)	15.10	17.52	19.04
CV_g (%)	11.52	5.46	12.19

[1] The degrees of freedom for replicates, progenies and residual were 3, 29 and 87, respectively. **p< 0,01.

Genetic parameters estimates for height, diameter and leaf-storey number of the progenies are shown in Table 2. A moderate genetic variability for height and leaf-storey number can be observed. On the other hand, a reduced variability for diameter can also be verified, which can be attributed to the initial phase of growth. These can be inferred from the additive genetic variation estimates (36.8258; 0.0891 and 0.3379), as well as from the narrow sense heritability on a plant basis (0.2190; 0.0243 and 0.1752) for the three traits, respectively (Table 2). These values, except the second one, are in accordance with the mean values of individual heritabilities for forest tree species (including Hevea) reported by Cornelius (1994).

Table 2. Estimates of the narrow sense heritability coefficients within blocks on a plant basis ($\hat{h}_i^2$), and progeny means basis ($\hat{h}_{mp}^2$), additive genetic variance ($\hat{\sigma}_a^2$), environmental variance among plots ($\hat{\sigma}_{plot}^2$), residual variance within plots (environmental + non additive, ($\hat{\sigma}_e^2$), individual phenotypic variance ($\hat{\sigma}_p^2$), for traits height, diameter and leaf storey number in rubber tree progenies, in Ponta Porã City, Mato Grosso do Sul state.

Heritability/variances	Height (cm)	Diameter (mm)	Leaf-storey number
($\hat{h}_a^2$)	0.22	0.02	0.18
($\hat{h}_{mp}^2$)	0.51	0.19	0.52
($\hat{}_a^2$)	36.83	0.09	0.34
($\hat{}_{plot}^2$)	21.13	0.02	0.15
($\hat{}_e^2$)	110.17	3.56	1.44
($\hat{}_p^2$)	168.12	3.67	1.93

It should be emphasised the high magnitudes of the heritability of progeny means for height and leaf-storey number, suggesting high genetic progress in response to selection using progeny information. These results corroborate those of Moreti et al. (1994), Boock et al. (1995) and Costa et al. (2000a, 2000b). Although the population has a narrow genetic basis, it is in the initial phase of development and the values obtained for the parameters might become more expressive at later ages. This might happen especially with diameter, whose parameters mentioned in the literature show greater values than the ones obtained in this paper. Continuous evaluations in different ages will be essential in planning the improvement strategy.

Phenotypic and genetic values for the 20 best progenies and genetic gain predicted for the five best progenies based on their genetic values are shown in Table 3.

Table 3. Phenotypic and additive genetic values of the 20 best progenies evaluated and predicted genetic gains with selection of the five best progenies for plant height (cm), diameter (mm) and leaf-storey number of the rubber tree progenies in Ponta Porã city, Mato Grosso do Sul state.

Progenies	Phenotypic values			Genetic values (μ + a)			Genetic gain (%)		
	height	diameter	leaf-storey	height	diameter	leaf-storey	height	diameter	leaf-storey
1	85.50	9.50	8.01	59.20	5.64	5.45	6.50	0.16	0.68
2	82.00	9.43	7.91	58.96	5.63	5.33	6.38	0.16	0.62
3	81.50	9.00	7.34	58.68	5.62	5.32	6.25	0.16	0.60
4	81.00	8.42	6.90	58.67	5.61	5.30	6.18	0.16	0.59
5	80.00	8.12	6.71	58.61	5.60	5.29	6.12	0.16	0.58
6	78.50	8.01	6.27	58.48	5.59	5.27			
7	78.08	8.00	5.53	58.36	5.50	5.26			
8	77.50	7.89	5.12	58.35	5.49	5.25			
9	77.00	7.32	4.98	58.34	5.48	5.23			
10	76.50	7.21	4.83	58.27	5.47	5.20			
11	76.03	7.13	4.57	58.12	5.46	5.00			
12	76.00	6.93	4.31	58.07	5.45	4.90			
13	75.70	5.82	4.16	57.92	5.43	4.86			
14	75.50	5.54	3.98	57.91	5.41	4.81			
15	75.00	5.34	3.90	57.90	5.40	4.78			
16	74.80	4.77	3.83	57.86	5.39	4.75			
17	74.55	4.72	3.52	57.84	5.37	4.71			
18	74.20	4.01	3.35	57.72	5.36	4.69			
19	74.01	3.93	3.32	57.66	5.35	4.62			
20	73.14	3.86	3.21	57.65	5.32	4.60			

It can be observed that the progenies whose seeds were collected from progenies 1 (85.50), 2 (82.00), 3 (81.50), 4 (81.00) e 5 (80.00) showed additive genetic and phenotypic values higher than the remaining progenies evaluated. Taking as an example plant height, the predicted genetic values are expressive if compared to the average obtained in the population (52.69). This maximises the genetic gains with selection, as showed in the referred Table 3 (genetic gain with selection of the five best progenies: 6.50; 6.38; 6.25; 6.18 and 6.12). The referred values follow the same tendency of superiority in relation to the averages of the other two traits.

Tables 4 and 5 show the predicted genetic values for height and diameter, which were obtained through selection with overlapping generations for the 20 best progenies and respective seedlings within progenies.

It is important to state that there are three strategies that can be adopted for seedling seed orchards, using the liner mixed model methodology or Reml/Blup: a) tested seed orchard (1,5 generation), with parent selection; b) seedling seed orchards, with selection of the individuals in the experiment (second generation seedling seed orchards); c) Orchard with overlapping generations, which is a recent modality. This orchard is made of a mixture of individuals selected in the experiment with some superior parents.

In this case, only a single ranking by predicted genetic values is made and the superior materials are included in the seed orchard, regardless if they belong to the current generation or to the previous one (Resende, 2002a).

It can be observed for height among the 20 best selected individuals to be included in the seed orchard with overlapping generations, one of them, the sixth individual in the top-ranking for that trait (identified by 'zero' on the 'tree' column), stands for seed parent 3. This shows that, in general, individuals of the current generation tended to be better than those belonging to the previous one, as expected. Nevertheless, the seed parent 3 is still superior to many individuals of the current generation and should be maintained in the improvement population.

On the other hand, for plant diameter, among the 20 best individuals selected to compose the seed orchard with overlapping generations, four of them (identified by 'zero' on the 'tree' column) stand for parents, and the best overall individual is a parent of the previous generation.

Table 4. Genetic values predicted for plant height, obtained by selection with overlapping generations, for the 20 best individuals of rubber tree progenies, in Ponta Porã city, Mato Grosso do Sul state.

Progenies	Seedling	Predicted additive genetic effect (a)	Genetic gain	New average
3	3	6.50	6.50	59.20
15	4	6.26	6.38	59.08
13	1	5.98	6.25	58.95
13	3	5.97	6.18	58.88
6	3	5.91	6.12	58.82
3	0	5.84	6.08	58.78
13	4	5.78	6.03	58.73
7	3	5.66	5.99	58.69
15	2	5.65	5.95	58.65
8	2	5.64	5.92	58.62
2	3	5.57	5.89	58.59
3	4	5.42	5.85	58.55
21	4	5.37	5.81	58.51
3	5	5.22	5.77	58.47
3	3	5.22	5.73	58.43
3	5	5.22	5.70	58.40
13	3	5.16	5.67	58.37
15	3	5.14	5.64	58.34
11	5	5.02	5.61	58.31
7	5	4.96	5.57	58.27

Table 5. Genetic values predicted for plant diameter (mm), obtained by the selection with overlapping generation, for the 20 best individuals of rubber tree, in of Ponta Porã city, Mato Grosso do Sul state.

Progenies	Seedling	Predicted additive genetic effect (a)	Genetic gain	New average
21	0	0.20	0.20	5.68
21	2	0.16	0.18	5.66
21	4	0.16	0.17	5.65
2	0	0.16	0.17	5.65
21	3	0.15	0.17	5.65
3	0	0.15	0.16	5.64
21	1	0.15	0.16	5.64
21	3	0.15	0.16	5.64
2	3	0.15	0.16	5.64
2	2	0.14	0.16	5.64
21	1	0.14	0.16	5.64
21	4	0.14	0.16	5.64
21	5	0.14	0.15	5.63
4	1	0.14	0.15	5.63
3	3	0.14	0.15	5.63
4	0	0.14	0.15	5.63
2	4	0.14	0.15	5.63
21	5	0.13	0.15	5.63
3	5	0.13	0.15	5.63
2	5	0.13	0.15	5.63

Conclusions

The are significant genetic variability among and within the progenies. This is an essential condition for establishing a genetic improvement program and it could be effectively exploited to increase height and diameter associated with future rubber production.

The moderate values of the coefficient of genetic variation suggest adequate genetic gain from selection in the population after the application of a precise selection procedure.

The predicted genetics values for height and diameter obtained through selection with overlapping generation and individual within progenies is an important strategy that can be adopted for seedlings in seed orchards, using the Reml/Blup methodology.

Acknowlegments

The authors are grateful to the CNPq and UCDB by financial support for Flávio Luiz Hilário Rego, Adriana Zanirato Contini and Raul Alffonso Rodrigues Roa.

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