Stability measurements and Yield responses of Maize (*Zea mays L*.) hybrids across two environments using AMMI Model

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ABSTRCT

Grain yield of 15 maize genotypes were tested in a randomized complete block design replicated three times under water stress condition across two environments. This was to assess the genotype × environment interactions (GE) for grain yield and other agronomic traits using additive main effects and multiplicative interaction model (AMMI) and different stability models. Combined analysis of variance across the two locations revealed that genotypes were significant among all traits. The stability analyses indicated that sensitivity index, superiority index, static stability, Wricke'secovalence, mean square deviation from regression and AMMI stability values showed close similarity and effectiveness in detecting stable genotypes over the environments. However, genotype G3, G4 and G11 were found to be more stable while G1, G5 and G14 were adapted to specific environments.

Keywords: *Zea mays*, genetic superiority, Grain yield, GE interaction, AMMI model.

Introduction

Maize (*Zea mays* L.) is the most important grain crop in the world and is produced in various environments. It is one of the most economically important cultivated plants in the world and the main energy source for animal feed, oil, and bio fuel (Das *et al.*, 2019). Owing to the great economic contribution of maize as food for humans and livestocks and raw materials for industries, it production has received a boost and support in Nigeria.

Maize is grown on a wide range of environments in Nigeria; this however is responsible for the variance in the performance of a genotype across environments. Hence, genotypes that are superior in one environment may not be superior in other environments due to genotype-by-environment interactions (GE) (Makumbi *et. al*., 2015). In view of this, researchers are utilizing available genetic resources to reconstruct the ideotype of the plant in order to meet the increasing requirements of the population through improvement in grain quality and yield (Bello *et al.*, 2010).

Yield of maize is determined by the correct application of production inputs and its interaction with environment as well as other agricultural production factors (Bocianowski *et al*., 2019b). Its Successful production depends on genotype and environmental effects as well as genotype-environment (GE) interaction (Das *et al.,* 2019). The complexity of yield is the result of different genotypic reactions to changing environmental conditions during plant development. It is better to have knowledge of the genetic behavior of maize yield to enable the breeders control the genetic advance for the crop.

The use of Additive main effects and multiplicative interaction analysis (AMMI) and genotype main effect plus genotype x environment interaction (GGE) to evaluate the relationships which exist between genotype and environment provide insight into the extent of the GE reaction in a given study. AMMI has been used to investigate genotype x environment interactions for grain yield (Zobel *et al*. 1988; Kassa *et al.*, 2013, Parent *et al*., 2017, Bocianowski *et al*., 2019b) and GGE for the analyses of grain yield and stability in tropical maize (Cooper and DeLacy 1994, Yan *et al.,* 2000). The AMMI model combines the analysis of variance for the genotype and environment main effects and the principal component analysis (*PCA*) with multiplicative parameters in a single analysis (Zobel *et al.*, 1988). The objective of this study was to assess genotype by environment interaction for yield of 15 maize (*Zea mays* L.) hybrids grown in southern guinea savanna of Nigeria using the AMMI model.

Materials and Methods

Fifteen F1 crosses were studied in a randomized complete block design with three replications in two locations between December 2018 and March 2019 (Adunu field $7^{o}9^{1}$E, latitude $9^{o}35^{1}$ N and 476 m above sea level and Jebba field $4^{o}51^{1}$E, latitude $9^{o}7^{1}$ N and 53 m above sea level) (table 1).Each entry was planted in a single row plot of 5 m long and 0.75 m apart with the hills spaced

0.25 m apart. Two seeds were initially planted per hill but were subsequently thinned to one plant per hill at 4 weeks after emergence to give a plant population of 53,333 plants per hectare. Furrow irrigation system was used to supply water to the field. The experiments received water every three days for the first five weeks. Water application was stopped for another five weeks and re-watering continued till the end of the experiment. Standard cultural practices including weed control throughout the growing season were followed. Fertilizer was applied to each location at the rate of 120 kg N ha^{-1}, 60 kg P_2O^5 ha^{-1} and 60kg K_2O in splits doses.

Data collected and statistical analysis

Data collection

The data recorded from each plot included; days to anthesis, i.e. days from planting to when 50 % of the plants shed pollen and days to silking ,were days from planting to when 50 % of the plants had extruded silks. Anthesis–silking interval (ASI), was determined as the difference between days to silking and days to anthesis. Plant height, was measured in centimeters as the distance from the base of the plant to the height of the first tassel branch, while ear height was determined by measuring a representative plant from the ground to the insertion of the top ear. Seed weight (100grain), as the weight of 100 seed shelled from harvested cob in grams and cob length was measured as the length of the peeled cob measured to the nearest centimeter and cob diameter was taken as the diameter of the peeled cob measured at the middle part of the cob to the nearest centimeter. Numbers of grains per row were counted on five randomly selected cobs and averaged for each genotype and Numbers of grains row per cob, were counted on five randomly selected cobs and then averaged for each genotype. Yield per plant were calculated as weight of the total grains per plot divided by the total number of plants in that plot after threshing at 13% moisture content

Statistical analysis

Analysis of variance (ANOVA) for all traits was done separately for each location, and combined across locations using Cropstat 2008 series.

Genotype main effect and genotype X environment (GGE) biplot analysis was calculated using the AMMI model. The AMMI model equation is: Yij = μ + Gi +Ej + Ej + k ikjk + Rij. Where Yij is the value of i^{th}genotype in the j environment; μ is the ground mean; Gi is the deviation of the i^{th}genotype from the ground mean; Ej is the deviation of g environment from the ground

mean; k singular value for pc axis k; ik and jk are the pc score for axis of k of the i^{th}genotype and in the environment; and Rij and residual and error term.

GGE biplot was computed as: Yij – Ej = k ikjk + Rij. Where Yij is the value of i^{th}genotype in the j environment; Ej effect of environment; = k singular value of pc axis k; ik and jk are the pc score for axis of the i^{th} genotype and i^{th} environment; Rij residual.

Performance stability of each genotype was determined after testing the significance of the genotype by environment interaction. This was achieved by using yield data, univariate stability parameter such as Wricke'secovalence, genetic superiority index, static stability, mean square deviation from regression.

Table 1. List of hybrids used for the study

S/No	CODE	HYBRID
1	G1	(W.DT STR Syn/TZL COMP1-W) F2 x TZL COMP1-W C6/DT-SYN-1-W
2	G2	(W.DT STR Syn/TZL COMP1-W)F2 x DT SYN2-W
3	G3	(W.DT STR Syn/TZL COMP1-W) F2 x DT Syn-1 F2
4	G4	(W.DT STR Syn/TZL COMP1-W) F2 x DT SYN 13-W F1
5	G5	(W.DT STR Syn/TZL COMP1-W) F2 x DT SYN2-W F1
6	G6	DT SYN2-W F1 x TZL COMP1-W C6/DT-SYN-1-W
7	G7	DT SYN2-W F1 x DT SYN2-W
8	G8	DT SYN2-W F1 x DT Syn-1 F2
9	G9	DT SYN2-W F1 x DT SYN 13-W F1
10	G10	DT SYN 13-W F1 x TZL COMP1-W C6/DT-SYN-1-W
11	G11	DT SYN 13-W F1 x DT SYN2-W
12	G12	DT SYN 13-W F1 x DT Syn-1 F2
13	G13	DT Syn-1 F2 x TZL COMP1-W C6/DT-SYN-1-W
14	G14	DT Syn-1 F2 x DT SYN2-W
14	G15	DT SYN2-W x TZL COMP1-W C6/DT-SYN-1-W

G: Genotype

Results and Discussion

Analysis of variance

Combined analysis of variance across the two locations revealed that genotypes were significant among all traits; this reflects the presence of genetic variability (Table 2). In a similar study, Abera, *et al.*, (2004) found significant differences among maize genotypes for similar traits in multi location trials. Makumbi *et al.*,2015, stressed that the performance of a genotype can vary from one environment to another. Environment was found significant for all traits except days to

silking, and ear height indicating environment as important source of variation and Genotype x Environments were significant for all the traits except days to tasseling, days to silking, number of grain row per cob, number of grains per row and number of grain per cob (Table2). However, Abd El- Wahed *et al*., 2015 finds out that exposing maize plant to drought stress at tasseling stage, lead to substantial reduction in yield and yield components such a kernel number per row, kernel weight, kernels per cob, grain yield per plant, biological yield per plant and harvest index. There were, therefore differences in the performance of the genotypes at the different locations. GE was highly significant for plant height and ear height at P=0.001 and significant for ASI, W.100, cob length, cob diameter and grain yield per plant at P= 0.05. Grain yield of the genotypes varied with locations. The lowest yield of 5.44–30.28g per plant was obtained at Adunu location, and the highest yield of 9.88–32.96g per plant was recorded at Jebba the second location (Table 3). Four genotypes, G1, G14, G5 and G6 yield above the location average at the two locations.

Table 2 Mean squares and degrees of freedom from ANOVA for grain yield and agronomic traits for 15 maize hybrids, under water stressed condition across two locations in Nigeria

Source of variation	Df	Mean square											
		Days to Tassel (Days)	**Days to Silk (Days)**	**A S I (Days)**	**plant height (cm)**	**Ear height (cm)**	**W. 100 Grain g/plot**	**No of grain rows per cob**	**No of grains per row**	**Cob length (cm)**	**Cob diameter (cm)**	**No of grains/ear**	**Grain yield/plant (g)**
Replication	2	17.055NS	2.457NS	21.600*	195.989NS	6.839NS	0.325NS	4.308NS	17.745*	0.599NS	0.041NS	5727.562*	2.460NS
Genotype	14	150.748*	274.840*	41.899**	1257.539**	182.546**	21.721**	56.433**	34.454**	5.099**	12.236**	16434.576**	192.065**
Environment	1	395.683*	66.995NS	151.217**	1283.462*	45.213NS	13.611*	188.327**	155.026**	210.345**	183.669**	20869.974*	186.480**
Genotype & Environment	14	62.170NS	76.184NS	11.378*	1404.408**	216.888**	5.092*	5.363NS	5.514NS	4.861*	3.871*	2995.454NS	7.787*
Error	58	53.852	73.505	5.52	253.524	34.336	2.736	3.798	5.316	1.533	1.243	1645.147	4.424
CV%		10.28	11	36.08	19.91	22.9	20.7	20.37	27.89	11.98	12.03	41.6	15.55

Df: Degree of freedom, ASI: Anthesis and silking interval, W.100: Wight of 100 seed, CV: Coefficient of variation.

Table 3 Mean grain yield (g/cob) of maize hybrid across two locations under water stress condition

	Genotype		MEAN	
S/No	Code	Hybrid	Jebba	Adunu
1	G1	(W.DT STR Syn/TZL COMP1-W) F2 x TZL COMP1-W C6/DT-SYN-1-W	32.96	30.28
2	G2	(W.DT STR Syn/TZL COMP1-W)F2 x DT SYN2-W	13.88	8.72
3	G3	(W.DT STR Syn/TZL COMP1-W) F2 x DT Syn-1 F2	11.66	8.30
4	G4	(W.DT STR Syn/TZL COMP1-W) F2 x DT SYN 13-W F1	14.25	12.00
5	G5	(W.DT STR Syn/TZL COMP1-W) F2 x DT SYN2-W F1	16.64	13.75
6	G6	DT SYN2-W F1 x TZL COMP1-W C6/DT-SYN-1-W	15.72	13.1
7	G7	DT SYN2-W F1 x DT SYN2-W	11.35	9.44
8	G8	DT SYN2-W F1 x DT Syn-1 F2	9.88	10.56
9	G9	DT SYN2-W F1 x DT SYN 13-W F1	14.00	10.70
10	G10	DT SYN 13-W F1 x TZL COMP1-W C6/DT-SYN-1-W	14.19	10.20
11	G11	DT SYN 13-W F1 x DT SYN2-W	14.34	10.20
12	G12	DT SYN 13-W F1 x DT Syn-1 F2	11.67	5.44
13	G13	DT Syn-1 F2 x TZL COMP1-W C6/DT-SYN-1-W	13.26	9.90
14	G14	DT Syn-1 F2 x DT SYN2-W	17.96	20.95
15	G15	DT SYN2-W x TZL COMP1-W C6/DT-SYN-1-W	12.77	7.82
		MEAN	**14.97**	**12.09**

Result on table 4 showed that genotypes react differently to environments. Genotypes with code G1, G5 and G14 recorded highest yield per plant while genotype G3, G12 and G7 recorded least yield per plant. The combined analysis revealed that genotypes with low superiority value showed superiority (G1, G5 and G14) over others with high values, indicating average stability (Table 4). Furthermore, Finlay and Wilkinson (1963) and Eberhart and Russell (1966) considered genotypes with high mean yield and genotype sensitivity, static stability, ecovalence stability and mean square deviation from regression closer to zero to be stable. Therefore, static stability identified G7, G8 and G6 as more stable across the locations. Wricke'secovalence (1962) postulate that genotype with smaller values of ecovalence are stable since they have little tendency of fluctuation across environments. Hence genotype G3, G4 and G11 were found more stable. While mean square deviation found G1, G14 and G6 to be more stable

Table 4. Mean value for yield, sensitivity, superiority and stability coefficient for hybrids under water stress condition across two locations.

Genotype Code	Mean Yield	Rank	Genotype Sensitivity	Rank	Genotype superiority	Rank	Static stability	Rank	Ecovalence Stability	Rank	Mean square deviation	Rank
G1	23.46	1	-4.74	1	66.50	1	92.98	14	136.38	15	0.87	1
G2	11.49	9	1.92	12	203.70	9	15.31	10	3.52	10	2.36	12
G3	9.98	13	1.17	8	234.20	13	5.63	6	0.11	1	1.36	8
G4	12.94	7	0.65	7	174.50	7	1.77	5	0.50	2	0.70	7
G5	23.35	2	6.67	15	68.30	2	184.45	15	133.30	14	0.82	15
G6	13.55	5	0.31	5	163.60	5	0.41	3	1.95	5	0.23	5
G7	9.66	14	0.15	3	241.70	14	0.10	1	2.97	9	2.05	3
G8	10.96	10	0.28	4	213.90	10	0.31	2	2.17	7	0.13	4
G9	13.21	6	1.75	11	170.10	6	12.62	9	2.30	8	1.33	11
G10	10.94	11	0.51	6	214.00	11	1.09	4	0.99	4	1.96	6
G11	12.27	8	1.44	9	187.50	8	8.56	7	0.79	3	0.54	9
G12	9.82	15	3.04	14	242.30	15	38.28	13	17.23	12	0.92	14
G13	13.93	4	2.80	13	160.00	4	32.51	12	13.44	11	47.39	13
G14	17.10	3	-2.67	2	118.80	3	29.59	11	55.89	14	0.75	2
G15	10.30	12	1.72	10	228.00	12	12.25	8	2.14	6	3.96	10

G: Genotype

The box plot for grain yield under water stressed condition in the two location expressed disparity between the two locations. The result in figure 1 is showing the distribution pattern of grain yield per plant of 15 maize plants. Meanwhile the box plot suggests that varieties react differently within each environment in the two locations. At Adunu location most of the varieties showed no different reaction to the environment; however at Jebba location majority of the varieties has similar reaction but negative.

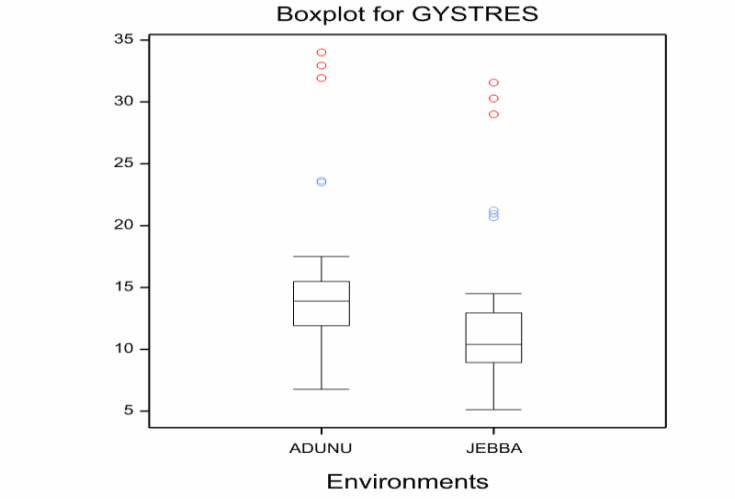

Figure 1

The AMMI biplot (Figure 2) showed that the environmental scores are joined to the origin by side line and location with long vectors exerting strong interaction and large range of genotype performance. The result shows that certain genotypes in one environment produced higher yield than others, similar result was reported by Makumbi *et al.*, 2015, Bocianowski *et al*, 2019a. Identification of the best genotypes at each location was based on the GGE biplot analysis. The bi-plot analysis was also used to assess the stability of the genotypes. The bi-plot analysis gave a visual assessment of GE based on grain yield which explained 100 % score (PC1 = 61.73 and PC2 = 38.27 %) of the total variation across the two environments (Fig. 2). The genotypes close to zero are considered as generally adaptable to all locations. Similarly genotypes close to the origin of the axes are more stable than the most distant ones, since they contributed only little to the interaction. The genotypes that had least contribution to GxE interaction and considered stable were G4, G6 and G9. Other than these, genotypes (G7 and G8) were not strictly close to the origin, but have relatively lower values of static stability and were identified as stable genotypes (Table 4). It has been reported that, if angle between two genotype vectors is less than 90 degrees, the genotypes are positively correlated, either doing well or badly in the same environment. But if the degree between two genotypes vectors is greater than 90, then they performed differently over environments. Figure 2 showed that G6, G14 and G1are positively correlated while G5 and G14 and G1 were negatively correlated, however, there is no correlation between G5 and G15, G11 and G6.The large environment vectors expressed by the bi-plot explained the high discrimination for the hybrids across Adumu and Jebba environment. Adunu was the least discriminating of the two environments, as evidenced by the short environment vector. Generally, the distribution of genotype in bi-plot space showed that there was genetic diversity among the genotypes for grain yield.

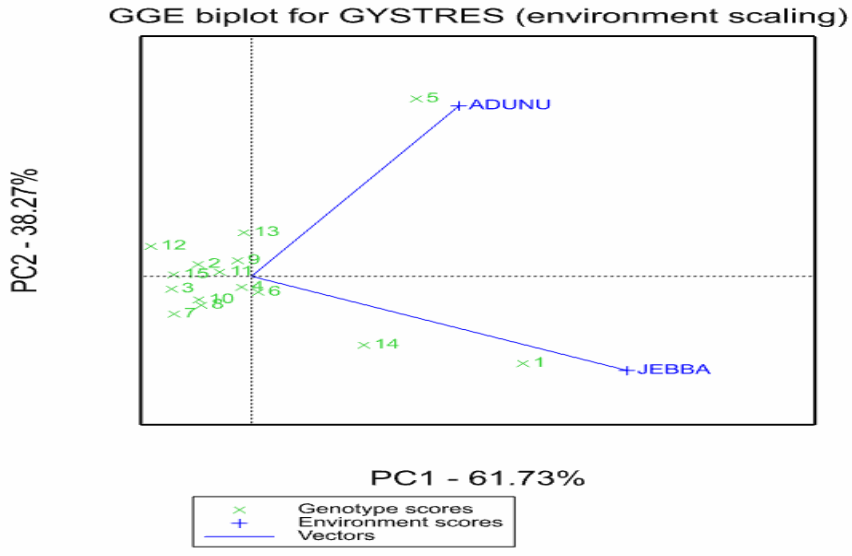

Fig. 2 The Environment vector bi-plot showing environmental differences discriminating 15 hybrids for grain yield at two test environments during 2018 season in Nigeria.

A set of lines intersecting the side of polygon at right angle of the origin of the bi-plot divide it into sectors, which is further sub divided into target environment comprising of one or more environments.

The two locations used in this study, revealed two sectors with two environments and different hybrids identified using a scatter plot (Fig. 3). Makumbi *et. al.*, 2015 reported that vertex genotype in each sector represents the highest yielding genotype in the location within that particular sector. In this study, the vertex genotypes were G1, G5, G7, G12 and G14. Performances of individual genotype could be assessed based on their positions relative to the X and Y axis. The best genotypes are considered to be those that have high yield with stable performance in most localities. In this regard, genotypes G1, G5 and G14 were the vertex entry that fell in the sector of the two locations, indicating that these genotypes were the highest yielding in these locations. However, genotypes G7 and G12 did not have any location falling in the sectors where they were located, suggesting that these entries were low yielding in the two locations (Fig. 3).

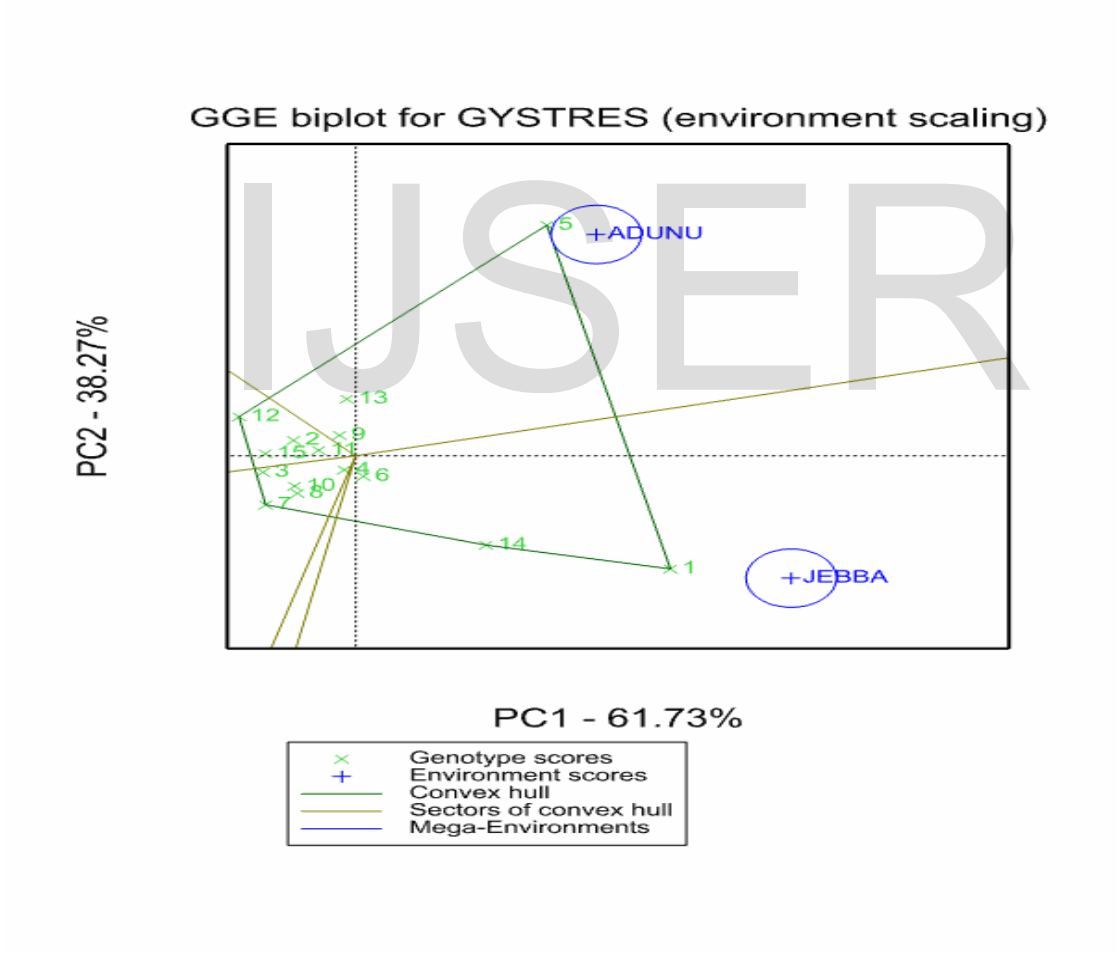

Fig. 3 Bi-plot showing distinct hybrids for the two different environments for grain yield during 2018 dry seasons in Nigeria

Conclusion

In conclusion AMMI analysis identified significant GE interaction of grain yield and high genotype stability value. Wricke'secovalence coefficient identified genotype G3, G4 and G11 to be more stable. Forthermore genotypes G1 and G5 were identified as the highest yielding in their various localities. However none of the high yielding genotypes showed stability character. Therefore, genotype G1, G5, and G13 should be subject to further testing.

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