Evaluation of Maize Grain Yield and Yield Stability Under Drought Stress by Ammi Analysis

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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 Additive main effects and multiplicative interaction (AMMI) and GGE-biplot are the most informative models. The objective of this study was to estimate the G×E interaction in 55 maize genotypes to identify maize genotypes of stability and/or adaptability across two irrigation treatments at two locations 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 for Feddan Yielg data showed highly significant due to treatments, genotypes and environments this pointed out that all sources of variance are important in analysis, however genotypes contributed with (48.36%) in treatments variances, the environment contributed with (44.0%) in treatments variance also interaction principal component axis (IPCA) accounted for (53.52% and 39.44%) respectively, were found to be highly significant, the (IPCA1 and IPCA2) together with had a total (92.96%) variances of the interaction. GGE biplot analysis environments showed that the genotype (10, 20, 32 and 36) was found promising in normal irrigation treatment at Assuit location in descending order. The genotypes (22, 27 and 44) was promising in normal irrigation treatment at Minia location in descending order. The genotypes (14, 17, 25, 45 and 49) are suitable to stress irrigation treatment at Minia location. The genotypes (6 and 50) are suitable to drought irrigation

treatment at Assuit location. The polygon reflects that G11, G33, G34, G53, and G56 are poor grain yielding and not suitable to either of the environments and relationships between genotypes and environments showed that the environments with a small angle between them are highly positively correlated, and they provide similar information on genotypes. Present investigations showed that N1 and N2 for grain yield. The two environments S1 and S2 are similar; they had small angle between them and they provide similar information on genotypes. In contrast, either N1 or S1 and N2 or S2 were dissimilar, since the angle was obtuse, 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 N1 and N2 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 N1 and N2 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, S1 and N2 are the most unstable.

Keywords: AMMI, Combining ability, Drought stress, Maize and Relative water content.

Introduction

To improve any quantitative traits, we should know not only what proportion of the total variation among plants is a direct result to genetic differences but also the nature of genetic variation. Different procedures are available to estimate the inheritance of quantitative traits. The diallel cross system of common usage in this respect for its power and versatility. They are widely used applied simultaneously without restriction that the number of parental combinations, including or excluding parents. Thus, the techniques of analysis can be contrast on the basis of their return in terms of information produced (**Ahmed et al., 2017; El-Hosary 2014**). The types of combining ability and superiority relative to check hybrid and their interaction across environments are essential in developing breeding strategies (**Turkey et al., 2018**). Furthermore, the magnitude of genetic components for confirmed characters would

rely fundamentally upon the environmental flexion's under which the breeding populations will be tested. When information on these points is available, the breeder can decide which of the numerous breeding procedures is most likely to succeed (**El-Hosary 2014; El-Hosary et al., 2018**). The essential final stage in most applied plant breeding programs is the evaluation of promising hybrids over diversified environments (locations and irrigations treatments).

Determining stability for elite crosses across various environmental conditions with the ultimate goal of improving some quantitative characters in maize is important to support and confirm the results of half diallel analysis and estimate the interaction of genotypes across environment and determine the best variety for the best environment. As quantitative inherited trait, grain yield performance of a genotype often varies from one environment to another, leading to a significant genotype x environment (GxE) interaction which can severely limit gain of selecting superior genotypes. Understanding the interaction of those factors and how they affect grain yield is crucial for maintaining high yield (**Fan et al., 2007; Dehghani et al., 2009**). Using principal components model as multivariate analysis, graphical model have been extensively used including GGE biplot (**Yan, 2001**). This method give a set of functional graphs that visualize help the plant breeders to explore the interrelationships among studied environments, among tested genotypes and the association between genotypes and environments.

The main objectives of this study were to: 1) estimate type and relative amount of the genetic variance components and their interaction with planting dates, 2) estimate the relative superiority than one check variety for grain yield plant-1 and 3) evaluate yield stability of the elite hybrids derived from half diallel cross analysis along with one check hybrid at two locations under different irrigations treatment date at each location.

Materials and Methods

This study reported here in was carried out at environmental research and studied Institute (ESRI), Sadat University, and the crosses season was done in private land Minia governorate during successive season 2019, and the F1 was evaluated in two locations at Minia and Assuit governorates during successive season 2020. One commercial hybrid ARC-GH 128 and ten inbred lines were used in this study and

these inbred lines were obtained from Agriculture Research Center (ARC) the name and pedigree for ten inbred lines.

In the first summer season 2019, seeds of the ten (10) inbred lines were split sown on 1th May and 8th to avoided differences in flowering time and secure enough hybrids seed at special locations at Menia governorate. All possible cross combinations without reciprocals were made between 10 inbred lines by hand method giving a total of 45 genotype in the season 2019 commercial check hybrid single cross ARC-GH 128 (SC 128) will be evaluated in the second season.

In the second summer season 2020 the two experiments were conducted at the two locations under two independent experiments normal irrigation and drought, by irrigation every 12 days and water-stress (drought environment) irrigation every 21 days. Planting dates was 15th June 2020 at Menia locations and the second location in 20th June 2020 at Assuit location.

The ten inbred lines and 45 F1s were separately grown randomly in randomized complete block design (RCBD) with three replications. The experiment was fertilized by organic maters before planting and a rate of 120 unit of N/feddan split in three dosses before the first three irrigations. All other agricultural practice were done as normally practiced in the two locations. Plots were two ridges 10 m long and the spacing between ridges and hills were 70 and 25 cm, respectively. To adjust the plant stand, two kernels were planted/hill on one side of the ridge then seedlings were later thinned to one plant/hill.

The other cultural practices were followed as usual for ordinary maize field in the area. Mean data were calculated after recorded measurements on 15 plants chosen at random from each plot for parents, F_1 crosses and ARC-GH128, except days to 50% silking where the mean of plot was used. The following traits were measured at flowering stage; leaf proline content (mg g^{-1}) determined according to protocol of **Bates et al. (1973)** as a physiological indicator of plant status under the implemented water stress treatments., relative water content (RWC%) estimated according to the protocol of **Barrs and Weatherley (1962)**, then compensation account in the following formula:

Table 1. Name and Pedigree of the studied inbred lines maize genotypes.

Inbred line number	Pedigree	Origin
Check variety	ARC-GH-128	
P1	G-308A-S.C.U1202	Egypt
P2	RG-5 g.s (sanjuan × ci 64) (S.C.14)	Egypt
P3	RG-8 g.s (sanjuan × ci 56) (S.C.14)	Egypt
P4	G-221 D White composite (S.C.16)	Egypt
P5	G-241 A Ellis 19S1	Egypt
P6	RG-15 g.s (syn.Laposta × Ci64)	Egypt
P7	RG-9 g.s (sanjuan × ci 55) (S.C.12)	Egypt
P8	G-308A-S.C.U1232	Egypt
P9	RG-17 g.s (syn.Laposta × Ci45)	Egypt
P10	G-201 D White composite (S.C.11)	Egypt

Characters studied

Agronomic characters

1. Days to tasseling
2. Days to silking
3. Plant height (cm)
4. Ear height (cm)
5. Leaf Angel
6. Leaf rolling
7. Leaf proline content (mg)
8. Relative water content (RWC %)

Yield and yield component
1. Ear weight /plot (Kg)
2. Kernel FW/plot (kg)
3. No. of row/ear
4. No. of kernel/row
5. Number of kernels/ear
6. 100 kernel weight
7. No. of ear/plot
8. Drought susceptibility index.
9. Feddan yield/kg.
10.

Data analysis

Obtained data were analyzed using AMMI model (**Gauch and Zobel, 1996**). Results of AMMI analysis were presented by biplot graphs: AMMI1 biplot − abscissa representing average grain yield data of genotypes and average data of environments and ordinate representing the effects of interaction (IPCA1); and AMMI2 biplot representing estimates of IPCA1 and IPCA2 on the abscissa and ordinate, respectively.

AMMI analysis was processed by R software, version 2.15.2 (Rdevelopment core team, 2005). Following mathematical model was applied (**GAUCH, 1988**):

$$Yij = \mu + Gi + Ej + \sum_{k-1}^{n} \alpha ik \ \lambda k \ \gamma jk + \theta ij$$

where: i = 1,2... 10, j = 1,2...4, Yij – presents grain yield of the i - genotype in the j - environment; μ – the grand mean, Gi – genotypic effect, Ej – environmental effect, λk – eigen values of principal component analysis (PCA) axis k, αikи γjk – are i – genotype and j - environment of PCA score for PCA axis k, θij – a residue, n – number of PCA axis contained in the model.

Correlations between IPCA1 or IPCA2 scores and grain yield, relative maturity group or the amount of precipitation in June was determined by Pearson's coefficients.

Results and Discussion

Additive main effects and multiplicative interaction (AMMI) model 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 2)**.

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

With regard Feddan Yielg data showed highly significant due to treatments, genotypes and environments this pointed out that all sources of variance are important in analysis, however genotypes contributed with value of 48.36% in treatments variances, the environment contributed with value of 44.0% in treatments variance also interaction principal component axis (IPCA) accounted for 53.52% and

39.44% respectively, were found to be highly significant. the (IPCA1 and IPCA2) together with had a total of 92.96% variances of the interaction (**Table 2**).

Table 2. Additive main effects and multiplicative interaction analysis of variance for grain yield/feddan of 55 maize genotypes across two irrigations treatment at two locations.

Source	d.f.	Feddan Yield/kg		
		S.S	M.S.	SS%
Total	659	21042.00	31.92	
Treatments	219	19860.00	90.66**	94.38**
Genotypes	54	10176.00	188.46**	48.36**
Environments	3	9258.00	3086.76**	44.00**
Block	8	984.00	123.12**	4.68**
Interactions	162	426.00	2.64**	2.02**
IPCA 1	56	228	4.08**	53.52**
IPCA 2	54	168	3.12**	39.44**
Residuals	52	24.00	0.48	5.63
Error	432	198.00	0.48	

GGE Biplot analysis environments the polygon view of GGE biplot for grain yield. **Fig. 1** 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
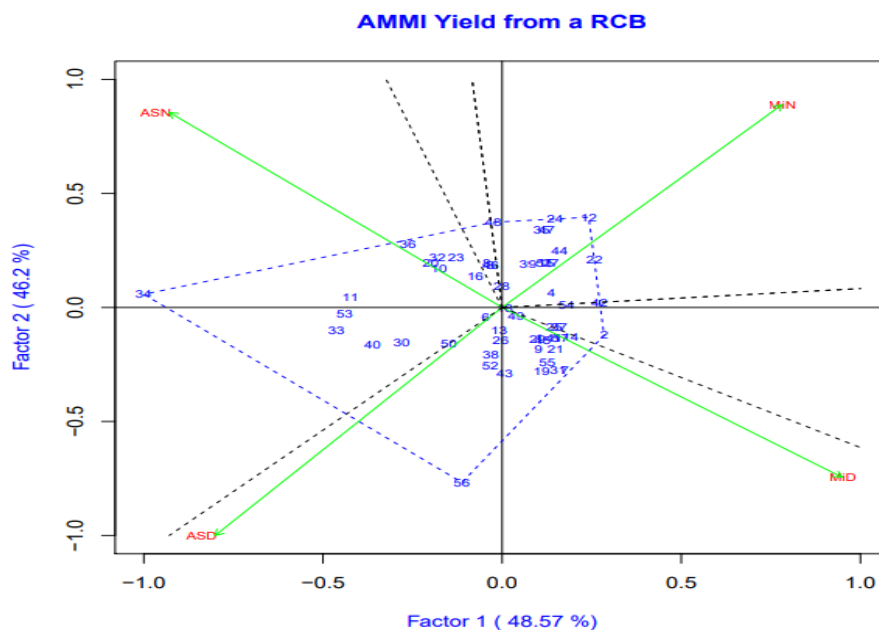
Fig. 1. Polygon view of GGE biplot showing the (G+G×E) interaction effect for grain yield of 55 maize genotypes for two irrigations treatment at two locations.

is important if a researcher has to make decisions and conclusions about specific correlations among environments and genotypes.

The genotypes 10, 20, 32 and 36 were found promising in normal irrigation treatment at Assuit location in descending order. The genotypes 22, 27 and 44 was promising in normal irrigation treatment at Minia location in descending order. The genotypes 14, 17, 25, 45 and 49 are suitable to stress irrigation treatment at Minia location. The genotypes 6 and 50 are suitable to drought irrigation treatment at Assuit location. The polygon reflects that G11, G33, G34, G53, and G56 are poor grain yielding and not suitable to either of the environments. An important feature of the GGE biplot was also predicted. In mega-environment 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)**.

Fig. 2 illustrates vector view of relationship between genotypes and 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 N1 and N2 for grain yield. Fig. 2 were considered to be similar as they had small angle between them. Also, the two environments S1 and S2 are similar; they had small angle between them and they provide similar information on genotypes. In contrast, either N1 or S1 and N2 or S2 were dissimilar, since the angle was obtuse, 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 N1 and N2 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 N1 and N2 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), S1 and N2 are the most unstable (**Yan and Kang 2003; Badu Apraku et al., 2011**). Through differences in performances of different genotypes. The results revealed that N1 and N2 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 N1 and N2 lied closest to the origin. Therefore, contributed the least to GEI; these environments are the most representative (stable) environments, but with poor discriminating ability as indicated in Fig. (2), S1 and N2 are the most unstable (**Yan and Kang 2003; Badu Apraku et al., 2011**).
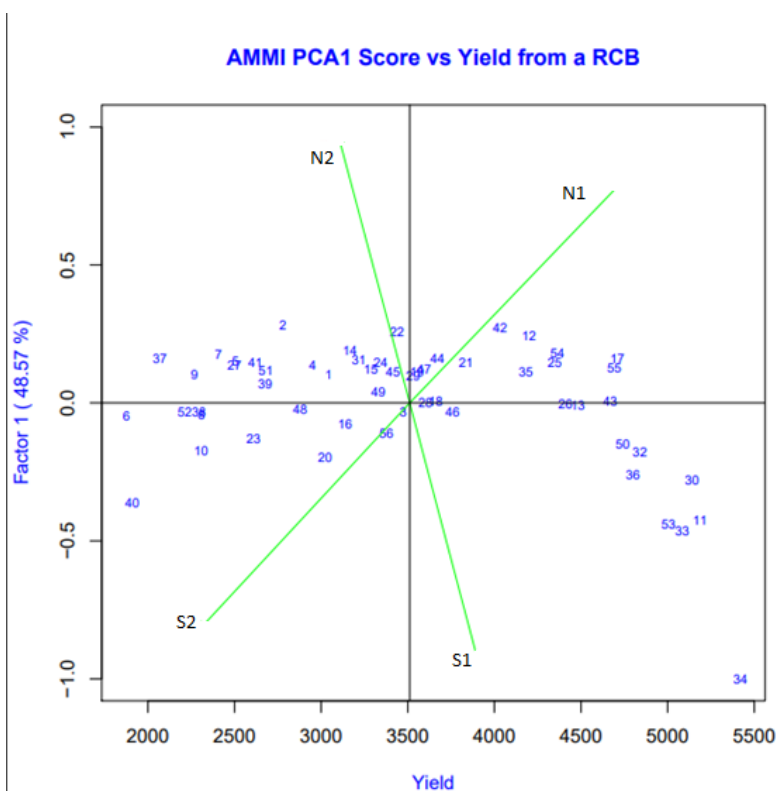
Fig. 2. The AMMI biplot showing relationship between genotypes and mega environments for grain yield.

Conclusion

The objective of this study was to estimate the G×E interaction in 55 maize genotypes to identify maize genotypes of stability and/or adaptability across two irrigation treatments at two locations using the AMMI and GGE-biplot models. The results revealed that N1 and N2 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 N1 and N2 lied closest to the origin. 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 N1 and N2 gave more information on the tested genotypes than the other environments.

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