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# Grain yield potential and stability of some open-pollinated varieties, exotic hybrids and promising single crosses of maize (*Zea mays* L.) in Central Sudan

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**Key words:** Grain, Stability, Yield, Open-pollinated, Exotic hybrids, Maize, Sudan.

**Abstract**

Maize (*Zea mays* L.) in the Sudan is a promising cereal crop with the potential usefulness for both human beings and livestock. In this study, 13 maize genotypes were evaluated over two consecutive seasons (2013 and 2014) at three locations, viz. Gezira, Rahad and Elsuki research stations farms of the Agricultural Research Corporation (ARC), under irrigation. The objectives were to evaluate these genotypes for grain yield potential and stability and henceforth identifying the highest yielding and stable genotypes for the different environments. A wide range of genetic variability was observed among the genotypes for most of the studied traits. The significant environment, genotype and genotype x environment (GE) component of interaction indicated wide differences among the environments and differential genotypic behavior to the test environments. Moreover, the three open pollinated genotypes HSD-5158, PR-89B-5655 and S99TLWQHG"AB, in addition to the exotic hybrids JKH 56 and PAC 745 were not significantly different in grain yield among themselves, but showed the highest grain yield, 2048, 1838, 2040, 1819 and 1858kg/ha, respectively, when compared to the rest of the genotypes. They out-yielded than the local check, Hudeiba-2 (1728kg/ha) by 18.5%, 6.4% 18.0%, 5.0% and 8.0%, respectively. The regression coefficients of the five genotypes were 0.591, 1.346, 1.136, 1.227 and 1.158. The results also indicated that, HSD-5158 and S99TLWQHG"AB showed taller plants (150 and 174cm) and they were late maturing compared to the rest of the genotypes. The results on the other hand, showed that, AMMI and pattern analysis have higher efficiency in partitioning and analyzing stability studies compared to regression analysis. PCA1and PCA2 in AMMI accounted for 55.8% and 20.3% and together they accounted for 76.1% of the GE sum of squares. This study concluded that, the five genotypes, HSD-5158, PR-89B-5655, S99TLWQHG"AB, JKH 56 and PAC 745 showed grain yield superiority and stability under the test environments. They could be grown successfully in the irrigated central clay plains of the Sudan. It is suggested to grow these genotypes under rain-fed conditions in southern Gadaref and the Blue Nile State for more than two seasons to test them for yield potential and stability.

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## Introduction

Maize (*Zea mays* L.) originated in Central America and was introduced to West Africa in the early 1950s by the Portuguese traders (Dowswell *et al.,* 1996). It ranks as one of the world's three most important cereal crops and cultivated in a wide range of environments more than wheat and rice because of its greater adaptability (Koutsika-Sotiriou, 1999). Maize is currently produced on nearly 100 million hectares in 125 developing countries and is among the three most widely grown crops in 75 of those countries (FAOSTA, 2010). By 2050 demand for maize will double in the developing world, and maize is predicted to become the crop with the greatest production globally, and in the developing world (Rosegrant *et al.,* 2008). In large parts of Africa maize is the principle staple crop; accounting for an average of 32% of consumed calories in Eastern and Southern Africa, rising to 51% in some countries.

Maize is an important source of carbohydrates since the maize seed consists of 70% starch and 10% protein. It is also used as a source for extracting edible oil. White maize is mostly used for human consumption, mainly milled as a meal which is then cooked to be eaten as porridge, or as grits. Yellow maize is used as animal feed in the dairy, pork, poultry and feedlot industries. The distribution between white and yellow maize is 60% to 40%, respectively.

In the Sudan, maize is a promising cereal crop with the potential usefulness for both human beings and livestock (Salih *et al.*, 2008). It ranks the fourth important cereal crop after sorghum, wheat and pearl millet. It is normally grown as a rainfed crop in Kordofan, Darfur and in small irrigated areas in the Northern states (Ishag, 2004). Although maize is emerging as an important cereal crop, the vast majority of farmers still practice recycling seeds of open pollinated varieties (OPVs) without continuous maintenance measures. Abdalla *et al.* (2010) reported that the lack of adapted lines with high yield potential and good resistance to water stress are the major limiting factors for maize production in the Sudan. Maize can occupy an important position in the economy of the country due to the possibility of blending maize with wheat for bread making and the increase in the demand of maize for poultry feed and for forage as well as its great potential for export to provide new source of hard currency.

Farmers and scientists usually seek for improved high yielding and adapted maize cultivars (hybrids and /or OPVs) and other essential agronomic traits. The grain yield superiority of such cultivars should be reliable over a wide range of environmental conditions and years. Moreover, the occurrence of genotype x environment interactions (GEI) should be at minimal.

In fact multi-location yield trials play an important role in plant breeding and agronomic research. Data from such trials have three main objectives: a) to accurately estimate and predict yield based on limited experimental data, b) to determine yield stability and the pattern of response of genotypes across environments; and c) to provide reliable guidance for selecting the best genotypes or agronomic treatments for planting in future years and at new sites (Crossa, 1990).

Various studies have been conducted to analyze the effect of G x E interaction on the Sudanese maize varieties. However, the changing environmental conditions in the Sudan, the expansion of maize to new agro-ecologies coupled with inadequate maize varieties available for the different environments necessitate accurate and continuous study of G x E interaction for a dynamic crop improvement program. Hence, the main objectives of this study is to evaluate 13 maize genotypes (open pollinated varieties, exotic hybrids and promising single crosses) under different environments for grain yield and its related attributes and henceforth identifying the most high yielding and stable genotype(s). The specific objectives are to measure grain yield potential for the maize genotypes under different environments, estimate genotype x environment interactions (G x E) through the behavior of these genotypes in an array of locations and environments, and measure grain yield stability among different maize genotypes.

## Materials and methods

*Experimental sites*

This experiment was conducted at three locations, i.e. Gezira (GRS), Rahad (RRS) and Elsuki (ERS) research stations of the Agricultural Research Corporation (ARC) of the Sudan for two consecutive seasons 2013 and 2014.The three sites were located in the central clay plains of the Sudan.

*Plant material*

The plant material used consisted of 13 maize genotypes. Eight out of the genotypes (3 single cross and 5 open- pollinated varieties). The rest of the genotypes were three exotic hybrids and one released exotic hybrid, in addition, to one released open – pollinated cultivar. The name, origin and status of the 13 genotypes used in the study are presented in Table 1.

**Table 1.** List of maize genotypes used in the study.

| Entry no. | Entry type | Pedigree and Origin |
|---|---|---|
| 1 | Open pollinated variety | HSD-5158 (ARC-Sudan) |
| 2 | Open pollinated variety | PR-89B-5655(CIMMYT) |
| 3 | Open pollinated variety | S99TLWQHG"AB-##(CIMMYT) |
| 4 | Open pollinated variety | S99TLWQ-1(CIMMYT) |
| 5 | Open pollinated variety | POOL15QPM-IR-##(CIMMYT) |
| 6 | Hybrid | JKH 56 (India) |
| 7 | Hybrid | PAC 740 (India) |
| 8 | Hybrid | PAC 745 (India) |
| 9 | Single cross(4x3x2012) | RING-A- S1-1 BAILO-O2 SIYQ x RING-A- S1-1) (ARC-Sudan) |
| 10 | Single cross (3x2x2012) | BAILO-O2 SIYQ x RING-A-S1-1 CORRALE10-02 SIYQ x RING-A- S1-2) (ARC-Sudan) |
| 11 | Single cross (7x6x2012) | SOBSIY-HG AB x RING-A-S1-1* BAILO-O2 SIYQ x RING-B- S1-1) (ARC-Sudan) |
| 12 | Check 1(hybrid) | Golden – 1 (ARC-Sudan) |
| 13 | Check 2(OPV) | Hudeba - 2 (ARC-Sudan) |

*Experimental layout and crop management*

The experiment was arranged in a randomized complete block design with three replicates in the two seasons and at the three locations. The plot size was maintained as 20m$^2$, i.e. of 5 ridges, 0.8m wide and 5m long. The land of the experiments was prepared using disk plowing, harrowing, leveling and then ridging to 80cm apart. Sowing date was the first week of July at the three locations in both seasons. Seeds were sown at the rate of 3- 4 seeds per hill. The plants were thinned to one plant per hill two weeks after sowing. A dose of 86-kg N/ha was applied in split equal doses after thinning and before flowering. The crop was irrigated at intervals of 10-14 days, and plots were kept free of weeds by hand hoeing.

*Parameters measured*

The growth and development parameters, i.e. days to 50% tasselling and silking, plant and ear heights were taken from five plants randomly selected from each plot. The yield components measured (ear length, number of kernels/ear and 100 kernel weight) were taken as the average of 5 ears taken randomly from each plot at harvest. The grain yield was assessed from the total number of harvested cobs in each plot as kg/ plot area and then converted to kg/ha.

*Statistical analysis*

The collected data were subjected to the individual analysis of variance (ANOVA) procedure using the IRRISTAT computer package at each location and combined across locations.

*Stability analysis*

The stability analysis was performed for grain yield combined across five environments (Gezira Research Station, 2013, Rahad Research Station, 2013, Elsuki Research Station, 2013, Elsuki Research Station, 2014 and Rahad Research Station, 2014). The joint regression analysis proposed by Eberhart and Russell, 1966 was adopted to estimate the stability parameters which include slope or regression coefficient (bi) and deviation from regression ($S^2di$), in addition to mean grain yield of each genotype.

Similarly, the Additive Main Effect and Multiplicative Interaction (AMMI) analysis was carried out to show the stability and pattern of adaptation of maize genotypes to the test environments. 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 genotype-environment interaction (GE) by principle components analysis (PCA). The IRRISTAT software was used to conduct the AMMI analysis

(IRRI, 2005) according to Zobel and Gausch, 1988 and Nachit *et al*, 1992 the equation of AMMI model.

## Results and discussion

*Genotype x Environment interaction (G x E)*

Mean square of genotypes across locations for season 2013 showed significant (P = 0.05) difference for all characters studied (Table 2). Similar results were shown for season 2014 with the exception of ear height and number of kernels per cob. In season 2013 season, location differences were highly significant (P = 0.01) for all characters except ear length and significant (P = 0.05) for days to silking in 2014 (Table 2).

The interaction of genotype x location was quite variable, i.e. significant (P = 0.05) for days to 50% silking, plant height, ear height, kernels weight and highly significant (P = 0.01) grain yield, while, non – significant for the rest studied characters, in both seasons (Table 2).

The interaction of genotype x season was also quite variable, e.g., at Gezira location, in 2013 season, genotypes showed significant differences (P = 0.05) for almost all characters except for ear height, while 50% of the characters (days to 50% tasselling and silking, plant and ear heights) showed non - significant differences at the same location in season 2014 (Table 3). At Rahad location, ear height, number of kernels/cob, 100– kernels weight and grain yield showed significant differences in both seasons (Table 3), while the interaction of the rest of the characters was variable. The current results of significant G x E for almost all characters were partially in accordance with those of Sallah *et al.* (2002) who found that GXE interaction was significant for grain yield, days to 50% silking and plant height of elite maize drought tolerance composites. The interaction effect of genotype x location was highly significant for most traits except days to50% tasselling, ear length (cm), and number of kernels/ row in both season, and this may be due to genetic factors. Hohls (2001) reported that, G x E interactions resulted in inconsistent differences between genotypes across environments, which was caused either by differential responses of the same set of genes to changes in environment or expression of different sets of genes in different environments. Ibrahim *et al.*, (1998) suggested that the ranking of genotypes was not the same at different locations. They studied the effects of minimum and maximum temperatures, rainfall and relative humidity on the G x E interaction in corn yield.

The significance of genotype x environment indicated that genotypes responded differently to environment and some are environment specific. Also, this finding indicated the importance of these components in affecting the phenotypic performance of the evaluated maize genotypes.

From the present study, and from the basis of the importance of genotype x environment interactions as shown we can conclude that, maize genotypes show differential responses, when grown under different environments, suggesting that maize genotypes should be tested over a number of environment (years and locations) to assure the selection of the suitable genotype or genotypes for each location.

**Table 2.** Mean squares of locations, genotypes, and their interactions for 13 maize genotypes, grown at Gezira, Rahad and Elsuki Research Stations in 2013and 2014 growing seasons.

| Traits | 2013 2014 | | | | | |
|---|---|---|---|---|---|---|
| | L | G | LXG | L | G | LXG |
| Days to50% tasselling | 112.01** | 16.11** | 11.00 ns | 68.32** | 7.4* | 4.09 ns |
| Days to50% silking | 101.84** | 8.51* | 10.84* | 62.82* | 7.06** | 4.13 * |
| Plant height (cm) | 4494.08** | 2.36* | 150.59 * | 10086.82** | 186.42* | 54.47 * |
| Ear height (cm) | 3024.21** | 224.25** | 65.33 * | 10041.33** | 88.13ns | 39.21* |
| Ear length (cm) | 157.11** | 5.76** | 1.99 ns | 3.57ns | 11.47** | 1.54 ns |
| Number of kernels per ear | 1675.49** | 62.93** | 15.69 ns | 833.65** | 51.16ns | 58.84 ns |
| 100-kernel weight (g) | 367.45** | 9.85* | 13.41 * | 280.82** | 12.81* | 12.23 * |
| Grain yield (kg/ha) | 2866.22** | 3493.39** | 2750.23** | 527.69** | 2730.99* | 9107.77** |

**Table 3.** Mean squares for eight characters in 13 maize genotypes evaluated at Gezira (GRS), Rahad (RRS) and Suki Research Stations (SRS) in two seasons (2013 and 2014).

| Traits | 2013 2014 | | | | |
|---|---|---|---|---|---|
| | GRS | RRS | SRS | GRS | RRS |
| Days to 50% tasselling | 53.04 ** | 56.45 ns | 55.37 ns | 49.25 ns | 47.24 ns |
| Days to 50% silking | 57.23** | 59.44 ns | 58.22* | 52.34 ns | 50.20* |
| Plant height (cm) | 176.21 * | 109.09 ns | 145.31ns | 158.41 ns | 180.03 ns |
| Ear height (cm) | 65.10 ns | 48.21* | 60.34* | 68.21 ns | 90.09 ns |
| Ear length (cm) | 17.06* | 14.14* | 16.29* | 18.25** | 18.10* |
| Number of kernels / cob | 34.01** | 23.03* | 32.28* | 44.10* | 37.28* |
| 100-kernel weight (g) | 24.21* | 18.12* | 20.08* | 24.14* | 20.06* |
| Grain yield (kg/ha) | 2739.44 ** | 1105.11* | 1477.12* | 2228.26* | 1708.33** |

*,** Significant at 0.05 and 0.01 probability levels, respectively, ns: not significant.

*Grain yield (kg/ha)*

The genotypes showed significant differences in grain yield at the three locations and in both seasons (Table 4). In both seasons, the open -pollinated genotypes showed the highest grain yield across locations, followed by the hybrids and then the two checks. The two open –pollinated genotypes, HSD-5158 and S99TLWQHG"AB in particular, showed higher grain yields of 1851, 1905, 2245 and 2176kg/ha in 2013 and 2014, respectively. The two hybrids, JKH 56 and PAC 745 came second and obtained medium grain yield of 1786 and 1930kg/ha in 2013 and in 2014, respectively. On the other hand, the two checks (Golden-1 and Hudeiba-2), showed the lowest grain yield combined across locations in both seasons (Table 4).

The high yield potential of the two open- pollinated genotypes, HSD-5158 and S99TLWQHG"AB could be attributed mainly to larger ears length, heaviest and higher number of kernels/ cob recorded by the two genotypes. The high values showed by the two open-pollinated genotypes in the three yield components (ear length, number of kernels/cob and 100- kernels weight) was reflected in the high grain yield potential of the above two open –pollinated varieties (HSD-5158 and S99TLWQHG"AB. Furthermore, the above three characters are important yield components positively correlated with high grain yield in maize.

In fact, HSD- 5158 showed high yield potential in preliminary and advanced yield trials conducted at Gezira Research Farm. Therefore, it is selected as a local high yielding and promising open- pollinated variety, identified by maize breeding program over the last few years. The second open pollinated genotype S99TLWQHG"AB was an introduction from CIMMYT and also selected due to high grain yield potential and better agronomic performance in preliminary and advanced yield trials. Accordingly, the high grain yield of these two open –pollinated genotypes than the rest of the tested genotypes was expected in this study.

Also, taller plants and relatively late flowering of the two genotypes could be responsible for the high grain yields of these two varieties. Usually, late maturing maize genotypes coupled with taller plants exhibited high grain yield potential.

On the other hand, higher grain yield of 2217kg/ha was obtained at Rahad site in 2014 compared to Gezira (1476kg/ha). However, the highest grain yield (2289kg/ha) was obtained at Elsuki in 2013. Such finding could be attributed to favorable environmental conditions, (i.e. adequate and even distribution of rainfall) at Rahad in 2014 and at Elsuki site in 2013.

The superiority in grain yield of the open-pollinated genotypes over hybrids in this study, in particular, the check hybrid Golden-1 was not expected because yield advantage of maize hybrid cultivars was well known and documented by several research workers. For example, the check hybrid Golden-1 used in this study was in fact tested for two seasons (2010/2011-2011/2012) with other hybrids in the same environments and showed high yield potential and grain yield stability. Therefore, it was released in 2013 for commercial use in the central clay plains of the Sudan (Mohammed *et al.* 2015).

Another possible reason could be, the standard cultural practices adopted in the trial. For example, the amount of nitrogen fertilizer applied to the trial was about 86kg N/ha (187kg/ha urea). This nitrogen rate is probably not sufficient and optimum for the hybrid varieties, since maize hybrid cultivars are more responsive to high nitrogen rates than the open-pollinated varieties. Accordingly, inferior grain yield showed by the hybrids in this study is expected and justified. Moreover, such a result agreed well with that of Heisey *et al.* (1998) who reported that, the yield advantage of hybrids is expressed only under optimum management practices.

**Table 4.** Mean grain yield (kg/ha) of 13 maize genotypes evaluated at Gezira Research Station (GRS), Rahad Research Station (RRS) and Elsuki Research Station (SRS) in two summer seasons (2013 and 2014).

| Genotype | Grain yield (kg/ha) | | | | | | |
|---|---|---|---|---|---|---|---|
| | 2013 | | | | 2014 | | |
| | GRS | RRS | SRS | Combined | GRS | RRS | Combined |
| HSD-5158 | 1673 | 1591 | 2289 | 1851 | 2102 | 2388 | 2245 |
| PR-89B-5655 | 1450 | 1162 | 2191 | 1601 | 1952 | 2187 | 2070 |
| S99TLWQHG"AB | 1751 | 1577 | 2385 | 1905 | 2059 | 2293 | 2176 |
| S99TLWQ-1 | 1521 | 1039 | 2214 | 1591 | 1487 | 2283 | 1885 |
| POOL15QPM-IR | 1096 | 0996 | 2185 | 1425 | 1582 | 2179 | 1881 |
| JKH 56 | 1608 | 0999 | 2099 | 1568 | 1845 | 2258 | 2052 |
| PAC 740 | 1600 | 1200 | 2243 | 1681 | 1660 | 2103 | 1882 |
| PAC 745 | 1551 | 1527 | 2281 | 1786 | 1656 | 2204 | 1930 |
| RING-A-SI-1 | 1393 | 0987 | 2320 | 1567 | 1652 | 2170 | 1911 |
| BAILO-02SIYQ | 1604 | 0992 | 2250 | 1615 | 1424 | 1867 | 1646 |
| SOBSIY-HG AB | 1322 | 0977 | 2074 | 1457 | 1357 | 1857 | 1607 |
| Golden-1 | 1077 | 0978 | 1920 | 1325 | 1423 | 1855 | 1639 |
| Hudeiba-2 | 1605 | 1167 | 2206 | 1659 | 1560 | 2035 | 1797 |
| Mean | 1476 | 1103 | 2289 | 1617 | 1707 | 2217 | 1901 |
| S.E.± | 177.6** | 141.5* | 158.2* | 114.6** | 135.8* | 126.4* | 137.0** |
| C.V.% | 20.8 | 22.9 | 16.3 | 16.3 | 13.9 | | 17.5 16.1 |

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

*Grain yield stability*

Evaluation of varieties and hybrids of any breeding program aims at identifying genotypes that consistently produce stable yields over a range of diverse environments. The mean grain yields of the tested genotypes over the five environments ranged from 1482kg/ha as minimum to the 2048kg/ha as maximum, with overall mean grain yield of 1761kg/ha (Table 5). Five genotypes, namely, HSD-5158, PR-89B-5655, S99TLWQHG"AB, JKH 56 and PAC 745, recorded higher grain yield of 2048, 1838, 2040, 1819 and 1858kg/ha than the overall mean grain yield (1767kg/ha) of all genotypes (Table 14). They out-yielded the best check, Hudeiba-2 (1728kg/ha) by 18.5%, 6.4%, 18.0%, 5.0 and 8.0%, respectively. However, the two genotypes, HSD-5158 and S99TLWQHG"AB (OPVs) showed the highest grain yield (2048 and 2040kg/ha) and exceeded Golden-1 and Hudeiba-2 in grain yield by 38.19%, 18.51%, 37.65% and 18.10%, respectively.

On the other hand, the genotype x environment (G x E) was significant for grain yield and justify grain yield stability analysis to identify the most stable and adapted genotype(s) to the test environments. Two stability methods were performed for grain yield stability analysis. These are the joint regression approaches as outlined by Eberhart and Russell (1966) and the additive main effect and multiplicative interaction model (AMMI).

*Eberhart and Russel's stability model (1966)*

In this model, the deviation from regression is used to assess unpredictable part of variability of any genotype with respect to environment that could not be predicted by the regression. It is a measure of reliability of the linear regression. Eberhart and Russel (1966) defined the stable genotype as one with $b_i = 1$, $S^2d = 0$ and higher mean grain yield than the overall mean grain yield. From Table (5), the results showed clear differences in slopes of the regression lines between tested genotypes and checks. Some regression coefficients (b) exceeded unity while others were less than one. The regression coefficient (slope) ranged from 0.55 for Golden – 1 to 1.35 for S99TLWQHG"AB (Table 5). From this study, the five genotypes, HSD-5158, PR-89B-5655, S99TLWQHG"AB, JKH 56 and PAC 745, that showed higher mean yield than the overall mean obtained regression coefficients of 0.591, 1.346, 1.136, 1.227 and 1.150, respectively. Accordingly, the most stable genotypes were S99TLWQHG"AB and PAC 745 according to Finlay and Wilkinson (1963). However, considering the three parameters of stability together, i.e. mean yield, regression coefficient and deviation from regression, only JKH 56 was the most stable genotype as proposed by Eberhart and Russell (1966). Furthermore, the yield of Hudeiba-2, POOL15QPM-IR, JKH 56, PR-89B-5655 and Golden-1 can be predicted due to relatively small values of $S^2di$ of these genotypes.

In fact, small values of deviation from regression close to zero with bi > 1.0 is an indication of high yield stability and adaptation of genotypes to high yielding environments, while these having bi < 1.0 are stable and adapted to low yielding environments as considered by Becker and Leon (1988).

Therefore, as the five genotypes, HSD-5158, PR-89B-5655, S99TLWQHG"AB, JKH 56 and PAC 745 showed grain yield superiority and stability, they could be successfully grown in the irrigated cropping systems in central Sudan, however, they need further testing under high rain fall conditions, i.e. southern Gadaref and southern Blue Nile State for yielding ability and stability.

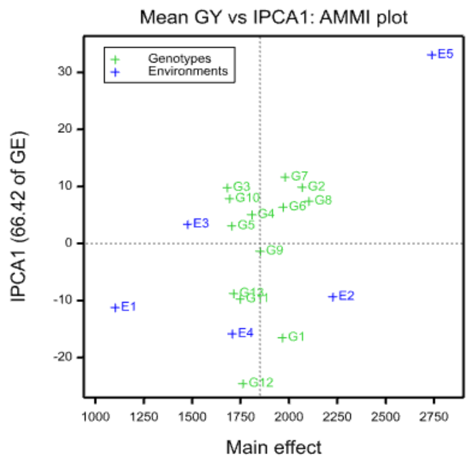
*AMMI bi-plot of the first two principal component axes (PCA1 and PCA2)*

To further explain the GE and stability, a bi-plot between the PCA1 and PCA2 scores were given in (Fig. 2). AMMI bi-plot of the first two principle component axes is a powerful way of detecting important scores of GE effects (Zobel *et al.* 1988). This analysis represents stability of the genotypes across environments in terms of principle component analysis. It is used to identify broadly adapted genotypes that offer stable performance across sites, as well as genotypes that perform well under specific conditions. In this study, the first two principal component axes (PCA1 and PCA2) in bi-plot analysis explained a large proportion of the variation 76.1% of the total GE sum of squares (Table 6). On this AMMI bi-plot, genotypes and environment having PCA values close to zero (near the origin) have small interaction effects, whereas those having large positive or negative PCA values (distant from zero) largely contribute to GE interaction (Yau, 1995). Hence the genotypes HSD-5158, S99TLWQ-1, PAC 740 and PAC 745 were the most interactive, while the genotypes POOL15QPM-IR, BAILO-02SIYQ, Golden-1 and Hudeiba-2 were the least interactive. On the other hand, environment E-3 and E-5 appeared at far distance from the origin (large PCA score), hence they had large interaction effects; whereas E-1, E-2 and E-4 had small interaction effects (Fig. 2).

Genotypes HSD-5158 were more stable and responsive for good environments (1 and 4), while the genotypes POOL15QPM-IR and RING-A-SI-1* were responsive and suitable for E-2 environment. Hence, in this investigation, visual observations of AMMi bi-plot analysis enable to identify genotypes and testing environments that exhibited major sources of GE interaction as well as those that were stable. Similar result was reported by Sneller *et al* (1997). AMMI model is more effective in partitioning interaction SS than the linear regression techniques resulting in increased precision equivalent to the number of replication by a factor of two to five. Such gain may be used to reduce cost by reducing the number of replications, to include more treatments in the experiment or to improve efficiency in selecting the best genotypes. In this study, comparing the effectiveness of joint regression and AMMI analysis for analyzing GE interaction, it was found that PCA1 in AMMI accounted for the GE sum of squares by 55.8%, while regression analysis accounted for GE sum of squares by 21.9%. Hence, AMMI analysis was superior to regression techniques in accounting for GE sum of squares and more effective in partitioning the interaction sum of squares. From this study the genotypes S99TLWQ-1, POOL15QPM-IR, JKH 56 and RING-A-SI-1 were more stable and high yielding genotypes under E2 and E5.

**Table 5.** Stability parameters for grain yield (kg/ha) of 13 maize genotypes evaluated at Gezira, Rahad and Elsuki Research Station in two summer seasons (2013 and 2014).

| Genotypes | Yield (kg/ha) | bi | $S^2di$ |
|---|---|---|---|
| HSD-5158 | 2048 | 0.591 | 56543.33 |
| PR-89B-5655 | 1835 | 1.346 | 26869.11 |
| S99TLWQHG"AB | 2040 | 1.136 | 71730.20 |
| S99TLWQ-1 | 1738 | 1.100 | 30758.80 |
| POOL15QPM-IR | 1653 | 1.204 | 14948.57 |
| JKH 56 | 1819 | 1.227 | 24209.08 |
| PAC 740 | 1782 | 1.152 | 69149.30 |
| PAC 745 | 1858 | 1.150 | 66736.20 |
| RING-A-SI-1 | 1739 | 1.158 | 37858.52 |
| BAILO-02SIYQ | 1631 | 1.011 | 67541.73 |
| SOBSIY-HG AB | 1532 | 0.746 | 43899.76 |
| Golden-1 | 1482 | 0.554 | 27773.33 |
| Hudeiba-2 | 1728 | 0.624 | 12476.00 |
| Mean | 1761 | | |




Grain yield mean kg/fedan

**Fig. 1.** The AMMI bipolt of the main and the PCA1 effects of both genotypes and environments on grain yield of 13 maize genotypes grown in five environments. Genotypes are indicated by triangles while environments are represented by circles.

**Table 6.** AMMI analysis of variance of the significant effects of genotypes (G), and environment (E) and genotype- environment interaction (GE) on grain yield (kg/ha) and the partitioning of the GE into AMMI scores.

| Source of variation | DF | SS | MS | Efficiency (%) |
|---|---|---|---|---|
| Environment (E) | 4 | 64383752 | 16095938 | |
| Genotypes (G) | 12 | 4032387 | 336032 | |
| GE I | 48 | 11130349 | 231882 | 98.6 |
| PCA1 | 15 | 7393067 | 492871** | 55.8 |
| PCA2 | 13 | 1997376 | 153644 | 20.3 |
| Residual | 20 | 1739906 | 86995 | |

DF, degree of freedom; SS, sum of square, MS mean square and Efficiency% percentage of GE sum of squares. *,** Significant at 0.01 probability levels, ns: not significant.

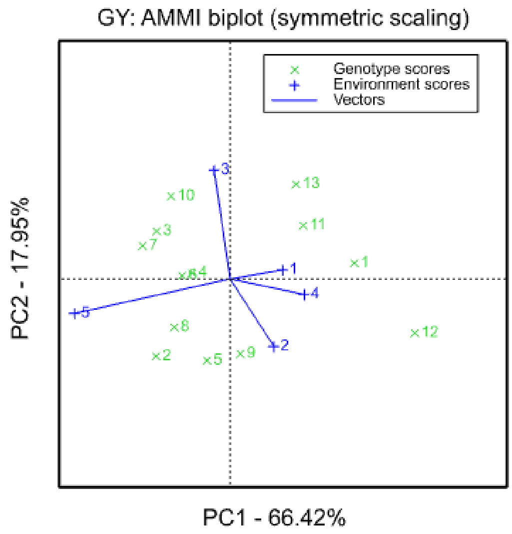



**Fig. 2.** AMMI bi-plot of the PCA1 and PCA2 axes for grain yield of 13 maize genotypes grown in five environments. Genotypes are indicated by triangles while environments are represented by circles.

## Conclusions

The significant environment, genotype, and genotype x environment component of interaction indicated wide differences between the environments and differential genotypic behavior under the test environments. The five genotypes, HSD-5158, PR-89B-5655, S99TLWQHG"AB, JKH 56 and PAC 745 showed grain yield superiority and stability under the test environments, therefore, they could be grown successfully in the irrigated central clay plains of the Sudan.

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