

Comparison of regression and AMMI analyses for assessing yield stability of maize inbred lines

A. Ndiaye¹, S. K. Vasal², S. Mclean², and J. Crossa²

¹ISRA. CNRA BP : 53 Bambey • (Senegal)

²CIMMYT, Apdo Postal 6-641, C.P. 06600, D. F., México

Abstract

Several statistical techniques have been developed for the analysis of the interaction of genotypes with environments (G x E). One method that has been used extensively is regression analysis. The objectives of this study were to i) compare the some of the methods available for assessing yield stability in the hope of identifying genotypes with wide stability of performance as well as good mean performance and ii) quantify the probability of successful selection of a genotype when using the additive main effect and multiplicative interaction (AMMI) technique compared with the regression technique. The regression technique used in this study is particularly effective in emphasising the actual trend of variety yield responses to a range of natural environments. The results of AMMI method agreed with the modified regression method analysis 80 and 95% of the time for white and yellow lines, respectively for selecting the best lines adapted to favorable environments. The two techniques poorly agreed when selection was for genotypes adapted to poor environments. However, AMMI method was more effective in detecting specific adaptability for specific environments.

Résumé

Plusieurs techniques statistiques ont été développées dans le cadre de l'étude de l'interaction génotype x milieu et la méthode de régression linéaire a été largement utilisée. L'objectif de cette étude est de comparer les résultats obtenus à partir de quelques méthodes dans l'espoir d'identifier des génotypes performants et à large adaptabilité et ii) de quantifier la probabilité de sélectionner un génotype en utilisant les valeurs prédites par la méthode AMMI comparée à celle obtenue par les techniques de régression. La technique de régression est particulièrement efficace pour mettre l'accent sur la tendance du rendement d'une variété dans plusieurs environnements. Les résultats obtenus par la méthode AMMI concordent presque avec ceux de la méthode de régression modifiée (dans 80 et 95% des cas pour les lignées blanches et jaunes respectivement) quand il s'agit de sélectionner les

meilleures lignées adaptées à des environnements favorables et seulement de façon partielle pour celles adaptées à des milieux défavorables. Cependant, la méthode AMMI paraît plus efficace dans l'identification d'une adaptabilité spécifique et pour un environnement spécifique.

Introduction

Over the last decade, CIMMYT Lowland Tropical Maize Subprogram has developed several productive maize (*Zea mays* L.) inbred lines with good combining ability. Sources of the lines include original populations, inbreeding tolerant populations, recycled elite lines, and recycled early generation lines reconstituted through the forward and reverse inbreeding procedure (FRIP). Inbred lines are evaluated for combining ability as from the S_3 or S_4 stage and are also tested *per se* in line evaluation trials (LETs) across many locations in collaboration with national programs in developing countries. Yield data have been used to examine many approaches to the analysis of stability.

Of the numerous statistical techniques developed to analyse the interaction of genotypes with environments ($G \times E$), the regression analysis has been extensively used. This was first introduced by Mooers (1921) and was given prominence by Yates and Cochran (1938) who used the mean performance of all genotypes grown in an environment as a suitable index of productivity of the environment. The performance of each genotype was plotted against this index for each environment, and simple regression was fitted by least squares to summarise the genotype's response.

Finlay and Wilkinson (1963) used the regression technique to examine the yield stability of various barley (*Hordeum vulgare* L.) genotypes. They considered regression slopes and overall yield level of genotypes as important stability criteria.

Eberhart and Russell (1966) also used a linear regression approach to determine yield stability in maize. In addition to the regression slopes (b-values) and mean yield, they considered deviations from the regression line as another important component of varietal stability. A variety is considered stable when its b-value is close to 1.0 with a minimum sum of squared deviations. Varieties with b-values significantly different from unity are not stable; those with high b-values are considered to be responsive to high-yield environments and vice versa for those with low b-values.

Multivariate methods have also been used in analysing stability in plant breeding. Crossa *et al.* (1988a) applied the principal coordinate analysis, proposed by Wescott (1987), to determine varietal stability in two international trials (EVT 12 and EVT 13) evaluated over 1979 - 1983. The results showed that four and three stable varieties had been derived from CIMMYT Population 22 and Population 43, respectively. Also

eleven selections derived from Population 28 showed good levels of stability in both high and low yielding environments. Crossa *et al.* (1990) also used the Additive Main Effect and Multiplicative Interaction (AMMI) method, with additive effect for genotypes and environments and the multiplicative terms for genotype x environment interaction, for analysing data from international maize cultivar trials. Results showed that AMMI increased the precision of yield estimates to a level equivalent to increasing the number of replications by a factor of 2.6.

Considerable confusion has arisen from the fact that the various methods of stability analysis have engendered many different measures of stability. Some of the studies reported in the literature showed that different measures of stability are similar but not identical in classifying test genotypes and/or environments. In some other cases, the test genotypes and environments are classified differently by the different stability measures.

This study was conducted to:

- compare the results of three methods of assessing yield stability in an attempt to identify wide stability of performance as well as good mean performance;
- quantify the probability of successful selection of a genotype when using AMMI predictive values, compared with the probability of selection based on the predictive values of regression techniques and/or treatment means.

The methods considered include the linear regression approach as suggested by Finlay and Wilkinson (1963) and modified by Eberhart and Russell (1966); the AMMI method, and the method proposed by St-Pierre *et al.* (1967).

Materials and methods

Stability of grain yield (kg/ha) was analysed for one white and one yellow inbred line evaluation trials (LETs) tested at ten locations in 1991. Due to missing data at some locations, data for 9 and 8 locations were used to analyse the stability of the white (LEW9404) and the yellow lines (LETY9405), respectively.

The trials had been conducted using a partially balanced lattice design with three replications at each location. The two checks were excluded from the analysis. Grain yield was adjusted to 15% moisture content. A combined ANOVA was carried out for grain yield. The following stability analyses were performed using the means of the three replications.

The method of St-Pierre *et al.* (1967). This method defines stability of a genotype as the percentage of the test environments in which the

performance Of the genotype is better than the mean performance Of all genotypes evaluated.

The AMMI analysis. AMMI was performed using MATMODEL (Gauch, 1987; Crossa (1990). This model first fits additive effects for genotypes (G) and environments (E) by the usual additive analysis of variance procedure. Thereafter, it fits multiplicative effects for genotype-environment (G x E) interaction by principal components analysis (PCA).

The linear regression approach. Environments were subdivided, according to AMMI method, into two major groups: those with positive G x E interaction and those that had negative G x E interaction. The stability parameters proposed by Eberhart and Russell (1966) were then calculated for each line in each group. Lines that had across location mean yield equal to or larger than the grand mean were selected. Genotypes were then classified based on their regression coefficients.

Results

AMMI method

White lines. For the white inbred line trials, AMMI analysis showed that environments, genotypes, and G x E interaction were highly significant ($P < 0.001$) and accounted for 46, 24, and 30% of the treatment sum of squares respectively (Table 1). In the biplot (Fig.1) the principal component axis 1 (PCA1) genotypes (environments) that appear almost on a perpendicular line have similar interaction patterns. Genotypes (environments) with large positive or negative PCA1 scores have large interactions whereas genotypes (environments) with PCA1 scores close to zero have small interactions. Crossa *et al.* (1990) pointed out that genotypes and environments with PCA1 scores of the same sign produce positive interaction effects, whereas combination of PCA1 scores with opposite signs have negative specific interactions

Table 1. Additive main effects and multiplicative interaction analysis of variance for grain yield (kg ha^{-1}) of 119 white inbred lines of maize, including the first two interaction principal component axes (PCA1 and PCA2).

Source of variation	df	Sums of squares ($\times 10^6$)	Mean squares
Treatment combinations	1070	1262.44	1.17
Genotype (G)	118	300.47	2.54**
Environment (E)	8	579.02	72.38**
G x E	944	382.94	0.40**
interaction PCA1	122	127.04	1.02**
interaction PCA2	123	77.11	0.62**
Residual	696	1721.77	0.25

** $P < 0.001$.

Fig1: Biplot of the yield means and the first principal component axis of the 119 white lines • 9 locations

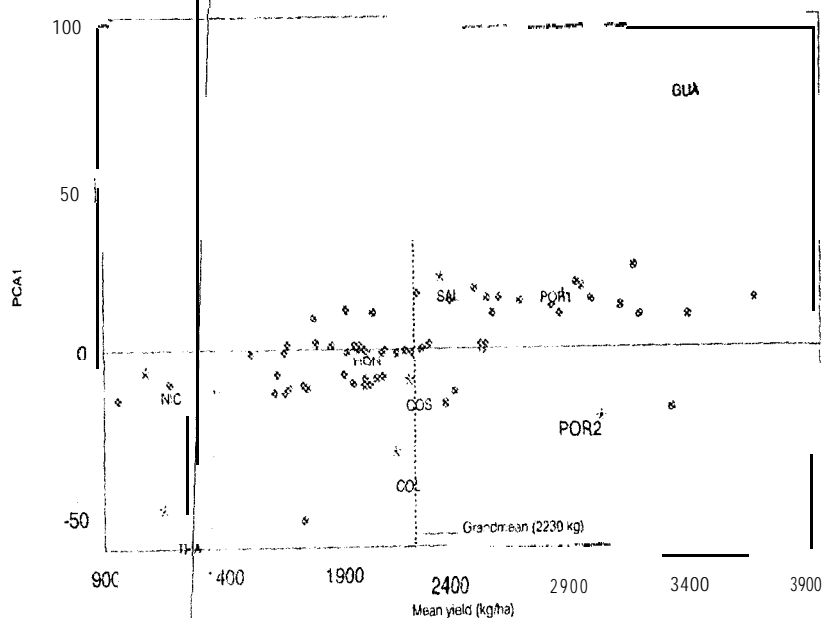


Table 2. Mean grain yield (kg/ha) of the top 20 white inbred lines adapted to favorable environments

Entries n°	Overall				
	Mean	Mean yield ¹	Guatemala	Salvador	Poza Rica
1	2643.9	3668.4	5967.1	2181.3	2996.7
3	2782.8	-1023.1	5171.6	3198.9	2996.7
7	3151.4	4225.8	5631.1	3134.0	3912.3
16	2009.6	4277.1	5804.0	3815.6	3211.7
17	3350.6	3271.5	5532.4	3714.4	3567.6
20	3625.0	5123.1	6517.0	5155.8	3896.5
24	3126.7	4703.9	6632.9	3734.6	3738.2
28	2277.9	3669.3	4715.2	2310.7	3982.1
32	2886.7	4306.9	5776.2	3352.0	3792.6
33	2030.8	2899.1	4257.3	1872.6	2567.4
37	2948.0	4194.6	5305.1	2961.8	4316.8
39	2534.2	3898.2	4329.8	3617.9	3746.9
53	1920.1	3010.9	3816.5	2300.9	2707.4
56	2818.1	3883.4	4385.4	3570.7	3714.0
73	2561.9	3784.8	4000.3	3210.4	3343.8
92	1786.6	2937.8	3672.5	2294.8	2846.2
98	2459.7	3734.1	5604.9	2781.4	2816.0
99	2159.8	3648.2	4877.2	3121.0	2946.4
114	3009.8	4302.3	5615.7	3329.1	3969.0
118	2509.6	3897.7	4179.6	3422.8	4090.7

¹Mean across the three selected sites in the group.

Using the amount of interaction and its sign as a stability parameter, genotypes could be divided into three groups from Figure 1:

Group 3 consists Of genotypes with high positive interaction. These are well adapted to favorable environments such as Guatemala, Salvador and Poza Rica 1 (POR1). Table 2 gives the mean yield of the top 20 white lines adapted to favorable environments. The overall mean yield varied from 1786 kg/ha for line 92 to 3625 kg/ha for line 20 whereas the mean yield over favorable environments varied from 2899 kg/ha for line 33 to 5123 kg/ha for line 20. Only lines 28, 33, 53, 92 and 99 had overall mean yield lower than the grand mean (2230 kg/ha). These lines were predominantly derived from Population 21 and from recycled lines.

Group 2 includes genotypes and ~environments with near-zero interaction (Table 3). Included in this group were the more stable lines and they performed well at the Honduras site. Only five of them had mean yields larger than the grand mean. About 25% of the lines were selections from Popula tion 21.

Group 3 consists of genotypes and environments with higher negative interactions (Table 4). They are adapted to unfavorable environments like Costa Rica, Nicaragua, Thailand, Colombia and Poza Rica 2 (POR2). The AMMI 2 model captured 86% of the treatment combination sum of squares. PCA1 and PCA2 explained 33.2 and 20.1% of the G x E interaction, respectively.

Table 3. Mean grain yield (kg/ha) of the 20 most stable white inbred lines in Honduras.

Entries n°	Overall mean.	Honduras
2	2190.0	2272.b
15	2493.0	2256.7
18	2077.3	2304.4
26	2163.3	1811.2
40	1661.5	1054.7
47	2482.6	2704.3
63	1793.8	1913.9
68	1923.7	2101.6
70	1972.4	976.4
72	2069.3	1752.7
76	2266.3	2675.3
79	2236.1	2142.7
84	2503.9	2385.0
89	1519.9	1988.2
95	1932.7	960.2
96	1968.1	2078.1
101	2130.7	2123.7
103	1995.1	2263.7
110	1852.4	1729.4
116	1971.9	7390.3

Table 4. Mean grain yield (kg/ha) of the 20 white lines adapted to unfavorable environments.

Entry n°	Overall mean	Mean yield ¹	Costa Rica	Nicaragua	Thailand	Colombia	Poza Rica 1
22	1741.1	1623.8	1253.2	524.0	1068.8	2264.9	3011.9
43	1949.2	1859.6	1746.2	1881.1	533.0	2630.5	2507.3
44	1677.7	1520.9	1942.1	573.8	1699.2	934.8	2554.6
46	2372.9	2176.6	2862.2	312.5	2052.4	2712.9	2942.9
48	1616.1	1596.9	2220.9	419.9	2153.8	942.3	2247.7
58	2335.1	2445.9	2267.4	659.5	3065.1	2066.3	-1171.3
60	1369.8	1232.5	1211.4	558.0	314.7	1532.9	2545.5
64	1629.5	1461.5	1469.2	424.0	627.0	1527.5	3259.7
80	1751.3	1696.4	1380.6	1104.2	1737.1	1494.1	2770.8
82	1992.5	1823.8	2353.1	1571.4	ix-i.7	1572.5	2227.5
83	1910.3	1684.9	2096.4	455.0	860.0	2160.8	2833.2
83	2071.8	2082.5	2860.6	1222.5	1281.3	1704.9	3343.0
87	960.1	1021.5	1487.3	552.3	397.1	1172.3	1498.5
PS	1660.3	1584.8	2253.2	267.1	1935.9	1235.3	2232.5
105	2041.5	1918.1	2214.3	1348.5	1065.9	2165.7	2796.1
107	1997.2	1815.8	2644.9	1096.3	1252.3	1228.2	2857.2
111	1176.3	1174.2	1242.4	1009.5	0.0	827.4	2791.9
113	3010.3	2039.9	1806.3	1029.3	736.8	3244.5	3332.7
115	3276.3	3635.9	1984.8	1417.4	3779.4	5535.3	5462.6
119	1741.8	2900.4	1601.5	425.1	3966.7	5498.7	3010.1

¹Mean across the five selected sites in the group.

Yellow lines. For the yellow lines, genotypes, environments and G x E interaction mean squares were statistically significant (Table 5) and accounted for 19, 55 and 26% of the treatment combination sum of squares, respectively. The AMMI 2 model captured 89% of the treatment sum of squares. PCA1 and PCA2 explained 36.4 and 20.5% of the G x E interaction, respectively. In the same manner as for the white lines, three groups could be distinguished based on the nature of the G x E interaction.

Table 5. Additive main effects and multiplicative interaction analysis of variance for grain yield (kg ha⁻¹) of 119 yellow inbred lines of maize, including the first two interaction principal components (PCA1 and PCA2) axis.

Source of variation	df	Sum of squares (x 10 ⁶)	Mean squares
Treatment combinations	951	1224.77	1.29
Genotype (G)	118	232.51	1.97 **
Environment (E)	7	668.37	95.48 **
G x E	826	323.89	0.39 **
Interaction PCA1	124	117.91	0.95 **
Interaction PCA2	122	66.23	0.54 **
Residual	580	139.74	0.24

Group 1. Table 6 contains the means yield of the top 20 yellow lines adapted to favorable environments such as Guatemala, Dominic

Republic and Poza Rica1 (POR1). The mean yield over these environments varied from 2773 kg/ha for line 97 to 5777 kg/ha for line 12. These lines were derived mainly from Population 24 (46%) and population 36. Only lines 24, 79 and 97 yielded below the grand mean.

Table 6. Mean grain yield (kg/ha) of the top 20 yellow lines adapted to favorable environments.

Entries n°	Overall mean	Mean yield ¹	Guatemala	Rep. Dom.	Poza Rica 1
9	3538.8	5039.7	4239.8	6435.0	4144.3
12	3712.8	4802.4	4826.8	5233.1	4345.2
14	4074.3	5774.4	5698.5	6424.1	5209.6
19	2434.6	3034.8	1995.5	4069.	9 3038.9
24	2427.7	3181.6	2522.5	3886.2	3136.2
32	2133.5	2830.5	2248.4	3622.0	2391.2
41	2622.9	3466.9	1888.8	3878	8 4633.2
44	2390.1	3374.9	3104.3	4092.6	2927.7
46	4024.5	5438.5	4515.7	6073.7	5726.1
47	2280.4	3236.0	2870.7	3730.n	3106.6
48	3703.5	3445.5	2672.1	4292.9	3371.4
52	2398.5	3436.7	3383.7	3921.7	3004.6
62	2283.3	3130.9	2308.7	4627.8	2456.1
66	3874.3	5067.1	4178.3	6461.4	4561.6
77	2752.1	3737.5	3850.3	3407.6	3954.6
78	2517.0	3504.7	3156.4	4057.9	3299.7
79	2559.2	3440.5	3322.4	4470.7	2528.5
92	2080.0	2925.3	2156.0	4150.2	2469.7
97	2745.4	3607.6	2047.3	5569.2	3201.2
	2003.5	2773.4	1880.1	3384.7	3055.3

¹Mean across the three selected sites in the group.

Group 2 included the yellow lines with near-zero interaction. The mean yield response varied from 1644 kg/ha for line 83 to 3011 kg/ha for line 3 (Table 7). At Poza Rica 2, 50% of these lines had an overall mean yield below the grand mean (2252 kg/ha)

Group 3 consists of 20 yellow lines adapted to unfavorable sites like Cuba, Thailand and Colombia (Table 8). The mean yield response over these locations varied from 1160 kg/ha for line 86 to 2211 kg/ha for line 112.

The AMMI method is useful for selecting locations for regional trials based on the G x E interaction. Locations could be grouped based on environmental index and similarity in G x E interaction. In our study, three groups can be constituted as shown in Fig. 1.

For the white lines, Group 1 included Nicaragua and Thailand; Group 2 Honduras, Salvador, Costa Rica and Colombia; and Group 3, Poza Rica and Guatemala. The site at Guatemala had the highest positive interaction and could be considered as a specific fourth group.

For the yellow lines, only two groups were identified (Fig. 2). Group 1 included Cuba, Thailand and Panama while Group 2 had Guatemala, Poza Rica 1, Poza Rica 2, Colombia and Dominican Republic.

Table 7. Mean grain yield (kg/ha) of 20 stable yellow lines at Poza Rica 2

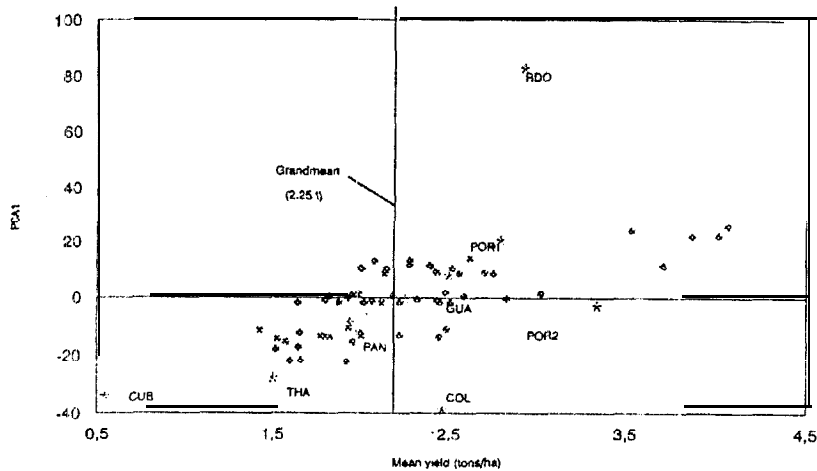
Entries n°	Overall mean	Poza Rica 2
5	3021.6	4307.1
7	2829.7	3960.4
13	2321.1	3269.8
26	2219.7	3073.5
28	1989.7	2926.8
29	2482.4	2707.2
31	2061.7	4297.1
34	2508.3	4598.9
36	2117.7	3610.1
38	2448.8	3690.4
43	2430.2	4165.8
50	2185.9	4220.4
51	1928.5	2653.6
64	1796.7	3409.0
74	2586.9	3179.2
76	1879.8	2059.7
83	1643.8	2393.5
85	1955.7	2708.7
95	1822.7	2448.1
101	2018.4	2367.0

Table 8. Mean grain yield (kg/ha) of 20 yellow inbred lines adapted to unfavorable environments

Entry n°	Overall mean	Mean yield ¹	Panama	Cuba	Thailand	Colombia
20	2143.7	1737.8	1986.4	461.2	1430.5	3073.2
21	1596.5	1609.1	1237.3	584.2	2050.3	2564.4
27	1428.6	1398.0	1372.9	621.0	1024.2	1773.9
35	1775.3	1410.4	3481.6	523.0	1313.8	2323.2
52	1574.7	1440.8	1675.7	206.1	1660.1	2221.4
53	1528.8	1379.9	1896.1	783.4	1308.3	1531.6
56	1647.5	1554.x	1454.0	779.1	2167.4	1818.7
60	1914.7	1601.8	1558.8	788.6	1799.9	2259.9
69	1518.8	1332.9	1493.5	584.6	434.9	2818.6
81	1660.5	3713.5	1-M. 1	413.3	2088.7	2865.9
84	2222.2	1803.7	16X1.3	544.4	2872.1	2116.9
86	1654.1	1160.0	1223.1	601.1	1399.1	1416.4
88	2445.5	2039.2	1657.1	799.4	2105.0	3595.4
96	1825.6	1681.7	1638.2	201.6	2177.7	2709.4
100	1751.1	1524.2	1891.7	338.1	1317.2	2549.9
110	1932.4	1538.0	1502.6	589.5	1357.3	2702.7
111	1992.6	1898.5	1882.2	904.1	2493.3	2312.3
112	2487.9	2211.8	2015.2	488.0	1234.0	5109.9
113	1918.9	1649.3	1066.5	389.6	2419.3	2721.9
114	2005.6	1678.8	1924.9	0.0	1765.1	3025.0

¹Mean across the four selected sites in the group.

Fig.2 : Biplot of the yield means and the first principal component axis of the 119 yellow lines • 8 locations



For both white and yellow line trials, environmental effect dominated the analysis. The $G \times E$ interaction sum of squares was about 1.4 times larger than the genotype sum of squares. The importance of the environmental effect is illustrated by partitioning the locations as shown in Figs. 1 and 2. Clearly, the trials involved a wide range of environments that need to be characterized in terms of climatic factors as well as biotic and or abiotic constraints for a biological explanation of the genotype \times environment interaction.

Regression analysis

The regression approach makes it possible to classify genotypes, on the basis of their b -values, as responding or adapted to high yielding sites (b_{HYS}) or to low yielding sites (b_{LYS}). Site means for grain yield ranged from 1076 kg/ha at Nicaragua to 3402 kg/ha at Guatemala for the white lines. Mean grain yields of the yellow lines varied from 546 kg/ha in Cuba to 3341 kg/ha in Poza Rica 2. According to the b -values, 58% of the white lines and 49% of the yellow lines had slopes larger than 1.0 in high yielding sites and cannot be considered as ideal genotypes.

For the white lines, 28% are ideal lines (ID) with mean yield over locations varying from 2236 to 3350 kg/ha; 32% are best for the high yielding sites (HYS) with across-location mean yield ranging from 2236 to 3442 kg/ha. The remaining 40% are best for low yielding sites (LYS); across-location mean yield varied from 2212 to 4408 kg/ha.

For the yellow lines, 33% are best for favorable environments with mean yield varying from 2275 to 4074 kg/h; only 5% can be considered as ideal with mean yield ranging from 2508 kg/ha for line 34 to 2687 kg/ha for line 1. The remaining 62% are best for low yielding sites, the across-location mean yield ranged from 2269 to 3712 kg/ha.

Although white lines 8, 14 and 25, and yellow lines 3, 13, 15, 23, 33, 34, 38 and 39 were classified in high-yield environments, we do not consider them as ideal genotypes in spite of their high across locations mean yield. This indicates that good average performance does not signify good adaptability and vice-versa.

Furthermore, 30% of the white lines are selections from Population 21 and 22% came from recycled lines; 24% of the yellow lines were derived from Population 24, 23% were from recycled lines and 18.5% from Sint-Amarillo TSR.

Figures 3 and 4 provide the relationship of genotype adaptation (regression coefficient) and genotype mean yield for the white and the yellow lines, respectively. Using the generalised interpretation of $G \times E$ analysis as reported by Finlay and Wilkinson (1963), each group of lines may be classified as shown in Table 9. The proportion of lines that were adapted to the highly favorable environments was greater than 50% in each group. Similarly, the percentage of environments in which the performance of each genotype was better than the mean performance of all genotypes varied from 44 to 100% and 38 to 100% for the white and the yellow lines, respectively.

Table 9. Percentage and ranges of grain yield (kg/ha) of lines specifically adapted to highly favorable ($b > 1.0$), all ($b = 1.0$), and unfavorable ($b < 1.0$) environments.

Inbred Group	Favorable env. ($b > 1.0$)			All env. ($b = 1.0$)			Unfavorable env. ($b < 1.0$)		
	%	Yield	range	%	Yield	range	%	Yield	range
White	52	2236	3477	24	2232	3625	24	2236	4408
Yellow 6	5	2280	4077	27	2233	2997	8	7299	2827

Fig.3: Biplot of the mean yield and the coefficients of regression b_i for the 119 white lines across 9 locations

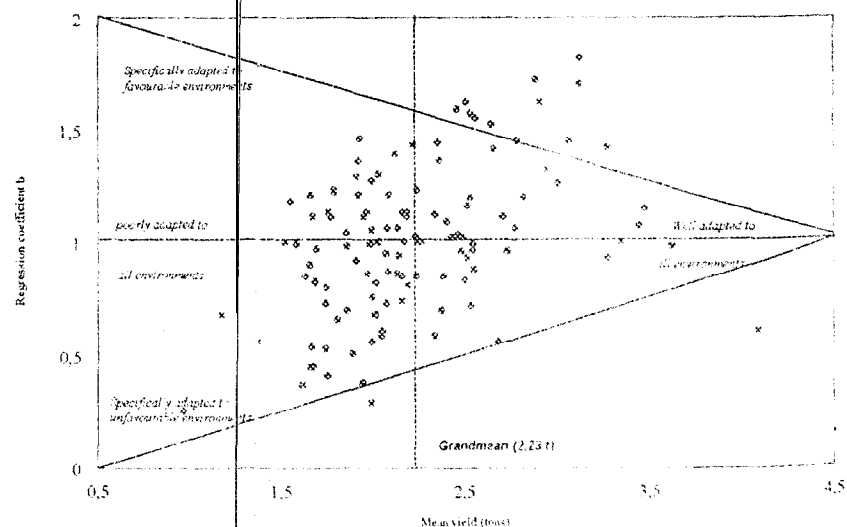
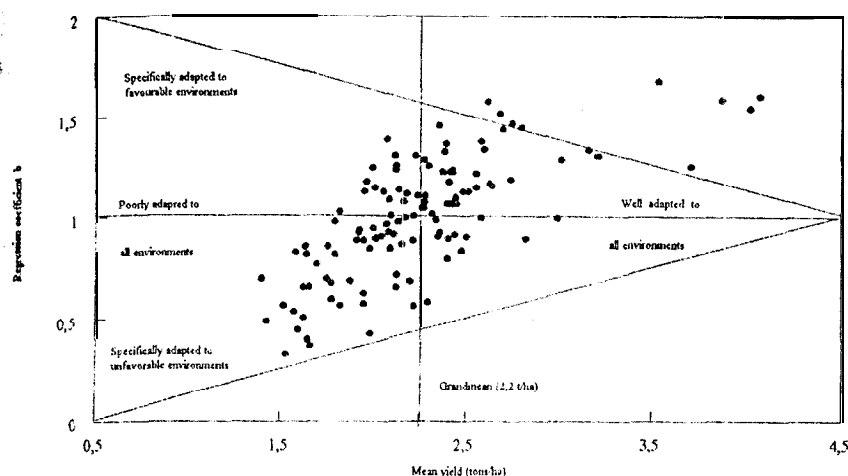


Fig.4 : Biplot of the mean yield and the coefficients of regression b_1 for the 199 yellow lines across 8 locations.



Discussion

$G \times E$ interactions limit the accuracy of yield estimates and complicate the identification of genotypes for general adaptation to a large number of environments. Maize breeders are therefore concerned about the accuracy with which $G \times E$ is quantified. The methods evaluated in our study yielded similar but not identical results.

Results of AMMI analysis of trials involving both white and yellow endosperm lines allowed the grouping of genotypes and/or environments based on their interactions. The first two principal components accounted for 53.3 and 56.9% of the interaction sums of squares for the white and the yellow lines, respectively.

Environmental effects dominated the performance of the lines in this study thus highlighting the importance of location variability as a principal factor in the trial network. It is therefore necessary to find a good approach to select homogeneous locations for international trials. AMMI method could be used for this purpose. The principle underlying this approach would be to decide which locations, rather than how many, are essential to clearly reveal the structure of $G \times E$ interaction truly present among the sample of lines and environments involved in the trials.

The regression technique used in this study is particularly effective in emphasizing the actual trend of varietal yield responses to a range of environments. According to Finlay and Wilkinson (1963), the two important indices in this type of analysis are the regression coefficient and the variety mean yield over all environments. The environmental response of all the genotypes tested can be studied by plotting these two indices together as coordinates in a two-dimensional scatter diagram.

As was found in our study, it seems that genotypes with $b < 1.0$ usually have mean yield over locations below the grand mean. Eberhart and Russell (1966) noted that in situations where there are no surplus productions that can be stored, or where long-term storage is not possible, such varieties may be the most desirable. For the developed countries, however, the breeder usually wants varieties that produce well above average in all environments. Hence, he desires varieties with a high mean yield, unit regression coefficient ($b = 1$) and small (near zero) deviation from regression. Analysis other than regression is required to obtain an overall picture of how stability and mean yield are to be traded off.

The results of AMMI analysis agreed well with the modified regression analysis for selecting the best white (about 80%) and yellow lines (about 95%), adapted to favorable environments, and only partially for those that are adapted to poor environments. However, the AMMI method was more efficient in detecting adaptability to specific environments. As suggested by Crossa *et al.* (1990), in plant breeding, the appropriate gain in precision achieved with AMMI provides a tool for selecting better genotypes and therefore achieving higher realized progress from selection. In addition, Crossa *et al.* (1990) suggested the need for research to determine the general usefulness of the AMMI model for analysing yield trials in agronomy and plant breeding.

In the methods proposed by Finlay and Wilkinson (1963) and St-Pierre *et al.* (1967), the average yield across all genotypes in an environment is used as an assessment of that environment except that the latter approach is expressed in terms of percentage. St-Pierre *et al.*'s approach agrees with the modified regression method only in detecting high yielding genotypes (overall mean yield superior to the grand mean) but does not provide the keys for distributing genotypes into types of adaptability.

Conclusion

The comparison of different methods for assessing yield stability indicated that the coefficient of regression, b -value, may be considered as a stability parameter even though it would be difficult to define an optimum value. In favorable environments, the agriculturists would choose genotypes with b -values greater than 1.0. On the other hand in unfavorable environments, they could choose genotypes with b -values smaller than 1.0 but with acceptable yield potential. Finally, the desirable value for the b coefficient is a function of crop management. Nevertheless, the AMMI method gives more satisfactory results than regression analysis in detecting specific adaptability to specific environments.

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