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Soybean stability and adaptability in Southern and Central Brazil

Marco Antonio Rott de Oliveira[1*], Valéria Carpentieri Pípolo[2], Ivan Schuster[1], Dorival Vicente[1], Marisa Dellagostin[1], and Edson Feliciano de Oliveira[1]

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ABSTRACT - *The use of effective methodologies for the identification of more stable lines with wide adaptation is an indispensable tool in genetic improvement. Diverse methods of estimation are presently available, each one with specific features. This study evaluated the adaptability and stability of 21 soybean lines/cultivars grown in 78 environments in the southern and central regions of Brazil, between 2001 and 2003, using four methodologies. In the stability analyses, the four methods led to the same results. In the analyses of adaptability, the methods Eberhart and Russel (1966) and of Cruz et al. (1989) presented basically the same results, though the latter presented additional information regarding the adaptability of lines to favorable and unfavorable environments. The analysis by the AMMI method led to the establishment of the models AMMI3 (Central Region) and AMMI4 (southern region), making the analysis of adaptability by biplots very complex. Six stable lines were identified in the central region and two in the South.*

Key words: *Glycine max*, genetic improvement, genotype x environment interaction, yield.

INTRODUCTION

Soybean in Brazil is grown in a latitude range of 32º south to 4º north and improvement programs target the development of cultivars adapted to a wide range of environments. The interaction between genotypes and the different environments is one of the main obstacles in the selection of competitive soybean genotypes apt for a wide range of cultivation. On the other hand, the genotypes x environments interaction is also a great opportunity for the selection of positive interactions to associate plant traits with predictable environment conditions, making the identification of adapted, high-yielding genotypes possible (Duarte and Vencovsky 1999).

Univariate methods that use simple and multiple regression were, over the last years, the most widely used statistical methods to evaluate the effect of interaction that involves different test genotypes and environments (Mauro et al. 2000, Prado et al. 2001). According to Zobel et al. (1988) and Crossa (1990), linear regression explains, for the most part, only part of the complex variation caused by interaction. Furthermore, little information is obtained on specific interactions of genotypes and environments. To overcome these limitations, Crossa (1990) suggested the application of multivariate methods such as the AMMI (additive main effects and multiplicative interaction analysis) procedure. This model combines additive components for the principal genotype effects and environments, with multiplicative components for the effects that involve genotypes x environments interaction. In the AMMI approach the measures of phenotypic stability are based on ranks and the graphic presentation of the results provides a more in-depth analysis of the genotype effects x environments interaction (Zobel et al. 1988; Duarte and Vencovsky 1999). The AMMI method is

[1] COODETEC – Cooperativa Central de Pesquisa Agrícola, C. P. 301, 85.813-450, Cascavel, PR, Brasil. * E-mail: marco@coodetec.com.br
[2] Departamento de Agronomia, Universidade Estadual de Londrina, C. P. 6001, 86.051-990, Londrina, PR, Brasil

applied in studies on the genotype x environment interaction in crops such as barley (Pinnschmidt and Hovmoller 2002), maize (Ajibade et al. 2002 and Pixley and Bjarnason 2002), wheat (Kaya et al. 2002), soybean (Oliveira et al. 2003), and common bean (Carbonell et al. 2004), among others.

The objective of this study was to evaluate the stability and adaptability of two sets of elite soybean lines with contrasting regions of adaptation and to verify the effectiveness of the multivariate method AMMI in relation to the univariate methods of Wricke (1964), Eberhart and Russel (1966) and Cruz et al. (1989) to determine the stability of the evaluated lines.

MATERIAL AND METHODS

Seventeen elite soybean lines of the soybean breeding program of COODETEC (Cooperativa Central de Pesquisa Agrícola) were evaluated plus four control cultivars in 78 experiments, during the harvests of 2001 and 2002 in the Central Region states (MG, MT, GO, and BA) and in the harvests of 2001, 2002 and 2003 in a region covering the states of RS, SC, PR, SP, MS and Paraguay (here denominated southern region) (Table 1). The trials of the central region comprised 12 and the trials of the southern region 10 genotypes, with one common line to both regions. The trials were set up in the randomized block design with three replications for each environment. Each plot consisted of four 5.0 m long rows, spaced 0.40 m apart and 0.20 m in-between plants. The two mid rows were harvested, disregarding 0.5m on either end, amounting to a useful area of 3.2 m^2. Grain weight (kg ha^{-1}) was adjusted to 13% moisture.

For the analysis of adaptability and stability, the methods of Wricke (1964), Eberhart and Russel (1966), Cruz et al. (1989) and AMMI (Gauch 1988) were used. The methods of Wricke (1964), Eberhart and Russel

Table 1. Identification of the lines/cultivars and the site of experimentation

Genotypes		Environments							
Code#	Line/cultivar	Code	Location£	Code	Location	Code	Location	Code	Location
G1	CD 96-231	E1	Alto Taquari-MT(1)	E22	Sonora-MS(2)	E43	Arapoti-PR(2)	E64	Campos Novos-SC(3)
G2	CD 96-3461	E2	Batatais-SP(1)	E23	Tupaciguara-MG(2)	E44	Campo Mourão-PR(2)	E65	Cruz Alta-RS(3)
G3	CD 97-1027	E3	Conc. do Alagoas-MG(1)	E24	Arapoti-PR(1)	E45	Cascavel-PR(2)	E66	Cachoeira do Sul-RS(3)
G4	CD 97-1039	E4	Goiatuba-GO(1)	E25	Batatais-SP(1)	E46	Dourados-MS(2)	E67	Cascavel-PR(3)
G5	CD 97-1367	E5	Guairá-SP(1)	E26	Cândido Mota-SP(1)	E47	Golondrina-PY(2) §	E68	Carazinho-RS(3)
G6	CD 97-1403	E6	Nova Ponte-MG(1)	E27	Campo Mourão-PR(1)	E48	Guarapuava-PR(2)	E69	Dourados-MS(3)
G7	CD 97-1420	E7	Primavera do Leste-MT(1)	E28	Campos Novos-SC(1)	E49	Mafra-SC(2)	E70	Guaíra-SP(3)
G8	CD 97-1509	E8	Rondonópolis-MT(1)	E29	Cruz Alta-RS(1)	E50	Maracaju-MS(2)	E71	Guarapuava-PR(3)
G9	CD 204	E9	Rio Verde-GO(1)	E30	Cascavel-PR(1)	E51	Mariópolis-PR(2)	E72	Mafra-SC(3)
G10	CD 211	E10	Sonora-MS(1)	E31	Dourados-MS(1)	E52	Não-Me-Toque-RS(2)	E73	Mariópolis-PR(3)
G11	MG/BR 46 Conquista	E11	Uberlândia-MG(1)	E32	Golondrina-PY(1)§	E53	Ponta Porã-MS(2)	E74	Palotina-PR(3)
G12	CD 96-556	E12	Alto Taquari-MT(2)	E33	Lagoa Vermelha-RS(1)	E54	Paranavaí-PR(2)	E75	Rolândia-PR(3)
G13	CD 97-1022	E13	Batatais-SP(2)	E34	Maracaju-MS(1)	E55	Ponta Grossa-PR(2)	E76	Santo Inácio-PR(3)
G14	CD 97-1024	E14	Chapadão do Céu-GO(2)	E35	Ponta Grossa-PR(1)	E56	Palotina-PR(2)	E77	Santa Rosa-RS(3)
G15	CD 98-1799	E15	Cristalina-GO(2)	E36	Palotina-PR(1)	E57	Sidrolândia-MS(2)	E78	Umuarama-PR(3)
G16	CD 98-2100	E16	Goiatuba-GO(2)	E37	Rolândia-PR(1)	E58	Santa Rosa-RS(2)		
G17	CD 98-2619	E17	Gaíra-SP(2)	E38	Sidrolândia-MS(1)	E59	Vacaria-RS(2)		
G18	CD 98-2731	E18	Nova Ponte-MG(2)	E39	Selbach-RS(1)	E60	Abelardo Luz-SC(3)		
G19	CD 98-2994	E19	Rondonópolis-MT(2)	E40	Umuarama-PR(1)	E61	Arapoti-PR(3)		
G20	CD 206	E20	Roda Velha-BA(2)	E41	Vacaria-RS(1)	E62	Comodoro-MS(3)		
G21	CD/FAPA 1425-73	E21	São Gabriel do Oeste-MS(2)	E42	Abelardo Luz-SC(2)	E63	Cândido Mota-SP(3)		

Lines and cultivars of G1 to G12 were cultivated in the trials of Central Brazil, and of 12 to 21 in trials of the south of Brazil
£ Location of E1 to E23: Central Brazil. Location of E24 to E78: Southern region. (1) 2001/2002; (2) 2002/2003; (3)2003/2004
§ Golondrina:Paraguay

(1966) and Cruz et al. (1989) were applied as described by Cruz et al. (2004), and the analyses realized using the software package Genes (Cruz 2001). The AMMI approach was applied as described by Duarte and Vencovsky (1999), and the analyses realized with the software Stability (http://www.dex.ufla.br/danielff/dff02.htm). The biplots were established using the software Statistica (StatSoft 1995).

RESULTS AND DISCUSSION

In the individual analyses of each one of the 23 environments of the Central Region, 10 presented a significant genotype effect, evidencing genetic variations among them in all environments. The variation coefficients varied from 8.11% to 33.29%. In the joint analysis of variance, where each experiment represented an environment, the genotype effects, environment and the genotypes x environments interaction were significant. The sum of squares of the genotype x environment interaction represented 15.32% of the sum of squares of treatments, and 13.05% of the total sum of squares.

In the trials of the southern region, the genotype effect was significant in 25 of the 55 experiments and the variation coefficients ranged from 5.98% to 20.54%. In this set of experiments the effects of the genotype, environment and the genotypes x environments interaction were significant as well. The sum of squares of the interaction represented 13.60% of the sum of squares of treatments and 11.74% of the total sum of squares.

Table 2 presents the results of the stability and adaptability analyses obtained with data from the central and southern region by the methods proposed by Wricke (1964), Eberhart and Russel (1966) and Cruz et al. (1989).

According to the ecovalence method (Wi^2) proposed by Wricke (1964) the most stable genotype is the one that presents the lowest Wi (%) index. For the data obtained by the 12 lines/cultivars studied in the 23 environments in the central region, the genotypes G8, G3, G2, G5, G9, and G7 were the most stable and the genotypes G4, G1 and control G11 (MG/BR 46 Conquista), although the least stable, were the most productive (Table2). Similar results were obtained by Prado et al. (2001) who evaluated the performance of cultivar MG/BR 46 Conquista in the Cerrado region of Rondônia, which presented a high Wi^2 index (13.30) and was the most productive.

In the environments of the southern region, control G20 (CD 206) was the most stable and the least productive (2870 kg ha^{-1}). Note that this productivity was only 5.1% inferior to line G19, which was the most productive (3026 kg ha^{-1}) and presented good stability as well (Table 2).

The method of Eberhart and Russel (1966) uses a regression of each genotype mean in each environment, in relation to the environmental index. By this method, an inclination of the straight line of regression (β_1) indicates the adaptability of a genotype, and the deviations around the straight line indicate stability. The determination coefficient of the regression is also related with the predictability of the genotype performance.

Of the 12 evaluated genotypes in the 23 environments of the central region, genotype G4 was adapted to favorable environments (in other words, it is a demanding line, but responds to improved cultivation conditions) Genotypes G5 and G6, with a similar performance to control G11, were adapted to the unfavorable environments, that is, they were more robust, but did not respond alike when the environment was improved. The other tested genotypes presented wide adaptability. In relation to stability, the genotypes G1, G4, G6, G10, G12, and control G11 were little stable (exactly the same lines/cultivars identified as little stable by the Wi index). Line G4, although little stable, presented reasonable predictability, since the determination coefficient of the regression in relation to the environmental indices was 88%. All other genotypes evaluated in the central region (G2, G3, G5, G7, G8 and G9) presented good stability. Interestingly, the four most productive genotypes were little stable. The most productive genotype among those of high stability was G5, which is the fifth most productive.

Of the 10 lines/cultivars evaluated in the southern region, line G15 is adapted to unfavorable environments and quite stable and predictable. Line G12 is adapted to favorable environments and little stable. The other lines in evaluation presented wide adaptability but low stability, barring control G20, which is quite stable and predictable. Its mean yield was however the lowest of all. The estimates of stability once more coincide with those obtained by the Wi index, since line G15 and control G20 were the most stable by this analysis.

The method proposed by Cruz et al. (1989) also uses linear regression of the mean of each genotype in relation to an environmental index, but in this approach the straight line of regression has two segments, one for the unfavorable and the other for the favorable environments. The inclination of the segments is given by β_1 for the unfavorable environments and by $\beta_1 + \beta_2$ for the favorable environments.

Table 2. Mean grain yield (kg ha-1) and estimates of parameters of adaptability and stability of 12 soybean genotypes, evaluated in 23 environments in Central Brazil, in the crop years 2001/2002 and 2002/2003 and of 10 soybean genotypes, evaluated in 55 environments in the South of Brazil in the crop years 2001/2002, 2002/2003 and 2003/2004

Genotype	Mean (kg ha-1)	Wricke (1964)	Eberhart and Russel (1966)			Cruz et al. (1989)			
		Wi (%)	β_1	s^2d	R^2(%)	β_1	$\beta_1+\beta_2$	MSE	R^2(%)
G1	3155	12.56	1.11	140206.57**	81.9	1.09	1.23	682626.53**	82.07
G2	2972	5.49	0.94	18887.09	88.1	0.94	0.93	305396.01	88.11
G3	3043	4.07	1.00	-4282.31	91.6	1.01	0.95	231411.84	91.69
G4	3304	13.27	1.29**	92549.09**	88.8	1.27**	1.47*	527237.43**	89.00
G5	3194	5.94	0.85*	10537.29	86.7	0.85*	0.82	278956.75	86.71
G6	2976	9.26	0.82**	64221.93*	79.3	0.85*	0.57*	426667.77**	80.29
G7	2884	6.42	1.02	38093.80	87.8	1.03	0.92	363027.36	87.87
G8	3065	4.05	1.00	-4629.84	91.7	1.02	0.88	226733.87	91.84
G9	2819	6.28	1.11	25797.94	90.6	1.12	1.05	326108.62	90.59
G10	3272	10.29	1.05	106668.94**	82.7	1.05	1.00	581077.01**	82.75
G11	3260	13.22	0.79**	125606.03**	71.1	0.72**	1.27	559992.61**	74.79
G12(C)	3298	9.15	1.02	87470.44**	83.5	1.04	0.89	515610.64**	83.67
G12(S)	3007	17.52	1.12**	103851.00**	82.54	1.15**	0.97	469472.97**	82.84
G13	3008	9.51	0.95	35207.21**	85.90	0.95	0.96	267751.15**	85.91
G14	2999	9.87	0.94	37887.04**	85.25	0.92	1.00	274436.04**	85.34
G15	2912	7.14	0.90*	8918.24	88.74	0.91*	0.88	187215.44	88.75
G16	3004	10.93	1.00	50038.09**	85.24	1.02	0.89	308729.64**	85.45
G17	2970	11.08	0.96	50333.85**	84.06	0.96	0.95	314067.06**	84.06
G18	2914	9.98	1.02	40822.00**	86.97	1.02	1.05	284678.90**	86.98
G19	3026	8.66	1.07	25839.33*	89.68	1.09	1.01	237491.16*	89.75
G20	2870	5.56	1.08	-3848.02	93.42	1.07	1.10	148130.42	93.43
G21	2916	9.74	0.97	38253.38**	85.93	0.92	1.18	259425.08**	86.83

G1 to G12(C) – Central Region, G12(S) to G21 – Southern region
G12(C) and G12(S) stand for the same line
MSE: Mean Square Error, not significant
*, ** significant at 5% and 1% probability, respectively, by the t test

Among the 12 genotypes evaluated in the 23 environments of the Central Region, genotypes G5, G6 and control G11 were the most adapted to unfavorable environments (β_1 smaller than 1). G5, with a similar performance to control G11, has wide adaptability to favorable environments ($\beta_1+\beta_2$ equal to 1). G6 presented low adaptability to favorable environments. Line G4 is most adapted to favorable environments ($\beta_1+\beta_2$ higher than 1), but does not as well in the unfavorable environments (β_1 higher than 1). The other evaluated genotypes had wide adaptability (β_1 and $\beta_1+\beta_2$ equal to 1). The results were in line with the ones obtained by the method of Eberhart and Russel (1966), whereas the method of Cruz et al. (1989) provided some additional information in relation to the genotypes G5, G6 and G11. According to the method of Eberhart and Russel (1966), these lines are adapted to unfavorable environments. The method of Cruz et al. (1989) showed that G6 is not adapted to favorable environments, while G5 and G11, besides adapted to unfavorable are widely adapted to favorable environments as well.

The results obtained regarding stability by the method of Cruz et al. (1989) in the experiments of the Central Region were exactly the same as those obtained by the method of Eberhart and Russel (1966), which coincides with the method of Wricke (1964).

For the 10 genotypes evaluated in the southern region, line G15 is adapted to unfavorable environments, as indicated by the method of Eberhart and Russel (1966). However, this genotype presents wide adaptability to favorable environments. Genotype G12, which by the method of Eberhart and Russel (1966) was indicated as adapted to favorable environments, was indicated as not adapted to unfavorable environments by the method of Cruz et al. (1989), and with wide adaptability to favorable environments. All other genotypes presented wide adaptability to favorable and unfavorable environments, while only line G15 and control G20 were considered stable.

The analysis of variance by the AMMI method (Table 3) defined AMMI model 3 for the environments of the Central Region, and AMMI4 for the southern region. These models retain 68.79% and 66.18% of the sum of squares of the genotypes x environments interaction (Table 4) for the environments southern and central region, respectively. A proposition of the analysis by the AMMI approach is to recover only what is considered "standard" in the sum of squares of the interaction and to disregard what is considered noise. For both datasets, around one third of the sum of squares of the genotypes x environments interaction consisted of noise.

The biplots of the AMMI analysis are presented in the Figures 1 and 2, considering the scores in function of the selected AMMI model. In this kind of biplot, the most stable genotypes must be close to the origin and the least stable more distant from the origin. The genotypes G2, G3 G5, G8, and G9 were the most stable in the environments of the central region of Brazil (Figure 1). AMMI analysis also evaluated the environment stability; among the 23 environments of the central region, the most instable were A5, A13, A14, A15, A16, A17, A18, A19 and A22. Genotypes and stable environments appeared in the same region in the biplots (near the origin). Since most environments are positioned in this region, one may say that the five genotypes identified as the most stable also presented wide adaptability. The analyses by the methods of Eberhart and Russel (1966) and Cruz et al. (1989) identified that line G4 is adapted to favorable environments. By the AMMI biplot (Figure 1), this line was associated to environment A15 in plot A, and to the environments A6 and A21in plot B. There is no pattern of a simultaneous association of this line with any specific environment in the two biplots. Lines G5, G6 and control G11, indicated for unfavorable environments by the above-described methods, did not present consistent association with specific environments in the biplots of Figure 1 either, except for G5, which appears close to the origin in both biplots, near most environments, expressing wide adaptability.

The biplot analysis for the 10 evaluated genotypes in the southern region (Figure 2) is a little more complex, since three biplots must be considered to include the first four principal components the AMMI4 model requires. Line G15 and control G20 were the most stable (appear close to the origins in the three biplots). Lines G12, G17 and G18 were the most instable (distant from the origin in

Table 3. Joint analysis of variance of 12 soybean lines/cultivars grown in 23 environments in Central Brazil in the crop years 2001/2002 and 2002/2003, and of 10 soybean lines/cultivars raised in 55 environments in the South of Brazil in the crop years 2001/2002, 2002/2003 and 2003/2004, by the AMMI method

Sources of variation	Central Region				Southern region			
	df	MS	Fc	Pr>Fc	df	MS	Fc	Pr>Fc
Genotypes(G)	11	1945152.83	8.30	0	9	490711.59	3.12	0.00101
Environments(E)	22	27719380.78	118.35	0	54	17454740.89	111.07	0
G x E	242	471974.58	2.01	0	486	306644.89	1.95	0
CP1	32	1246575.85	5.32	0	62	630926.57	4.01	0
CP2	30	796379.51	3.40	0	60	439973.76	2.80	0
CP3	28	528252.80	2.25	0.00029	58	314733.83	2.00	0.00002
CP4	-	-	-	-	56	265318.65	1.69	0.00141
Deviation	152	234506.31	1.00	0.48642	862	85750.60	0.54	1
Error	550	234216.14			1098	157145.08		

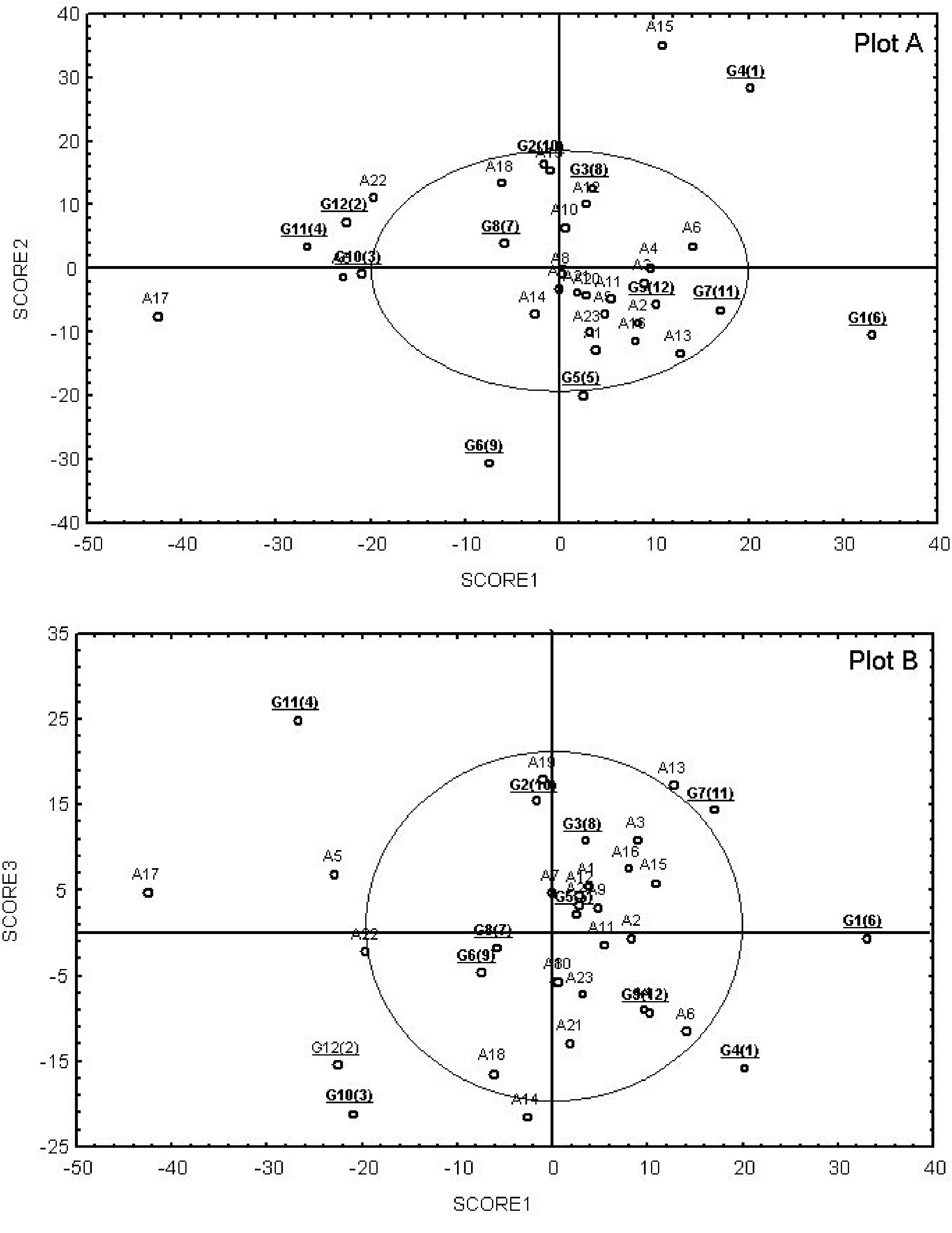

Figure 1. Biplot of AMMI analysis, considering the first three Principal components for stability of 11 soybean lines evaluated in 23 environments in Central Brazil in the crop years 2001/2002 and 2002/2003. The ellipse delimits the most stable genotypes (G underlined) and environments (A). Numbers in brackets indicate the relative position of each genotype, in the mean of the 23 environments

the three biplots), with exception of G15 and control G20. All lines appear instable in at least one biplot. This result was also observed in all evaluation methods of stability used above. All 55 evaluated environments can be considered stable based on the three biplots of Figure 2. Based on the position of the lines and environments in the biplots, line G15 and control G20 can be considered as of wide adaptability, since their positions are in the same region as most of the environments. By the methods of Eberhart and Russel (1966) and Cruz et al. (1989), line G15 was classified as adapted to unfavorable environments, and line G12 adapted to favorable environments, while the other lines presented wide adaptation. The biplots did not show this pattern and, with exception of line G15 and control G20, no consistent association of genotype with specific environment could be obtained across the three biplots.

In the analysis of stability, all methods presented similar results. In the analyses of adaptability results obtained by the methods of Eberhart and Russel (1966) and of Cruz et al. (1989) were very similar. By the latter it was however possible to obtain more complete information. For example, by the method of Eberhart and Russel (1966), line G5 and control G11 were classified as adapted to unfavorable environments, while by the method of Cruz et al. (1989) these genotypes were classified as of specific adaptability to unfavorable environments and of wide adaptability to favorable environments. So, by the method of Eberhart and Russel (1966), G5 and G11 would only be recommended for the unfavorable environments. The additional information provided by the bi-segmented regression of the method of Cruz et al. (1989) however recommended them for the unfavorable as much as for favorable environments. The same was true for line G15, evaluated in the southern region. Line G12, on the other hand, when evaluated in the southern region by the method of Eberhart and Russel (1966) was classified as of specific adaptability to favorable environments, but when evaluated by the method of Cruz et al. (1989), it becomes evident that this line is not adapted to unfavorable environments, but rather presents wide (and not specific) adaptability to favorable environments.

The analysis of adaptability through the biplots of the AMMI analysis is not a simple task when more than one biplot should be taken into consideration in the evaluation. This is the case when the AMMI model to be used is greater than AMMI2. Besides, when a large number of genotypes and/or environments is evaluated, the high number of points in the biplot makes the identification of each individual point difficult and the analysis becomes even more trying. The AMMI analysis has quite strong statistical proprieties, since it eliminates the “noises” of the genotypes x environments interaction, and concentrates the analysis only on the “standard” of this interaction. Besides, environment stability can be evaluated, making the elimination of little stable environments possible. In the present analysis however, where two datasets of different regions were considered,

Table 4. Decomposition of $MS_{G \times E}$ and percentage of explanation of each eigenvalue, in the stability and adaptability analysis of 12 soybean lines/cultivars in Central Brazil, and of 10 lines/cultivars in the South of Brazil, by the AMMI method

Principal component	Central Region			Southern region		
	Eigenvalues	% Explanation	% Accumulated	Eigenvalues	% Explanation	% Accumulated
1	13296.809	34.92	34.92	13039.149	26.25	26.25
2	7963.795	20.92	55.84	8799.475	17.71	43.96
3	4930.359	12.95	68.79	6084.854	12.25	56.21
4	3961.668	10.41	79.20	4952.614	9.97	66.18
5	2441.900	6.41	85.61	4012.832	8.08	74.26
6	1814.725	4.77	90.38	3799.683	7.65	81.91
7	1239.927	3.26	93.63	3388.307	6.82	88.73
8	845.364	2.22	95.86	3100.743	6.24	94.97
9	726.901	1.91	97.76	2498.812	5.03	100.00
10	501.796	1.32	99.08			
11	349.369	0.92	100.00			

the AMMI analysis did not present an additional contribution to the joint analyses for the estimates of stability and adaptability of soybean lines and cultivars, but rather made the interpretation more difficult, in function of the obtained AMMI models.

The analyses of stability and adaptability by the methods of Eberhart and Russel (1966) and of Cruz et al. (1989) present more simplified applications. They make it possible that statistical tests identify the most stable genotypes and the environment group to which they are most adapted more precisely. Of the two, the method proposed by Cruz et al. (1989) presents more in-depth information on adaptability. However, this method requires the use of a larger number of environments in the analysis, to permit the separation of the environments in two groups (favorable and unfavorable) as well as regression with each group.

Among the lines evaluated in the central region, line G5 can be indicated as the regionally most appropriate, owing to its good adaptability to unfavorable environments and general adaptability to favorable environments, besides being stable. Besides, the mean was high, only 3.3% below the best mean. Line G1, which presented the highest mean, must only be indicated for favorable environments.

For the southern region, line G15 presented the same traits as line G5 above, however was one of the least productive. Still, the productivity was only 3.8% inferior to the most productive line.

Line G12 is present in the experiments of both regions. In the central region, its mean was the second highest (3298 kg ha^{-1} or 0.18% less than the highest mean), and the adaptability was wide in favorable as much as unfavorable environments. However, its stability was low. In the southern region, its mean ranked fourth (3007 kg ha^{-1} or 0.63% lower than the highest mean), with wide adaptability to favorable environments, but not recommended for unfavorable environments. It also presented low stability in the southern region. Besides, the line presents resistance to Soybean Cyst Nematode *Heterodera glycines* Ichinohe and the root-knot nematodes *Meloidogyne javanica* (Treub) Chitwood and *M. incognita* (Kofoid and White) Chitwood. For these traits and for its performance in the 78 test environments, this line can be recommended for cultivation in the entire central region of Brazil and favorable environments of the southern region. This is probably the first time that a soybean line/cultivar can be recommended for cultivation in such a wide region, spreading from Rio Grande do Sul to Mato Grosso and Bahia.

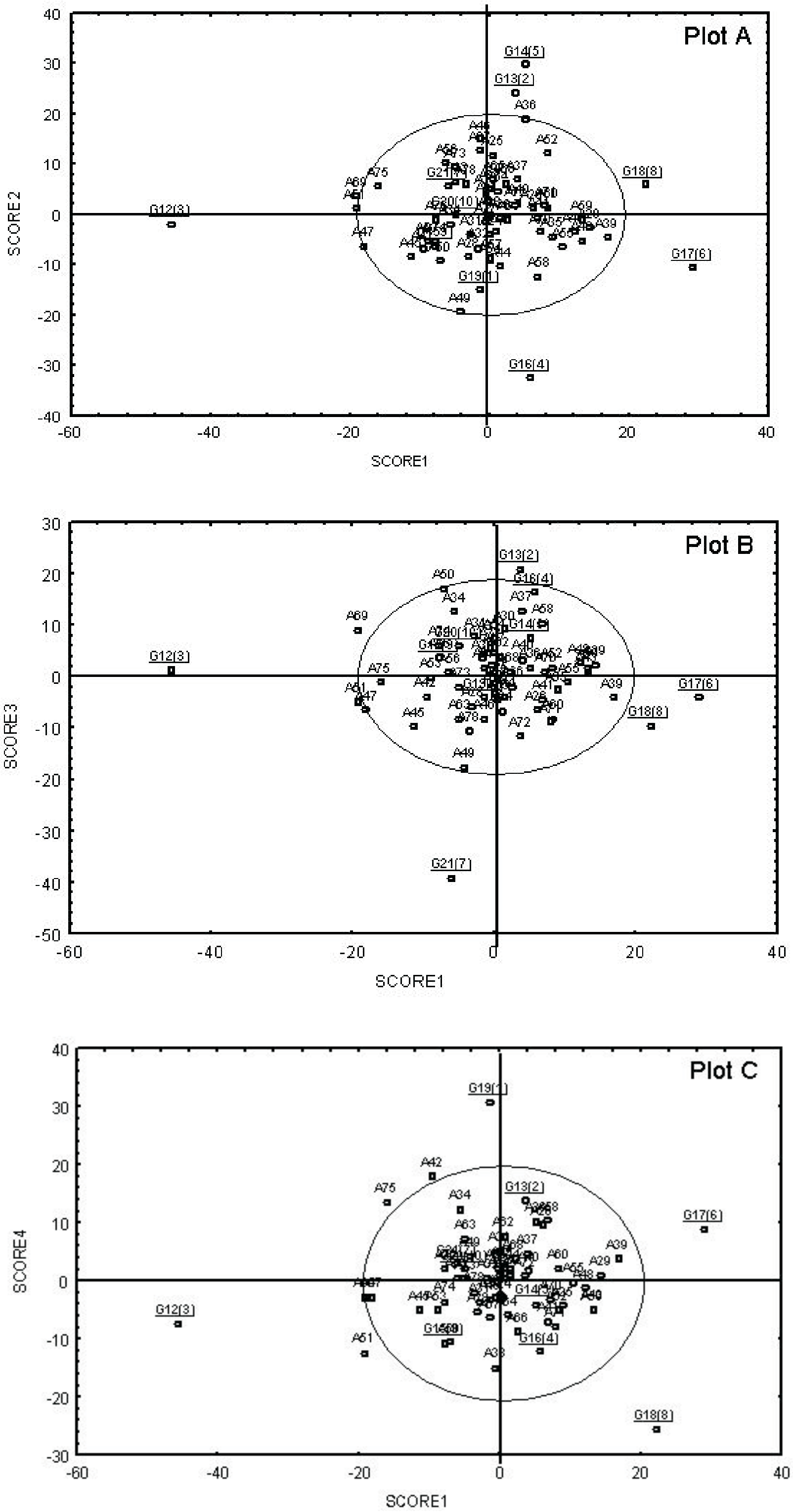

Figure 2. Biplot of the AMMI analysis, considering the first four principal components for stability of 10 soybean lines/cultivars evaluated in 55 environments in the southern region of Brazil in the crop years 2001/2002, 2002/2003 and 2003/2004. The ellipse delimits the most stable genotypes (G underlined) and environments (A). Numbers in brackets indicate the relative position of each genotype, in the mean of the 55 environments

Estabilidade e adaptabilidade de soja nas regiões sul e central do Brasil

RESUMO - *O uso de metodologias eficientes na identificação de linhagens mais estáveis e com ampla adaptação é ferramenta indispensável no melhoramento genético. Diversos métodos de estimação estão atualmente disponíveis, cada qual com propriedades específicas. Neste trabalho foram avaliadas a adaptabilidade e estabilidade de 21 linhagens/cultivares de soja conduzidas em 78 ambientes nas regiões sul e central do Brasil, entre 2001 e 2003, utilizando quatro metodologias. Nas análises de estabilidade, os quatro métodos apresentaram os mesmos resultados. Nas análises de adaptabilidade, os métodos Eberhart e Russel (1966) e de Cruz et al. (1989) apresentaram basicamente os mesmos resultados, porém o último apresentou informações adicionais em relação à adaptabilidade das linhagens nos ambientes favoráveis e desfavoráveis. A análise pelo método AMMI produziu os modelos AMMI3 (região central) e AMMI4 (região sul), tornando complexa a análise de adaptabilidade pelos biplots. Foram identificadas seis linhagens estáveis na região Central e duas na região Sul.*

Palavras-Chave: *Glycine max*, melhoramento genético, interação genótipo x ambiente, produtividade.

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