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Association among stability measurements in rubber tree traits

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ABSTRACT

The simultaneous use of different methods of stability analysis is becoming more widely used in the selection of genotypes in breeding programs. Knowing how these different methods are associated can contribute to a more efficient selection. The objective of the present study was to assess association among different methods of stability analysis in the rubber tree [*Hevea brasiliensis* (Willd. ex Adr. de Juss.) Muell.-Arg.], using different traits and different groups of genotypes for the same trait. Two open-pollinated progeny populations (POP1 and POP2) and a group of clones (Group 1) were analyzed. POP1 contained 22 progeny, assessed in the municipalities of Pindorama, Votuporanga and Jaú, São Paulo state, Brazil. POP2 included 30 progeny assessed in Selvíria, Mato Grosso do Sul state, Votuporanga and Colina, São Paulo state, Brazil. Group 1 consisted of 25 clones assessed in Votuporanga. The following traits were assessed in POP1: girth, rubber yield, bark thickness and number of latex vessel rings. Rubber yield was assessed in POP2 and Group 1 clones. The following methods of stability analysis were used: Wricke; Eberhart and Russell; Lin and Binns; AMMI (Principal Additive Effect and Multiplicative Interaction) and HMRPGV (Harmonic Mean of the Relative Performance of the Genetic Values) predicted by Blup (Best Linear Unbiased Prediction). The Spearman correlation was used to verify the association between the stability parameters. Three scenarios were observed; in the first, some parameters did not show significant association in any of the analyses: Eberhart and Russell with Lin and Binns; Eberhart and Russell with HMRPGV; Wricke with HMRPGV; AMMI with Lin and Binns and AMMI with HMRPGV. In the second, some parameters showed significant associations in all the analyses such as: Wricke with AMMI, Lin and Binns with HMRPGV. Finally, in the third, the significance of association varied according to the analysis: Eberhart and Russell with Wricke, Eberhart and Russell with AMMI and Wricke with Lin and Binns. Therefore, the association among some stability parameters varies according to the trait and/or the group of genotypes analyzed. The association observed in one analysis cannot be applied to another analysis. In this data analysis is possible to observe that the AMMI method can be used with HMRPGV or Lin and Binns. In addition, Eberhart and Russell can be used with HMRPGV or Lin and Binns, since they offer differentiation and provide additional approaches to the study of stability.

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1. Introduction

In breeding programs, when assessing genotypes in different environments, there is often significant effect of the genotype x environment interaction. Environments are sometimes different locations and sometimes different assessment periods. When there is significant effect, the stability and adaptability analyses are complementary.

Several studies have been conducted on stability in the rubber tree in the last decade. In some studies, the stability between location was assessed (Gonçalves et al., 2009; Gouvêa et al., 2013; Verardi et al., 2009) and in other studies, stability in time (Gonçalves et al., 2008; Vinod et al., 2010; Priyadarshan et al., 2008; Gouvêa et al., 2013, 2012, 2011; Silva et al., 2014). In some of these studies the genotypes assessed were progeny (Gonçalves et al., 2009; Gouvêa et al., 2013 Verardi et al., 2009) and in others they were

clones (Gonçalves et al., 2008; Vinod et al., 2010; Priyadarshan et al., 2008; Gouvêa et al., 2012, 2011; Silva et al., 2014). A single method of stability analysis was used in most of the studies, but the simultaneous use of different methods has become more frequent, for example, as in those by Priyadarshan et al. (2008), Gouvêa et al. (2012) (e 2011) and Silva et al. (2014).

The simultaneous use of different stability methods with the assessment of correlation between the parameters estimated from these methods has been observed in several studies, such as those by Gouvêa et al. (2012), Sahin et al. (2011), Segherloo et al. (2008), Mohammadi and Amri (2008) and Mohebodini et al. (2006). In these studies assessments were made on a single group of genotypes and a single trait.

Several characters contribute to the production of rubber. According to Henon and Nicolas (1989), the number of latex vessels is the character that most influences latex production. Genetic and phenotypic correlations between yield and number of latex vessel rings were verified by Gonçalves et al. (2005). Silva et al. (2012) observed genetic correlations between bark thickness and girth growth. According to Gonçalves and Fontes (2012), girth growth is also associated with various aspects in the genetic improvement of rubber. The early opening of the panel and 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. Therefore, the importance of identifying progeny with stability for these traits.

An assessment that considers the correlation between stability parameters by analyzing different traits and different groups of genotypes may supply complimentary information to the studies already carried out. Thus the objective of the present study was to assess the correlation between different methods of stability analysis in the rubber tree using different traits and different groups of genotypes for the same trait.

2. Material and methods

2.1. Plant material and experimental information

POP1 consisted of 22 open-pollinated progeny, obtained from 22 parental clones selected phenotypically in a H. brasiliensis clone population from Asia and Africa, established in the Campinas Experimental Center (CEC), Agronomic Institute (IAC). The three progeny tests were set up in Experimental Stations of Pindorama, 21°13′S, 48°56′W and 560 m altitude, in Jaú latitude 22°17′S, 48°34′W and 580 m altitude and in Votuporanga, latitude 20°25′S, 49°50′W and 480 m altitude. A randomized block design was used with six replications and ten plant-linear plots with 2 × 2 m spacing. POP2 consisted of 30 open-pollinated progeny from Asian clones, IACs and other genotypes selected previously. The three progeny tests were set up in Selvíria, experimental field that belongs to Paulista State University at Unesp, Ilha Solteira-SP, latitude de 20°20′S, 51°23′W and 370 altitude and in Experimental Stations of Colina-SP latitude 20°43′S, 48°32′W and 569 m altitude and Votuporanga-SP. A randomized block design was used with three replications and 10 plants per plot with 3.0 × 3.0 m spacing in Selvíria-MS, and 2.0 × 2.0 m spacing in Colina and Votuporanga. Group 1 of clones consisted of 25 clones, one Malayan, eight Amazon (IAN, Fx, RO) and 16 local clones (IAC). The experiment was assessed in Votuporanga in a randomized block design with three replications, using eight plants per linear plot in 7.0 m × 3.0 m spacing.

2.2. Traits assessed

2.2.1. Rubber yield

The data for the progeny rubber yield were obtained by the modified Hamaker Morris-Mann (HMMm) precocious test for three-year-old seedlings (Tan and Subramaniam, 1976). The panel was opened 15 cm above ground level, using the S/2 system (half spiral cut) and d/3 (interval between tapping, that is, one 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 tappings on the individuals of each progeny. The results were expressed in grams of dry rubber per tapping per tree ($g\,s^{-1}\,a^{-1}$). In POP2 there was stimulation with ethefon at 2.5% concentration. The clone group (Group 1) yield data were registered starting in the seventh year, for the trees that presented trunk girth greater than 45 cm, measured 1.2 m above the rootstock. The data were recorded by means of latex from one tapping, randomly collected twice a month, dried under normal shade and ventilation conditions throughout the evaluation period, fastened by a wire on each tree. The total annual weight of rubber per tree was divided by the number of coagulates. The system used was that of tapping ½S d/4 6 d/7.11 m/y.ET 2,5% Pa La 8/y–half spirals tapping (½S), carried out at four-day intervals (d/4), with rest on Sundays (6d/7), tapping 11 months per year (11 m/y), stimulated with 2.5% ethephon (ET 2.5%) applied to the panel (Pa) on the gutter with coagulates (La), eight times a year (8/y). The assessment period for girth was once a year in six years

2.2.2. Girth

Girth was measured at, 50 cm above ground level, using a tape measure. The data from the third year were assessed because early selection is made in the third year.

2.2.3. Bark thickness

To measure the bark thickness, three barks samples were collected from each plant, using a gouge, measured with a digital packymeter and the mean expressed in millimeters. The measurements were made in the third year.

2.2.4. Number of latex vessel rings

The number of latex vessel rings was assessed from bark samples that were blocked in histological paraffin sections and stained. The radial longitudinal type of histological cut was used. To obtain this cut the cambium rings were placed in parallel position in relation to the workbench at the time of inclusion in paraffin. The samples were sectioned in a microtome (Leitz mod. 1512) 125 micras thick, dehydrated in 90% ethylic alcohol and stained with Sudan III. The number of latex vessel rings was counted under an optical microscope (Olympus CBA) with 10x magnification.

2.3. Statistical analysis

2.3.1. Between locations joint analysis

Before carrying out the between location joint analyses of variance, homogeneity was verified the residual variances, using the analysis of individual variance. The criteria used were described by Pimentel-Gomes (2000) where homogeneous variances present a ratio between the greatest and smallest residual mean square lower than seven. Joint analyses of variance and joint deviation analysis were carried out

The model used in the between location joint analysis of variance of POP1 and POP2 is expressed by the equation:

$$\mathbf{Y}_{ijk} = \mu + (\mathbf{B/A})_{jk} + \mathbf{G}_i + \mathbf{A}_j + \mathbf{GA}_{ij} + \mathbf{E}_{ijk}, \text{where}:$$

$\mathbf{Y}_{ijk} = \boldsymbol{\mu}$ = general mean of the experiment; $(\mathbf{B/A})_{jk}$ = effect of block **k** within environment **j**; observation in the **k**-th block, assessed on the **i**-th genotype and **j**-th environment; $\mathbf{G}_i$ = effect of genotype **i** (i = 1, 2, . . . n); $\mathbf{A}_j$ = effect of environment **j** (**j** = 1,2. . .n); $\mathbf{GA}_{ij}$ = effect

of genotype I an environment j interaction and E_{ijk} = random error associated to observation **ijk**.

When the environment and genotype interaction (G × A) was significant, the stability methods of Wricke, Eberhart and Russell, AMMI uni-multivariate analysis and the nonparametric method by Lin and Binns were used.

The joint deviation analysis and the x^2 test on the values of the maximum likelihood values (LTR) were used to verify the significance of the effect of the G × E interaction by the mixed linear model. When the G × E interaction was significant, the analysis of stability and adaptability by the MHPRVG method was used predicted by Blup (Best Linear Unbiased Prediction).

The mixed linear model, described in Resende, (2007a), used in the genotype × location interaction, is expressed by the equation:

$Y = Xr + Zg + Wp + Ti + e$, where :

Y is the data vector, r is the replication effects vector (presumed fixed) added to the general mean, g is the genotypic effect vector presumed random, p is the plot effect vector s (random), i is the vector of the effects of the G × E interaction (random), and e is the vector of errors or residues (random). The uppercase letters represent the incidence matrices for the referred effects.

2.3.2. Analyses of measurements repeated in time

For Group 1 clones, the univariate analysis of variance in the split plot design was used to assess the means repeated in time after using the sphericity test (Mauchly, 1940). When the Mauchly test results were not significant, the experiment was analyzed in the form of sub split plot and the significance of the G × E interaction for measurements repeated in time was verified by the F test. When the G × E interaction was significant, analyses were made using the methods by Wricke, Eberhart and Russell, AMMI and the nonparametric method by Lin and Binns.

The significance of the G × E interaction for measurements repeated in time was also observed in the mixed models, starting with the x^2 values from the analysis of the maximum likelihood ratio LTR(x^2) obtained in the deviation analysis. When the G × E interaction was significant, the MHPRVG method was used through the models for measurements repeated in time.

In the analysis of variance in the split plot design, the plots were represented by the genotype and the subplots by the measurements. In these analyses the genotype and environments were considered fixed.

The model used is expressed by the equation:

$Y_{ijk} = \mu + B_j + P_i + \varepsilon_{ij} + S_k + \theta_{jk} + PS_{ik} + \delta_{ijk}$, where :

μ = general mean, B_j = effect of the j-th block ($j = 1,2...n$); P_i = effect of the i-th plot ($i = 1,2...n$); ε_{ij} = random error a; S_k = effect of the k-th subplot; θ_{jk} = random error b; PS_{ik} = effect of the interaction of the i-th plot with the j-subplot and δ_{ijk} = random error c.

In the analysis of measurements repeated in time by the mixed linear model used for Group 1 clones, the analysis model of genotype × measurement interaction for clones was described in Resende, (2007a) expressed by the equation:

$Y = m + Zg + Wp + Ti + Qs + e$, where

Y is the data vector, **m** is the effect of the effects of the measurement-replication combinations assumed as fixed added to the general mean, **g** is the genotype effect vector assumed as random, **p** is the plot effect vector assumed as random, **i** is the vector of the effects of the measurement genotype interaction, **s** is the vector of the permanent environment effect vector assumed as random and **e** is the error or residue vector assumed as random. The uppercase letters represent the incidence matrices for the referred

effects. The vector **m** includes all measurements in all the replications and adjusts simultaneously for the effects of the replication, measurement and replication measurement interaction.

2.3.3. Stability statistical models

2.3.3.1. Wricke method.
In the Wricke method, described by Cruz et al. (2006), the parameter Wi is estimated partitioning the sum of squares of the G × E interaction in the parts due to the genotypes. The partitioning is made using the following statistical model:

$$Wi = \sum_j \hat{G}A_{ij}^2 = \sum_j Y_{ij} - \left(\bar{Y}i. - \bar{Y} + \bar{Y}..\right)^2, \text{ where:}$$

Wi: contribution of genotype **i** in the total of the interaction, Y_{ij}: is the mean of genotype **i** in environment **j**; $\bar{Y}_{i.}$: mean of genotype **i**; $\bar{Y}_{.j}$: mean of environment **j**; $\bar{Y}_{..}$: general mean.

This method partitions the sum of squares of the interaction attributed to each genotype and the genotype that presented the lowest ecovalence estimate is considered the most stable.

2.3.3.2. Eberhart and Russell method.
The Eberhart and Russell method is based on analysis of simple linear regression. The linear regression model for this methodology is:

$Y_{ij} = \mu_i + b_i I_j + d_{ij} + \bar{e}_{ij}$, where :

Y_{ij} = is the mean observed of genotype **i** in environment **j**; μ_i = is the general mean of genotype **i**; b_i = is the coefficient of regression of genotype **i**; I_j = is the environmental index **j**; d_{ij} = is the deviation of the regression of genotype **i** in environment **j**; $\bar{e}_{ij}$ = is the mean error associated to the mean.

The environmental index is calculated by $I_j = \bar{Y}_{.j} - \bar{Y}_{..}$, with $\sum_{j=1}^{n} I_j$,

n is the number of environments.

In this method each variety is characterized by $\hat{\beta}_i$ = coefficient of regression and by $\hat{\sigma}_{d_i}^2$ = variance of the deviations of regression, that is, the stability parameters.

2.3.3.3. Lin and Binns method.
In the nonparametric analysis by the Lin and Binns method described by Cruz (2006), the genotypes are characterized by the parameter **Pi** associating stability and productivity that defines as superior the cultivar with performance close to the maximum in several environments. In this method, the **Pi** measurement is adopted as the mean quadratic distance between genotype **i** and the genotype with maximum response in environment **j**, as follows:

$$Pi = \sum_{j=1}^{n} (Y_{ij} - M_j)^2 / 2a, \text{ where:}$$

Pi = estimate of the stability parameter of cultivar **i**; Y_{ij} = productivity of genotype **i** in environment **j**; **n** is the number of environments; M_j = maximum response observed among all the cultivars in environment **j**; **a** is the number of environments. In this method the most stable genotype presents P_i close to zero.

2.3.3.4. AMMI analysis.
AMMI uni-multivariate analysis is described by Duarte and Vencovsky (1999). This analysis includes additive components to study the main effects of genotype and environments and multiplicative components to study the G × E interaction. In the principal components analysis, the variation contained in these significant components is called standard and that contained in the non-significant components is called noise. The following model was used for the AMMI methodology:

$$Y_{ij} = \mu + g_i + e_j + \sum_{k=1}^{n} \lambda_k \gamma_t \alpha_{jk} + \rho_{ij} + \varepsilon_{ij} \qquad , \text{ where:}$$

Table 1
Mean squares (MS) of the joint analysis of variance carried out in the third year on the girth (G), rubber yield (RY), bark thickness (BT) and number of latex vessel rings (NLVR) of 22 rubber tree open-pollinated progeny (POP1) assessed in Jaú, Pindorama and Votuporanga in the state of São Paulo, Brazil and latex production of 30 rubber tree open-pollinated progeny (POP2) assessed in Selvíria in the state of Mato Grosso do Sul and in Colina and Votuporanga in the state of São Paulo, Brazil.

Source of variation		G	RY	NLVR	BT		RY
	D.F.	M.S.				D.F.	M.S
	POP1					POP2	
		(cm)	(g t^{-1} t^{-1})	(un)	(mm)		(g t^{-1} t^{-1})
Blocks/locations	15	7.60	0.22	1.39	0.52	6	8.87
Blocks	5	5.32	0.18	1.13	0.2	2	6.13
Blocks × locations	10	8.73	0.24	1.52	0.64	4	10.23
Progeny	21	97.45**	0.80**	0.93**	2.31**	29	11.47**
Locations	2	2,207.41**	4.60ns	0.55ns	0.08ns	2	1,667.67**
Progenyx Locations	42	8.66*	0.27**	0.34**	0.48**	36[1]	10.06**
Error	315	4.65	0.08	0.14	0.12	77[1]	3.62
Means		21.81	0.81	3.09	3.76		4.36
CV%		9.98	35.71	12.15	9.3		29.02

(g t^{-1} t^{-1}) = g tapping^{-1} tree^{-1}; ns, *, ** - non-significant and significant by the *F* test at 0.05 and 0.01 probability, respectively; [1] values in adjusted because of the heterogeneity of the residual variances, D.F. = Degrees of freedom. C.V = Coefficient of variation.

$Y_{i,j}$ = mean genotype response **i** (i = 1, 2,... g genotype) in environment **j** (j = 1, 2,... a environments); μ = general experimental mean; g_i = fixed effect of genotype **i**; e_j = fixed effect of environment **j**; λ_k = k-th single value (scale) of the original interaction matrix (denoted by G × E interaction); γ_{ik} = element corresponding to the **i**-th genotype in the **k**-th vector singular column of the GE matrix; α_{jk} = element corresponding to the **j**-th environment in the **k**-th vector singular line vector of the GE matrix GA; ρ_{ij} = noise associated to the term **(ga) ij** of the classic interaction of genotype **i** with environment **j**; ε = mean experimental error.

2.3.3.5. Harmonic mean of the relative performance of the genetic values—MHPRVG. In the concept of mixed models, the MHPRVG method predicted by Blup (Best Linear Unbiased Prediction) described by Resende (2007b) includes the simultaneous analysis for yield, stability and adaptability. According to the author, the MHPRVG method should be applied preferentially on the original data, obtaining the Blup(s) for the genotype values (general mean + genotype effects). There is a mixed linear model that gives the genetic values for each experimental situation that involves the G × E interaction.

2.3.4. Analysis of correlation
The stability parameters estimated by the different methods were compared by the Spearman correlation analysis. The stability parameters $\hat{\sigma}_{d_i}^2$ variance of the deviation from the regression by Eberhart and Russell and IPCA 1 of the AMMI analysis were used in the correlation analyses which considered only absolute values (without + or -).

3. Results and discussion

The joint analyses of variance (Table 1) showed significant progeny and progeny × location (P × L) interaction for the traits girth, rubber yield, number of latex vessel rings and bark thickness in POP1 and for rubber yield in POP2. The significance of the progeny effect is an indication of genetic variability and shows favorable condition for selection. The significance of the P × L effect indicates that the relative performance of the progeny was not the same in the locations assessed. Because of these significances the analyses of stability and adaptability using the methods by Wricke, Eberhart and Russell, Lin and Binns and AMMI analysis were carried out.

The deviation analysis (Table 2) also showed significant effect for progeny and the P × L interaction for girth, rubber yield, number of latex vessel rings and bark thickness in POP1 and for rubber yield in POP2. Due to the significances observed in the analysis of deviance, the stability and adaptability were analyzed by the HMRPGV model predicted by BLUP.

The Mauchly test was used as a preliminary analysis prior to split plot analysis to verify the clone × year interaction in rubber yield in Group 1. This test verifies whether a population presents homogeneous and nil residual correlations, a condition known as sphericity. The results were non-significant (Pr > x^2 = 0.2014), indicating that the sphericity was not violated by significant values, permitting the use of split plot design analysis to verify the C × Y interaction. Freitas et al. (2008) assessed measurements repeated in time in sugarcane and recommended the univariate model with a split plot in time scheme because it is easy to apply and interpret, emphasizing the importance of meeting the sphericity condition. The importance of using the Mauchly test as analysis prior to analysis of variance in assessing measurements repeated in time was

Table 2
Joint analysis of deviance of assessments carried out in the third year for the girth (G), rubber yield (RY), bark thickness (BT) and number of latex vessel rings (NLVR) of 22 rubber tree open-pollinated progeny (POP1) assessed in Jaú, Pindorama and Votuporanga in the state of São Paulo, Brazil and latex production of 30 rubber tree open-pollinated progeny (POP2) assessed in Selvíria, in the state of Mato Grosso do Sul and in Colina and Votuporanga in the state of São Paulo, Brazil.

Effect	POP1								POP2	
	G (cm)		RY (t g^{-1} t^{-1})		NLVR (un)		BT (mm)		RY(t g^{-1} t^{-1})	
	Deviance	LTR (x^2)	Deviance	LTR (x^2)	Deviance	LTR (x^2)	Deviance	LTR (x^2)	Deviance	LTR (x^2)
Progeny	15,024.40+	42.98**	724.99+	8.96**	2.228.50+	8.69**	2.188.04+	18.11**	3.954.77+	26.29**
Progeny × Location	14,990.87+	9.45**	727.97+	11.94**	2.242.87+	23.01**	2.231.27+	61.34**	3.958.74+	30.26**
Plot	15,017.86+	36.44**	727.26+	11.23**	2.276.68+	56.87**	2.203.23+	33.30**	3.928.60+	0.12ns
Complet model	14,981.42	–	716.03	–	2.219.81	–	2.169.93	–	3.928.48	

g t^{-1} t^{-1} = g tapping $^{-1}$ tree^{-1}; LTR (x^2) = x^2 of the likelihood ratio test (LRT) tabulated with degree of freedom equal to a 1: 3.84 and 6.63 for the levels of significance of 0.05 and 0.01, respectively + Deviance of theme fitted model without the referred effects.

Table 3

Mean square (MS) of the joint analysis of variance in the split plot in time for rubber yield (RY) corresponding to six years yield used in the assessment of 25 rubber tree genotypes in Votuporanga, São Paulo state, Brazil.

Source of variation	D.F.	RY (g t^{-1} t^{-1}) MS
Blocks	2	164.65
Clones	24	2,002.37**
Residual A	48	241.86
Years	5	1,2670.79**
Residual B	10	29.95
Clones × years	120	177.16**
Residual C	240	30.48
General mean		40.71
C.V%—Error A		38.20
C.V%—Error B		13.44
C.V%—Error C		13.55

g t^{-1} t^{-1} = g tapping $^{-1}$ tree^{-1}; ** significant at 0.01 in the F test. DF. = Degrees of Freedom; C.V. = Coefficient of Variation.

Table 4

Joint analysis of deviance by the means repeated in time of rubber yield (six years) corresponding to 25 rubber tree clones assessed in Votuporanga, São Paulo state, Brazil.

Effect	Deviance	LTR(x^2)
Clones	10,214.86	37.84**
Clones × Years	10,559.78	382.76**
Plot	10,177.07	0.05ns
Permanent environment	10,715.95	538.93**
Complet Model	10,177.02	

g t^{-1} t^{-1} = g tapping $^{-1}$ tree^{-1}; LTR (x^2) = x^2 of the likelihood ratio test (LRT) tabulated with degree of freedom equal to a 1: 3.84 and 6.63 for the levels of significance of 0.05 and 0.01, respectively; n.s. = Not significant.; +Deviance of theme fitted model without the referred effects.

also emphasized by Xavier and Dias (2001). The approach of mixed linear models, such as the predicted analysis by BLUP, is another way of assessing measurements repeated in time and has recently been used by some authors Freitas et al. (2011), Ferreira et al. (2012) and Gouvêa et al. (2013).

Analysis of variance in the split plot design was carried out to verify the P × L interaction (Table 3) and deviation analysis for measurements repeated in time (Table 4) to verify the same interaction by the approach of mixed linear models. In both analyses significant clone effect was observed, that permitted clone selection by temporal analysis. In both the approaches significant P × L interaction was also observed, indicating that the relative performance of the clones was not the same in the different years. Because of the significance of the clone effect and the C × Y interaction in the analysis of the variance in the split plot design in time design stability was analyzed by the methods of Wricke, Eberhart and Russell, Lin and Binns and AMMI analysis. Due to the significances observed in the deviation analysis, the stability and adaptability were analyzed using the HMRPGV model predicted by BLUP.

Table 5 shows the coefficients of correlation among the stability parameters, assessing for different traits within the same population. Table 6 shows the coefficients of correlation among the stability parameters, for rubber yield, assessing POP1, POP2 and Group 1 clones. In these approaches three scenarios were observed in relation to the significance of the association. In the first scenario, some parameters did not show significant association in any of the analyses such as: $\hat{\sigma}^2_{di}$ .with Pi; $\hat{\sigma}^2_{di}$ with HMRPGV; Wi with HMRPGV; IPCA1 with Pi and IPCA1 with HMRPGV. In the second scenario, some parameters showed significant associations in all the analyses such as: Wi% with IPCA1, Pi with HMRPGV. It is emphasized that the negative coefficients of correlations between Pi and HMRPGV are attributed to the fact that there are more stable Pis with values closer to 0 and in the HMRPGV the genotypes with the

Table 5

Spearman coefficients of correlation obtained between the stability and adaptability parameters of the 22 rubber tree progeny assessed in Jaú, Pindorama and Votuporanga, São Paulo state, Brazil.

Traits/parameters	Wi%	IPCA 1	Pi	HMRPGV
Girth				
$\hat{\sigma}^2_{d_i}$	0.23	0.27	0.00	−0.01
Wi%		0.82**	0.25	−0.25
IPCA 1			0.19	-0.16
Pi Geral				−0.98**
Number of latex vessel rings				
$\hat{\sigma}^2_{d_i}$	0.22**	0.27	0.08	0.01
Wi%		0.46 *	0.19	−0.07
IPCA 1			-0.04	0.14
Pi				−0.96**
Rubber yield				
$\hat{\sigma}^2_{d_i}$	0.29	0.45*	−0.05	0.27
Wi%		0.89**	0.02	0.26
IPCA 1			-0.06	0.25
Pi				-0.82**
Bark thickness				
$\hat{\sigma}^2_{d_i}$	0.49*	0.21	0.17	−0.05
Wi%		0.44*	−0.03	0.13
IPCA 1			−0.18	0.28
Pi				−0.97**

*,** Significant at 0.05 and 0.01 probability.$\hat{\sigma}^2_{d_i}$ = Deviation of the regression coefficient by the methods by Eberhart and Russell; Wi = stability parameter by the Wricke method; IPCA1 = first principal component obtained in the AMMI analysis; Pi= stability mean in Lin and Binns; HMRPGV = harmonic mean of the relatives performance of the genetic values predicted by Blup.

greatest values are the most stable and adapted. Finally, in the third scenario, the significance of the association between the parameters varied. In Table 5 significant association between $\hat{\sigma}^2_{di}$ and Wi was observed only for the traits number of latex vessel rings and bark thickness. Table 6 shows that significant association between $\hat{\sigma}^2_{di}$ and Wi is observed only for rubber yield in Group 1 clones, there is no association for rubber yield in POP1 and POP2. The significant

Table 6

Spearman coefficients of correlation obtained between the stability and adaptability parameters estimated in the assessment of the latex production of a population of 22 open-pollinated progeny (POP1) assessed in Jaú, Pindorama and Votuporanga, São Paulo, of 30 rubber tree open pollination progeny is (POP2) assessed in Selvíria, Mato Grosso do Sul and in Colina and Votuporanga, São Paulo, Brazil and rubber yield assessed for six years in 25 clones (Group 1) assessed in Votuporanga, São Paulo, Brazil.

Genetic material/parameter	Wi%	IPCA 1	Pi	HMRPGV
POP1				
$\hat{\sigma}^2_{d_i}$	0.29	0.45*	−0.05	0.27
Wi%		0.89**	0.02	0.26
IPCA 1			−0.06	0.25
Pi				−0.82**
POP2				
$\hat{\sigma}^2_{d_i}$	0.30	0.33	0.00	−0.04
Wi%		0.86**	−0.06	0.08
IPCA 1			0.00	-0.06
Pi				−0.92**
Grupo 1				
$\hat{\sigma}^2_{d_i}$	0.85**	0.72**	−0.34	0.24
Wi%		0.77**	−0.42*	0.33
IPCA 1			−0.21	0.10
Pi				−0.92**

*,** Significant at 0.05 and 0.01 probability.$\hat{\sigma}^2_{d_i}$ = Deviation of the regression coefficient by the method by Eberhart and Russell; Wi = stability parameter by the method by Wricke; IPCA1 = first principal component obtained in the AMMI analysis; Pi = stability mean in Lin and Binns; HMRPGV = harmonic mean of the relative performance of the genetic values predicted by Blup.

association between $\hat{\sigma}_{di}^2$ and IPCA1 was observed for rubber yield in POP1 (Table 5 but not for the other traits. In the assessment of rubber yield (Table 6 significant association was observed between IPCA1 for POP1 and Group 1, but it was not observed for POP2. The significant association between Wi and Pi was observed only for rubber yield in Group 1 clones (Table 6 In the other analyses (Tables 5 and 6) the association between these parameters was not significant. It can be inferred from these results that the association among some stability parameters varies according to the trait analyzed and/or with the group of genotypes analyzed.

The association between the Wricke (Wi) method and the AMMI analysis (IPCA1), observed in the present study were also observed by Silva and Duarte (2006) in a similar study on soybean. The strong association between methods makes unnecessary use them simultaneously. Association between the methods by Eberhart and Russell ($\hat{\sigma}_{di}^2$) and Lin and Binns (Pi) were found by Carbonell et al. (2007), when assessing common bean yield. In this work this association was not observed, are methods that can be used simultaneously.

In the present study, the association between the parameters by Eberhart and Russell and IPCA1 of AMMI depended on the analysis, Silva and Duarte (2006), assessed soybean yield and found low association between these methods. The authors suggested simultaneous use of these methods to generate differentiated approaches in the G × E interaction process.

There was no association between the AMMI (IPCA1) and HMRPGV methods. A similar situation was reported by Silva et al. (2011) in carrot. Thus, the methods should be used simultaneously to offer different and complementary approach.

From the results observed, it was verified that there are methods that show strong association, such as the methods by Wricke (Wi) and AMMI (IPCA1) analysis, and Lin and Binns (Pi) and HMRPGV. In the first case, the association can be explained because both use the genotype contribution for the G × E interaction, as already emphasized by Silva and Duarte, 2006. However, the AMMI analysis is the most indicated, these authors recommend AMMI analysis because this method discards noise on GE interaction. Gouvêa et al., 2011, observed that Wricke method selects stable genotypes among those who have low production performance, undesirable situation in improvement. In the second case, Lin and Binns (Pi) and HMRPGV have in common the fact of considering the genotype performance and selecting stable and adapted genotypes among those with best performance. According to Resende (2007b), HMRPGV predicted by best linear unbiased prediction is similar to the method by Lin and Binns, but the first offers results as means-predicted that are interpreted as genetic values of yield, stability and adaptability and allows estimated the genetic gain with selection of the best progeny. The strong association between HMRPGV and Lin and Binns makes it unnecessary to use them simultaneously.

The lack of association among some stability methods indicates that the general ranking for stability varied from one method to another. But it is important to emphasize that different methods may agree on genotype selection for stability, in this case the best classification for stability are the same from one method to another, even though the general ranking is not. The stable performance of some genotypes identified by different methods has already been reported by Mohammadi and Amri (2008), Priyadarshan et al. (2008), Gouvêa et al. (2012), Carbonel et al. (2007) and Sahin et al. (2012), that makes the selection more reliable, which, allied to the fact that the association among some stability parameters varies depending on the genotype group and/or trait analyzed, reinforces the importance of the simultaneous use of different methods of stability analysis.

4. Conclusions

Thus the present study contributes to these stability studies by showing that association among some stability parameters varies according to the trait analyzed and/or the genotype group analyzed. Consequently the association among stability parameters observed in one analysis cannot be applied in another analysis. In this data analysis is possible to observe that the AMMI method can be used with HMRPGV or Lin and Binns. In addition, Eberhart and Russell can be used with HMRPGV or Lin and Binns, since they offer differentiation and provide additional approaches to the study of stability. This simultaneous use of no-associated methods is useful to increase security in the selection of genotypes, considering that stability is one of the goals of genetic improvement.

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