Annual growth increment and stability of rubber yield in the tapping phase in rubber tree clones: Implications for early selection

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ABSTRACT

The annual girth or diameter growth in the tapping phase is an important trait associated with rubber production, resistance to wind breakage and wood production. The main objective of the present study was to assess the temporal stability of rubber tree genotypes for both natural rubber production and annual girth growth in the post-tapping phase. The phenotypic and genetic correlations of these variables over the years of evaluation were estimated in a rubber tree breeding program. Thirty-two clones were assessed along with the control genotype RRIM 600 for two traits, annual production and girth growth, which were evaluated for five and six years, respectively. A randomized complete block design, with effectively split-plots in time, was used with three replicates, six trees per plot, spaced at 7 m × 3 m. We observed that negative genetic correlations of the accumulated annual girth growth with the accumulated rubber yield ($r_g = -0.58$, $P < 0.01$), and high stability of yield with AMMI statistics explaining 96% of interactions. The study concluded that early selection in the first year of rubber yield may reduce the evaluation time of clones in a rubber tree breeding program. There was a negative phenotypic correlation between annual girth growth and yield. The study allowed differentiation of the genotypes assessed for temporal stability and overall performance for yield during tapping. Genotype selected for stability of production it is not the same as those selected just for annual growth. The stability of annual girth growth correlates negatively with the stability of yield.

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1. Introduction

In Brazil, rubber tree [*Hevea brasiliensis* (Willd. ex Adr. de Juss.) Müell-Arg.] plantations are expanding to areas considered free from south American leaf blight disease wilt caused by the fungus *Microcyclus ulei* (P. Henn) V. Arx., including the southeast where the rubber tree shows great adaptability to varied ecological conditions (Gonçalves and Marques, 2008).

Year-to-year climatic variations, in addition to the diversity of sites where rubber tree is cropped, evaluations need to be conducted over several years to fully understand genotype × environment interaction, so that a comprehensive picture is obtained of the genotype by environment interactions. Here, environment is represented by "year" (G × Y) allowing for estimation of temporal stability of genotypes providing greater safety in recommending clones.

In rubber tree breeding programs desirable genotypes are such that in addition to high yield they should have both vigorous growth and yield stability during the tapping phase. According to Koo et al. (2007), the advantage of selecting superior genotypes by stability analysis is that stable genotypes are reliable across the environments, reducing the genotype-environment interaction.

To improve rubber plantation productivity, basic knowledge about the genetic traits of the plant populations of the species of interest is necessary for efficient selection and to conduct well-targeted crossings. Quantitative data analyses economically import traits that are useful to estimate genetic variances, type of genetic action involved, heritability and genetic correlations, so that the results obtained can be used to predict genetic gains after successive selection cycles. The quantitative information, besides widening the understanding of rubber tree genetics and its reproductive characteristics, also assists to determine the best selection strategy overcoming problems and difficulties in superior genotype selection. The main objectives of rubber tree breeding is to increase yield and vigor through methods that can shorten the breeding cycle of the crop, estimate the genetic parameters and correlates these traits (Gonçalves et al., 2006).

Silva et al. (2012), studying open-pollinated progenies, concluded that the annual trunk girth increment and virgin bark

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thickness are variables that are genetically correlated and a simultaneous selection for increase in the two variables. This study also concluded that progeny-mean hereditability for the rubber yield trait and annual trunk girth increment were superior to individual- and within-progeny heritabilities. This can be the basis of a strategy to increase the genetic gain in the rubber tree.

To make this recommendation as reliable as possible, a detailed study is needed on the temporal stability of the genotypes and with respect to their economically important traits (Cruz, 2006). Adaptability and stability analyses are, therefore, statistical procedures that allow identification of the cultivars with more stable performance that respond predictably to the environmental variations (Silva and Duarte, 2006).

The objective of the present study was to assess the temporal stability of rubber tree genotypes for natural rubber production, annual girth growth in the post-tapping phase, phenotypically and genotypically correlating these variables along the years of reviews in a breeding program for the species.

2. Materials and methods

Thirty-two rubber tree genotypes belonging to the Instituto Agronômico de Campinas (IAC) breeding program were assessed along with the control genotype (RRIM 600). That is the most planted clone in Brazil and around the world (Table 1) to responses of interest corresponded to five years' rubber yield and six years of annual girth growth. The experiment was conducted at the Jaú Experimental Station, Brazil (22°17′S latitude, 48°64′W longitude) located at an altitude of 580 m, in moderate A eutrophic, red–yellow clay soil, with sandy/medium texture. The predominant climate in the region is the Aw type (Koppen) with a defined dry season, 21.6 °C mean annual temperature, mean annual relative humidity of around 70%, with extremes of 77% in February and 59% in August. The annual mean rainfall is 1344 mm with 74% of the rainfall from October to March and 26% from April to September (INPE-CPTEC, 2013).

A randomized complete block design was used with three replicates and six trees per plot in a 7 m × 3 m spacing. The trees began to be tapped at 7 years of age. The system used to assess the first annual rubber yield was 1/2S d/4, 5d/7, 11 m/y, ET 2.5% Pa (8/y)—tapping in a half spiral (1/2S), performed at four-day intervals (d/4), for 11 months of the year (11 m/y), using Ethefon (ET) with 2.5% active ingredient applied on the regenerating recently tapped panel (pa) eight times a year (8/y) (Dijkman 1951). After tapping, latex was collected in plastic cups provided for each tree. This system is widely standardized and documented in the literature (Gouvêa et al., 2011; Gonçalves et al., 2011; Vijayakumar et al., 2000).

To assess girth growth in the tapping phase, annual measurements were taken of plant vigor expressed in girth growth. Six years' growth data were analyzed in the post-tapping period. The trunk girth (cm) was measured at 120 cm above the soil, using a piece of tape. Annual girth growth was calculated by subtracting from the circumference of one year. Individual-year analyses of variance were carried out to assess the genetic variability among the clones and the experimental accuracy, followed by joint analysis of variance across years.

Joint analysis of variance was carried out using the randomized complete block design with split-plot in time model, consisting of fixed effects for genotypes and environments; in this case environment was represented by year. The model fitted this analysis was: $Y_{ijk} = \mu + g_i + a_j + b_k + (ga)_{ij} + (gb)_{ik} + (ab)_{jk} + (gab)_{ijk} + e_{ijk}$ where: Y_{ijk}: is the observed value of the ith genotype in the fixed year in the kth replicate; μ is the average mean; g_i is a fixed effect of the ith genotype ($i = 1, 2,\ldots g$); a_j is a effects of the jth year ($j = 1, 2,\ldots,a$); b_k is a fixed effect of the kth block ($k = 1, 2,\ldots,b$); $(ga)_{ij}$ is the fixed interaction between ith genotype with the jth year; $(gb)_{ik}$ is the interaction between ith genotype with the kth block; $(gab)_{ijk}$ is the interaction between genotype, year and replicate, e_{ijk} is the experimental error.

The analyses of variance were carried out using the ANOVA procedure of the SAS program (SAS Institute, 2002).

Further analyses were carried out using the AMMI methodology. AMMI analysis is a combination of univariate methods (analysis of variance) with multivariate methods (main component analysis and single-value partitioning) (Zobel et al., 1988). The SAS manual (SAS Institute, 2002) was used as described in Duarte and Vencovsky (1999). The proposed model was: $Y_{ij} = \mu + g_i + e_j + \sum_{k=1}^{n} \lambda_k \gamma_{ik} \alpha_{jk} + \rho_{ij}$ where: Y_{ij} is the mean response of the ith genotype in jth environment; μ is the average mean; g_i is the fixed effect of the ith genotype ($i = 1, 2,\ldots,g$); e_j is the fixed effect of the jth environment j ($j = 1, 2,\ldots,a$); λ_k is the square root of the kth eigenvalue of the matrices (**GE**)(**GE**)' and (**GE**)'(**GE**) (of non-equal eigenvalues); γ_{ik} is the ith term (related to genotype i) of the kth eigenvector of the (**GE**)(**GE**)'; α_{jk} is the jth term (related to environment j) of the kth eigenvector of the (**GE**)'(**GE**); ρ_{ij} is the error term.

Complementing the principal components analysis AMMI also was used the analysis-the linear regression Eberhart and Russell (1966). The model used for this methodology was the following: $Y_{ij} = m_i + b_i l_j + d_{ij} + \bar{e}_{ij}$ where: Y_{ij} =is the observed mean of genotype i in environment j; m_i = general mean of genotype i; b_i = coefficient of regression of genotypic i; l_j = environmental index j; d_{ij} = deviation of the regression of i genotype in environment j; $\bar{e}_{ij}$ = mean error associated to the average general.

Table 1
Means of rubber yield (RY, g.tree^{-1} tapping) and annual girth growth (AGG, cm y^{-1}) of 33 genotypes in five years of assessment rubber production and six years for annual girth growth.

ID	Genotypes	RY	AGG	ID	Genotypes	RY	AGG	ID	Genotypes	RY	AGG
01	IAC 400	95.16[*]	4.30	12	Pind 060/87	39.15	3.14	23	Pind 512/88	42.02	4.38
02	IAC 401	79.22[*]	2.75	13	Pind 141/87	66.82	2.74	24	Pind 673/88	53.45	2.71
03	IAC 403	63.38	3.37	14	Pind 147/87	44.35	3.95	25	Vot 056/88	55.70	4.17
04	IAC 404	66.18	3.29	15	Pind 161/88	40.94	4.74[*]	26	Vot 061/88	62.83	4.07
05	IAC 417	69.64	3.54	16	Pind 218/88	26.61	4.53	27	Vot 171/88	50.54	3.53
06	IAC 424	42.50	3.38	17	Pind 237/87	28.06	4.09	28	Vot 211/88	50.30	2.73
07	IAN 873	56.36	3.28	18	Pind 267/88	50.84	2.94	29	Vot 237/88	53.71	3.86
08	PB 235	74.17	3.67	19	Pind 282/87	28.23	3.37	30	Vot 272/88	59.15	3.09
09	GU 198	79.94[*]	3.58	20	Pind 300/87	53.84	3.51	31	Vot 275/88	53.59	3.37
10	GU 176	45.75	3.13	21	Pind 302/88	58.10	3.52	32	1-2-56-77	43.05	4.30
11	Pind 14/88	39.12	3.08	22	Pind 373/88	50.56	4.62	33	RRIM 600	66.16	
	Overall Average	54.22	3.47								
	CV$_{(\%)}$	16.44	43.63								

[*] Significant for $P < 0.05$ Dunnett test with respect to the control genotype RRIM 600.