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# AMMI AND GGE BIPLOT ANALYSES FOR YIELD STABILITY OF NINETEEN MAIZE GENOTYPES UNDER DIFFERENT NITROGEN AND IRRIGATION LEVELS

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## Abstract

Genotype-by-environment (G×E) interaction reduces the correlation between genotypic and phenotypic parameters and complicates progress of selection. Among several models proposed for evaluation of the G×E interaction, the AMMI and GGE-biplot are the most informative models. The objective of this study was to estimate the G×E interaction in 19 maize hybrid cultivars and populations and to identify maize genotypes of stability and/or adaptability across 12 environments (combination of two irrigation regimes × three soil N levels × two years) using the AMMI and GGE-biplot models. A randomized complete block design was used in each environment with three replications. The AMMI analysis of variance indicated that the genotype (G), environment (E) and G×E interaction had significant influence (pd"0.01) on maize grain yield. Based on AMMI model, SC-30K8 (G2), SC-131 (G4) and SC-10 (G1) could be considered stable across the test environments and among the five highest grain yielding genotypes in this experiment. SC-101(G3) and SC-30N11 (G6) had the highest and second highest yield, but were considered average in stability and the most unstable genotypes, respectively. The optimum water and N environment E7 (WW-HN, 2017) is the most stable based on IPCAe-1, IPCAe-2 and ASV scores; hence it was the least interactive environment for grain yield, and is considered the ideal environment for selecting genotypes which can be adaptable for water stress and low N conditions. The water stressed environments E10 and E4 indicated both good discriminating ability and representativeness, making them ideal and best environments for testing the maize genotypes. Based on GGE-biplot method, SC-101(G3) is the winning genotype for the first mega-environment which consists of five environments. SC-30N11 (G6) is the winning genotype for the second mega-environment which consists of seven environments. These genotypes are the most adapted to the respective mega environments.

***Key words:*** *Zea mays*, G × E interaction, Mega environment, Grain yield, adaptability

## Introduction

Maize (*Zea mays* L.) ranks the second amongst cereal crops grown in Egypt with regard to the harvested area and production after wheat. According to FAOSTAT (2020), Egypt in 2017 grew 920,601 hectares and produced 7.1 million tons of grains, with an average yield of 7.72-ton $ha^{-1}$. According to the same report, Egypt ranks fourth in the world with respect to average productivity after the USA (11.084 ton $ha^{-1}$) Canada (10.524 ton $ha^{-1}$), and France (8.749 ton $ha^{-1}$), where the maize harvested area of these countries was large. However, the local production of maize is not sufficient to satisfy the local consumption, which is about 16 million tons, because Egypt imported in 2017 about 8.33 million tons of maize grains with an import value of 1723.2 million US dollars (FAOSTAT, 2020). To reach the self-sufficiency of maize production in Egypt, efforts are devoted to extend the acreage of maize and to improve the maize productivity from the unit area. Extending maize growing is only available in the deserts, where sandy soil is suffering from its low water-holding capacity; *i.e.* soil moisture stress and deficiency in nutrients, particularly nitrogen, *i.e.* Low-N stress.

A major challenge of maize production in Egypt is lack of stable varieties. For the last four decades, a number of hybrid maize varieties were developed and released for growing in the Valley and Delta as well as in the new reclaimed soils. The single and three-way cross hybrid varieties should be tested for stability and adaptability in

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these environments, which differ in soil fertility, climate, N and water availability. Adaptability is the response of the genotypes to the differences between the locations, while stability represents the response of genotypes to variations between years (Lin and Binns, 1994).

Genotype-by-environment (G×E) interaction is reflected in inconsistent crop yield across environments. Variations in climate change and soil properties and the inherent potential of genotypes are among the major factors for variable crop yield (Al-Naggar *et al.,* 2018c and 2019). Fortunately, the possibility exists to find or develop stable and high-yielding genotypes (fit genotypes) for the mega-environments (Gauch and Zobel, 1997). Additive main effect and multiplicative interaction (AMMI) model (Crossa *et al.,* 1990 and Ebdon and Gauch, 2002) and genotype plus genotype-by-environment (GGE) biplot model (Blanche *et al.,* 2007; Sharma *et al.,* 2014 and Yan *et al.,* 2007) are frequently applied procedures for genotype, environment and genotype-by-environment analysis based on crop attributes. AMMI separates the genotype and environment main effects and the GEI effects (Gauch *et al.,* 2008) and provides much insight into GEI (Crossa *et al.,* 1990). The GGE biplot emphasis on genotype and genotype-by-environment interaction becomes efficient in the mega-environment analysis and genotype evaluation which includes attribute-based genotypes ranking (Yan *et al.,* 2007).

It is important to show the relationship between genotypes and environments for selected traits graphically by use of a genotype by genotype by environment (GGE) biplot that allows visual assessment of genotype by environment interaction (GEI) pattern of multi-locational or multi-environment data (Yan *et al.,* 2000 and Yan and Hunt, 2002). GGE is the most recent approach for analysis of GEI and increasingly being used in GEI studies in plant breeding research (Butran *et al.,* 2004). The model was proposed by Yan *et al.,* (2000), and has shown extensive usefulness and a more comprehensive tool in quantitative genetics and plant breeding (Yan, 2001 and Yan and Rajcan, 2002). The model covers very critical areas in the study of stability of multi-locational trials, like the which-won-where pattern, mean performance and stability of genotypes, discriminating ability, mega-environment investigation, and representativeness of environments. The GGE method emphasizes on two concepts, whereby in the first concept, it clearly points out that even though the measured yield is a result of combination effect by Genotype (G), Environment (E) and genotype x environment interaction (GEI), only G and GEI are relevant and must be considered simultaneously when evaluating genotypes, thus the name GGE. The second concept is based on the biplot technique which was developed by Gabriel (1978) which is used to estimate and show the GGE of MEYT, hence the name GGE biplot. The GGE biplot is made by the first two principal components (PC), PC1 and PC2 also known as the primary and secondary effects, respectively. This is derived from subjecting the environment centered yield data (due to GGE) to singular value decomposition. This now makes it very easy for one to see which genotype won in which environments, thus facilitating mega-environment (ME) identification (Yan *et al.,* 2000 and Yan 2001). This is facilitated in the form of a polygon to visualize the interaction patterns between genotypes and environments (Yan and Kang, 2003), whereby furthest genotypes are connected from the biplot origin such that all genotypes are contained in the polygon (Kaya *et al.,* 2006). Some genotypes will be located on the vertices of the polygon and they are either the best or the poorest in one or more environments (Yan *et al.,* 2000, Yan and Kang, 2003 and Yan and Tinker, 2006). The rays are drawn perpendicular to the sides of the polygon dividing it into sectors, such that the vertex genotype in each sector is also the best genotype for sites whose markers fall into respective sector so that sites within the same sector share the same winning genotype (Yan *et al.,* 2000 and Yan, 2002). GGE biplot is a visual display of the G+GE of multi-environmental data where groups of locations with similar cultivar responses are presented and it identifies the highest yielding varieties for each group. The present study was done to analyze yield data on 19 maize hybrid cultivar and populations from across twelve environments conducted under combinations of two irrigation regimes × three nitrogen (N) levels × two years in Giza location. The objectives were (i) to identify maize genotypes with stable and high yield performance across different environments by using AMMI analysis, (ii) to measure the correlation among the twelve test environments, (iii) to determine whether the test-environments belong to a single mega environment or not and (iv) to rank environments based on discriminating ability and representativeness by using the GGE biplot analysis.

## Materials and Methods

This study was carried out in the two successive growing seasons 2016 and 2017 at the Agricultural Experiment and Research Station of the Faculty of Agriculture, Cairo University, Giza, Egypt (30°02'N latitude and 31°13'E longitude with an altitude of 22.50 meters above sea level).

**Breeding materials**

Seeds of 19 maize (*Zea mays* L.) genotypes (9 single crosses, 5 three-way crosses and 5 open-pollinated populations) obtained from Agricultural Research Center (ARC) (13 genotypes), Hi-Tec Company (3 genotypes), Pioneer-Corteva Company (2 genotypes), Fine Seeds Company (one genotype), were used in this study table 1.

**Experimental procedures**

Sowing date was April 24$^{th}$ in the 1$^{st}$ season (2016) and April 30$^{ht}$ in the 2$^{nd}$ season (2017). Sowing was done in rows; each row was 4 m long and 0.7 m width. Seeds were over sown in hills 25 cm apart, thereafter (after 21 days from planting and before the 1$^{st}$ irrigation) were thinned to one plant/hill to achieve a plant density of about 24,000 plants/fed. Each experimental plot included two rows (plot size = 5.6 m$^2$).

Evaluation in each season was carried out under 12 environments (from E1 to E6 in the first season and from E7 to E12 in the second season), *i.e.* three nitrogen levels, *i.e.*, high-N (HN), medium-N (MN) and low-N (LN) by adding 120, 70 and 20 kg N/acre (285.6, 166.6 and 47.6 kg N/ha), respectively in two equal doses in the form of Urea 46% before 1$^{st}$ and 2$^{nd}$ irrigations and two irrigation regimes, *i.e.*, well-watered (WW) and water stress at flowering (WS) table 2.

**Experimental design**

A randomized complete blocks design with three replications was used for each environment. Well-watered environments were separates from water stress environments with an alley (4 m width), to avoid water leaching between plots.

**Water regimes**

The following two different water regimes were used:

**Well-watered (WW):** Irrigation was applied by flooding, the second irrigation was given after three weeks and subsequent irrigations were applied every 12 days.

**Water stress at flowering (WS):** The irrigation regime was just like well watering, but the 4$^{th}$ and 5$^{th}$ irrigations were withheld, resulting in 24 days' water stress just before and during the flowering stage.

**Fertilization regimes**

Nitrogen fertilization for each rate was added in two equal doses of Urea 46% before the first and second irrigation. Triple Superphosphate Fertilizer (46% $P_2O_5$) at the rate of 30 kg $P_2O_5$/acre (70 kg $P_2O_5$/ha), was added as soil application before sowing during the preparation of the soil for planting.

All other agricultural practices were followed according to the recommendations of ARC, Egypt. Weed control was performed chemically with Stomp herbicide just after sowing and before the planting irrigation and manually by hoeing twice, the first before the first irrigation (after 21 days from sowing) and the second before the second irrigation after 33 days from sowing). Pest control was performed when required by spraying plants with Lannate (Methomyl) 90% (manufactured by DuPont, USA) against corn borers.

**Soil analysis**

Physical and chemical soil analyses of the field experiments table 3 were performed at laboratories of Soil and Water Research Institute of ARC, Egypt.

Data of soil analysis table 3 showed that there were differences in physical and chemical analysis of the soil between the 1$^{st}$ and 2$^{nd}$ year of evaluation.

**Meteorological data**

The required weather data for the experimental site through the two growing seasons were obtained from Central Lab for Agricultural Climate, Agricultural Research Center at Giza, Governorate, Egypt (Table 4). Weather data table 4 showed some differences between 2016 and 2017 seasons especially in temperature.

**Data recorded**

**Grain yield plant$^{-1}$ (GYPP) (g)** was estimated by dividing the grain yield plot$^{-1}$ (adjusted at 15.5% grain moisture) on the number of plants plot$^{-1}$ at harvest.

**Biometrical analysis**

Each of the twelve environments was analyzed separately as a randomized complete block design (RCBD) and a combined analysis of variance across the twelve environments was performed on the basis of individual plot observation using the MIXED procedure of MSTAT ®. Prior to analysis, the data were tested for normality. Test for homogeneity of variances was done using Bartlett's test (Bartlett 1937). Least significant difference (LSD) values were calculated to test the significance of differences between means according to Steel *et al.,*

**Stability analyses**

Stability analysis of the 19 maize genotypes was carried out for grain yield/plant across 12 environments, representing the combinations of two irrigation regimes × three soil nitrogen levels × two years. Two different approaches were adopted for estimating the stability parameters, namely AMMI analysis and GGE biplot method of stability analysis (Yan *et al.,* 2000). AMMI

and GGE biplot models were computed using the GeneStat-17.1.13780 software program.

**Additive means effect and multiplicative interaction (AMMI) model:**

The AMMI model is as follows:

$$Y_{ger} = \mu + \alpha_g + \beta_e + \Sigma n \lambda n \gamma gn \delta en + \varepsilon_{ger} + \rho_{ge};$$

where Yger was the observed yield of genotype (g) in environment (e) for replication (r); Additive parameters: μ was the grand mean; αg is the deviation of genotype g from the grand mean, βe is the deviation of the environment e; Multiplicative parameters: λn was the singular value for interaction principal component axis (IPCA) n, γgn was the genotype eigenvector for axis n, and εen is the environment eigenvector; εger is the error term and ρge are PCA residuals. Accordingly, genotypes with low (regardless of the sign) IPCA scores showed general or wider adaptability, while those with high IPCA scores showed specific adaptability (Gauch and Zobel, 1996).

**AMMI Stability Value (ASV)**

The ASV is the distance from the coordinate point to the origin in a two- dimensional plot of IPCA1 scores against IPCA2 scores in the AMMI model (Purchase, 1997). Because the IPCA1 score contributes more to the G×E interaction sum of squares, a weighted value is needed. This was calculated for each genotype and each environment according to the relative contribution of IPCA1 to IPCA2 as follows:

$$ASV = \{[(SS_{IPCA1} \div SS_{IPCA2}) \text{ (IPCA1 score)}]^2 + (\text{IPCA2 score})^2\}^{1/2}$$

Where $SS_{IPCA1} / SS_{IPCA2}$ was the weight given to the IPCA1-value by dividing the IPCA1 sum of squares by the IPCA2 sum of squares. The larger the ASV value, either negative or positive, the more specifically adapted a genotype was to certain environments. A smaller ASV value indicated a more stable genotype across environments (Purchase, 1997). The AMMI model was performed using the Genestat-17.1.13780 software.

**GGE Biplot analysis (Yan *et al.*, 2000)**

To evaluate the phenotypic stability and adaptability, the GGE biplot analysis was performed, considering the simplified model for two main components. In this approach, the effects of genotype (G) and genotype by environment (GE) were considered as random in the model. In this case, the best linear unbiased prediction (BLUP) of G and GE effects are calculated.

The components of genotypic variance, of the variance of G×E interaction and residual were estimated by the method of restricted maximum likelihood (REML). For analysis of variance the software package SAS 9.2 version was used. GGE biplot software was used to explain relationship between genotype and locations graphical (Yan and Kang, 2003).

The model for a GGE biplot (Yan, 2002) based on singular value decomposition (SVD) of the first two principal components is:

ξν.η

$$Y_{ij} - \mu - \beta_j = \lambda_1 \xi_{i1} \eta_{j1} + \lambda_2 \xi_{i2} \eta_{j2} + \varepsilon_{ij} \quad (1)$$

where $Y_{ij}$ is the measured mean (DBH) of genotype i in environment j, μ is the grand mean, $\beta_j$ is the main effect of environment j, $\mu + \beta_j$ being the mean yield across all genotypes in environment j, λ1 and λ2 are the singular values (SV) for the first and second principal component (PC1 and PC2), respectively, $\xi_{i1}$ and $\xi_{i2}$ are eigenvectors of genotype i for PC1 and PC2, respectively, $\eta_{j1}$ and $\eta_{j2}$ are eigenvectors of environment j for PC1 and PC2, respectively, εij is the residual associated with genotype i in environment j.

PC1 and PC2 eigenvectors cannot be plotted directly to construct a meaningful biplot before the singular values are partitioned into the genotype and environment eigenvectors. Singular-value partitioning is implemented by,

$$g_{i1} = \lambda_1^{f1} \xi_{i1} \text{ and } e_{ij} = \lambda_1^{1-f1} \eta_{1j} \quad (2)$$

Where F1 is the partition factor for PC1, theoretically F1 can be a value between 0 and 1, but 0.5 is most commonly used.

To generate the GGE biplot, the formulae (1) was presented as:

$$Y_{ij} - \mu - \beta_j = g_{i1}e_{1j} + g_{i2}e_{2j} + \varepsilon_{ij} \quad (3)$$

If the data was environment-standardized, the common formula for GGE biplot was reorganized as follows:

$$Y_{ij} - \mu - \beta_j/s_j = \Sigma g_{i1}e_{1j} + \varepsilon_{ij} \quad (4)$$

Where, $s_j$ is the standard deviation in environment j, l =1, 2,…,k, $g_{i1}$ and $e_{1j}$ are PC1 scores for genotype i and environment j, respectively. We used environment standardized model (4) to generate biplot of "which-won where". For the analysis of relationship between the trials, genotype and environment evaluation, we used unstandardized model (3). The GGE biplot model was performed using the Genestat-17.1.13780 software.

## Results and Discussion

**Additive main effects and multiplicative interaction (AMMI) model**

**AMMI analysis of variance**

Combined analysis of variance revealed highly

significant (P≤0.01) variances due to environment, genotype, genotype × environment interaction and interaction principle component axes (IPCAs) (Table 5). This result revealed that there was a differential yield performance among the maize genotypes across testing environments and the presence of strong genotype by environment (G×E) interaction. As G×E interaction was significant, further calculation of genotype stability is possible.

The differential ranking of genotypes across different environments has been reported in most multi environment trials in West and Central Africa (Ifie *et al.,* 2015). According to Moghaddam and Pourdad (2009), highly significant GEI for grain yield under the multiple-stress and non-stress environments indicates differential responses of the hybrids and the need to identify high-yielding and stable hybrids across the test environments.

The analysis of variance table 4 showed that genotype (18.23%), environment (50.23%) and GEI (30.71%) effects were significant (P ≤ 0.01). Even though the proportion of the environment is the largest, genotype and GEI effects have paramount importance for genotype evaluation (Yan and Kang, 2003). Furthermore, GEI effect was larger (30.71%) than the genotypic effect (18.23%), indicating a high loss of potential genetic gain (Rono *et al.,* 2016). Thus, the potential of genotypes was more exploited if the best performed genotypes were identified for the specific environments. As the pooled ANOVA showed the presence of GEI for the maize grain yield, it means a breeder faces challenge of selection genotypes for advancement and or release, hence further testing for genotypes with wider and specific adaptation and locations with good discriminating ability and representativeness should be done. This is similar to the study which was done by Gasura *et al.,* (2015), where they tested 20 sorghum varieties and there was a large effect of GEI about seven times larger than the effect of genotypes. AMMI ANOVA showed that IPCA1 accounted for 44.29% and IPCA2 accounted for 34.12%, both accounting for a sum of 78.41% table 3 and this showed similarity with study of Gasura *et al.,* (2015), where PC1 and 2 explained 36.8 and 29.5%, respectively.

The presence of a significant G×E interaction also suggested differential responses of the genotypes across the test environments and the need to identify high-yielding and stable genotypes across the contrasting environments (Badu-Apraku *et al.,* 2003, 2011a; Oyekunle and Badu-Apraku 2013 and Adu *et al.,* 2019). Several authors also reported significant G×E interaction and thus stability analysis for bread wheat (Sial *et al.*,, 2000) and finger millet (Misra *et al.,* 2009 and Lule *et al.,* 2014) was possible.

Substantial percentage of G×E interaction was explained by IPCA-1 (12.73%) followed by IPCA-2 (5.94%) table 4. The interaction effect was concentrated in the first two IPCA scores (60.78%) explaining the magnitude of interaction effect on yield. The remaining IPCA axes (residual) contributed only 39.22 % to G×E interaction. Because of their maximum, the first two principal components (IPCA-1 and IPCA-2) were used to plot a 2-dimensional GGE biplot. Gauch and Zobel (1996) suggested that the most accurate model for AMMI can be predicted by using the first two IPCAs. Several authors took the first two IPCAs for GGE biplot analysis since because the greater percentage of genotype by environment interaction (GEI), in most cases, were explained by the first IPCA such as for maize (Wonde and Labuschagne, 2005; Choukan, R. 2010; Badu-Apraku *et al.,* 2012), bread wheat (Asnake *et al.,* 2013), common bean (Abeya *et al.,* 2008), finger millet (Lule *et al.,* 2014) and grain sorghum (Al-Naggar *et al.,* 2018 a, b). This indicated that AMMI biplot model is the best fit for this data set, which is in agreement with Adugna, (2007), Misra, *et al.,* (2009) and Al-Naggar *et al.,* (2018a).

A large sum of squares shows that environments were diverse, influencing yields differently which was in harmony with the findings of Reddy *et al.,* (2014) in sweet sorghum production. Identification of adaptable, stable, and high yielding genotypes under different environmental conditions prior to release has been reported by Lule *et al.,* (2014) to be the first and foremost steps for plant breeding. Environment expresses most of the total yield variation while genotype and genotype by environment interactions were less effective (Mortazavian *et al.,* 2014). The soil's constituents such as moisture content, mineral availability and pH that is an integral part of environment cause large annual variation in yield performance of a crop. GEI can be reduced by identifying genotypes that are most stable (Eberhart and Russell, 1966).

**AMMI Stability Value (ASV)**

The IPCA1, IPCA2 scores and AMMI stability values (ASV) of 12 environments and 19 maize genotypes are presented in tables 6 and 7, respectively. Environments and genotypes with least ASV and IPCA scores (either negative or positive) are considered the most stable. According to ASV, the environment E7 (well-watered, High-N, 2017 season) was the most stable and the highest grain yielding table 5, followed by E8 (well-watered, Medium-N, 2017 season), which was the third highest grain yielding. The two environments E7 and E8 are therefore considered the most stable based on IPCAe-1 and ASV scores; hence they were the least interactive environments for grain yield. On the contrary, environment E10 (Water stressed, High-N, 2017 season) was the most unstable based on IPCAe-1, IPCAe-2 and

ASV scores, but was the second highest yielding and the environment E4 (water stressed, high N, 2016 season) was the second most unstable based on IPCAe-1 and ASV scores and attained the third lowest GYPP, hence they were the most interactive environments for grain yield.

The greater IPCA-1 shows greater discriminating ability of an environment. This gives the importance of determining the discriminating ability to enhance separation through differences in performances of different genotypes. The results revealed that E10 (WS-HN, 2017 season) and E4 (WS-HN, 2016), which are water stressed environment in the two seasons (2016 and 2017) gave more information on the tested genotypes than the other environments. So this study provides important information on selecting and releasing best and ideal genotypes which are good for production in specific and widely adapted environments as well as determine the most effective and necessary environments which gives more information on varieties in future breeding trials.

Furthermore, the $IPCA_g$ scores of genotypes in AMMI analysis indicate stability of genotypes across environments; high $IPCA_g$ scores (either negative or positive) are unstable while those with low scores are stable (Hagos and Abay, 2013).

An ideal genotype should have high mean grain yield and small ASV. Accordingly, SC-168 followed by Midland population, SC-30K8, SC-131, TWC-1100 and SC-10 showed the lowest ASV and IPCAg-1. The grain yield/ plant was below average for SC-168 and TWC-1100, the second lowest for Midland, the third highest for SC-30K8 and the fourth highest for SC-131 and the fifth highest for SC-10. These results revealed that these genotypes are showing relatively better stability than the rest of genotypes. However, stability needs to be considered in combination with yield (Farshadfar, 2008). Thus, SC-30K8 (G2), SC-131 (G4) and SC-10 (G1) could be considered stable and among the five highest grain yielding genotypes in this experiment. It is worthy to note that the single cross SC-10 (G1) is considered as check cultivar in registration trials of new released cultivars of maize; both SC-10 (G1) and SC-131 (G4) are bred by Agricultural Research Center of the Ministry of Agriculture, Egypt.

Furthermore, SC-101 (G3) bred by Fine Seed Company and SC-30N11 (G6) bred by Pioneer-Corteva Company were the highest and second highest yielding genotypes (216.5 and 182.5 g per plant, respectively) but with average and high ASV score (9.30 and 20.97, respectively). Therefore, these genotypes (SC-101 and SC-30N11) could be identified as good genotypes to validate for yield performance and specific adaptability to rich environments (well-watered and high N). The results of ASV further confirmed that TWC-352 (G13), TWC-360 (G14),

**Table 1:** Designation, origin and grain color of maize genotypes under investigation.

| Genotype No. | Designation | Origin | Genetics Nature | Grain Color |
|---|---|---|---|---|
| G1 | SC-10 | ARC-Egypt | Single cross | White |
| G2 | 30K8 | Pioneer-Corteva | Single cross | White |
| G3 | SC-101 | Fine seeds, Egypt | Single cross | White |
| G4 | SC-131 | ARC-Egypt | Single cross | White |
| G5 | SC-2031 | Hi-tec, Egypt | Single cross | White |
| G6 | SC-30 N11 | Pioneer-Corteva | Single cross | Yellow |
| G7 | SC-168 | ARC-Egypt | Single cross | Yellow |
| G8 | SC-176 | ARC-Egypt | Single cross | Yellow |
| G9 | SC-2055 | Hi-tec, Egypt | Single cross | Yellow |
| G10 | TWC-310 | ARC-Egypt | 3-ways cross | White |
| G11 | TWC-321 | ARC-Egypt | 3-ways cross | White |
| G12 | TWC-1100 | Hi-tec, Egypt | 3-ways cross | White |
| G13 | TWC-352 | ARC-Egypt | 3-ways cross | Yellow |
| G14 | TWC- 360 | ARC-Egypt | 3-ways cross | Yellow |
| G15 | American Early Dent | ARC-Egypt | Population | White |
| G16 | Giza-2 | ARC-Egypt | Population | White |
| G17 | Nubaria-355 | ARC-Egypt | Population | White |
| G18 | Original Midland | Kensas - USA | Population | Yellow |
| G19 | Reid Type Composite | USA | Population | Yellow |

**Table 2:** Characterization of the 12 environments used in this investigation.

| Environment | Water status | Water Designation | Nitrogen level | Nitrogen Designation | Year | Environment Designation |
|---|---|---|---|---|---|---|
| E1 | Well-Watered | WW | High N | HN | 2016 | WW-HN, 2016 |
| E2 | Well-Watered | WW | Medium N | MN | 2016 | WW-MN, 2016 |
| E3 | Well-Watered | WW | Low N | LN | 2016 | WW-LN, 2016 |
| E4 | Water stressed | WS | High N | HN | 2016 | WS-HN, 2016 |
| E5 | Water stressed | WS | Medium N | MN | 2016 | WS-MN, 2016 |
| E6 | Water stressed | WS | Low N | LN | 2016 | WS-LN, 2016 |
| E7 | Well-Watered | WW | High N | HN | 2017 | WW-HN, 2017 |
| E8 | Well-Watered | WW | Medium N | MN | 2017 | WW-MN, 2017 |
| E9 | Well-Watered | WW | Low N | LN | 2017 | WW-LN, 2017 |
| E10 | Water stressed | WS | High N | HN | 2017 | WS-HN, 2017 |
| E11 | Water stressed | WS | Medium N | MN | 2017 | WS-MN, 2017 |
| E12 | Water stressed | WS | Low N | LN | 2017 | WS-LN, 2017 |

A.E.D. (G15), Giza-2 (G16) and TWC-321 (G11), were unstable and not adaptable and that Midland (G18) was consistent low yielder across environments.

Odewale *et al.,* (2013) reported that two out of the five coconut genotypes grown across nine environments in southern Nigeria showed smaller ASV and thus better stability. Farshadfar (2008) noted that three out of 20 bread wheat genotypes evaluated gave smaller ASV and higher grain yield than the grand mean and thus better relative stability. Lule *et al.,* (2014) identified three out of 32 genotypes of finger millet that had better grain yield, but with high ASV and thus good genotypes to validate for yield performance and specific adaptability. Stable genotypes follow genes that affect the trait in question and their expression relative to the environment being similar to average cultivar while unstable genotypes have genes that are challenged differently by a different environment (Ngeve and Bouwkamp, 1993).

**Table 3:** Soil analysis at 0-30 cm depth in the experimental fields at Giza in 2016 and 2017 growing seasons.

| Soil characteristics | 2016 season | 2017 season |
|---|---|---|
| **Physical analysis** | | |
| Silt % | 36.4 | 42.55 |
| Clay % | 305.3 | 36.15 |
| Fine sand % | 22.8 | 13.35 |
| Coarse sand % | 5.5 | 7.95 |
| Soil Type | Clay loam | Clay loam |
| Chemical analysis | | |
| pH (paste extract) | 7.92 | 7.95 |
| EC ($dSm^{-1}$) | 1.66 | 2.8 |
| SP | 62.5 | 61.5 |
| $CaCO_3$ % | 7.7 | 4.8 |
| Soil bulk density g $cm^{-3}$ | 1.2 | 1.15 |
| Soluble anions (mEqu/l) | | |
| $HCO_3$ | 0.71 | 8 |
| Cl | 13.37 | 12.75 |
| $SO_4$ | 0.92 | 7.25 |
| Soluble cations (mEqu/l) | | |
| $Ca^{++}$ | 4.7 | 12.04 |
| $Mg^{++}$ | 2.2 | 7.66 |
| $Na^{+}$ | 8.0 | 8.09 |
| $K^{+}$ | 0.1 | 0.197 |
| Available nutrients (mg/kg) | | |
| N | 182 | 371 |
| P | 6.35 | 8.86 |
| K | 398 | 409 |
| Zn | 4.34 | 6.55 |
| Mn | 9.08 | 10.12 |
| Fe | 10.14 | 15.2 |

Source: Central Lab for Soil Analysis, Agricultural Research Center, Cairo, Egypt, Meteorological data.

**Table 4:** Meteorological data during the two growing seasons of the experiment.

| Month | Temperature | | | RH % | Wind speed 2m(m/sec) | Sunshine duration (hr) |
|---|---|---|---|---|---|---|
| | Max. (°C) | Min. (°C) | Aver. (°C) | | | |
| **2016** | | | | | | |
| May | 34.6 | 19.1 | 28.9 | 38.7 | 3.4 | 13.4 |
| June | 38.6 | 22.5 | 33.5 | 31.7 | 2.0 | 13.9 |
| July | 36.6 | 24.3 | 32.6 | 46.3 | 2.1 | 13.8 |
| August | 37.2 | 23.8 | 32.5 | 44.3 | 3.5 | 13.0 |
| **2017** | | | | | | |
| May | 34.6 | 19.4 | 29.3 | 34.0 | 2.0 | 13.4 |
| June | 36.7 | 16.0 | 23.3 | 23.3 | 2.0 | 13.9 |
| July | 38.2 | 24.5 | 33.5 | 42.3 | 1.6 | 13.8 |
| August | 37.1 | 24.6 | 32.5 | 46.3 | 2.0 | 13.1 |

Source: Central Lab for Agricultural Climate, Agricultural Research Center, Giza Governorate, Egypt, Aver. = Average, Max. = Maximum, Min. = Minimum, RH % = Relative humidity.

**Table 5:** Additive main effects and multiplicative interaction analysis of variance for grain yield/plant of 19 maize genotypes across 12 environments.

| SOV | df | MS | Explained % |
|---|---|---|---|
| Blocks | 24 | 117 | 0.06 |
| Treatments | 227 | 15734** | 99.17** |
| Genotypes (G) | 18 | 36481** | 18.23** |
| Environment (E) | 11 | 164471** | 50.23** |
| Interaction (G×E) | 198 | 5585** | 30.71** |
| IPCA 1 | 28 | 16369** | 12.73** |
| IPCA 2 | 26 | 8223** | 5.94** |
| Residuals | 144 | 3012** | 12.04** |
| Error | 432 | 64 | 0.77 |
| Total | 683 | 5273 | |

*, ** Significant at $P \leq 0.05$ and $P \leq 0.01$, respectively.

**Genotypes grain yield *vs* IPCA-1(AMMI plot)**

Genotypes or environments located on the right-hand side of the midpoint of the axis main effects have higher yields than those on the left-hand side (Ngeve and Bouwkamp, 1993). In this study, genotypes No. 3, 6, 2, 4, 9, 1, 17, 16, 11, 8 and 5 Fig. 1 were generally high yielding as they were placed on right-hand side of midpoint representing grand mean. Similarly, Environments E7, E10, E8, E11, E9, E1 and E12 in descending order, were considered to be superior in grain yield Fig. 1.

SC-101 (G3) followed by SC-30N11 (G6) produced the best yield (216.5 and 182.5 g/plant, respectively) and attained moderate and high scores of IPCAg-1 (2.85 and -9.35, respectively), indicating that they were of average stability and unstable genotypes, respectively table 7 and

**Table 6:** Environment means, scores of IPCAe-1, IPCAe-2 and AMMI stability value (ASV) for grain yield/plant of maize.

| Environment | Mean | Variance | $IPCA_e$ [1] | $IPCA_e$ [2] | ASV |
|---|---|---|---|---|---|
| E1 | 157.3 | 3172 | -6.34 | 0.25 | -6.34 |
| E2 | 142.8 | 2065 | -3.53 | 0.38 | -3.53 |
| E3 | 117.4 | 1696 | -2.01 | 2.21 | -2.01 |
| E4 | 80.8 | 2002 | -7.41 | 5.40 | -7.42 |
| E5 | 77.3 | 1195 | -3.47 | 5.17 | -3.47 |
| E6 | 59.5 | 508 | -3.17 | 2.18 | -3.17 |
| E7 | 224.6 | 3620 | -0.71 | -7.18 | -0.71 |
| E8 | 197.3 | 2059 | 1.14 | -5.75 | 1.14 |
| E9 | 169.5 | 2953 | 4.72 | -2.19 | 4.72 |
| E10 | 206.5 | 6851 | 14.53 | 7.96 | 14.54 |
| E11 | 181.6 | 3226 | 2.07 | -1.66 | 2.07 |
| E12 | 153.9 | 2661 | 4.18 | -6.76 | 4.18 |
| Margin | 147.4 | 5273 | | | |

**Table 7:** Means, scores of IPCA-1 and IPCA-2 and AMMI stability value (ASV) of 19 maize genotypes for grain yield/plant.

| Genotype | Designation | Mean GYPP(g) | $IPCA_g$ [1] | $IPCA_g$ [2] | ASV |
|---|---|---|---|---|---|
| G1 | SC-10 | 172.10 | 2.08 | -0.19 | 4.47 |
| G2 | SC-30K8 | 176.10 | 0.66 | 3.31 | 3.60 |
| G3 | SC-101 | 216.50 | 2.85 | -7.02 | 9.30 |
| G4 | SC-131 | 173.50 | -0.51 | -3.60 | 3.76 |
| G5 | SC-2031 | 148.30 | -3.02 | -4.46 | 7.86 |
| G6 | SC-30N11 | 182.50 | -9.65 | 3.49 | 20.97 |
| G7 | SC-168 | 142.20 | 0.06 | -2.11 | 2.11 |
| G8 | SC-176 | 146.90 | 4.30 | 0.84 | 9.27 |
| G9 | SC-2055 | 168.60 | -2.12 | 0.07 | 4.54 |
| G10 | TWC-310 | 139.70 | -1.72 | -2.88 | 4.68 |
| G11 | TWC-321 | 150.40 | 4.90 | -2.85 | 10.89 |
| G12 | TWC-1100 | 122.70 | 0.92 | 3.61 | 4.12 |
| G13 | TWC-352 | 109.30 | -6.51 | 4.07 | 14.53 |
| G14 | TWC-360 | 124.60 | -7.83 | 2.65 | 16.99 |
| G15 | A.E.D. | 107.10 | 7.99 | 5.35 | 17.95 |
| G16 | Giza-2 | 158.50 | 4.99 | 6.02 | 12.28 |
| G17 | Nubaria | 165.50 | 4.44 | -1.69 | 9.66 |
| G18 | Midland | 100.10 | 1.41 | 1.24 | 3.28 |
| G19 | Reid Type | 95.60 | -3.26 | -5.85 | 9.11 |

Fig. 1. Genotypic stability is crucial in addition to grain yield (Naroui *et al.,* 2013). The two genotypes G2 (SC-30K8) from Pioneer-Corteva and G4 (SC-131) from ARC, Egypt produced the third and fourth highest yields in this experiment and attained low scores of IPCAg-1 (0.66 and -0.51, respectively), indicating that they were stable high yielding genotypes.

Genotypes with below average yield, such as SC-168 (G7), TWC-310 (G10) and TWC-1100 (G12) also showed small values of IPCA-1, indicating consistence in yield performance across locations. TWC-360 (G14) (124.6 g/plant), A.E.D. (G15) (107.1 g/plant) and TWC-352 (G13) (109.3 g/plant) were among the below average genotypes in grain yield, but attained relatively high IPCA-1 scores (-7.83, 7.99 and -6.51, respectively) table 7, Fig. 1. These results indicated inconsistent yield performance across environments, for these genotypes. Reid Type (G19) and Midland (G18) yielded the least grain (95.6 and 100.1 g/plant, respectively) and attained moderate IPCAg-1 scores (-3.26 and 1.41, respectively) implying that they were average in adaptability Fig. 1; table 7.

**Relationships between genotypes and environments**

Fig. 2 illustrates vector view of relationship between genotypes and mega environments for grain yield, in which environments are connected with biplot origin *via* lines. They also show the relationship among genotypes. This view of biplot aids in the understanding of interrelationship among environments. The cosine of the angle between the vectors of two environments approximates the correlation coefficient between them.

Environments with a small angle between them are highly positively correlated, and they provide similar information on genotypes. Present investigations showed that E1 (WW-HN, 2016 season) and E2 (WW-MN, 2016 season) for grain yield Fig. 2 were considered to be similar as they had small angle between them. Also, the two environments (E4 and E6), (E3 and E5), (E9 and E11) and (E11 and E12) are similar; they had small angle between them and they provide similar information on genotypes. In contrast, either (E1 or E2) and (E4 or E6) were dissimilar with E10 (WS-HN, 2017 season), since the angle was obtuse. Similarly, (E7 and E10) and (E5 and E8) were dissimilar, and they provide different information on genotypes.

The greater IPCA-1 shows greater discriminating ability of an environment. This gives the importance of determining the discriminating ability to enhance separation through differences in performances of different genotypes. The results revealed that E10 (WS-HN, 2017 season) and E4 (WS-HN, 2016), which are water stressed environment in the two seasons (2016 and 2017) gave more information on the tested genotypes than the other environments. So this study provides important information on selecting and releasing best and ideal genotypes which are good for production in specific and widely adapted environments as well as determine the most effective and necessary environments which gives more information on varieties in future breeding

trials.

E11 (WS-MN, 2017 season), E3 (WW-LN, 2016 season) and E2 (WW-MN, 2016 season) lied closest to the origin and, therefore, contributed the least to GEI; these environments are the most representative (stable) environments, but with poor discriminating ability as indicated in Fig. (2). On the contrary, E10 (WS-HN, 2017) and E4 (WS-HN, 2016) exhibited the highest contribution; they indicated both good discriminating ability and representativeness, making them ideal and best environments for testing the maize genotypes. These environments represent the water stress conditions in the first and second seasons. Environment E10 is the most unstable based on IBCAe-1 and IPCAe-2. Test environments which are discriminating like E10, E4 and E5 are important under circumstances when selecting genotypes that are specifically adapted if target environments can be divided into mega-environments. However, where the target environments cannot be divided into mega-environments such test environments like E10 can be useful for culling unstable genotypes across the contrasting environments (Yan and Kang 2003; Badu-Apraku *et al.,* 2011).

## GGE Biplot analysis

### Mega-environments (which-won-where)

The polygon view of GGE biplot for grain yield Fig. 3 indicates the best genotype(s) for each environment. The genotypes located on the vertex of a polygon are best or poorest genotypes in some or all environments, except left bottom quadrant (Hagos and Abay, 2013).

Which-won-where (Yan *et al.,* 2007) identified best winners for the mega-environment or sector. This enables the researcher to have specific and valid justification to recommend genotypes which are good for that particular environment (Gasura *et al.,* 2015). This also means the genotypes can be tested in those few mega-environments and still good yield data results can be obtained. The GGE biplot also gave information which is important if a researcher has to make decisions and conclusions about specific correlations among environments and genotypes.

The genotype G3 (SC-101) was found promising in E11, E7, E8, E9, E12 and E3 in descending order. The genotype G6 was promising in E4, E1, E5 and E6 environments in descending order. The genotypes G3, G1, G2, G17 and G4 are suitable to E11, E8, E12, E9, E3, E2 and E7. The genotypes G6, G5, G10 and G9 are suitable to E4, E5, E1 and E6. The polygon reflects that G19, G18, G15, G14, G13, G12, G8, G11, G7 and G16 are poor grain yielding and not suitable to either of the environments.

An important feature of the GGE biplot (which-won-where) was also predicted. In mega-environment

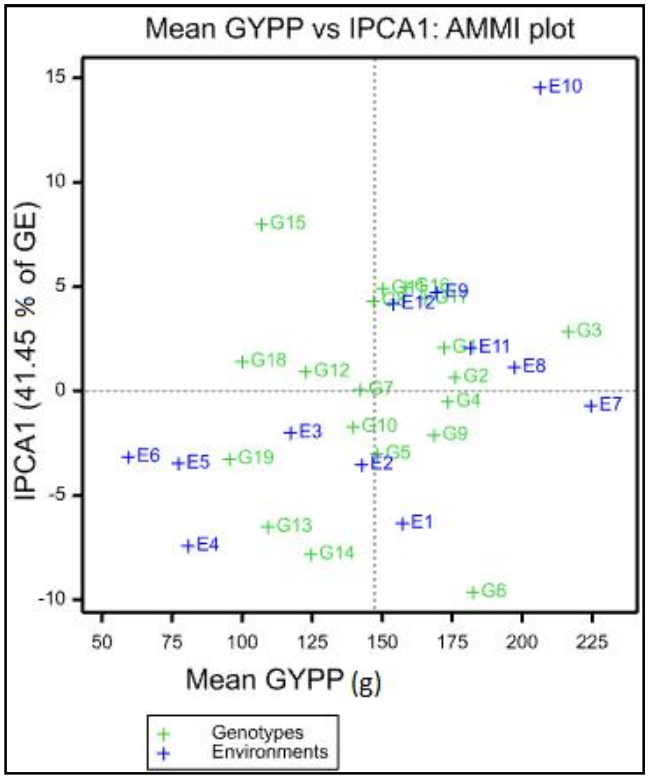


**Fig. 1:** The relationship between mean grain yield/plant (g) and IPCA-1 of 19 maize genotypes (G) evaluated under twelve environments (E).

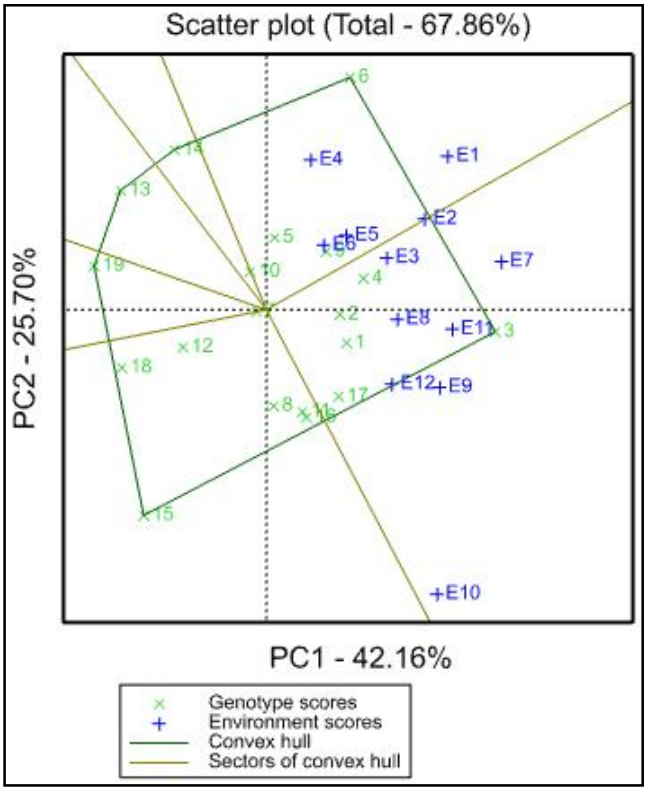


**Fig. 3:** Polygon view of GGE biplot (which–won–where) showing the (G+G×E) interaction effect for grain yield of 19 maize genotypes in 12 environments.

identification process, furthest genotypes are connected together to form a polygon, and perpendicular lines are drawn to form sectors which will make it easy to visualize the mega-environments. Environments in one sector having best-performing genotype can be considered as mega-environments for that genotype (Gebre and Mohammed, 2015). These results are in conformity with the findings of Reddy *et al.,* (2014) who observed high yielding and stable genotypes. Biplots were divided into six sectors in Fig. 3; genotypes which fall in same sector as with environment are said to be adapted to those environments.

The results Fig. 3 and 4 indicated two mega-environments, the environments, E1 (WW-HN, 2016), E2 (WW-MN, 2016), E4 (WS-HN, 2016), E5 (WS-MN, 2016), and E6 (WS-LN, 2016), formed one mega-environment; the most adapted genotypes to this mega environment are G6 followed by G5, G9 and G10. E11 (WS-MN, 2017), E7 (WW-HN, 2017), E8 (WW-MN, 2017), E3 (WW-LN, 2016), E9 (WW-LN, 2017), E12 (WS-LN, 2017) and E10 (WS-HN, 2017), formed another mega-environment; the most adapted genotypes to this mega environment are G3 followed by G4, G2, G1 and G17. The winning genotypes for each mega-environment are those positioned at the vertex. G3 is the winning genotype for the first mega-environment which consists of E1, E2, E4, E5 and E6. G6 is the winning genotype for the second mega-environment which consists of E11, E7, E8, E3, E9, E12 and E10. These genotypes are the most adapted to the respective mega environments.

The results of GGE biplot confirmed those of correlation analysis among the twelve studied environments for grain yield/plant, which indicated the strong phenotypic correlation (similarity) between E2 and E4 and between E1 and E3 and the dissimilarity between E5 and/or E6 and the rest of environments. As correlated environments provide similar information on test genotypes, when two or three environments are highly correlated, one of the environments in each pair could be dropped to reduce the cost of field evaluation without any loss of information (Adu *et al.,* 2019).

**Comparison plot for genotypes based on the concentric circle**

An ideal environment is the one which is on the intrinsic circle Fig. 5. So the non-stressed environment E7 (WW-HN, 2017) is considered the ideal environment. However, the water stressed environments E10 (WS-HN, 2017) and E4 (WS-HN, 2016) cannot be ideal environment for selecting genotypes which can be adaptable for water stress conditions. Fig. 5 shows the comparison plot for genotypes, and an ideal genotype is one which is near or at the center of the concentric circle. Hence in the study, the plot reflected that G3 (SC-101) is the most ideal genotype as shown by its position reflecting that this genotype has high mean grain yield and stability,

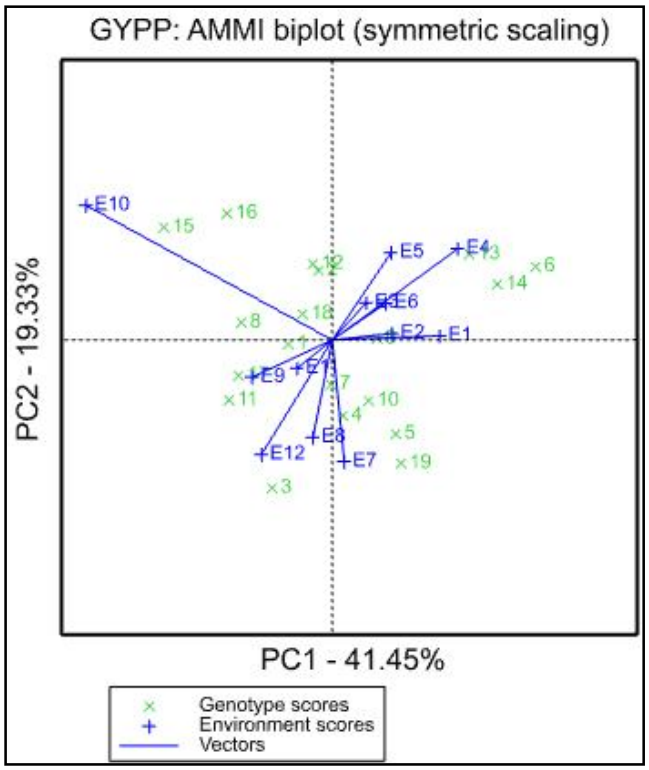


**Fig. 2:** The AMMI biplot showing relationship between genotypes and mega environments for grain yield.

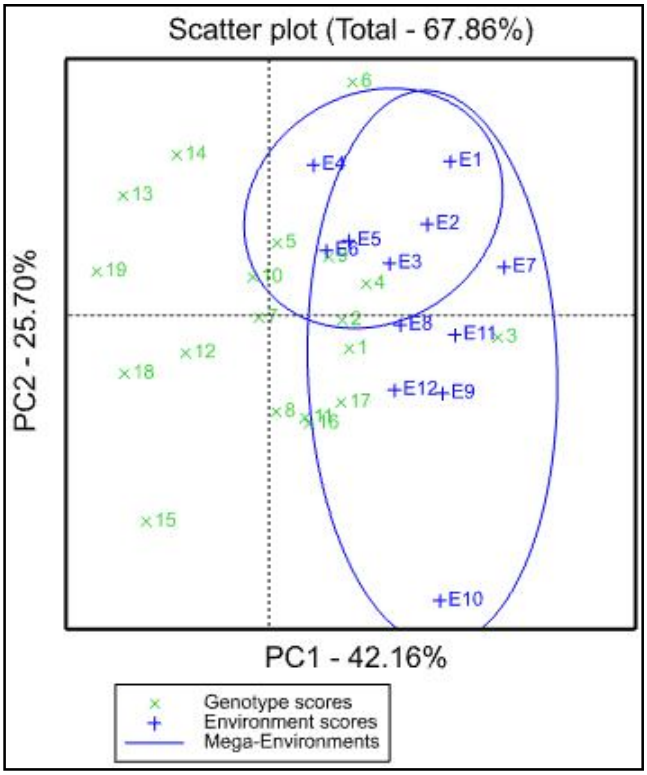


**Fig. 4:** Scatter plot of the relationship between PC1 and PC2 showing mega environments for grain yield.

followed by G4 (SC-131), G2 (SC-30K8), G1 (SC-10) and G9 (SC-2055). Good genotypes are those which are closer to the ideal genotype (G4, G2, G1 and G9). They are positioned closer to the ideal genotype. However, G19 (Reid Type), G18 (Midland), G15 (American Early Dent), G13 (TWC-352), and G14 (TWC-360) are the poorest genotypes in this experiment as their position in the plot are located far from the concentric circle.

The biplot analysis identified the discriminating ability and representativeness as well as the correlation of environments (Sujay *et al.,* 2014) and genotype average performance. The results showed the importance of testing and comparing genotypes so as to select the ones with specific and wide adaptation accordingly and environments which are representativeness to reduce experimenting costs by discarding unrepresentative locations and those with poor discriminating abilities.

The study results gave a better understanding of how biased a researcher can be if there is GEI and fails to do further GEI biplot analysis. The GGE have a lot of information which validates appropriate environment for testing and appropriate genotypes for selection and recommendation (Sujay *et al.,* 2014); there was effective evaluation of environments and genotypes and evaluation of genotypes based on the mean performance and stability across environments which is important required information for a researcher. Considering the great influence of the environment and genotype x environment interaction on grain yield of maize genotypes, further testing in additional environments across more seasons and broadening the genetic base of the genotypes is encouraged.

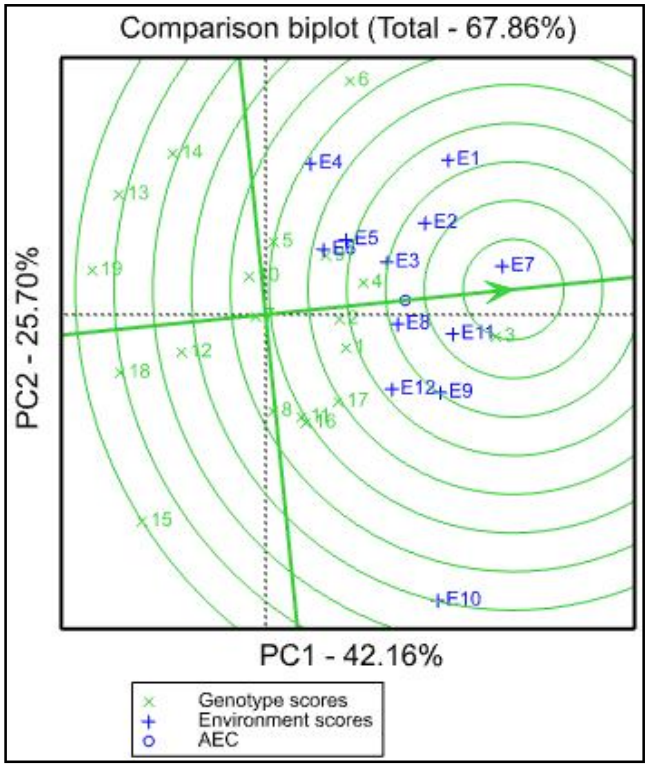


**Fig. 5:** The average environmental coordination (AEC) view to rank genotypes and environments relative to the center of the concentric circles.

## Conclusions

The results showed that the grain yield performance of the 19 genotypes of maize was significantly influenced by environment, genotype and their interaction. A further analysis on the adaptability and stability across the 12 environments was done. The non-stressed environment E7 (WW-HN, 2017) is the most stable based on IPCAe-1, IPCAe-2 and ASV scores; hence it was the least interactive environment for grain yield, and is considered the ideal environment for selecting genotypes which can be adaptable for water stress and low N conditions. The water stressed environments E10 (WS-HN, 2017) and E4 (WS-HN, 2016) indicated both good discriminating ability and representativeness, making them ideal and best environments for testing the maize genotypes. The results indicated two mega-environments, E1(WW-HN, 2016), E2 (WW-MN, 2016), E4 (WS-HN, 2016), E5 (WS-MN, 2016) and E6 (WS-LN, 2016), formed one mega-environment; the most adapted genotypes to this mega environment are G6 followed by G5, G9 and G10. E11 (WS-MN, 2017), E7 (WW-HN, 2017), E8 (WW-MN, 2017), E3 (WW-LN, 2016), E9 (WW-LN, 2017), E12 (WS-LN, 2017) and E10 (WS-HN, 2017), formed another mega-environment; the most adapted genotypes to this mega environment are G3 followed by G4, G2, G1and G17. Based on AMMI model, SC-30K8 (G2), SC-131 (G4) and SC-10 (G1) could be considered stable across the test environments and among the five highest grain yielding genotypes in this experiment. These have been identified as possible candidates for use as good germplasm in future breeding programs. SC-101(G3) and SC-30N11 (G6) had the highest and second highest yield, but were considered average stability and the most unstable genotypes, respectively. Based on GGE-biplot method, G3 is the winning genotype for the first mega-environment which consists of E1, E2, E4, E5 and E6. SC-30N11 (G6) is the winning genotype for the second mega-environment which consists of E11, E7, E8, E3, E9, E12 and E10. These genotypes are the most adapted to the respective mega environments. Considering the great influence of the environment and genotype x environment interaction on grain yield of maize hybrids and populations, further testing in additional locations across more seasons and N and water environments is encouraged.

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