

## Different methods to assess yield temporal stability in rubber

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**Abstract** – The objective of this work was to assess, during six years, the temporal stability of natural rubber yield of 25 superior *Hevea brasiliensis* genotypes, using the Wricke, Eberhart & Russell, Lin & Binns, additive main effect and multiplicative interaction (AMMI) analysis, and harmonic mean of the relative performance of the genetic values (HMRPGV) methods. The IAC 40 and IAC 300 genotypes were identified as stable and high yielding by the Eberhart & Russell, Lin & Binns, HMRPGV, and AMMI Biplot methods. The ranking of the other more stable genotypes identified by these analyses was altered. The observed results in the AMMI Biplot agreed with those observed in the Wricke method for identifying stable, but lower yielding genotypes. The simultaneous use of different methods allows a more accurate indication of stable genotypes. Stability analyses based on different principles show agreement in indicating stable genotypes.

**Index terms:** *Hevea brasiliensis*, genotype selection, genotype x year interaction.

## Diferentes métodos para avaliar a estabilidade temporal do rendimento em seringueira

**Resumo** – O objetivo deste trabalho foi avaliar, durante seis anos, a estabilidade temporal da produção de borracha natural de 25 genótipos superiores de *Hevea brasiliensis*, utilizando os métodos de Wricke, Eberhart & Russell, Lin & Binns, análise dos efeitos aditivos principais e interação multiplicativa (AMMI) e média harmônica da performance relativa dos valores genéticos (MHPRV). Os genótipos IAC 40 e IAC 300 foram identificados como estáveis e produtivos, pelos métodos de Eberhart & Russell, Lin & Binns, MHPRV e Biplot AMMI. Houve alteração no ordenamento dos demais genótipos mais estáveis identificados a partir dessas análises. Os resultados observados no Biplot AMMI mostraram concordância com os observados no método de Wricke para a identificação de genótipos estáveis, mas menos produtivos. A utilização simultânea de diferentes métodos permite a indicação mais precisa de genótipos estáveis. Análises de estabilidade baseadas em diferentes princípios mostram concordância na indicação de genótipos estáveis.

**Termos para indexação:** *Hevea brasiliensis*, seleção de genótipos, interação genótipo x ano.

### Introduction

The main source of natural rubber, *Hevea brasiliensis* (Willd. ex A. Juss.) Muell. Arg., is an important commercial species, which has been the object of genetic breeding to increase latex yield. However, this is a slow and laborious process, due to the perennial nature of the crop and to the several selection and assessment stages of the breeding cycle (Chandrasekhar et al., 2007; Priyadarshan et al., 2009). In one of these stages, the selection process involves assessing the adaptability and stability of genotypes in different environments.

Plant breeders usually estimate adaptability and phenotype stability parameters to assess new genotypes before recommending them as cultivars (Silva & Duarte,

2006). In the case of *H. brasiliensis*, the most desirable genotypes are those that show stability in vigor and high yield over the years and locations (Gonçalves et al., 2003). Genotype x year interaction in perennial crops represents the different responses of genotypes to changes in annual conditions. In genotype x year interaction, the relative performance of genotypes varies with the year (Gonçalves et al., 2005).

Several methods, involving different assessment parameters, biometric procedures, or information detailing of analyses, can be used to assess stability and adaptability (Cruz & Carneiro, 2006). In the method proposed by Wricke (1965), based on analysis of variance, the sum of squares of the interaction is divided into parts attributed to each genotype, and the genotype with the lowest estimate for ecovalence ( $\omega_1$ ) is considered

stable (Cruz et al., 2004). The method proposed by Eberhart & Russell (1966), based on linear regression, measures the response of each genotype to environmental variations. Regression coefficients of each genotype, regarding the environmental index of the deviations of this regression, represent the estimates of the adaptability and stability parameters (Cruz et al., 2004). In the nonparametric analysis by Lin & Binns (1988), the measurement used to estimate the stability and adaptability of cultivars is the mean of the square of the distance between the cultivar and the mean maximum response obtained in the environment (Cruz & Carneiro, 2006). The additive main effect and multiplicative interaction (AMMI) model combines a univariate method, i.e., analysis of variance for additive effects of genotype and environment, with a multivariate method, i.e., analysis of principal components for multiplicative effect of genotype x environment interaction (Gauch & Zobel, 1988). This method enables a more precise estimate of genotypic responses and an easy graphic interpretation of statistical analysis results by plot procedure (Zobel et al., 1988). According to Resende (2004), in the context of mixed models, the harmonic mean of the relative performance of the genetic values (HMRPGV), predicted by Blup, is an option for simultaneous selection based on yield, stability, and adaptability.

Recently, several methods have been used simultaneously to assess stability and adaptability in various crops, such as guarana (Nascimento Filho et al., 2009), cotton (Silva Filho et al., 2008), beans (Melo et al., 2007; Pereira et al., 2009a, 2009b), corn (Cargnelluti Filho et al., 2007), soybean (Silva & Duarte, 2006), sugarcane (Rosse et al., 2002), and eucalyptus (Resende et al., 2001). In some cases, these methods can be complementary, since the simultaneous use of different methods generates estimates with different approaches (Pereira et al., 2009b).

The most recent studies on stability and adaptability regarding *H. brasiliensis* have been based on the Finlay & Wilkinson (Gonçalves et al., 2009), Reml/Blup (Verardi et al., 2009), Eberhart & Russell (Gonçalves et al., 2008), and GGE-Biplot (Priyadarshan et al., 2008) methods. However, there is no record of different methods being used simultaneously.

The objective of this work was to assess, during six years, the temporal stability of natural rubber yield of 25 superior *H. brasiliensis* genotypes, using the Wricke,

Eberhart & Russell, Lin & Binns, additive main effect and multiplicative interaction (AMMI) analysis, and harmonic mean of the relative performance of the genetic values (HMRPGV) methods.

## Materials and Methods

A total of 25 genotypes were used in the experiment: one Malay clone (RRIM 600), eight Amazon clones (five IAN, two Fx, and one RO), and 16 local clones (IAC). The Amazon clones derived from crosses and selections made in Brazil by Ford and Instituto Agronômico do Norte (IAN); except RO 45, a primary clone, derived from unknown parents, from a collection in the state of Rondônia. The IAC clones are the result of crosses and selection by Instituto Agronômico de Campinas (IAC).

The experiment was set up in the experimental area of Pólo Regional Noroeste Paulista, at the Estação Experimental de Votuporanga, located in the northwestern region of São Paulo State, Brazil, at 20°25'S and 49°50'W, at 450-m altitude. The mean temperature during the growing season was 32°C, and the mean annual rainfall was 1,480 mm. The soil is classified as Paleudalf (Argissolo), with average nutrient status and poor physical structure. A randomized complete block design, with three replicates, was used. Each plot consisted of one row of six plants, with 7.0 m between rows and 3.0 m between plants. Rubber yield was assessed with half spiral tapping, at three-day intervals, five days a week, during eleven months of the year. Yield was measured by the amount of coagulated latex in the bowls, which were attached to each tapped tree and collected randomly twice a month; the latex was dried under normal shade and ventilation conditions during the assessment period. The total annual rubber yield per tree was divided by the number of coagulates, and the results were expressed in grams per tree per tapping.

Data were subjected to individual and joint analyses of variance. After verifying significant genotype x year interaction, analyses of genotype adaptability and phenotype stability were carried out using the Wricke (1965), Eberhart & Russell (1966), Lin & Binns (1988), AMMI (Zobel et al., 1988), and Blup prediction (HMRPGV) methods, described by Resende (2004). The analyses of the first three methods were carried out using the Genes program (Cruz, 2006), while the analyses of the fourth and fifth methods were done with

the SAS (SAS Institute, 2002) and the Selegen Reml/Blup (Resende, 2007) programs, respectively. The statistical models used in these analyses are described below.

The stability of the genotypes by the Wricke method was estimated by:

$$\omega_i = \sum_i \sum_j [Y_{ij} - (Y_{i.}/L) - (Y_{.j}/G) + (Y_{..}/GL)]^2,$$

in which:  $\omega_i$  is the contribution of the *i*th genotype in the total of the interaction;  $Y_{ij}$  is the mean of the *i*th genotype in environment *j*;  $Y_{i.}$  is the total of the *i*th genotype in all locations;  $Y_{.j}$  is the total of environment *j* considering all genotypes;

$$Y_{..} = \sum_i \sum_j Y_{ij},$$

in which: *G* is the number of genotypes assessed; and *L* is the number of experimental locations.

In the analysis by Eberhart & Russell (1966), the linear regression model was represented by:

$$Y_{ij} = m_i + b_i I_j + d_{ij} + \bar{\epsilon}_{ij},$$

in which:  $Y_{ij}$  is the observed mean of the *i*th genotype in environment *j*;  $m_i$  is the general mean of the *i*th genotype;  $b_i$  is the regression coefficient of the *i*th genotype;  $I_j$  is the *j*th environmental index;  $d_{ij}$  is the deviation of the regression of the *i*th genotype in the *j*th environment; and  $\bar{\epsilon}_{ij}$  is the mean error associated to the mean. With this methodology, two stability parameters were estimated: regression coefficient ( $\beta_i$ ), i.e., the regression of the performance of each genotype in different years on the annual mean over all genotypes, and variance of the deviation ( $\hat{S}_{di}^2$ ) from the regression line. The coefficient of determination ( $R^2$ ) for regression was used to determine how well the linear model fit the data. The environmental index was calculated by:

$$I_j = \bar{Y}_{.j} - \bar{Y}_{..}, \text{ with } \sum_{j=1}^n I_j = 0,$$

in which *n* is the number of environments.

In the method by Lin & Binns,  $P_i$  is the mean quadratic distance between genotype *i* and the genotype with maximum response in environment *j*, as follows:

$$P_i = \sum_{j=1}^n (Y_{ij} - M_j)^2 / 2n,$$

in which:  $P_i$  is the superiority index of the *i*th genotype;  $Y_{ij}$  is the yield of the *i*th genotype in the *j*th environment;  $M_j$  is the yield of the genotype with maximum response among all genotypes in the *j*th environment; and *n* is the number of environments. Modifications were used to discriminate  $P_i$  values for favorable and unfavorable environments, as reported in Cruz & Carneiro (2006).

The model below was used in AMMI analysis, which involves additive components to study principal effects, and multiplicative components to study interaction:

$$Y_{ij} = \mu + g_i + e_j + \sum_{k=1}^n \lambda_k \gamma_{ik} \alpha_{jk} + \rho_{ij} + \epsilon_{ij},$$

in which:  $Y_{ij}$  is the mean response of the *i*th genotype ( $i = 1, 2, \dots, G$  genotypes) in the *j*th environment ( $j = 1, 2, \dots, A$  environments);  $\mu$  is the general mean of the experiments;  $g_i$  is the fixed effect of the *i*th genotype;  $e_j$  is the fixed effect of the *j*th environment;  $\lambda_k$  is the *k*th singular value (scale) of the original interaction matrix (shown by GA);  $\gamma_{ik}$  is the element corresponding to the *i*th singular vector column of the GA matrix;  $\alpha_{jk}$  is the element corresponding to the *j*th environment in the *k*th singular vector line of the GA matrix;  $\rho_{ij}$  is the noise associated to the  $(ga)_{ij}$  term of the classic interaction of the *i*th genotype with the *j*th environment *j*; and  $\epsilon$  is the mean experimental error.

The HMRPGV from the program Selegen-Reml/Blup, which is used for complete block designs with temporal stability and adaptability, according to the statistical model number 79, was used in the joint selection for yield, stability, and adaptability of genetic materials:

$$y = Xm + Zg + Wp + Ti + Qs + \epsilon,$$

in which: *y* is the data vector; *m* is the vector of the effects of evaluation-replicate combinations (assumed as fixed) added to the general mean; *g* is the vector of the genotypic effects (assumed to be random); *p* is the vector of the plot effects (random); *i* is the vector of the effects of genotype x evaluation interaction; *s* is the vector of the permanent environment effects (random); and  $\epsilon$  is the error or residue vector (random). The uppercase letters represent the incident matrices for the referred effects. Genotypic effects were considered to be random due to the number of genotypes assessed, i.e., a total of 25. Resende & Duarte (2007) recommend treating genotypic effects as random when the number of treatments is equal to or greater than ten.

## Results and Discussion

Highly significant ( $p < 0.01$ ) effects were observed in the individual variance analyses of the genotypes for rubber yield each year, suggesting that the differences among the genotypes within each year were attributable to genetic causes. The joint analysis of variance showed highly significant effects ( $p < 0.01$ ) for genotypes, years, and genotype x year interaction, which indicates, respectively, presence of variability among genotypes, differences between years, and differences in the relative performance of genotypes in the years assessed.

Since the focus of the present study was to select stable genotypes over time, comparisons between the different methods of stability assessment concentrated mainly on the genotype with the best performance for the parameters assessed.

**Table 1.** Estimates of phenotypic stability obtained by the Wricke method, and mean rubber yield (grams per tree per tapping) of 25 *Hevea brasiliensis* genotypes assessed, during six years.

Genotype	Rubber yield <sup>(1)</sup>	Rank	Ecovalece ( $\omega$ ) <sup>(2)</sup>	(%)	Rank
IAN 4493	33.233	17	129.19	0.6077	1
IAC 307	42.632	9	197.66	0.9298	2
IAC 310	31.521	20	220.52	1.0373	3
IAC 313	39.437	12	254.06	1.1986	4
IAC 302	41.441	10	269.20	1.2663	5
IAC 309	34.384	16	328.06	1.5431	6
IAC 314	26.509	25	345.49	1.6252	7
IAN 6721	31.951	18	380.67	1.7906	8
IAC 308	39.768	11	381.93	1.7965	9
IAC 311	31.703	19	420.34	1.9772	10
IAN 6323	31.417	21	422.98	1.9897	11
RRIM 600	50.068	7	477.67	2.2469	12
IAC 316	30.92	22	560.19	2.6350	13
IAC 300	52.722	4	620.61	2.9193	14
IAC 312	29.003	23	678.07	3.1896	15
Fx 985	36.386	15	788.58	3.7094	16
IAN 3703	38.632	13	809.89	3.8096	17
IAC 306	28.616	24	984.64	4.4905	18
IAC 40	66.737	1	972.73	4.5756	19
Fx 3899	38.316	14	1031.10	4.8501	20
IAC 301	55.226	2	1497.40	7.0434	21
RO 45	51.494	6	1545.5	7.2696	22
IAC 56	54.398	3	1765.00	8.3025	23
IAC 303	52.591	5	3082.50	14.5000	24
IAN 3156	48.719	8	3124.40	14.697	25

<sup>(1)</sup>Mean yield of six years. <sup>(2)</sup> $\omega$ , stability parameter.

Table 1 shows the stability parameters ( $\omega$ ) obtained with the Wricke method, based on analysis of variance, in which the lowest values indicate greater stability. The most stable genotypes (IAN 4493, IAC 307, IAC 310, IAC 313, and IAC 302) were not amongst the highest yielding; the genotypes identified as least stable (IAN 3156, IAC 303, IAC 56, RO 45, and IAC 301) had better yields. According to Cargnelutti Filho et al. (2007), the Wricke method does not depend on the mean yield or on the response to variations in environmental conditions (adaptability); thus, methods based on analysis of variance may not be very efficient. Nascimento Filho et al. (2009) reported similar results to those obtained in the present study, but for guarana [*Paullinia cupana* var. *sorbilis* (Mart.) Ducke], while using a method based on analysis of variance. The authors verified that the clones with minimum variance among the environments were generally lower yielding and highly stable, but not of interest for breeding to increase yield. In the case of the genotypes used in the present study, which had been previously assessed and selected, even those with lower yields have potential for use. The results found for the most stable genotype agreed with those found in AMMI analysis. Silva Filho et al. (2008) and Silva & Duarte (2006) also observed agreement between the Wricke method and AMMI analysis in cotton and soybean, respectively.

The parameters obtained by the Eberhart & Russell method are shown in Table 2. High values were observed for the determination coefficient ( $R^2$ ), indicating that the genotypes fitted the stability model. Eighteen of the 25 genotypes assessed showed nonsignificant deviations from the regression ( $\hat{S}_{di}^2 = 0$ ), indicating stability. The Fx 3899, IAC 301, IAC 303, IAC 56, IAN 3156, IAN 3703, and RO 45 genotypes did not show stability. Regarding adaptability, six genotypes (IAC 303, IAC 56, IAC 40, RO 45, IAC 301, and RRIM 600) showed specific adaptability in favorable environments ( $\hat{\beta}_i > 1.0$ ), while genotypes IAN 3156, IAC 306, Fx 985, and IAC 314 showed specific adaptability for unfavorable environments ( $\hat{\beta}_i < 1.0$ ). The genotypes showed general adaptability ( $\hat{\beta}_i = 1.0$ ). According to Resende et al. (2001), genotypes with ( $\hat{\beta}_i = 1.0$ ) are only desirable if they have maximum yield. IAC 40, IAC 300, and the control RRIM 600 were among the highest yielding stable genotypes, and were considered stable by the Lin & Binns, HMRPGV, and AMMI1 biplot analyses. There was agreement among the genotypes that showed

specific adaptability in favorable environments by the Eberhart & Russell method and by the Lin & Binns method. Cargnelutti Filho et al. (2007), Silva Filho et al. (2008), and Nascimento Filho et al. (2009) found agreement between the Eberhart & Russell and Lin & Binns methods.

Table 3 shows the ranking of the genotypes according to the Lin & Binns method for stability, adaptability, and yield, with the alteration proposed by Cruz & Carneiro (2006), which separates clones with greater stability and phenotypic adaptability for favorable and unfavorable environments ( $<P_i$ ). IAC 40 was classified as the most stable and adapted genotype in favorable and unfavorable environments, whereas IAC 300 was among the most stable and adapted in

general and unfavorable environments. Genotypes IAC 303, IAC 56, IAC 301, and RRIM 600 showed specific adaptability to favorable environments, while IAN 3156, IAC 300, IAC 301, and RO 45 had specific adaptability to unfavorable environments. Besides identifying the most stable and adaptive genotypes among the highest yielding, the Lin & Binns method is easy to apply and interpret, and discriminates the best clones for performance in both favorable and unfavorable environments (Nascimento Filho et al., 2009; Pereira et al., 2009a).

In the analyses carried out by HMRPGV (Table 4), IAC 40 and IAC 300 were among the first genotypes for all the parameters assessed. The highest genetic values for stability were found for IAC 40, IAC 3156, IAC 300, IAC 301, and IAC 303, and the greatest adaptability was found for IAC 40, IAC 300, IAC 3156, IAC 301, and IAC 56. The genotypes that showed highest stability and adaptability were IAC 40, IAC 300, IAC 301, IAC 3156, and IAC 56. As observed by Maia et al. (2009), there are similarities among the rankings of these materials by the different methods. According to the authors, this could be a result of the positive correlation and the mean magnitude involving genotypic performance in the environments.

Five components were obtained by AMMI analysis (IPCA). There was significance up to the AMMI2 model, which was the first to associate significance for axles (IPCA) with nonsignificance for residue (noise). According to Gauch (1988), the first AMMI axles capture a greater percentage of pattern. The subsequent increase in dimensions (axles) results in a decrease in the percentage of pattern and in an increase in noise. Therefore, in spite of selection on a single axle, which explains a small portion of the original sum of squares of the genotype x environment interaction ( $SS_{G \times E}$ ), the capture of a greater percentage of pattern was expected. In the present study, the first axle (IPCA 1) explained 51.04% of the sum of squares of the interaction of the variation, and the second (IPCA 2) explained 33.12%, totaling 84.16% in the first two components. Figure 1 shows the AMMI1 biplot analyses for IPCA x rubber yield data and the AMMI2 biplot analyses for IPCA 1 x IPCA 2. According to Duarte & Vencovsky (1999), in AMMI analysis, the biplot is interpreted by the magnitude and the sign of the genotype and environment scores for the interaction axles. Thus, scores close to zero characterize genotypes and

**Table 2.** Estimates of phenotypic stability and adaptability obtained by the Eberhart & Russell method, and mean rubber yield (gram per tree per tapping) of 25 *Hevea brasiliensis* genotypes assessed, during six years.

Genotype	Rubber yield <sup>(1)</sup>	Rank	$\hat{\beta}_i$	$\hat{S}_{di}^2$	$\hat{R}_i^2$ (%)
Fx 3899	38.3161	14	0.7265	48.6314*	61.3825
Fx 985	36.3861	15	0.6478*	18.0133	69.1596
IAC 300	52.7217	4	1.1437	25.8523	85.3667
IAC 301	55.2256	2	1.3158*	82.2139**	77.9023
IAC 302	41.4411	10	0.8952	-1.3866	89.3772
IAC 303	52.5911	5	1.5952**	160.5526**	74.6954
IAC 306	28.6161	24	0.4983**	4.8952	66.5147
IAC 307	42.6317	9	1.1681	-10.9963	96.4821
IAC 308	39.7683	11	1.1093	7.8044	89.8646
IAC 309	34.3839	16	0.9109	4.1587	87.2256
IAC 310	31.5206	20	0.7356	-17.8916	96.9370
IAC 311	31.7033	19	0.9378	12.7089	84.4452
IAC 312	29.0028	23	0.7146	17.8020	73.2885
IAC 313	39.4367	12	1.1420	-4.5250	94.1934
IAC 314	26.5094	25	0.6635*	-16.6270	95.0171
IAC 316	30.9200	22	0.7343	10.2692	78.1839
IAC 40	66.7372	1	1.5485**	-3.9745	96.6544
IAC 56	54.3983	3	1.5661**	57.8997**	86.7083
IAN 3156	48.7189	8	0.3521**	150.2240**	13.2301
IAN 4493	33.2333	17	0.8120	-18.2022	97.6838
IAN 3703	38.6322	13	1.1446	41.5731**	81.4344
IAN 6323	31.4172	21	0.9318	12.7632	84.2536
IAN 6721	31.9506	18	1.0056	10.2136	87.0699
RO 45	51.4944	6	1.3888*	75.3584**	80.7889
RRIM 600	50.0683	7	1.3119*	-2.2406	94.9672

<sup>(1)</sup>Mean yield of six years.  $\hat{\beta}_i$ , regression coefficient.  $H_0, \hat{\beta}_i = 1$  and  $H_A, \hat{\beta}_i \neq 1$ . \* and \*\*Significant by the t test at 5 and 1% probability, respectively.  $\hat{S}_{di}^2$ : deviation of the regression coefficient.  $H_0, \hat{S}_{di}^2 = 0$  and  $H_A, \hat{S}_{di}^2 \neq 0$ . \* and \*\*Significant by the f test, at 5 and 1% probability, respectively.  $\hat{R}_i^2$ , determination coefficient.

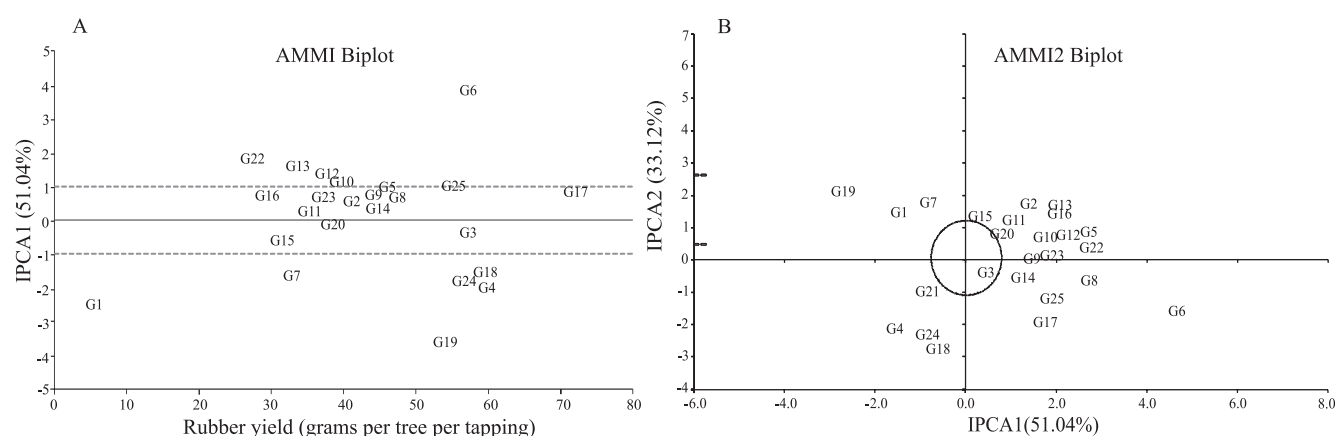
**Table 3.** Estimates of phenotypic stability and adaptability obtained by the Lin & Binns method, with the alteration proposed by Cruz & Carneiro 2006 and mean rubber yield (grams per tree per tapping) of 25 *Hevea brasiliensis* genotypes assessed, during six years<sup>(1)</sup>.

Genotype	Rubber yield	General Pi	Rank	Favorable Pi	Rank	Unfavorable Pi	Rank
IAC 40	66.7372	18.8244	1	6.9162	1	42.6409	1
IAC 301	55.2256	169.6429	2	192.6872	4	123.5543	4
IAC 300	52.7217	189.2094	3	243.2734	6	81.0813	3
IAC 56	54.3983	189.3249	4	169.4281	3	229.1185	6
RRIM 600	50.0683	219.5556	5	212.1379	5	234.3909	7
IAC 303	52.5911	220.6021	6	158.9637	2	343.8791	10
RO 45	51.4944	231.4335	7	252.5771	7	189.1463	5
IAN 3156	48.7189	392.1168	8	558.3374	12	59.6756	2
IAC 307	42.6317	407.0212	9	396.9746	8	427.1145	12
IAC 302	41.4411	449.8353	10	499.1332	10	351.2396	11
IAC 313	39.4367	501.9152	11	493.7025	9	518.3408	16
IAC 308	39.7683	503.7598	12	520.8373	11	469.6047	13
IAN 3703	38.6322	562.6114	13	607.4329	13	472.9684	14
Fx 3899	38.3161	588.9922	14	741.7744	14	283.4279	8
Fx 985	36.3861	630.8047	15	798.6014	17	295.2112	9
IAC 309	34.3839	682.6774	16	764.4721	15	519.0881	17
IAN 4493	33.2333	731.4238	17	834.6248	18	525.0219	18
IAN 6721	31.9506	775.1583	18	770.7880	16	783.8991	25
IAC 311	31.7033	787.6565	19	849.2486	20	664.4723	22
IAN 6323	31.4172	796.8074	20	841.1832	19	708.0559	24
IAC 310	31.5206	799.4209	21	927.4925	22	543.2777	19
IAC 316	30.9200	828.5439	22	919.5880	21	646.4557	21
IAC 312	29.0028	910.1217	23	1,062.0425	23	606.2803	20
IAC 306	28.6161	956.8838	24	1,195.7316	25	479.1881	15
IAC 314	26.5094	1,022.0931	25	1,180.9025	24	704.4743	23

<sup>(1)</sup>Pi, measure to evaluate phenotypic adaptability and stability.

**Table 4.** Estimates of harmonic mean of the genetic values (HMGV), relative performance of the genetic values (RPGV), and harmonic mean of the relative performance of the genetic values (HMRPGV) of 25 *Hevea brasiliensis* genotypes assessed, during six years.

Genotype	Order	HMGV	Genotype	Order	RPGV	Genotype	Order	HMRPGV
IAC 40	1	64.136	IAC 40	1	1.7971	IAC 40	1	1.7597
IAN 3156	2	46.394	IAC 300	2	1.3352	IAC 300	2	1.3271
IAC 300	3	43.210	IAN 3156	3	1.3297	IAC 301	3	1.2705
IAC 301	4	41.433	IAC 301	4	1.3014	IAN 3156	4	1.2579
IAC 303	5	38.766	IAC 56	5	1.2221	IAC 56	5	1.1982
RRIM 600	6	38.128	RO 45	6	1.2167	RO 45	6	1.1873
IAC 56	7	37.423	IAC 303	7	1.1990	IAC 303	7	1.1714
RO 45	8	37.279	RRIM 600	8	1.1551	RRIM 600	8	1.1528
IAC 302	9	33.038	IAC 302	9	1.0487	IAC 302	9	1.0331
IAC 310	10	32.400	IAC 307	10	0.9767	IAC 307	10	0.9639
IAN 4493	11	32.235	IAN 4493	11	0.9355	IAC 313	11	0.9302
Fx 985	12	31.790	IAC 313	12	0.9352	IAC 310	12	0.9246
IAC 309	13	31.155	IAC 310	13	0.9306	IAN 4493	13	0.9126
IAC 313	14	30.583	IAC 308	14	0.9226	IAC 308	14	0.9103
IAC 308	15	30.284	IAC 309	15	0.9103	IAC 309	15	0.9051
IAC 307	16	30.006	Fx 985	16	0.8821	Fx 985	16	0.8489
IAN 3703	17	27.197	IAN 3703	17	0.8400	IAN 3703	17	0.8192
IAC 306	18	26.265	Fx 3899	18	0.7959	IAN 6323	18	0.7821
IAN 6323	19	26.250	IAN 6323	19	0.7920	Fx 3899	19	0.7700
IAC 312	20	25.428	IAC 312	20	0.7827	IAC 312	20	0.7675
IAC 316	21	24.683	IAN 6721	21	0.7739	IAC 311	21	0.7311
IAC 314	22	23.952	IAC 311	22	0.7494	IAN 6721	22	0.7236
Fx 3899	23	23.718	IAC 306	23	0.7417	IAC 306	23	0.7200
IAC 311	24	23.393	IAC 314	24	0.7147	IAC 314	24	0.7114
IAN 6721	25	20.132	IAC 316	25	0.7118	IAC 316	25	0.6999



**Figure 1.** AMMI biplot analyses for data of IPCA x rubber yield and AMMI2 biplot analyses for IPCA1 x IPCA2. The following genotypes were evaluated: G1 (Fx 3899), G2 (Fx 985), G3 (IAC 300), G4 (IAC 301), G5 (IAC 302), G6 (IAC 303), G7 (IAC 306), G8 (IAC 307), G9 (IAC 308), G10 (IAC 309), G11 (IAC 310), G12 (IAC 311), G13 (IAC 312), G14 (IAC 313), G15 (IAC 314), G16 (IAC 316), G17 (IAC 40), G18 (IAC 56), G19 (IAN 3156), G20 (IAN 4493), G21 (IAN 3703), G22 (IAN 6323), G23 (IAN 6721), G24 (RO 45), and G25 (RRIM 600).

environments that contribute little to interaction, i.e., are stable. In the AMMI2 biplot, stable genotypes and environments are those whose points are close to zero for the two interaction axes (IPCA1 x IPCA2). The most stable genotypes in the AMMI biplot were IAC 310, IAN 4493, IAN 6721, IAC 313, IAC 314, and IAC 307, all with low yield. IAC 40 and IAC 300 were among the high yielding and stable genotypes, as observed in previous analyses. The results found for stable genotypes, but with lower yield, were in line with those found with the Wricke method. In AMMI2, genotypes IAN 4493, IAC 300, and IAC 314 were considered stable.

There was coherence among the most stable genotypes identified with the different analytical methods; however, the ranking of some genotypes was altered. IAC 40 and IAC 300 were considered the most stable in the analyses that associated stability to yield. From the breeder's point of view, processing data by several methods of adaptability and stability analysis, while considering the peculiarities of each method, is better for decision-making when indicating cultivars (Cargnelutti Filho et al., 2007). When the genotype x environment interaction results in the variation of unpredictable environmental factors, such as year to year variation, as was the case in the present study, breeders need to develop more stable genotypes that can perform reasonably well in a wide range of conditions. Such breeding

strategies can help rubber producers to avoid risks (Gonçalves et al., 2008).

## Conclusions

1. The simultaneous use of different methods leads to a more accurate indication of stable *Hevea brasiliensis* genotypes.
2. Stability analyses based on different principles show agreement in indicating stable *H. brasiliensis* genotypes.

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