Genotype-environment interaction in maize hybrids: an application of the AMMI model

Jaison Pereira de Oliveira*; Weber Neves Moreira Jr; João Batista Duarte; Lázaro José Chaves and José Baldin Pinheiro

Setor de Melhoramento Vegetal, Escola de Agronomia, Universidade Federal de Goiás (UFG), Caixa Postal 131, CEP 74001-970, Goiânia, GO, Brazil. (* Corresponding Author. E-mail: bictu@bol.com.br)

ABSTRACT

The genotype-environment interaction is generally recognized when the same genotype is assessed in different environments, having a decisive influence in cultivar recommendation. Maize hybrids that are only adapted to particular environments can become a limiting factor to seed production in large scale. One of the main objectives of breeders is the obtainment of a hybrid with high mean yield and good adaptation to different environments. The present study assessed the grain yield stability in thirty-six maize genotypes in ten environments located in Central Brazil in the 1999/2000 growing season. The analysis of variance (ANOVA) detected significance ($P<0.01$) for the genotype-environment interaction (GE). The AMMI model (additive main effects and multiplicative interaction) was used to assess the additive and multiplicative effects of the interaction. The results indicated homogeneity of environments assessed and high correlation of the hybrid genetic constitution with the yield stability of the three types studied -single, triple and double crosses maize hybrids. The first multiplicative component of the interaction explained more than half (50.6%) of the original sum of squares (SS_{GE}). Most of the environments were neutral in their contribution to the interaction. The Uberlândia environment contributed positively, while the environment in Patos de Minas contributed negatively to the GE interaction. Most of the genotypes also presented a low contribution to interaction. Some single crosses hybrids presented greater mean yield (10182.0 $kg.ha^{-1}$) while the double crosses hybrids presented greater stability to the environments studied.

KEY WORDS: *Zea mayz,* genotype-environment interaction, ammi model.

INTRODUCTION

One of the greatest challenges to maize breeders is the obtainment of a hybrid with high mean yield and the widest possible adaptation to the various environments so that the maize hybrids can be produced on large scale, lowering the production costs of the basic material and making it more accessible to producers. In the initial assessment, maize hybrids are tested in relatively few environments, and interaction can interfere in the performance results leading to errors in selection where promising materials are discarded because of the lack of a more careful analysis of the data obtained. The relative performance of the genotypes can be altered with changes in the environments and these different responses are due to the genotype-environment interactions (GE) because there are environments that are either more or less favorable to certain genotypes.

Several statistical analysis procedures have been used to better interpret these interactions, that is, to analyze the performance of the various environments and ascertain the genotype stability. The most used methods to interpret genotype stability are based on regression analyses (such as Finlay and Wilkinson, 1963; Eberhart and Russell, 1966; Silva and Barreto, 1985; Cruz et al., 1989; Brazil, 1990). Agronomic zoning is used to stratify environments in sub-regions within which the interactions are not significant (Brasil, 1990; Duarte and Zimmermann, 1991). These methods are dependent on the genotypes and environments under study and may not be informative if the linearity fails (Crossa, 1990).

The additive nature of the common analysis of variance (ANOVA) allows for an adequate description of the main effects (genotypic and environmental effects). However, the GE interaction (residue after fitting an additive model for these effects) may not be additive and other techniques are required to identify the existing relationships. The principal components analysis is a statistical procedure that gives a multiplicative model that can be used to diagnose and analyze the interaction, although it is also faulty in the identification of the main significant effects (Shafii and Price, 1998). In this sense, the

AMMI model (Crossa, 1990) is a method that combines, in a single model, the estimation of the main effects and multiplicative components for the effects of the GE interaction. More precise genotype-environment interaction estimates can be obtained with the AMMI model that makes it easier to interpret the results obtained (Duarte and Vencovsky, 1999).

The objective of this study was to use the AMMI analysis model to assess the stability of some maize hybrids and verify the influence of a sample of environments in Central Brazil (Goiás, Mato Grosso, Mato Grosso do Sul, Minas Gerais and São Paulo) in the productive performance of these genotypes.

MATERIAL AND METHODS

The experiments were conducted in the 1999/2000 summer growing season in the following locations: Bom Jesus-GO, Chapadão do Sul-MS, Montividiu-GO, Alto Garças MT, Uberlândia-MG, Cristalina-GO, Patos de Minas-MG, Unaí-MG, Casabranca-SP and Iraí de Minas-MG. These locations were chosen to represent the main maize cropping regions in Central Brazil. These are predominantly savannah areas (Cerrado) with altitudes varying from 500 to 1100m.

Thirty-six maize hybrids were assessed, of which thirteen of which were single, nine triple and fourteen double crosses maize hybrids. Thirty-one of these genotypes were experimental hybrids and the others were commercial hybrids, used as controls. A randomized complete block design was used with two replications by location. The plots were two 5 m rows spaced at 0.8 m, totaling 8 m^2 useful area. The stands of the plants in the experiments at Montividiu, Alto Garças, Uberlândia and Patos de Minas were corrected to average stand. The grain yield ($kg.ha^{-1}$) data was assessed and corrected to 13% moisture.

The analysis of variance (ANOVA) was used and the GE interaction was estimated by the AMMI model (Zobel et al., 1988; Duarte and Vencovsky, 1999). Thus, the mean response of the genotype i in environment j ($\boldsymbol{Y_{ij}}$) is modeled by: $Y_{ij} = \mu + g_i + a_j + \Sigma\lambda_k\gamma_{ik}\alpha_{jk} + \rho_{ij} + \bar{e}_{ij}$; where μ is a common constant to the responses (normally the general mean); $\boldsymbol{g_i}$ is the fixed effect of genotype i ($i = 1, 2, ..., g$); $\boldsymbol{a_j}$ is the fixed effects of environment j ($j = 1, 2, ..., a$); $\Sigma\lambda_k\gamma_{ik}\alpha_{jk}$ is the fixed significant effect or pattern of the specific interaction of the genotype i with environment j ($\boldsymbol{ga_{ij}}$), where λ_k is the k-th singular value (scalar), γ_{ik} and α_{jk} are the correspondent elements, associated to λ_k, of the singular vectors (rows vector and column vector) of the matrix of interaction estimated by ANOVA. For the same matrix, ρ_{ij} is the non-significant effect or noise of $\boldsymbol{(ga)_{ij}}$, which is an additional residue, and $\boldsymbol{e_{ij}}$ is the pooled experimental error, assumed independent and $e_{ij} \sim N(0, \sigma^2)$.

In this procedure, the contribution of each genotype and each environment to the GE interaction is assessed by use of the biplot graph display in which yield means are plotted against the scores of the first principal component of the interaction (IPCA1). The computational program for AMMI analyses is supplied by Duarte and Vencovsky (1999).

RESULTS AND DISCUSSION

By the F (Snedecor) test, applied according to the Gollob (1968) rule, only the first axis of interaction (IPCA1) was significant (1% probability). This led to the selection of the named AMMI1 model, which explained 29.79% of the sum of squares (SS_{GE}) (Tables 1 and 2). The first plus the second axes explained more than half (50.6%) of these sums of squares, but there were no further significant components after fitting the second axis (Table 1). Therefore, there was no need to further elaborate the model.

The results in Table 3 indicate homogeneity for yield of the environments assessed.

Table 4 shows the high correlation of the genetic constitution of the hybrids with the yield stability of the three types of hybrids studied. Most of the environments are neutral in the contribution to the interaction. The Uberlândia environment contributed positively, whereas the Patos de Minas environment contributed negatively to the GE interaction. Most of the genotypes also presented low contributions to interaction (Table 4).

Most of the genotypes presented a stability performance similar to what was expected, since they form the same genetic group (Figure 1). The control hybrids (G32 to G36) also presented similar performances in the environments used, which can be affirmed by the proximity of their points in Figure 1. One of the objectives of the seed producing companies has been to release hybrids with wide geographic adaptation that have yield volume and can assure a good average yield, even if the environments to be cropped are very heterogeneous. This is because the hybrids are exhaustively tested in their pre-commercial stages in several environments/years.

When the effect of the genotype-environment interaction was analyzed in the phenotypic responses, it was observed, for example, that G3 hybrid in Casa Branca (A9) produced 6636.82 kg.ha^{-1} (Table 5). In this case, the expected yield was determined basically by the main effects, 6637.30 kg.ha^{-1} (Table 6), because the term of the specific interaction, -0.48 kg.ha^{-1} (Table 7), is practically nihil. It could be affirmed that the performance of this hybrid was maintained in the other environments, characterizing it as a highly stable genotype.

The G17 hybrid presented good adaptation to the Uberlândia environment (A5). Its specific interaction, 5074.92 kg.ha^{-1} (Table 7), was the highest magnitude in this environment. Its predicted yield was 14682.97 kg.ha^{-1} (Table 5), that is, 9608.05 kg.ha^{-1} (Table 6) plus 5074,92 kg.ha^{-1}, indicating great effect of the specific interaction in the final response. The good adaptation of this genotype to this environment was

Table 1. Joint analysis of variance including the partitioning of the GxE interaction.

Source	DF	SS	MS	F	Pr > F
Genotypes	35	159648137.00	4561375.00	3.72	0.0001
Environment	9	1209036384.00	134337376.00	109.46	0.0001
Interaction GxE	315	386585217.00	1227255.00	0.77	1.0000
IPCA1	43	115194840.12	2678949.77	1.67	0.0071
Resídue AMMI1	272	271390377.12	997758.74	0.62	1.0000
Error pooled	344	551459418.86	1603079.70	-	-

Table 2. Multiplicative partitioning of the sum of squares of the GE interaction by the AMMI model analysis

Singular axis	Eingenvalue (λ_k^2)	Proportion ($\lambda^2_k/\Sigma\lambda^2_k$)	Acumuled proportion (%)
1	115194840.12	0.2980	29.80
2	806789389.28	0.2087	50.67
3	52262236.13	0.1352	64.19
4	41049552.46	0.1062	74.80
5	30945304.45	0.0800	82.81
6	26760759.29	0.0692	89.73
7	16335445.12	0.0423	93.96
8	13822699.99	0.0358	97.53
9	9535440.37	0.0247	100.00
Total	386585217.00	1.00	-

Table 3. Results of the mean yield of the environments and their respective scores on the first singular axis of GE interaction (IPCA1) by the AMMI model method.

Environment	Means (kg.ha^{-1})	IPCA1 (kg.ha^{-1})$^{1/2}$
Bom Jesus (BJS)	8017.65	-6.53
Chapadão do Sul (CHS)	9941.22	-9.28
Montividiu (MON)	8321.44	-6.01
Alto Garças (ATG)	11353.99	-21.74
Uberlândia (UBL)	9359.15	78.59
Cristalina (CRI)	10027.78	-24.17
Patos de Minas (PTM)	8136.92	-46.41
Unaí (UMA)	9557.51	3.87
Casabranca (CSB)	6462.33	-2.37
Irai de Minas (IRM)	4666.69	34.06

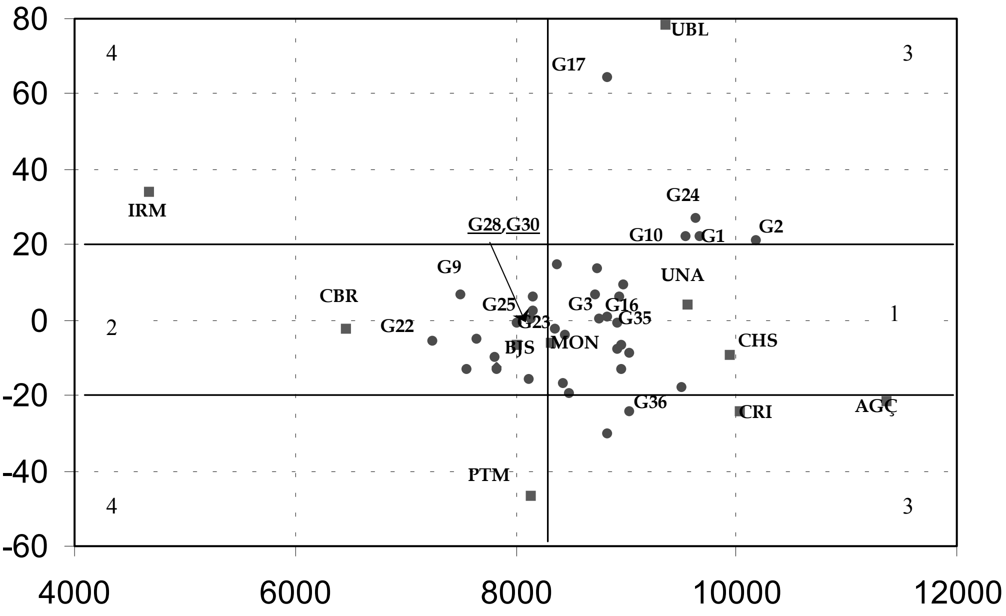

Figure 1. Mean yield (kg/ha) of the genotypes (G1 to G36) and respective environments studied (BJS, CHS, MON ATG, UBL, CRI, PTM, UMA, CSB, and IRM) against the first IPCA1 axis and graphic sectors (1 and 4).

also demonstrated by the proximity between the corresponding points in Figure 1.

This same genotype should not be recommended for the Patos de Minas environment (A7) because of the strong negative component of the specific interaction, -2996.95 kg.ha^{-1} (Table 7), which influences a reduction in the final yield of the genotype to that environment (Table 5).

Genotypes G3, G16, G25, G28, G30, G33, and G35 had a small contribution to the GE interaction while genotypes G1, G2, G10, G17, G234 and G36 contributed a lot to the GE interaction captured by the

Table 4. Results of the mean yield of the genotypes and their respective scores on the first singular axis of GE interaction (IPCA1) by the AMMI model method.

Genotypes [1/]	Means (kg.ha^{-1})	IPCA1 (kg.ha^{-1})$^{1/2}$	Genotypes	Means (kg.ha^{-1})	IPCA1 (kg.ha^{-1})$^{1/2}$
G1 (SH)	9672	22.42	G19 (SH)	8717	6.61
G2 (SH)	10182	21.08	G20 (SH)	7824	-12.87
G3 (SH)	8759	0.20	G21 (SH)	8914	-7.68
G4 (SH)	9500	-17.65	G22 (SH)	7237	-5.25
G5 (TH)	8149	6.01	G23 (SH)	8359	-2.10
G6 (TH)	8437	-16.48	G24 (SH)	9622	27.27
G7 (DH)	7828	-12.49	G25 (SH)	8017	-0.81
G8 (DH)	8110	-15.64	G26 (SH)	8377	14.61
G9 (DH)	7491	7.04	G27 (TH)	7644	-5.01
G10 (DH)	9538	22.10	G28 (TH)	8139	0.54
G11 (DH)	8954	-13.00	G29 (DH)	7555	-12.72
G12 (DH)	8956	-6.83	G30 (DH)	8161	2.50
G13 (DH)	8976	9.54	G31 (DH)	8478	-19.33
G14 (DH)	8941	6.18	G32-DKB333B (T)	8731	13.88
G15 (DH)	9038	-8.86	G33-P30F80 (T)	8453	-4.16
G16 (DH)	8823	1.15	G34-D766 (T)	8836	-30.33
G17 (SH)	8833	64.57	G35-TORK (T)	8928	-0.52
G18 (DH)	7810	-10.02	G36-AG6690 (T)	9033	-23.96

[1/] SH: single hybrid; TH: triple hybrid; DH: double hybrid; T: check hybrid.

first axis IPCA1 (Table 3). The Unaí (A8) and Casa Branca (A9) environments also had small contributed to the interaction and the Uberlandia (A5), Patos de Minas (A7) and Iraí de Minas (A10) environments contributed most (Table 3 and 7, Figure 1).

Considering all the genotypes, the greatest yield was observed in Alto Garças (A4) with a mean of 11353.99 kg.ha^{-1}, where all the genotypes produced over 10000.00 kg.ha^{-1} (Tables 4 and 5). On the other hand, the Iraí de Minas environment (A10) gave a lower mean yield 4666.69 kg.ha^{-1}, where the genotypes did not produce more than 7115.00kg.ha^{-1} (Tables 4 and 5).

When the genotypes and environments were classified in the four groups, as proposed by Avarez and Eyherabide (1996) (Table 8 and Figure 1), the genotypes with greater stability and high and low mean yields were grouped in sectors 1 and 2, respectively. In sectors 3 and 4 are the genotypes with lower stability and with greater and lesser yields,

Table 5. Expected yields for each combination of genotype and environment, according the selected AMMI model.

Genotype	Environment									
	A1	A2	A3	A4	A5	A6	A7	A8	A9	A10
G1	8959.03	10821.05	9274.47	11954.27	12209.50	10573.69	8183.99	10732.19	7496.96	6518.39
G2	9477.97	11343.66	9792.71	12493.55	12614.61	11116.21	8756.26	11237.21	8010.34	6983.05
G3	8191.30	10114.32	8495.20	11524.58	9549.99	10197.87	8302.52	9733.26	6636.82	4848.54
G10	8827.23	10690.13	9142.50	11827.35	12050.42	10447.54	8064.97	10597.05	7363.83	6373.59
G16	8249.26	10169.67	8553.65	11568.08	9688.89	10239.06	8322.56	9801.12	6698.74	4945.10
G17	7844.70	9591.04	8182.02	10198.85	14682.97	8716.10	5388.87	10056.32	6557.89	7114.96
G24	8877.42	10726.14	9195.38	11798.92	12540.60	10406.58	7909.04	10701.02	7435.52	6633.60
G25	7455.49	9381.29	7758.86	10804.21	8727.78	9479.95	7607.18	8986.89	5893.79	4071.53
G28	7568.98	9491.05	7873.05	10897.05	8956.79	9569.51	7666.54	9114.50	6015.92	4240.11
G30	7578.73	9495.41	7883.82	10876.92	9133.74	9544.62	7597.97	9144.68	6033.84	4329.59
G33	7914.08	9849.07	8215.71	11313.73	8901.34	9997.59	8199.30	9410.65	6341.46	4394.20
G35	8365.52	10290.52	8659.04	11709.80	9662.63	10384.85	8505.58	9899.96	6808.04	4993.40
G36	8323.44	10612.78	8914.78	12324.33	7924.79	11056.20	9698.45	9913.97	6968.46	4299.60

Table 6. Expected yields for each combination of genotype and environment due only to the main effects.

Genotype	Environment									
	A1	A2	A3	A4	A5	A6	A7	A8	A9	A10
G1	9105.54	11029.10	9409.33	12441.88	10447.03	11115.66	9224.80	10645.40	7550.22	5754.58
G2	9615.74	11539.31	9919.53	12952.08	10957.24	11625.86	9735.00	11155.60	8060.42	6264.78
G3	8192.62	10116.19	8496.41	11528.97	9534.12	10202.75	8311.89	9732.48	6637.30	4841.67
G10	8971.64	10895.21	9275.44	12307.99	10313.14	10981.77	9090.91	10511.50	7416.32	5620.69
G16	8256.79	10180.36	8560.59	11593.14	9598.29	10266.92	8376.06	9796.65	6701.47	4905.84
G17	8266.55	10190.12	8570.35	11602.90	9608.05	10276.68	8385.82	9806.41	6711.23	4915.60
G24	9055.60	10979.17	9359.40	12391.95	10397.10	11065.73	9174.87	10595.46	7500.28	5704.65
G25	7450.18	9373.75	7753.97	10786.53	8791.68	9460.31	7569.44	8990.04	5894.86	4099.22
G28	7572.53	9496.10	7876.32	10908.88	8914.03	9582.66	7691.80	9112.39	6017.21	4221.57
G30	7595.11	9518.68	7898.91	10931.46	8936.61	9605.24	7714.38	9134.97	6039.79	4244.16
G33	7886.89	9810.46	8190.69	11223.24	9228.39	9897.02	8006.16	9426.75	6331.57	4535.94
G35	8362.12	10285.69	8665.91	11698.46	9703.62	10372.24	8481.38	9901.98	6806.80	5011.16
G36	8466.86	10390.43	8770.65	11803.21	9808.36	10476.99	8586.13	10006.72	6911.54	5115.91

Table 7. Matrix of GE interactions for each combination of genotype and environment estimated by AMMI analysis.

Genotipe	Environment									
	A1	A2	A3	A4	A5	A6	A7	A8	A9	A10
G1	-146.50	-208.05	-134.86	-487.61	1762.46	-541.97	-1040.81	86.79	-53.25	763.81
G2	-137.77	-195.65	-126.82	-458.54	1657.37	-509.66	-978.74	81.61	-50.08	718.27
G3	-1.32	-1.87	-1.21	-4.39	15.86	-4.88	-9.37	0.78	-0.48	6.87
G10	-144.41	-205.08	-132.93	-480.64	1737.28	-534.23	-1025.93	85.55	-52.49	752.90
G16	-7.53	-10.69	-6.93	-25.06	90.60	-27.86	-53.50	4.46	-2.74	39.26
G17	-421.85	-599.08	-38.32	-1404.05	5074.92	-1560.58	-2996.95	249.90	-153.34	2199.36
G24	-178.18	-253.04	-164.07	-593.03	2143.50	-659.15	-1265.82	105.55	-64.77	928.95
G25	5.31	7.54	4.89	17.68	-63.90	19.65	37.73	-3.15	1.93	-27.69
G28	-3.55	-5.09	-3.27	-11.83	42.76	-13.15	-25.25	2.10	-1.29	18.53
G30	-16.39	-23.27	-15.08	-54.54	197.12	-60.62	-116.41	9.70	-5.96	85.43
G33	27.19	38.61	25.02	90.48	-327.06	100.57	193.14	-16.10	9.89	-141.74
G35	3.40	4.84	3.14	11.34	-40.98	12.60	24.20	-2.02	1.24	-17.76
G36	156.57	222.35	144.13	521.12	-1883.57	579.22	1112.33	-92.75	56.91	-816.30

Table 8. Relationship among the types of hybrids and environments and frequency of occurrence in the graphic sectors of performance.

Graphic sectors	Total Hybrids	Simple hybrids	Triple hybrids	Double hybrids	Environments
1	12 (33%)	6 (46%)	3 (33%)	3 (21%)	2 (20%)
2	17 (47%)	5 (38%)	2 (22%)	10 (71%)	3 (30%)
3	7 (20%)	2 (16%)	4 (45%)	1 (8%)	3 (30%)
4	0	0	0	0	2 (20%)
Total	36 (100%)	13 (100%)	9 (100%)	14 (100%)	10 (100%)

respectively. Thus we concluded that most of the single crosses fall in sector 1 and that 84% of these hybrids are distributed in sectors 1 and 2, presenting therefore, high mean yields and good stability. On the other hand, the double crosses hybrids were concentrated in sector 2, also showing good stability but a lower mean yield.

CONCLUSIONS

The results indicate homogeneity of the environments assessed and a high relationship of the yield stability with genetic constitution of the hybrids (single, triple and double crosses hybrids). The first two AMMI axes explained more than half (50.60%) of the original genotype-environment interaction. Most of the environments were neutral in the interaction contribution. The Uberlândia environment contributed positively, while the Patos de Minas environment contribeted negatively to the GE interaction. Most of the genotypes presented low contribution to interaction, although the single crosses presented greater mean yield, and the double hybrids showed greater yield stability for the environments studied.

RESUMO

Interação genótipo-ambiente em híbridos de milho: uma aplicação do modelo ammi

A interação genótipo x ambiente geralmente é constatada quando um mesmo genótipo é avaliado em vários ambientes, influenciando decisivamente na recomendação de cultivares. Híbridos de milho que tenham somente adaptação a determinados ambientes podem se tornar limitantes para a produção de sementes em grande escala. Um dos principais objetivos dos melhoristas é a obtenção de um híbrido com produtividade média elevada e boa adaptação a diferentes ambientes. No presente estudo foi avaliado a estabilidade da produção de grãos de trinta e seis genótipos de milho, em dez ambientes da região do Brasil Central, na safra 1999/2000. A análise de variância (ANOVA) detectou significância ($P<0,01$) para a interação genótipo x ambiente (GE). O modelo AMMI (additive main effects and multiplicative interaction) foi utilizado para avaliar os efeitos aditivos e multiplicativos da interação. Os resultados indicaram homogeneidade dos ambientes avaliados e uma alta correlação da constituição genética dos híbridos com a estabilidade produtiva dos três tipos estudados – híbridos simples, triplos e duplos. Os dois primeiros componentes multiplicativos da interação explicaram mais da metade (50,6%) da soma de quadrados original (SS_{GE}). A maioria dos ambientes se mostrou neutra na contribuição da interação. O ambiente de Uberlândia contribuiu positivamente para a interação, ao contrário do ambiente de Patos de Minas. A maioria dos genótipos também apresentou baixa contribuição para a interação. Alguns híbridos simples apresentaram maior rendimento médio (10182,0 $kg.ha^{-1}$), enquanto os híbridos duplos apresentaram maior estabilidade nos ambientes estudados.

REFERENCES

Alvarez, M. D. P. and Eyhérabide, G. H. 1996. Estabilidade del rendimento de híbridos comerciales de maíz en el área de la EEA pergamino. Revista de Tecnologia Agropecuaria. INTA Pergamino. 1(2):17-31.

Brasil, E. M. 1990. Comparação de métodos de controle da interação genótipo x ambiente em milho (Zea mays L.). M. S. Diss. Escola de Agronomia, Universidade Federal de Goiás, Goiânia.

Crossa, J. 1990. Statistical analyses of multilocation trials. Advances in Agronomy. 44:55-85.

Cruz, C. D.; Torres, R. A. A. and Vencovsky, R. 1989. Na alternative to the stability analysis proposed by Silva and Barreto. Revista Brasileira de Genética. 12:567-580.

Duarte, J. B. and Vencovsky, R. 1999. Interação Genótipos x Ambientes Uma Introdução à Análise "AMMI". Série Monografias, n.9. Sociedade Brasileira de Genética, Ribeirão Preto.

Duarte, J. B. and Zimmermann, M. J. de O. 1991. Selection of locations for common bean (Phaseolus vulgaris L.) germoplasm evaluation. Revista Brasileira de Genética. 14(3):765-770.

Eberhart, S. A. and Russel, W. A. 1966. Stability parameters for comparing varieties. Crop Science. 6:36-40.

Finlay, K. W. and Wilkinson, G. N. 1963. The analysis of adaptation in a plant-breeding programme. Australian Journal of Agricultural and Resource Economics. 14:742-754.

Gollob, H. F. 1968. A statistical model which combines features of factor analytic and analysis of variance techniques. Psychometrika. 33(1):73-145.

Shafii, B. and Price, W. J. 1998. Analysis of Genotype-by-Environment Interaction Using the Additive Main Effects and Multiplicative Interaction Model and Stability Estimates. Journal of Agricultural, Biological, and Environmental Statistics. 3(3):335-345.

Silva, J. G. C. and Barreto, J. N. 1985. Aplicação de regressão linear segmentada em estudos da interação genótipo x ambiente. p.49-50. In: Resumo do Simposio de Estatística Aplicada à Experimentação Agronômica, 1st, Cargill, Campinas.

Zobel, R. W.; Wright, M. J. and Gauch, H. G. 1988. Statistical analysis of a yield trial. Agronomy Journal. 80(1):388-393.

Received: November 12, 2002;

Accepted: January 27, 2003.