Assessment of Yield Stability and Adaptability of Parental Inbred Lines and F$_1$- Hybrids of Grain Maize (*Zea mays* L.) Using AMMI Analysis

Atif I. Abuali[1], Awadalla A. Abdelmula[2], Mutasim M. Khalafalla[3], Nada B. Hamza[4], Abdelwahab H. Abdalla[2] and Atif E. Idris[5]*

[1]*Enviromental, Natural Resources and Desertification Research Institute, National Centre for Research, P.O. Box 2404, Khartoum, Sudan.*
[2]*Department of Agronomy, Faculty of Agriculture, University of Khartoum, Shambat, Postal code: 13314, Khartoum, Sudan.*
[3]*Faculty of Public Health and Health Informatics, Umm AL-Gura University, P.O. Box (715), Makkah, Saudia Arabia.*
[4]*Commission for Biotechnology and Genetic Engineering, National Centre for Research, P.O. Box. 2404, Khartoum, Sudan.*
[5]*Department of Agronomy, College of Agricultural Studies, Sudan University of Science and Technology, Shambat, P.O. Box 71, Khartoum North, Sudan.*

Authors' contributions

This work was carried out in collaboration between all authors. All authors read and approved the final manuscript.

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ABSTRACT

This study was carried out to identify the yield stability and adaptability of the grain maize genotypes (parental inbred lines, F$_1$-hybrids and check varieties), using Additive Main Effects and Multiplicative Interaction (AMMI). A field experiment was executed during the winter and summer seasons of 2009 and 2010 at two locations, Shambat and Elrawakeeb, Sudan. A split-plot design with three replications was used to layout the experiment. The inbred lines and their F$_1$-hybrids were evaluated in the field under normal irrigation and water-stress conditions. The results showed that, highly significant differences were detected among genotypes, environments and for G×E interaction, indicated differential performance of genotypes over environments. Considering mean grain yield, and the Linear Regression parameters *bi* and S^2d values jointly, the F$_1$-hybrids

*Corresponding author: Email: atifelsadig@yahoo.com;

160×2, 160×3 and 6×3 gave above average mean of grain yield/ha and were most stable for grain yield/ha. AMMI analysis differentiated the genotypes (parental inbred lines and F_1-hybrids), based on their grain yield, into different adaptation pattern and stability. Based on AMMI analysis, the F_1- hybrids 66y×6 and 6×3 were highly stable with considerable high yield and adapted to favorable environments. However, the F_1- hybrids 160×66y and 160×3 exhibited the highest mean grain yield/ha (4.1 tons and 3.5 tons, respectively), with slightly low interaction scores, hence they are regarded as superior hybrids.

1. INTRODUCTION

Maize (*Zea mays* L.) (2n=20), which is also known as corn, belongs to the family Poceaceae. Maize is the third most important crop worldwide [1]. Maize grows over wider geographical and environmental ranges than any other cereal crop. It is grown at latitudes varying from the Equator to slightly Northern and southern of latitude 50⁰, from sea level to over 3000 meters elevation under heavy rainfall and semi – arid conditions, cool and very hot climates. About half of the world maize area is located in developing countries, where maize flour is a staple food for poor people and maize stalks provide dry season feed for farm animals [2]. Diversified uses of maize worldwide include: grain, starch products, corn oil and forage for animals [3].

In Sudan, although maize is of less importance than sorghum, wheat and millet as a staple human food, however, the crop plays a great role in food security for the people in Blue Nile and South Kordofan States [4]. The crop is grown in the two states by traditional farmers in small-holdings under rain-fed. Nowadays, different companies and individuals started to grow the crop at a large scale under irrigation or under rainfall in different parts of Sudan. However, the total cultivated area of maize in the Sudan increased from 17 thousand hectares in 1971 to 37 thousand hectares in 2010 [2]. The average grain yield of maize (1894 kg/ha) is far below that of the world (6 t/ha) [5]. The low productivity of maize was attributed to the low yield stability of the local open-pollinated cultivars [6].

Selection based on yield only, may not always be adequate when genotype by environment interaction is significant [7]. The presence of genotype by environment interaction (GEI) frequently changes the hybrid ranks in different environments due to cross interaction making their proper selection difficult. Therefore, it is essential that the genotype by environment interaction is taken into account, properly understood and analyzed. However, analysis of interaction of genotypes with locations and other agro-ecological conditions would help in getting information on adaptability and stability of performance of genotypes. The method commonly used for analysis of G×E interaction is the Linear Regression model of [8], in which the bi-values give information about adaptability and S2d is used as measure of stability of performance. Other workers [9], suggested the use of AMMI (Additive Main Effects and Multiplicative Interaction) approach as a measure of stability and adaptability. The AMMI model is a better model for analysis of GxE interaction in multiplication varietal trials [9]. It does not only give estimate of total GxE interaction effect of each genotype but also partitions it into interaction effects due to environments. The present study was undertaken to analyze GxE interaction and evaluate the adaptability and stability of maize

genotypes (parental inbred lines, their F1-hybrids and check varieties) for grain yield, using AMMI.

2. MATERIALS AND METHODS

2.1 Plant Material and Experimental Details

Plant material used in this study were consisted of seven parental inbred lines (66y, 160, 3, 2, 405, 277 and 6), thirteen F_1- hybrids and two standard commercial cultivars (Huediba-1 and Huediba-11) of maize crop (*Zea mays* L.). Field experiments were conducted to achieve the objectives of this study. The first field experiments were carried out during the winter and summer seasons of the two years 2009 and 2010 at the Experimental Farm of the Faculty of Agriculture, University of Khartoum at Shambat (32º:32´ E. Longitude, 15º:40´ N. Latitude and 380 meters above the sea level). The second field experiment (summer 2010) was carried out at Elrawakeeb Dry lands and Desertification Research Station, National Centre for Research, about 35 Km west of Khartoum (32º:15´ E. Longitude, 15º:25´ N. Latitude and 420 meters above the sea level), Sudan. The genotypes were evaluated under two levels of water treatment; namely normal irrigation every 7 days and water stress by irrigating every 21 days, and under four different environments namely: [Shambat winter season 2009 (SW09), Elrawakeeb summer season 2010 (ERS10), Shambat summer season 2010 (SS10) and Shambat winter 2010 (SW10)]. A split- plot design with three replications was used to execute these experiments. The water treatments were assigned to the main-plots and genotypes to the sub- plots. Each genotype (inbred line or hybrid) was grown in a 4×5 meters/plot at a seed rate of 3–4 seeds/hill on ridges during the last week of July for summer season and the first week of November for winter season. Each plot contains five ridges and data was taken from the plants grown on middle ridges. Thinning was carried out after a week from sowing, to raise two plants/hill. Hill-to-hill and ridge-to-ridge spacing was 20 and 70 cm, respectively. Agronomic and cultural practices, i.e., fertilizer application, weeding, irrigation and plant protection procedures were adopted when required according to recommendations. The grain yield (kg/ha) was calculated for each genotype, under each environment.

2.2 Statistical Analysis

The stability analysis was based on grain yield (kg/ha) data collected from 8 environments (2 locations x 2 seasons x 2 water treatments). Then G×E interaction, adaptability and yield stability parameters of genotypes, were estimated using the Linear Regression model of [8]. G×E interaction was also analyzed using Additive Main Effect and Multiplicative Interaction (AMMI) model [9], to identify adaptation pattern of the different genotypes in the eight macro-environments. This AMMI- analysis fits additive effects due to genotypes (G) and environments (E) by the usual additive analysis of variance procedure, and then fits multiplicative effects for genotypes – environment (GE) interaction by principal components analysis (PCA). The AMMI model is as follows:

$$Y_{ij} = \mu + g_i + e_j + \Sigma\lambda_k + \alpha_{ik} \, y_{jk} + R_{ij}$$

Where, Y_{ij} is the the yield of i – th genotypes in j-th environment; μ the overall mean, g_i is the effect of the i-th genotype; e_j is the effect of the j-th enviroment; λ_k is the square root of the ei gen value of the PCA axis k. Then α_{ik} and y_{jk} are the principle components scores for PCA axis k of the i th genotype and j-th environment, respectively, and R_{ij} is the residual.

Enviroment and genotype PCA scores are expressed as unit vector times the square root of λ_k (i.e., environment PCA= $\lambda_k^{0.05} y_{ik}$, genotype score = $\lambda_k^{0.05} \alpha_{ik}$ [9]. The aim of AMMI analysis is separate pattern from noise so as to identify that part of genotype × environmental interaction, which is reproducible. This may lead to better of the model is obtained by PCA ($\alpha_{ik} \times y_{jk}$). The practical advantage of AMMI is that the interactions can be modeled by only one or two PCA- axis.

It is possible to analyze genotype- environmental interaction graphically. The method to do this is called AMMI-biplot. The biplot shows the main effects means on the abscissa and principal component one (PCI) values as the ordinates. Genotypes (or environments) that appear almost on aperpendiculat line have similar means and those that fall almost on a horizontal line have similar interaction patterns. Genotypes (or environments) with large PCI scores (positive or negative) have high interactions, whereas genotypes (or environments) with PCI scores near zero have small interactions. As pointed by [9], the AMMI expected yield for any genotype and environment combination can be calculated from bipot. The interaction part is simply the genotype PCI score times the environment PCI score. Genotypes and environments with PCI scores of the same sign produce positive interaction effects, whereas, combination of PCI scores of positive sign negative specific interactions. The data on yield of the 7 inbred lines and their 13 F_1- hybrids in the eight – environments together were subjected to this analysis.

3. RESULTS

The combined analysis of variance for grain yield (kg/ha) revealed significant differences ($P<0.01$) between genotypes across all macro-environments Table 1. The combined analysis also revealed significant difference among testing environments, genotypes and G× E interaction Tables 1 and 2. The mean over the eight environments (µ) and the stability parameters; the regression coefficients (*bi*) and deviation from regression linearity (S^2d) were estimated for grain yield (kg/ha) and presented in Table 3.

Table 1. Sum of squares (SS), mean squares (MS) and variance components (var. comp.) from analysis of variance of 22 maize genotypes (parental lines, F_1- hybrids and check varieties) evaluated in eight macro–environments[1] for grain yield (kg/ha)

Var. comp	d.f	SS	EMS	Var. comp.
Environment[1]	7	231397413.4	1152782.7	
Rep with Env	16	18444523.7	9205690.4	28.7**[2]
Genotypes	21	193319498.1	924110.9	9.96**
Genotypes × Envir	147	135844304.4	450651.79	2.05**
Residual[3]	336	151149000.2		

[1]*Eight macro-environments (combination of 2 locations × 2 years × 2 treatments), see materials and methods (ERD$_0$S10, ERD$_1$S10, SS D$_0$10, SS D$_1$10, SW D$_0$09, SW D$_1$09, SW D$_0$10 and SW D$_1$10).*
[2]*, ** Significant at the 0.05 and 0.01 probability level, respectively*
[3]*Residual= deviations from regression*

3.1 Performance of the Inbred Lines and F_1-Hybrids

The mean (µ) grain yield (kg/ha) of the genotypes across the eight environments ranged from 1770 kg/ha for inbred line 66y to 2289 kg/ha for inbred line 2 and from 2389 kg/ha for hybrid 160×405 to 4070 kg/ha for hybrid 160×66y Table 3. Moreover, nine of the F_1- hybrids

exhibited mean of grain yield above the grand mean; these hybrids were 66y×277, 66y×6, 66y×2,160×6, 160×3,160×66y, 6×405 and 6×3 Table 3.

Table 2. Analysis of variance for regression of genotypes (parental lines, F_1 – hybrids and check varieties), on eight macro-environments[1]: Sum of squares (SS), mean squares (MS) and variance components (Var. comp.) for grain yield (kg/ha)

Sources of variation	d.f	S.S	MS	Var.comp
Total	527	186853738.6		
Genotypes	21	64439832.7	3068563.5	9.83**[2]
Env + in Geno × Envir	154	122413905.9	7948955	
Env. in linear	1	77132471.1		
Geno. × Env. (linear)	21	4057360.5	193207.6	0.62ns[2]
Pooled deviation	132	41224074.3	312303.6	
Residual[3]	352	56621174.6	160855.6	
Grand mean= 2621.85		R-squared= 0.663		CV. 26.50%

[1]*Eight macro-environments (combination of 2 locations × 2 seasons × 2 treatments), see material and methods ((ERD_0S10, ERD_1S10, SS D_010, SS D_110, SW D_009, SW D_109, SW D_010 and SW D_110).*
[2]**, **, ns =Significant at the 0.05 and 0.01 probability level and non-significant, respectively.*
[3]*Residual= deviations from regression*

3.2 Stability of the Parental Inbred Lines and F_1-Hybrids

Analysis of stability as measured by regression coefficient (*bi*) indicated that most of the genotypes had an average responsiveness Table 3. However, the range for (*bi*) among parental inbred lines was 0.78 - 1.20 and it was 0.73 – 1.62 for F_1- hybrids Table 3. The inbred line 6 had the smallest value (0.78) of *bi* and line 2 the highest (1.20) value. Among F_1- hybrids, the lowest (0.73) value of *bi* was exhibited by the hybrid 160×277 and the highest (1.62) by the hybrid 160×66y.

The deviation from regression (*S^2d*) among the parental inbred lines ranged from -61251 for inbred line 66y to 335769 for inbred line 3. The lines 66y, 2, 405 and 160 were not significantly different from zero, indicating stability of performance for these lines over different environments. S^2d of line 3 was significantly greater than zero indicating lack of stability in performance of this line. S^2d values of 66y×405, 160×2, 160×3, 160×277, 66y×3, 160×405 and 6×3 were not significantly different from zero, indicating stability of performance for these genotypes over different environments. S^2d of the F1-hybrids 66y×277, 66y×2, 160×6 and 160×66y were significantly greater than zero indicating lack of stability in performance of these hybrids. Considering mean value, *bi* and S^2d of these hybrids; 160×2 and 6×3 showed high mean value with non-significant deviation regression and scored regression coefficient less than unity. While, 160×3 also showed highest mean value with non-significant deviation from regression and scored regression coefficient above unity Table 3.

3.3 Adaptation of Inbred Lines and F_1-Hybrids

The AMMI analysis for the evaluated seven inbred lines and the thirteen F_1- hybrids is presented in Table 4. The analysis showed that, the variation due to environments (E), genotypes (G) and the genotype × environment interaction (G×E) was highly significant (P<0.01) and accounted for 41.3, 34.5 and 24.2% of the total sum of squares

(ESS+GSS+GEI SS), respectively Table 4. Large variation among the F_1-hybrids as well as the parental lines for grain yield (kg/ha) and their interaction to the environments was determined Table 4. The highest average grain yield (kg/ha) was obtained for the environment SSD_010 (3747 kg/ha) and the lowest (1620 kg/ha) for the environment $ERSD_110$ Fig. 1. Among the eight environments SWD_009 and SWD_109 exhibited the highest (+42.6 and +29.4) positive PCA scores, respectively, while, $ERSD_110$ and SSD_110 showed the highest (-32.4 and -10.6) negative PCA scores, respectively Fig. 1. However, the environment SWD_010 scored the smallest (-2.5) negative interaction (PCA scores). Among the lines, the largest (+5.3) positive score of PCA was shown by line 2 and the largest (-17.7) negative score was exhibited by inbred line 3 Fig. 1.

Table 3. Mean (μ), stability parameters (regression coefficient = *bi,* deviation from regression= *S²d*) for grain yield (kg/ha) for the 22 maize genotypes evaluated at eight environments

Genotypes	μ	*bi*	*S²d*
Parental lines			
66y	1770	0.81	-61251
277	2069	0.84	131316
3	1943	0.87	335769**
6	1792	0.78	65736
2	2289	1.20	-35511
160	1826	0.86	1456
405	2033	1.06	71587
Checks			
Huediba I	2706	0.87	28159*
Huediba II	2540	0.94	3247
F_1-hybrids			
66y×405	2588	1.06	44589
66y×277	2953	0.93	392928**
66y×6	3076	1.28	274151*
66y×2	3680	1.14	88292**
66y×3	2416	0.94	147562
160×405	2389	0.89	491296
160×277	2550	0.73	398917
160×6	2809	0.86	1410591**
160×2	2634	0.90	79307
160×3	3464	1.11	406943
160×66y	4070	1.62	32402**
6×405	3179	1.53	-42939**
6×3	2906	0.80	62472
Mean	2622	1.00	214708

The F_1-hybrids showed high variability in grain yield (kg/ha) and their interactions (PCA scores) to the different eight macro-environments Fig. 1. The hybrid 66y×2 exhibited the highest (+46.0) positive interaction (PCA score), whereas, the hybrid 66y×3 showed the highest (-15.1) negative PCA score. However, the hybrid 160×66y has the highest yield among all hybrids and moderate (+19.0) positive PCA score Fig.1. The hybrids which showed the smallest interactions (PCA scores) were 160×3, 66y×6 and 6×3 Fig.1.
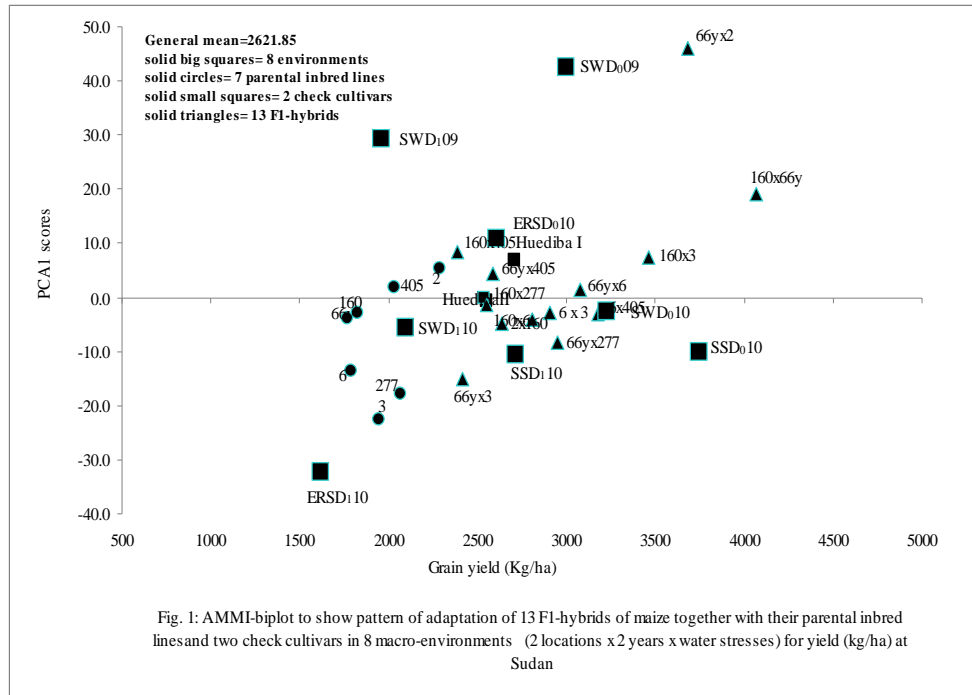
Table 4. Variance components of AMMI analysis for 22 genotypes (Parental inbred lines, F_1-hybrids and check varieties): Sum of squares (SS), mean squares (MS) and variance components (Var. comp.) for grain yield (kg/ha), averaged over three replications and across eight macro-environments

Sources	d.f	SS	MS	Var.comp
Total	527	730424739.8		
Environment	7	231397413.4	33056773.3	28.68**
Rep with in Env.	16	18444523.7	1152782.7	
Genotypes	21	193319498.1	9205690.4	9.96**
Genotypes × Env.	147	135844304.4	924110.9	2.05**
PCA 1	27	50281927.4	1862293.6	4.13**
PCA 2	25	35956537.1	1438261.5	3.19**
PCA 3	23	16304076.7	708872.9	1.57*
PCA 4	21	12871581.1	612932.4	1.36ns
PCA 5	19	11513085.0	605951.8	1.34ns
PCA 6	17	4935981.1	290251.8	0.64ns
PCA 7	15	3981116.0	265407.7	0.59ns
Residual	336	151419000.180	450651.79	
Grand mean = 2622		R- squared = 0.79		C.V= 25.60%

[1]*Eight macro-environments (combination of 2 locations × 2 years × 2 treatments), see materials and methods (SW D_009, SW D_109, SS D_010, SS D_110, ERD_0S10, ERD_1S10, SW D_010 and SW D_110). [2]Residual= deviations from regression*

., ** Significant at the 0.05 and 0.01 probability level, respectively. ns Non-significant.PCA: Principal Component Analysis*

Fig. 1: AMMI-biplot to show pattern of adaptation of 13 F1-hybrids of maize together with their parental inbred linesand two check cultivars in 8 macro-environments (2 locations x 2 years x water stresses) for yield (kg/ha) at Sudan

4. DISCUSSION

4.1 Yield Stability

The adaptability and stability of a genotype are useful parameters for recommending cultivars for known cropping conditions. [8], proposed an assessment of cultivar response to environmental changes using a linear regression coefficient and the variance of the regression deviations. In this study, the genotypes (parental inbred lines, F1-hybrids and check varieties) are grouped according to the size of their regression coefficients, less than, equal to, or greater than one and according to the size of the variance of the regression deviations (equal to or different from zero). Therefore, the genotypes with regression coefficients greater than one would be more adapted to favorable growth conditions; those with regression coefficients less than one would be adapted to unfavorable environmental conditions, i.e., to the water stress environments, and those with regression coefficients equal to one would have an average adaptation to all environments. Thus, genotypes with variances in regression deviations equal to zero would have high stability, whereas those with a variance of deviation from regression greater than zero would have low stability. Many stability models have been developed to identify the stable genotype. Eberhart and Russell [8] model is the one which has been used in maize and in other crops by several workers e.g. [10,11,12] in pearl millet. According to [8], a variety is said to be stable when regression coefficient (bi) is equal to one, deviation from regression (S^2d) is close to zero as possible with high mean performance.

In the present study, the combined analysis of variance revealed significant differences among the genotypes and environments for grain yield (kg/ha). Whereas, genotype × environments interaction was also significant for grain yield (kg/ha), indicating that genotypes interacted significantly with the environments. On the basis of stability parameters, regression coefficient (bi) could simply be regarded as the measure of response of a particular genotype and it was ranged from 0.78 to 1.06 for inbred lines and from 0.73 to 1.62 for F_1- hybrids. This large variation in regression coefficients indicates different responses of the genotypes to environmental changes. Also, these large variations in *bi*-values give the breeder an advantage to select genotypes for both adverse and favorable environments. The average deviation (S^2d) from linear regression response was greater for F_1- hybrids than for inbred lines. However, the hybrids 160×2, 160×3 and 6×3 exhibited high stability for grain yield (kg/ha) with higher mean performance across the environments. According, to their high yield and stability under drought stress conditions, the hybrids 160×2, 160×3 and 6×3 could be used for future breeding program to improve drought tolerance in maize. Many workers identified phenotypic stability for different characters in maize genotypes e.g. [13-17].

4.2 Adaptation of Inbred Lines and F_1- Hybrids

In the present study, AMMI analysis for grain yield (kg/ha) revealed that significant different was detected among the testing environments, genotypes and genotype × environment interaction. The large of sum squares for environments (41.3%) indicated that environments were different. However, most of variation in grain yield (kg/ha) in this study was caused by environments effect. Similar results were reported by [18-20]. The importance of the genotypes sum squares (34.5%) was large than that for genotypes × environment interaction (24.2%) indicating that genotypes were adapted among the most of testing environments. These results are useful in sustaining the plant breeder for determine the genotypes

performance for specific environments. Results from AMMI analysis also showed that the first principal component axis (PCA1) of the interaction was adequate to differentiate between the genotypes (parental inbred lines and F_1-hybrids) according to their adaptability. For example, the AMMI analysis showed that the most productive (3747 kg/ha) environment was $SSD_0 10$ and the less productive (1620 kg/ha) one was $ERSD_1 10$. On the other hand, environment $SWD_0 09$ showed the largest interaction score (+42.6) and environment $SWD_0 10$ showed the smallest interaction score (-2.5). This result indicates that Shambat winter season under normal irrigation ($SWD_0 10$) has less effect on genotypes performance, compared to other environments, whereas environment $ERSD_1 10$ exhibited the highest (-32.4) negative interaction score, indicating its high drought severity resulting in great reduction of the tested genotypes.

Based on mean performance (grain yield kg/ha), and according to AMMI biplot, the parental inbred lines and the different hybrids exhibited different pattern of adaptations. For example, the hybrid 66y×2 showed the highest positive interaction and more adapted to the favorable environment $SWD_0 09$, and $ERSD_0 10$. The hybrids 160x66y showed the highest yield and moderate positive interaction, indicating its stability and adaption also to the most productive favorable environments ($SWD_0 09$ and $ERSD_0 10$). However, the hybrids 66y×6, 160×2, 405×6 and 6×3 exhibited an interaction (PCA scores) closer to zero, indicating their high yield stability. Moreover, the hybrid 66y×3 showed considerable yield and adaptation to drought environments (e.g., $SWD_1 10$ and $ERSD_1 10$). Based on AMMI analysis, generally, the parental lines had inherited their adaptation as well as yield performance to their F_1-hybrids, e., g., inbred lines 3 and 277, which produced hybrids (66y×3 and 66y×277) with negative scores and low yields. Similar results were reported by [21,22], who analyzed the genotype-environment interactions and phenotypic stability of maize.

5. CONCLUSION

Maize genotypes vary in their response to variable environmental conditions. On the basis of stability parameters, the F1- hybrids 160×66y and 160×3 exhibited the highest mean grain yield/ha (4.1 tons and 3.5 tons, respectively), with slightly low interaction scores, hence they are regarded as superior hybrids. AMMI analysis approach based on grain yield was successful in discriminating the genotypes (parental inbred lines and their F1-hybrids) into different adaptation pattern. These results indicated that specific and wide adaptations are equally important in this study. Furthermore, the environments used for evaluation showed more variability, in both main effects and interactions, than the genotypes.

COMPETING INTERESTS

Authors have declared that no competing interests exist.

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