



Simultaneous selection of rubber yield and girth growth in young rubber trees



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ABSTRACT

The importance of the rubber yield from the rubber tree (*Hevea brasiliensis*) is already well known. Recently, the importance of girth growth and consequently wood rubber tree has been emphasized. Genotypes with greater girth growth produce greater volume of wood. Rubber tree timber can be used as raw material for a vast range of products, substituting wood from natural forests. Rubber tree genotypes that combine high yield and vigorous growth are of great interest for genetic improvement. Thus, the objective of the present study is the simultaneous selection in young rubber tree progenies for dual-purpose rubber yield and girth growth. Twenty-two progenies were used which were assessed at the field in two locations in a randomized experimental block design with three replicates and 3 m × 3 m spacing. The classic selection index was used; this index is a tool that allows all the characters of interest to be used simultaneously. The progeny effect was significant for both variables and in both locations, indicating progeny genetic variability and the possibility of selection. The progeny mean heritability (\hat{h}_p^2) was greater than the heritability based on single individual's level (\hat{h}_i^2) and within plot heritability (\hat{h}_w^2). The multicollinearity among the variables was low, so the variables could be used simultaneously to construct the selection index. Four progenies were selected with an 18% selection intensity, but the progenies were different in the two locations. The classic selection index was efficient in simultaneous selection of rubber yield and girth growth in progeny of young rubber trees. Simultaneous selection for rubber yield and vigor is important at the initial stages of genetic breeding and should be done per location. This selection contributes to identifying superior progeny for rubber yield and with potential for double purpose: wood and rubber production.

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1. Introduction

The importance of assessing the rubber yield of *Hevea brasiliensis* (Willd. ex A.D. de Juss.) Muell. Arg. is well known. Recently, the importance of rubber tree timber has been also emphasized (Naji et al., 2012; Shigematsu et al., 2011). In south-west Asia the rubber tree is one of the major economic crops, valued not only for the production of rubber, but also for timber (Silpi et al., 2006). When rubber production declines after 25 to 30 years of commercial exploitation, rubber tree timber can be used as raw material for a vast range of products, substituting wood from natural forests (Killmann and Hong, 2000). A character associated with timber production is the vigor, represented by girth growth. More vigorous genotypes consequently produce a greater volume of wood.

This character is also associated with various aspects in the genetic improvement of yield. The early opening of the panel and a good production are only possible in trees that grow vigorously in the juvenile phase. Good stem growth, during the tapping period, will maintain constant production and at the same time will reduce breakage by the wind (Gonçalves and Fontes, 2012). Thus genotypes with high rubber yield and girth growth are of great interest for genetic breeding (Gonçalves et al., 2009, 2003). Usually, these variables have always been analyzed separately. The simultaneous selection considering these two characters can help to identify progenies with potential for production of rubber and wood.

The goal of genetic breeding in plants can be defined as the final economic trait on which genetic gain is desired and can be a single trait or a combination of traits. Thus, when the objective of selection involves more than one trait, three selection systems can be adopted to obtain genetic gains in all the traits of economic importance and interest to the breeder, namely: (i) tandem selection; (ii) independent elimination levels and (iii) selection index (Resende, 2002). According to Resende (2002), in the first system, selection is made for a determined trait until the desired level is reached and

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Table 1
Location of the rubber tree progeny tests carried out in the experimental stations of Jaú and Votuporanga, São Paulo State, Brazil.

Characteristic	Jaú	Votuporanga
Spacing (m)	3.0 × 3.0	3.0 × 3.0
Total area (ha)	0.28	0.28
Elevation above mean sea level (m)	580	482
Latitude (S)	22°17'	20°25'
Longitude (W)	48°34'	49°59'
Annual mean temperature (°C)	21.6	22.3
Annual mean rainfall (mm)	1,344	1,480

then for other traits of interest. In the second system, minimal levels are established for each trait and all the individuals below this level are eliminated. In the selection index system, all the traits of interest are considered simultaneously.

The selection index permits the generation of genotypic aggregate on which selection is made, functioning as an additional trait, resulting from the combination of determined traits chosen by the breeder, on which simultaneous selection is to be made (Cruz and Regazzi, 2001). The index is obtained as linear combinations of the means of several traits and it is efficient because it allows assessment of all the available information and can attribute different weights to the traits studied and prioritizes attributes judged of greater importance by the researcher (Falconer, 1981).

The selection index was first introduced in plant breeding by Smith (1936) and later in the improvement of animals by Hazel (1943). This index is currently known as classic index or Smith and Hazel index. According to Cruz and Regazzi (2001) many models of selection indexes are available in the literature such as the classic index, desired gains index, base index, sum of the posts or ranks, free weights and parameters index and the multiple index.

Recent studies with selection indexes have been carried out on several species such as the acai palm (Teixeira et al., 2012), eucalyptus (Paula et al., 2002) and caribbean cherry (Paiva et al., 2002).

The objective of the present study is the precocious selection of rubber tree progenies for dual-purpose rubber yield and girth growth.

2. Materials and methods

The material consisted of 22 open pollination progenies, obtained from parental clones selected phenotypically in a *Hevea brasiliensis* population of Asian clones introduced in Brazil. The tests were set up in Experimental Stations in Jaú and Votuporanga. Table 1 shows the characteristics of the locations where the experiments were set up. A randomized block design was used with three replicates and ten-plant linear plots, in 3 m × 3 m spacing.

To assess the annual girth growth, measurements were taken annually for three consecutive years to assess the plant vigor. The girth was measured 50 cm above the soil, using a graded tape measure, and the measurements were expressed in centimeters. The annual girth growth increase was calculated by subtracting the girth of one year from the girth of the previous year and the results were expressed in centimeters.

Rubber yield was obtained by the Hamaker Morris-Mann (HMMm) test, modified for three-year-old plants. The plant panels were opened at 15 cm above the soil, using the S/2 (half spirals cut) and d/3 (tapping interval, that is, one tapping every three days), discarding the first five tapping samples that corresponded to the panel running in phase. Three tests were carried out of 10 descending cuts on the individuals of each progeny, with intervals of one month rest between the tests. The results were expressed per test, in grams, of dry rubber per tapping per tree ($g\ t^{-1}\ t^{-1}$).

The genetic parameters were obtained by the Reml/Blup method (maximum restricted likelihood/best linear unbiased prediction).

The statistical models used were described by Resende (2007). In the individual analysis, the model used was applied to open pollination progenies, with a mixed reproductive system, 22% self-fertilization rate (Furlani et al., 2005). The statistical model used was: $Y = Xr + Za + Wc + \varepsilon$, where Y is the data vector; r is the replication effects vector, assumed as fixed, added to the general mean; a is the individual additive genetic effects vector, assumed as random; c is the plot effects vector, ε is the random residual vector. The uppercase letters represent the incident matrixes for the effect. The significance of the progeny effect was verified on the values of the maximum likelihood ratio (LTR) obtained in the analysis of deviance.

The following genetic parameters were estimated: heritability at individual level, with 22% self-pollination rate: $\hat{h}_i^2 = [4\hat{\sigma}_g^2/(1+s)^2]/(\hat{\sigma}_g^2 + \hat{\sigma}_c^2 + \hat{\sigma}_e^2)$; heritability for the progeny-mean, considering complete survival: $\hat{h}_x^2 = \hat{h}_i^2 = (\hat{\sigma}_g^2)/[\hat{\sigma}_g^2 + \hat{\sigma}_c^2/b + \hat{\sigma}_e^2/(nb)]$; within plot heritability: $\hat{h}_w^2 = \{1 - [(1+s)^2/4]\}[4/(1+s)^2]\hat{\sigma}_g^2/\hat{\sigma}_e^2$; Coefficient of determination of the plot effects: $\hat{c}_{plot}^2 = \hat{\sigma}_c^2/(\hat{\sigma}_g^2 + \hat{\sigma}_c^2 + \hat{\sigma}_e^2)$; Accuracy in progeny selection, considering complete survival: $\hat{A}c = (\hat{h}_x^2)^{0.5}$; Coefficient of genetic variation: $CV_g(\%) = 100(\hat{\sigma}_g^2)^{0.5}/\mu$; coefficient of experimental variation: $CV_e(\%) = \{[(0.75 \cdot \hat{\sigma}_g^2 + \hat{\sigma}_e^2)/n] + \hat{\sigma}_c^2\}^{0.5}/\mu \cdot 100$, coefficient of relative variation: $CV_r = CV_g/CV_e$; where $\hat{\sigma}_g^2$ is the genetic variance, $\hat{\sigma}_c^2$ is the environmental variance among plots, $\hat{\sigma}_e^2$ is the environmental variance, b is the block, n is the number of plants per plot, s is the selfing rate, μ is the mean.

The classic selection index model described by Cruz (2006) is presented below:

$$\begin{aligned}
 H &= a_1g_1 + a_1g_2 + \dots a_n g_n \\
 &= \sum_{i=1}^n a_i g_i = g'a \quad \text{and} \quad I = b_1y_1 + b_2y_2 + \dots b_n y_n \\
 &= \sum_{i=1}^n b_i y_i = y'b \quad \text{where :}
 \end{aligned}$$

n is the number of traits in the index; H is the genotypic aggregate or linear combination of the unknown genotypic values; I is the index selection to be estimated; g' is the vector ($1 \times n$) of unknown genotypic values of the n traits considered; y' is the vector ($1 \times n$) of means; a is the vector ($n \times 1$) of weight (or values) previously established by the breeder; b is the vector ($n \times 1$) of the coefficients of weighting of the index. P is the phenotypic variance matrix ($n \times n$) and co-variances; G is the genetic variance matrix ($n \times n$), obtained at progeny mean level. Thus vector b is estimated by: $Pb = Ga$.

The annual mean of girth growth and rubber yield was used to construct the classic selection index. In the classic index, the weight vectors were established with their own experimental data, as used by Teixeira et al. (2012) and Paula et al. (2002). The genetic standard deviation was established as the weight vector. A selection intensity of 18% was practiced. To make the study of the selection indexes feasible, the multicollinearity diagnosis of the traits was carried out by the software Genes (Cruz, 2006), prior to obtaining the indexes. All the other analyses were carried out using the Selegen-Reml/Blup program (Resende, 2007).

3. Results and discussion

An essential stage in selection is to estimate genetic parameters of traits. The genetic parameters for annual mean girth growth and rubber yield in Jaú and Votuporanga are shown in Table 2.

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