

Genotype by environment interaction and stability analyses of grain yield of selected maize (*Zea mays* L.) genotypes in eastern and central Sudan

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ABSTRACT

In this study, 22 open pollinated maize genotypes introduced from International Maize and Wheat Improvement Center (CIMMYT) and International Institute of Tropical Agriculture (IITA) plus two local checks (Var113, Hudieba-2) were evaluated over two seasons (2017 and 2018) and four locations, *viz.* New Halfa, Kassala, Gezira and Elsuki Research Station farms of the Agricultural Research Corporation (ARC) of the Sudan. The objectives of this study were to determine magnitude of G x E interaction and identify high yielding and stable genotypes under different environments. Treatments were arranged in a randomized complete block design with three replicates. Combined analysis of variance revealed highly significant ($P < 0.01$) variation among environment, genotype, and genotype by environment interaction (GEI). This is an indication of inconsistency of genotypes in response to changing environment, the high influence of environment on yield performance among the maize genotypes and, also, the significant effect of environments indicated that the testing environments were significantly different from each other in yielding potential expression. AMMI analysis of variance for grain yield showed the environment contribution by (24.06%) of the total yield variation and genotypes explained only (9.84%) of the variation. Also, substantial percentage of G x E interaction sum of squares, explained by G x E (50.41%) followed by IPCAI (19.22%) and IPCA2 (15.52%) of the variation. Based on grain yield potential and statistical stability analyses, *i.e.* Eberhart and Russel model (1966) as well as the additive main effect

and multiplicative interaction (AMMI) analysis, revealed that, the genotypes TZBR Eld-4-WC1, BR9922-DMRSR, TZBR Comp1-w, TZBR Comp1-Y and TZBR YPOP STRCY were recommended for the high yielding favourable supplementary irrigation condition (over 3000 kg/ha) of New Halfa, Gezira and Elsuki while the genotypes TzBREld-3C5, TzBREld-4-WC1, HYDERAB, 97502 (RE) and ECA STRIGOFE-153 were recommended for the unfavourable low yielding (less than 1500 kg/ha) rainfed condition of Kassala.

INTRODUCTION

Maize (*Zea mays* L.) is widely grown in most parts of the world, over a wide range of environmental conditions, between latitudes of 58° North to 40° South of the equator (Thimothy *et al.*, 1988, Dowsnell *et al.*, 1996; Golam *et al.*, 2011). Maize is one of the most important food crops worldwide, serving as staple food, livestock feed, and industrial raw material (Troyer, 2006).

Among cereal crops, maize has the highest average yield (4.7 t/ha) and remains third after wheat and rice in total area 177 (million ha) and production 967 (million tons) in the world (DACNET, 2014). However, among the developing economies, maize ranks first in Latin America and Africa but third after mild rice and wheat in Asia (CIMMYT, 1989; Dowsnell *et al.*, 1996). Maize is one of the widely cultivated crops in Africa; its share of the global maize production is very low, mainly due to low average yield per unit area (Heisey and Edmeades, 1999; Pingali and Pandey, 2001).

In Sudan, it is grown as a rainfed crop in Kordofan, Darfur and in small irrigated areas in the Northern State (Ahmed and Elhag, 1999). It is grown mainly as feed crop (both grain and forage) and rarely as food crop. Lack of improved seeds is one of the major problems hindering maize production in the Sudan. This may be partially explained by the low yield levels (below 1 ton/fed) reported for maize in the Sudan (Mohammed and Tambal, 2012).

Developing high yielding varieties adapted to more diverse environments is a major objective of breeders. However, environmental conditions affect the yield performance of a genotype. Hence, genotype

performance is a function of the genotype and the nature of the production environments (Cooper and Byth, 1996). In addition, performance of a genotype is also determined by the G x E interactions, which is a differential response of genotypes to changes in environment (Crossa, 1990; Vargas *et al.*, 1999). Also, it is defined as the inconsistency of relative performance of genotypes over environments (Hill *et al.*, 1998). Hence, multi environment trials (MET) are essential because of the existence of genotype by environment interactions which complicate genotype evaluation, selection and for this reason, analysis of genotype by environment data from MET trials has been an important component of plant breeding and cultivar recommendation. Therefore, plant breeders have been striving to develop genotypes with grain yield and other desirable characters over a wide range of different environmental conditions.

Lack of stable high yielding cultivars is one of the major bottlenecks for production and productivity of maize in Sudan. Identification of adaptable, stable and high yielding genotypes under varying environmental conditions prior to release as a cultivar is the first and foremost step for plant breeding. The current study involved the evaluation of 24 maize genotypes from CIMMYT (International Maize and Wheat Improvement Centre, Mexico), IITA (International Institute of Tropical Agriculture, Nigeria) and Sudan to determine the magnitude of GXE interaction of advanced maize genotypes, and determine the stability and yield performance of advanced maize genotypes at multiple locations in order to identify stable high yielding candidate cultivar (s) for possible release.

MATERIALS AND METHODS

The experiment was conducted for two seasons (2017/18 and 2018/19) at four locations, *viz.* New Halfa, Kassala, Gezira and Elsuki Research Stations of the Agricultural Research Corporation (ARC) of the Sudan.

The plant material used in this study consisted of 22 genotypes of maize introduced from the CIMMYT and IITA plus two local checks; Var113 and Hudieba-2 (Table 1).

The experiments were laid out in a randomized complete block design with three replicates. Each entry was represented by a plot of 2 rows. Each row was 5 m long with spacing of 20 x 80 cm between holes and rows, respectively, giving a total plot area of 8.0 m². The recommended cultural practices of the Agricultural Research Corporation of the Sudan were followed in both years to raise a good crop. Sowing date was the second week of July at New Halfa, the third week of July at Gezira and Elsuki, and the first week of August at Kassala.

During the two seasons, the crop was healthy and no pest, infestations were reported, consequently, no protection measures were taken. At physiological maturity, when the leaves and husks of the plant started to turn yellow and dry, each plot was harvested separately and then grain yield and its components were measured.

The analysis of variance was used to study differences among genotypes within each season, location and combined. Regression coefficient of Eberhart and Russell model (1966) and the additive mean effect and multiplicative interaction model (AMMI) were used to study grain yield stability of the different maize genotype in eight environments (four locations x two seasons) using Genstat 2012 statistical package.

Stability analyses of grain yield of selected maize genotypes

Table 1. Plant material used in the study [22 open-pollinated genotypes of maize plus two local checks (Var113 and Hudeiba-2)].

Entry no.	Pedigree	Seed color	Origin
1	TZBR Eld-3C5	White	IITA
2	TZBR Eld-4-WC1	White	IITA
3	TZBR Eld-4-YC1	Yellow	IITA
4	BR9922-DMRSR	White	IITA
5	BR9943- DMRSR	White	IITA
6	BRTZL ComP4DMRSR	White	IITA
7	Ama TZBR-WC3	White	IITA
8	TZBR ComP1-W	White	IITA
9	TZBR ComP2-W	White	IITA
10	TZBR ComP1-Y	Yellow	IITA
11	SOB SIY	Yellow	CIMMYT
12	98 TZEE- W STR 99TZEE-YQ P MC CO	Yellow	CIMMYT
13	2004 TZEE-Y POP STR CY	Yellow	CIMMYT
14	TZEE-Y POP STR CY	Yellow	CIMMYT
15	TZEE-Y POP QPM CO	Yellow	CIMMYT
16	POP EV-3	Yellow	CIMMYT
17	503 SLWMBR-1	White	CIMMYT
18	503 SIWAB -2	White	CIMMYT
19	HYDER ABAD 97 502 (RE)	White	CIMMYT
20	ECA QVE -2	White	CIMMYT
21	ECA QVE-6	White	CIMMYT
22	ECA STRIGOFF -153	White	CIMMYT
23	Var-113 (check)	White	Sudan
24	Hudieba-2 (check)	Yellow	Sudan

RESULTS AND DISCUSSION

Genotype by environment interaction (GEI)

The effects of season on days to 50% tasseling and silking, plant height, ear diameter, number of kernels per row, 100-kernel weight and grain yield were significant, while that of location were very highly significant for all the studied traits (Table 2). Also, the effects of genotypes and their interaction with location (GXL) were very highly significant ($P \leq 0.01$) for all the characters under study. The influence of genotypes on plant and ear height, number of rows per ear, number of kernels per row as well as grain yield varied significantly with season (SXG) (Table 2). The second degree interaction effects of season, location and genotypes (SXLXG) were significant for almost all the traits with the exception of number of rows per ear and 100-kernel weight.

Table 2. Mean square of seasons (S), locations (L), genotypes (G) and their interactions for 24 maize genotypes combined over two seasons and four locations, grown at New Halfa, Kassala, Gezira and Elsuki Research Stations Farms during summer season of 2017 and 2018.

Trait	S	L	G	LxG	SxG	Sx LxG
DT	1906***	569.49***	70.81***	6.60***	3.16 ns	7.50***
DS	2066.46***	542.76***	72.10***	6.45***	2.99 ns	7.75***
PH	4742.62*	36294.52***	526.46***	163.47***	134.43***	119.96***
EH	277.51 ns	12670.41***	444.69***	130.34***	101.24***	99.63***
ED	1.20*	24.09***	0.239***	0.11***	0.056 ns	0.072**
EL	6.520 ns	647.84***	8.44***	3.61***	2.075 ns	2.25**
NRE	1.41 ns	19.8234***	3.1019***	2.0078***	1.0765*	0.6758 ns
NKR	327.278*	3226.001***	52.791***	26.619***	12.008*	23.619***
KW	414.462*	4558.504***	17.750***	12.253***	5.331*	3.996 ns
GYD	4393653*	111583793***	634805***	709527***	255527***	288795***

*, **, *** = Significant at 0.05, 0.01 and 0.001 levels of probability, respectively. NS = Not significant.

DT= days to 50% tasseling; DS= days to 50% silking; PH = plant height; EH = ear height; ED = ear diameter; EL = ear length; NRE = number of rows per ear; NKR = number of kernels per row; KW= 100 kernel weight (g); GYD = grain yield (kg/ha).

Grain yield stability

Evaluation of genotypes across environments and through analysis of G x E interaction help to identify those with stable performance as well as to delineate environments based on genotypic response.

In this study, combined analysis of variance showed that genotype, environment, and their interaction (GEI) were significant ($P < 0.01$) (Table 4). Hence, in this study, two stability methods have been used as stability measurements. These are Eberhart and Russell's stability model (1966) and the additive main effect and multiplicative interaction model (AMMI).

Eberhart and Russell's stability model (1966)

According to this model, a stable variety is defined as one with highest mean yield, regression coefficient (b_i) = 1.0 and $S^2d_i = 0$. Therefore, regression coefficient (b_i) is considered as an indication of the response of the genotype to varying environments and in most cases the deviation from regression (S^2d_i) is taken as a parameter for stability rather than (b_i) which is more about responsiveness of genotypes. Also, if the regression coefficient of genotype (b_i) was close to one ($b_i=1.0$) and deviation from regression of zero ($S^2d_i=0$) and grain yield higher than overall mean yield, genotype was adapted in all environments, whereas genotype with (b_i) more than one ($b_i > 1.0$) was more responsive or adapted to high yielding environments, and any genotype with significantly lower than (1.0) was adapted to low yielding environments.

Therefore, in this study, the results from Eberhart and Russell model (1966) showed the regression coefficients (slope) ranged from 0.65 for genotype 19 and 20, respectively to 1.27 for genotype 8 and absolute values of (S^2d_i) ranged from 18707 to 484686 for genotypes 22 and 1, respectively (Table 3). Furthermore, in this study, the 15 highest yielding genotypes were 7, 19, 2, 9, 13, 8, 15, 3, 18, 4, 21, 1, 22, 14 and 10, recorded grain yield higher than the general mean (2422 kg/ha) of the trials (Table 3). Hence, genotypes with ($b_i > 1.0$) and mean grain yield higher than the general mean were 2, 7, 8, 9, 14 and 18, indicating that these were more responsive or adapted to environmental changes and, therefore, suitable for high yielding environments (favorable environments), whereas genotypes with b_i lower than one ($b_i < 1.0$) but low yielding (below the

general mean) were 5, 6, 11, 17, and 20. This means that these genotypes have better response under unfavorable environments but are unstable.

Genotypes with ($b_i=1.0$) and deviation from regression close to zero ($S^2_{di}=0$) and high yielding (higher than the general mean) are genotypes 1 (2603 kg/ha), 3 (2557 kg/ha), 4 (2569 kg/ha), 21 (2587 kg/ha) and 22 (2605 kg/ha). These findings indicated that these genotypes are more responsive under all environments and stable. From these findings, the most stable genotypes with lowest deviation were genotypes 1, 3, 4, 21 and 22 when the yield regression coefficient and the deviation from regression were considered together (Table 3).

Additive main effects and multiplicative interactions (AMMI) analysis model

Combined analysis of variance can quantify GXE interaction and describe the main effects but does not explain the interaction effect (Asnake *et al.*, 2013). Genotype by environment interaction was quantified using the most common procedure; i.e. pooled analysis of variance, which partitions the total variance into its component parts (genotype, environment, GEI and pooled error). In this study, the combined ANOVA for 24 maize genotypes (OPVs) evaluated across eight environments based on the AMMI model is presented in Table 4. Results from combined analysis of variance revealed highly significant ($P \leq 0.01$) variation among environment, genotype, and genotype by environment interaction and IPCAs axes. This indicates that the big influence of environment on yield performance among the maize genotypes and also the significant effect of environments indicated that the testing environments were significantly different from each other for yielding potential expression.

In this study, the AMMI analysis of variance for grain yield showed the environment contribution by 24.06% of the total yield variation and genotypes explained only 9.84% of the variation. Also, substantial percentage of G x E interaction sum of squares, explained by G x E (50.41%) followed by IPCA1 (19.22%) and IPCA2 (15.52%) of the variation (Table 4). The first two IPCAs accounted 34.74% of the total G x E interaction sum of squares. However, most of the variation was explained by the first two principle components (IPCAs) according to Crossa (1990). This result was in agreement with that of Alberts, (2004)

Stability analyses of grain yield of selected maize genotypes

who reported that the IPCA1, IPCA2 axes explained (68.08%) and (31.92%) of the total G x E.

Table 3. Stability parameters for grain yield of 24 maize genotypes evaluated at New Half, Kassala, Gezira and Elsuki.

Genotype	Mean (kg/ha)	SLOPE	MS-DEV
1	2603	1.0	484686
2	2452	1.21	191240
3	2557	1.03	22891
4	2569	1.09	218205
5	2319	0.86	95951
6	2332	0.89	129047
7	2427	1.16	39948
8	2489	1.27	234632
9	2458	1.18	46682
10	2626	0.98	188462
11	2318	0.88	126523
12	2302	1.01	58121
13	2472	0.84	71927
14	2613	1.17	173925
15	2495	0.92	273644
16	2292	1.23	59690
17	2108	0.85	235734
18	2564	1.11	119122
19	2446	0.65	307650
20	2166	0.65	76375
21	2587	1.03	297207
22	2605	1.03	18707
23	2148	1.04	92079
24	2174	0.88	75464
Mean	2422		

Slope of regression of variety means on site index.

MS-DEV= deviation from regression component of interaction.

Table 4. The additive main effect and multiplicative interaction (AMMI) analysis of variance of the significant effects of genotype (G), environment (E) and genotype X environment interaction (GE) on grain yield (kg/ha) and the partitioning of the GE into AMMI scores.

Source of variation	Df	SS	MS	F	Efficiency (%)
Environment (E)	7	35680567	5097223	75.80**	24.06
Genotype (G)	23	14600507	634805	7.30**	9.846
Interaction (GEI)	161	74761283	464356	5.34**	50.41
PCA1	29	28508534	983053	11.30**	19.22
PCA2	27	23016019	852445	9.80**	15.52
Residual	105	23236730	22130	2.54	
Total	296	148279087			

DF = degree of freedom; SS= sum of square; MS= mean square and efficiency (%) = percentage GE sum of squares.

*, **, *** Significant at 0.05, 0.01 and 0.001 levels of probability, respectively.

PCA1= first principal component.

PCA2 = second principal component.

AMMI biplot of the first two principal component axes (PCA1and PCA2)

In this study, high variation was observed between genotypes for grain yield and their reaction to the environment (Tables 5 and 6). Grain yield between environments studied ranged from 1129 kg/ha for E-4 to 3496 kg/ha for E-6 and E-7, respectively. The highest average yield was obtained in E-6 and E-7 followed by the E-5, whereas E-3 and E-4 (had obtained the lowest grain yield). Also E-1, E-5, E-6, E-7 and E-8 exhibited the largest absolute PCA1 score (i.e. had the highest interaction effect), whereas the smallest PCA1score was shown by E-3 and E-4, respectively (i.e. had the least interaction effect) based on the AMMI bi-plot, G and E having PCA values close to zero have small interaction effects, whereas those having large positive or negative PCA absolute values largely contribute to GE interaction. Hence, E-1, E-5, E-6, E-7 and E-8 were the

most interactive, while E-3 and E-4 were the least interactive among the eight environments (Table 5 and Fig. 2). E-5 was the most interactive among the eight environments.

Furthermore, the IPCA scores of a genotype in the AMMI analysis indicate the stability of a genotype over environments. The greater value of the IPCA score, either positive or negative means the genotype is more specifically adapted to certain environments, whereas the lower value of the IPCA score or (close to zero) means the genotype is more adapted and stable over all environments. Therefore, in this study among the eight major environments that comprised of (N1 and N2), (K1 and K2), (G1 and G2) and (S1 and S2) for two seasons combined the best genotypes were selected according to AMMI estimate. At New Halfa (N1 and N2), the best genotypes were (G2, G4, G8, G10 and G14), whereas in Gezira environments (G1 and G2), were (G4, G10, G14, G15, G18, G19 and G 21), also in Elsuki environments (S1 and S2), were (G1, G13, G19 and G22), while in Kassala environments (K1 and K2) were (G1, G3, G19 and G22). Hence, depending on the results of IPCA scores, genotypes (G1, G2, G4, G8, G10, G13, G14, G15, G18, G19, G 21 and G22) which have greater IPCA scores and high yielding, therefore, can be considered as widely adapted and specifically adapted to certain environments, and also adapted to the higher yielding on more favorable environments, whereas the genotypes (G1, G3, G8, G19, and G22) which have small and close to zero IPCA scores can be considered as the most stable or adapted genotypes over all environments as presented in Table 6.

Table 5. PCA1 and PCA2 scores for the eight growing environments of 24 maize genotypes.

Environment	Number of environments	E.-Mean	1PCAe [1]	1PCAe [2]
G1	1	2306	23.07147	- 42.25036
G2	2	2417	- 18.43050	- 9.53251
K1	3	1424	5.80560	5.98746
K2	4	1129	3.03956	15.34841
N1	5	3305	- 32.00962	0.49798
N2	6	3496	- 20.01402	- 3.97957
S1	7	3496	19.24244	13.04043
S2	8	2303	19.29507	20.88818

PCA1= first PC axis. PCA2 = second PC axis

G1, G2 = Gezira; K1, K2= Kassala; N1, N2 = New Halfa and S1, S2= Elsuki.

AMMI crosses sites analysis

AMMI having the bi-plot feature, genotypes and environments are plotted on the same diagram, facilitating inference about specific interactions of individual genotypes and environments by using the sign and magnitude of PCA1 values. Any genotype with a PCA1 value close to zero (near the origin) has small interaction effects, shows general adaptation to the tested environments. A large genotypic PCA1 score (distant from zero), large contribution to GE and reflects more specific adaptation to environments with IPCA1 scores of the same sign. Accordingly, in this study, the AMMI model biplot based on IPCA1 and the genotype means for 24 maize genotypes was constructed to show the performance and association of the genotypes (Fig.1.) and the eight environments were shown based on IPCA1 values of the environments mean (Fig. 2).

Stability analyses of grain yield of selected maize genotypes

Table 6. First four AMMI selections per environment season (2017 and 2018).

Number	Environment	Mean	Score	1	2	3	4
1	G1	2306	23.07	G15	G21	G18	G19
2	G2	2417	-18.43	G14	G4	G10	G21
3	S1	2303	19.24	G19	G1	G13	G22
4	S2	2993	19.30	G1	G19	G22	G13
5	K1	1424	5.81	G1	G22	G19	G3
6	K2	1129	3.04	G1	G8	G22	G3
7	N1	3305	-32.01	G4	G2	G14	G8
8	N2	3496	-20.01	G14	G4	G10	G2

Environments, namely G1, G2 = Gezira; K1, K2= Kassala; N1, N2 = New Halfa
S1, S2= Elsuki; Genotypes name from G1 to G22 as presented in Table 1.

Fig.1 shows that genotype 10 was the highest yielding followed by genotypes 14, 22, 21,18,4 and 3, whereas genotype 4 was the most stable genotype as it is the closest to the PCA axis and can be considered as adaptable to environments. On the other hand, genotype 21 was the least stable as it is far from the IPCA1axis, due to its high mean grain yield can be considered as a responsive genotype for a specific environment. Among the eight environments K1 and K2 were the most stable environments when IPCA were close to zero, whereas G1 environment was far distant from the origin (Fig. 2).

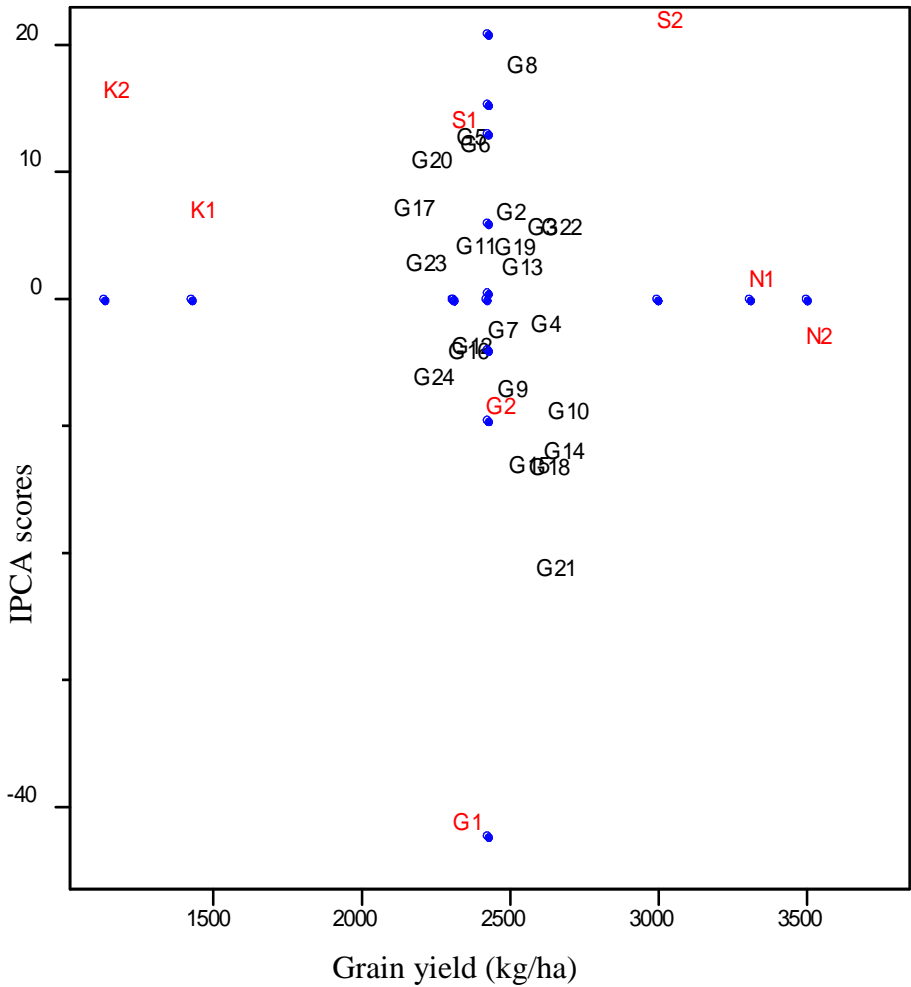


Fig. 1. The AMMI bi plot of the main and the PCA1 effects of both genotypes and environment on grain yield of 24 maize genotypes grown in eight environments. Genotypes are indicated by +G.

Stability analyses of grain yield of selected maize genotypes

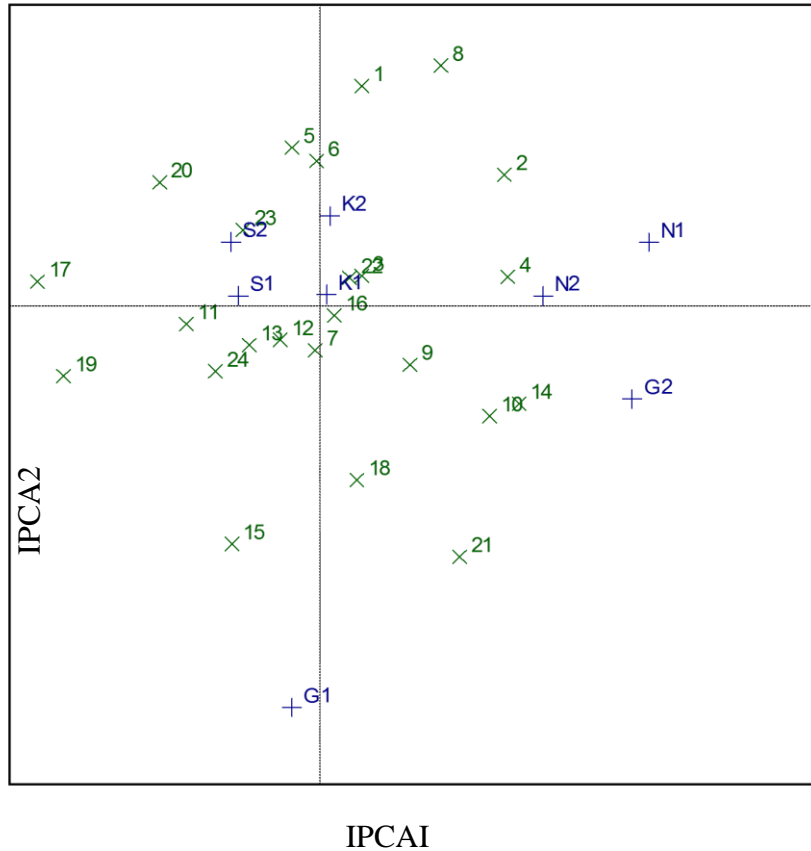


Fig. 2. The AMMI bi-plot of the PCA1 and PCA2 axes for grain yield of 24 maize genotypes grown in eight environments. Genotypes are indicated by X.

CONCLUSIONS

The results of this study indicated:

1. Significant differences were found among the 24 maize genotypes for most of the studied traits in each season and location separately and across them showing large variation among the genotypes.
2. The genotypes performance differed with environments.
3. Both Eberhart and Russel model and AMMI analysis showed that genotypes, TZBR Eld-4-YC1 .BR9922 DMRSR, TZBR Comp1-Y, TZBR YPOP STRCY, 503 SIWAB-2, ECA STRIGOFE-153 were the highest yielding and stable genotypes over locations and seasons.

4. For specific environments, genotypes TZBR Eld-4-WC1, BR9922-DMRSR, TZBR Comp-1-w, TZBR Comp-1-4-Y and TZBR YPOP STRCY were stable and high yielding (over 3300 kg/ha) under the favorable supplementary irrigation conditions. Genotypes TZBREld -3c5, TZBREld-4-WC1, HYDERAB, 97502 (RE) and ECA STRIGOFE-153, were low yielders (less than 1500 kg/ha) but stable under the unfavorable rainfed conditions.

RECOMMENDATION

Based on grain yield potential and stability, the genotypes TZBR Eld-4-YC1, BR9922-DMRSR, TZBR Comp-1-w, TZBR Comp1-Y and TZBR YPOP STRCY were recommended for the favorable supplementary irrigation conditions of New Halfa, Gezira and Elsuki while the genotypes TZBREld -3c5, TZBREld-4-WC1, HYDERAB, 97502 (RE) and ECA STRIGOFE-153 were recommended for the unfavorable low yielding rainfed conditions of Kassala.

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