



Comparison between different selection methods of rubber trees



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ABSTRACT

The purpose of this study was to compare estimates of genetic gain using three different selection methods (between and within, combined selection and Multi-Effect Index) for the cultivation of rubber trees (*Hevea brasiliensis*), analyzing the variability rubber yield and the annual girth growth, evaluated at three locations. The population consisted of 22 open pollinate progenies from different regions of rubber cultivation in the State of São Paulo (Jaú, Pindorama and Votuporanga). The experiment was arranged in a randomized block design with 6 replications, 10 plants per plot and spacing of 2 m × 2 m. The individual narrow-sense heritability (\hat{h}_r^2) and heritability of progeny means (\hat{h}_{mp}^2) were mean and high, respectively, for all variables at the three sites, indicating little environmental influence on the variables. The within and between selection method proved more promising in Jaú, while at the other locations, gains were higher by the Multi-Effect Index, with genetic gain of over 100%. The combined selection obtained medium gains, in some cases very close to those of the Multi-Effect Index. The multi-effect selection index can increase the genetic gains, maximizing selection and enabling a reduction in the breeding cycle of the species.

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1. Introduction

One of the difficulties with studies of perennial species are the long breeding cycles, requiring a search for alternatives that make breeding programs of these species more dynamic and precise. The rubber tree [*Hevea brasiliensis* (Willd. ex A.Dr. Than Juss.) Muell. Arg.] is an example, since a cycle (until the final recommendation of a new cultivar) lasts more than 25 years.

Knowing the genetic characteristics of the study populations is essential to make selection more effective. Qualitative data are useful to estimate the genetic variation, and based on heritability data and genetic correlations between economically important variables, the genetic gains can be estimated after successive selection cycles. Quantitative data determine the selection strategies best-suited to overcome difficulties in the selection of superior genotypes and broaden the knowledge on the genetic structure of rubber (Silva et al., 2012).

The selection of characters in the juvenile stage can be an efficient method of maximizing the genetic gain, while minimizing the breeding cycle (Adams et al., 2007). The genetic gains can be predicted by several selection methods. These methods differ from each other in the way the selection is carried out, whether

the selection is at the plant, the progeny and/or at the population level, and can result in different estimates of genetic gain.

The direct selection between and within progenies is an alternative to estimate the genetic gains since both the best progenies as well as the best plants within progenies are selected. For David et al. (2003) combined selection creates an index value for each tree based on individual and progenies performance weighted according to individual and progenies heritabilities, respectively. The selection by the Multi-Effect Index is based on the multiplication of the phenotypic values at the level of plants, plot means, progeny means, block means and overall mean, by the weighting coefficients of the (heritability) indices (Resende and Higa, 1994).

In view of the different possible selection methods, this study aims to compare the estimates of genetic gains of vigor and yield of three of them (between and within, combined selection and Multi-Effect Index) for rubber trees, evaluated at three locations, to contribute to a basis for future breeding programs of the species.

2. Material and methods

2.1. Material

The population consisted of 22 open pollinate progenies derived from phenotypically selected parental clones in a population of *H. brasiliensis* from Asia, and grown on experimental fields in three regional centers of the São Paulo Agency of Agribusiness (APTA),

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Table 1
Descriptive variables of the experimental sites of progeny testing in Brazil.

Descriptive variables	Locations		
	Jaú	Pindorama	Votuporanga
Spacing (m)	2 × 2	2 × 2	2 × 2
Planting density	1 row × 10 plants 10 plants/plot	1 row × 10 plants 10 plants/plot	1 row × 10 plants 10 plants/plot
Experimental design	RBD ^a	RBD ^a	RBD ^a
Number of replications	6	6	6
Altitude (m)	580	560	450
Latitude (S)	22° 17'	21° 13'	20° 25'
Longitude (EE)	48° 34'	48° 56'	49° 59'
Temperature (annual mean)	21.6°	21°	22.3°
Annual rainfall (mm) (annual mean)	1.344	1.390	1.480
Soil type	Ferralsol	Acrisol	Lixisol
Terrain	Flat	Flat	Flat

^a Randomized block design.

which represented different regions of rubber cultivation in the State (Jaú, Pindorama and Votuporanga) (Table 1).

The experiment was established in a randomized block design with 6 replications, 10 plants per plot and spacing of 2 m × 2 m.

2.2. Methods

The traits measured in the progeny tests at all sites were:

- (a) *Dry rubber yield*: obtained by the Hamaker Morris-Mann test (HMM) modified for three-year-old seedlings, based on the average dry rubber yield of 30 tappings per plant. The tapping panel was opened 15 cm above the ground, using a ½S d/3, with a total of 35 tappings, discarding the first five tapping samples that corresponded to the adaptation of the panel. The indication ½S stands for a half-spiral cut and d/3 indicates the interval between tappings, in this case, one tapping every three days.
- (b) *The stem girth*: determined at 50 cm from the ground with a measuring tape (in cm).

2.2.1. Estimates of genetic and phenotypic parameters

Estimates of genetic and phenotypic parameters were computed with the genetic-statistical software Selegen – Reml/Blup,

developed by Resende (2007) for the improvement of perennial plant species, applied to the open pollination progeny tests, in a randomized block design with several plants per plot at several locations and a single population. Expressed in matrix terms, the statistical model is given by: $y = Xb + Za + Wc + e$, where b is the vector of fixed block effects, a is the vector of random effects of genotypic matrices, c is the vector of random effects of common environments of plots, where e is the vector of random errors. Genetic parameters were estimated the following formulas: $\hat{h}_r^2 = \hat{\sigma}_2 / (\hat{\sigma}_\alpha^2 + \hat{\sigma}_p^2 + \hat{\sigma}_e^2)$ (individual narrow-sense heritability); $\hat{c}_p^2 = \hat{\sigma}_r^2 / (\hat{\sigma}_\alpha^2 + \hat{\sigma}_p^2 + \hat{\sigma}_e^2)$ (correlation due to the common environment of the plot); $\hat{h}_{mp}^2 = 0.25\hat{\sigma}_\alpha^2 / [(0.25\hat{\sigma}_\alpha^2) + (\hat{\sigma}_p^2/b) + (\hat{\sigma}_e^2/(nb))]$ (mean progeny heritability); $\hat{\sigma}_f^2 = \hat{\sigma}_a^2 + \hat{\sigma}_p^2 + \hat{\sigma}_e^2$ (individual phenotypic variance); $CV_g(\%) = \left(\sqrt{\hat{\sigma}_\alpha^2 / (x)} \right) \times 100$ (individual genetic variation coefficient); $CV_e(\%) = \left[\left(\sqrt{c^2 + \hat{\sigma}_{plot}/n} \right) / \bar{x} \right] \times 100$ (coefficient of environmental variation within the plot), $GG(\%) = (GG/\bar{x}) \times 100$ (Genetic gain in percentage).

2.2.2. Estimates of genetic gains

2.2.2.1. *Between and within, direct and indirect selection*. The estimated gains between and within, direct and indirect selection

Table 2
Estimates of the genetic parameters for the variables annual girth growth (cm) (GiGr), rubber yield (g/pl) (RY) based on analysis at the plant level of 22 rubber progenies tested at three locations in Brazil.

Locations	Variable	Estimates											
			\hat{h}_r^2	\hat{h}_{mp}^2	\hat{h}_{ad}^2	\hat{r}_{aa}	c_p^2	$\hat{\sigma}_a^2$	$\hat{\sigma}_{parc}^2$	$\hat{\sigma}_f^2$	$\hat{\sigma}_e^2$	CVg (%)	CVr
Jaú	GiGr	I	0.73 ± 0.15	0.82	0.86	0.91	0.17	1.12	0.27	1.53	0.14	12.12	0.88
		II	0.13 ± 0.06	0.55	0.11	0.74	0.07	0.32	0.17	2.39	1.89	10.35	0.45
		III	0.31 ± 0.09	0.77	0.27	0.88	0.05	5.49	0.93	17.58	11.15	10.50	0.75
	RY	I	0.01 ± 0.03	0.08	0.01	0.28	0.08	0.01	0.01	0.13	0.12	3.42	0.12
		II	0.09 ± 0.08	0.51	0.07	0.71	0.03	0.04	0.02	0.47	0.41	10.33	0.41
		III	0.12 ± 0.08	0.58	0.09	0.76	0.04	0.12	0.04	0.99	0.84	13.55	0.48
Pindorama	GiGr	I	0.59 ± 0.12	0.84	0.59	0.91	0.10	0.57	0.09	0.95	0.29	8.91	0.92
		II	0.14 ± 0.06	0.47	0.13	0.68	0.16	0.61	0.69	4.33	3.04	11.21	0.38
		III	0.39 ± 0.10	0.84	0.33	0.92	0.02	11.38	0.73	29.39	17.29	12.16	0.93
	RY	I	0.59 ± 0.14	0.88	0.54	0.94	0.03	0.21	0.01	0.36	0.13	33.29	1.13
		II	0.64 ± 0.14	0.89	0.59	0.94	0.03	0.31	0.01	0.49	0.16	32.78	1.19
		III	0.40 ± 0.11	0.83	0.35	0.91	0.03	0.32	0.03	0.80	0.45	23.11	0.91
Votuporanga	GiGr	I	0.67 ± 0.14	0.84	0.70	0.92	0.11	0.81	0.14	1.22	0.26	11.24	0.95
		II	0.27 ± 0.09	0.76	0.23	0.87	0.04	0.95	0.14	3.54	2.44	9.16	0.72
		III	0.58 ± 0.13	0.91	0.51	0.95	0.06	13.88	0.14	23.83	9.81	11.00	1.27
	RY	I	0.33 ± 0.11	0.84	0.27	0.92	0.01	0.05	0.01	0.14	0.09	25.87	0.93
		II	0.29 ± 0.10	0.82	0.23	0.90	0.01	0.07	0.01	0.26	0.18	23.60	0.87
		III	0.19 ± 0.08	0.75	0.15	0.87	0.01	0.13	0.01	0.66	0.53	19.91	0.71

\hat{h}_r^2 is the individual narrow-sense heritability; \hat{h}_{mp}^2 is the mean heritability of the progeny; \hat{h}_{ad}^2 is the additive heritability within a plot; \hat{r}_{aa} is the accuracy; c_p^2 is the coefficient of determination of the plot effects; $\hat{\sigma}_a^2$ is an additive genetic variance; $\hat{\sigma}_{parc}^2$ is an environmental variance between plots; $\hat{\sigma}_f^2$ is an individual phenotypic variance; $\hat{\sigma}_e^2$ is the residual variance; $C\%$ is the genetic gain; $CVg\%$ is the coefficient of genetic variation and CVr is an index of relative variation = $CVg\%/CVe\%$.

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