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EVALUATION OF MAIZE HYBRID IN MULTI-LOCATIONAL TRIAL USING GGE BIPLOT AND AMMI MODEL

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ABSTRACT

This study was executed to assess the twenty-one single cross maize hybrids with three local checks (BHM-12, BHM-13 and BHM-14) in five locations of Bangladesh for its adaptability and stability and also to study the genotypes and environment interaction. Yield data of twenty-four maize hybrids was analyzed through the additive main effects and multiplicative interaction (AMMI) and GGE biplot methods. Considering the grain yield, b_i~1 and S^2d_i~0 value, it was observed that G10 and G16 were the higher yielding and suitable across the environments. On the other hand, G20 and G14 were higher yielding but were responsive to favorable environments. Among the five locations, the environment of Hathazari was the poorest, whereas Barishal and Dinajpur were the most favorable environments for maize production. When hybrids were compared with ideal genotypes, it was observed that G14, G16, G10, and G20 were closed to the ideal genotypes so that they can be more desirable than other tested hybrids. The AMMI biplot indicated that G24, G16, G13, G17 and G14 were positioned adjacent to the biplot's origin which indicated their stability in performance across environments. Finally, stability analysis with the help of GGE and AMMI statistics identified two hybrids G14 and G16 that could be used as reference for future crop improvement program.

Keywords: AMMI Model, environment, GGE biplot, maize, stability

INTRODUCTION

Maize (*Zea mays* L.) is a crop of utmost importance for having its versatile uses along with wider adaptability and stands second position after rice in Bangladesh Maize is one of the prime staples crops for the nutrition of the world's population. Maize produces 1,170 million metric tons grain by covering more than 180 million hectares of land in all over the world (Ahmed et al., 2020). It is one of the leading productive C_4 plant with higher response of photosynthesis and it has the eminent potential for production of carbohydrate in unit area/day. Shiferaw et al. (2011) reported that animal feed industries utilized about 70% of total maize production and intensified growth of population of this sector will set off the need of meat and eggs as a protein source which eventually stimulated the production of maize. Maize is also exploited in the food industry as sweeteners and food additives, which is a further significant end-user part of maize (Gulati et al., 2008). Maize plant's stem and foliage can be used as livestock feed. Husk, stalk and shelled cobs are usable as fuel (Ahmed et al., 2011). Maize has a potential nutritional value that contains about 72% starch, 10% protein, and 4% fat, supplying an energy density of 365 Kcal/100 g (Hasan et al., 2018). At present, 4.7 million tons (BBS, 2021) have been produced in Bangladesh against around two million tons of annual demand (Islam et al., 2022). So there has been a crucial requirement to increase its yield, quality and production area to break the cycle of poverty during frequent climatic extreme conditions. Two factors influencing yield increase are modern management practices and plant breeding, which has a major impact on production.

Maize grows over a broad extent area with regard to the genotype by environment interaction (GEI) that hinders the pointing out of high-yielding and stable genotypes (Akcura et al., 2011). Genotype by environment interaction (GEI) deals with the various responses of genotypes across a broad environmental range. The prime focus of the new hybrid is to look for higher and stable yield in both favorable and unfavorable environmental conditions (Katsenios et al., 2021). The identification of maize varieties that are stable (hybrid's response across various environments) plays a major role in the enhancement of farmers' acceptability as well as the adoption of elite new varieties.

Genotype is supposed to be better adapted or stable if it has a higher mean yield and low fluctuation in yielding capability across diverged locations. The effect of genotype and environment interaction becomes more apparent during multi-location and multi-year trials for estimation and prediction of yield on the basis of based on defined experimental data. According to Lu'quez et al. (2022), higher yielding and better stable cultivar can be identified when cultivars are grown in various environments,

The GEI analysis has been conducted by various statistical methods such as stability analysis following AMMI model; principal component analysis (PCA) and linear regression analysis; ANOVA and GGE biplot analysis (Nzuve et al., 2013). GGE biplot analysis i.e. genotype main effect (G) and interaction of G × E (Hossain et al., 2018; Kizilgeci et al., 2019) is one of the convenient tools for geneticists and plant breeders that identifies superior genotypes (stable and high yielding) over multiple locations as well as by using graphical axes to detect the best suitable location for a particular genotype (Akcura et al., 2011).

The AMMI model is also a functional method that combines ANOVA and PCA, and the resulting output is a biplot that evaluates GE interactions graphically (Kaya et al., 2006). The results of AMMI analysis are regarded potential to evaluate the performance of yield of different genotypes under multi environment trials and to determine the suitable environments for all studied genotypes [Li et al., 2006; Agahi et al., 2020; Mafouasson et al., 2018 and Hongyu, et al, 2014]. Due to its high accuracy of results and contribution for understanding interaction between genotypes and environment, this model is extensively used by the researchers (Gauch, 2013). It also provides information for evaluation of improved cultivar, recommendations and selection of tested environment (Abay and Bjornstad, 2009).

Therefore, the aim of this research to find out the high yielding stable hybrids using AMMI and GGE biplot method which could have wide or specific adaptation in tested environment.

MATERIALS AND METHODS

Experimental sites

The study was executed by exploiting multi-location trials in five locations viz., Regional Agricultural Research Station (RARS), Rahmatpur, Barishal; RARS, Jashore; RARS, Jamalpur; RARS, Hathazari, Chittagong and Wheat Research Centre (WRC), Nashipur, Dinajpur during rabi season of 2018-19. The agro-climatic description of five experimental sites used in the study was given in Table 1. The environments had different soil texture (pH ranges from 5.2-7.5) and variable microclimate condition. Jashore location had a well-drained and clay loam structure of soil with pH 7.5 whereas Dinajpur has sandy clay loam soil and pH was 5.21.

Table 1. Agro-climatic description of five experimental sites used in the study

Particulars	E_1	E_2	E_3	E_4	E_5
Location	Rahmatpur Barishal	Jashore	Jamalpur	Hathazari, Chittagang	Nashipur, Dinajpur
Lattitude (decimal)	22.7875	23.1869	24.9354	22.5016	25.7524
Longitude(decimal)	90.2945	89.1874	89.9356	91.7936	88.6733
Soil type	Silty clay	Clay loam	Loamy	Silty loam	Sandy clay loam
pH	7.0	7.5	5.8	5.76	5.21
Climate					
Maximum temp. (^{O}C)	33.5	32.1	31.6	29.7	33.6
Minimum temp. (^{O}C)	25.2	22.9	22.4	23.4	23.4
Average rainfall (mm)	141.96	109.75	171.46	243.04	158.53

Experimental treatments and design

Twenty-one white maize hybrids (developed through the local cross) and three checks BARI hybrid maize (BHM-12, BHM-13 and BHM-14) were used in this study. Seven white kernelled maize inbred lines (CML-330, CML-332, CML-322, CML-311, CML-331, CML-518, CML-383) were used as a parental line then the lines were crossed in a half diallel fashion excluding reciprocals to produce 21 F_1's in the previous rabi reason 2017-2018. The experiment was laid out in a randomized complete block design with three replications in five locations.

Experimental procedure

Two seed per hill and each line were sown in two row plot with 4m long. The unit plot size was 4m×1.2m. In the field, 1.5 m distance from block to block, 60 cm from row to row, and 25 cm from plant to plant was kept. Fertilizers were applied in the form of urea-Triple Super Phosphate-Muriate of Potash-Gypsum-Zinc Sulphate- Borax @550-600-250-200-50-25kg ha−1respectively. Before sowing, one third of urea and the full doses of Triple Super Phosphate- Muriate of Potash, Gypsum, Zinc sulphate and borax were applied. The remaining two-thirds of urea was applied in two equal segments at the knee height stage and about one week prior to silking. The entire field management approaches were standard to assure favorable growing environments.

Data collection

Harvesting was started on 20th April 2019, depending upon the maturity of the plants, i.e., when plants showed visible signs of drying, the husk cover was entirely dried, and the grains were completely matured. Grain maturity was pointed out from the milk line of kernels or a black layer formation at grain and placenta's junction. To estimate grain yield (GY), ten middle plants from each row were harvested to avoid border effects and adjusted at 15 % moisture.

Statistical Analysis

Data collected from all tested locations were pooled and the presence of significant G×E were deal with analysis of variance. The stability parameters, regression coefficient (b_i) of the genotype over environmental indices and deviation from regression (S^2d_i) were calculated in accordance with Eberhart and Russel (1966). Using Cropstat 7.2 program, all collected data were processed and analyzed.

GGE Biplot and AMMI Model

The GGE biplot was constructed in view of the simplified model for two main components centered on the environment (PC1 and PC2) to evaluate stability and adaptability (Yan, 2007). The GGE biplot multiplicative model is close to the AMMI multiplicative model (Sousa et al., 2015). Principal components formed by putting environment-centered means to singular value decomposition (SVD). Then the first principal component (Axis 1) scores were laid out against their respective value/scores for the second principal component (Axis 2) to create biplot (Mohammadi et al., 2010; Hossain et al., 2018).

AMMI model analysis was done by using analysis of variance and principal component analysis for measuring stability and genotype environment interactions (Gauch, 1988; Yan et al., 2007).

The model equation is:

$$Y_{ij}= \mu + G_i + E_j+\sum_{k=1}^{n} \lambda k \; \alpha ik \; \gamma jk + e_{ij}$$

Where: Y_{ij} is the average yield of the ith genotype in the jth environment and is the overall mean yield; μ denotes the grand mean; G_i stands for the effect of genotype i; Ej is the effect of environment j; λ_k is the k^{th} singular value of the original matrix interaction; α_{ik} and γ_{jk} signify the genotype and environment principal component scores for axis k; n is the number of principal components kept in the model and e_{ij} stands for the average experimental error associated with observation, assumed to be independent.

RESULTS AND DISCUSSION

The full joint analysis of variance (Table 2) displayed considerable effects for genotypes, environment and the interaction between genotype and environment (GXE). Genotype's mean sum of squares were highly significant for yield that indicated the presence of genetic variation. Environment was the extensive initiator of variation for grain yield. The mean sum of squares for environments were highly significant suggesting that yield was significantly influenced by environments. Since the environment and G x E interactions was found significant which specify diverse environment and tested hybrids which implied differential responses of genotypes to different environments, it is necessary to find out the G×E interaction (Silveira et al., 2016; Ilker et al., 2018). The AMMI model is a powerful tool that can perfectly analyze genotype environment interaction. Different studies have been reported considerably different G×E interactions in maize grain yield (Carson et al., 2002; Makumbi, 2005; Menkir and Adepoju, 2005).

Table 2. Full joint analysis of variance for grain yield data inclusive of the partitioning of the G×E interaction of twenty-four maize hybrids

Source of variation	df	Mean sum of squares
Genotypes (G)	23	16.66**
Environment (E)	4	7.35**
Interaction (G x E)	92	2.01**
AMMI Component 1	26	3.38**
AMMI Component 2	24	1.62
AMMI Component 3	22	1.54
AMMI Component 4	20	1.23
Residuals	23	1.79

Assessment of phenotypic index and stability parameters

The grain yield in five locations, as well as overall mean yield coupled with phenotypic index (P_i), environmental index (I_j), regression coefficient (b_i), and deviation from regression (S^2d_i) value, are presented in Table 3. The mean grain yield ranged from 6.91 t ha^{-1} to 11.75 t ha^{-1}. In case of phenotypic index, fourteen hybrids displayed positive phenotypic index while rest of the hybrids had negative index for yield. Thus, positive phenotypic index represented the higher yield and negative represented the lower yield. Again, the rich or favorable and poor or unfavorable environments are reflected by positive and negative environmental index (I_j) for this character, respectively. The range of environmental indices for grain yield was -0.37 to 0.51 which reflected the variation in performance from one location to another. Thus, the environment of Hathazari was the poorest, whereas Barishal and Dinajpur were the most favorable environmental for maize production. The environmental mean for grain yield ranged from 9.79 t ha^{-1} to 10.67 t ha^{-1}. The differences in b_i value ranges from 0.08 to 3.75 reflected the response of tested hybrid and indicated that these materials responded differently in different environment. The adaptability in performance across the location for all the genotypes was indicated by the non-significant regression coefficient value (b_i) different from unity. When $b_i=1$ and mean yield high, then the genotypes are well adapted to all environment; when $b_i=1$ and mean yield low, the genotypes are poorly adopted to all tested environments. A regression coefficient value significantly less than unity indicates, either, a lower than average response to high yielding environments or a better than average performance in low-yielding environments. Among the studied materials, G14 (11.75 t ha^{-1}), G16 (11.51 t ha^{-1}), G20 (11.43 t ha^{-1}) and G10 (11.28 t ha^{-1}) produced highest yield. Considering grain yield, b_i~1 and S^2d_i~0 indicated that G14 and G16 were the higher yielding and suitable across the environments. These results were in line with the reports of Kaundal and Sharma (2006). On the other hand, G20 & G10 were given higher yield but were responsive to favorable environments. Rahman et al. (2010) were also recorded significant differences of adaptability and yield stability in maize genotypes.

Table 3. Estimates of stability parameters for yield (t ha^{-1}) of twenty-four maize hybrids at five locations

Crosses	Yield (t ha^{-1})					Overall mean	P_i	b_i	S^2d_i
	BSL	JSR	DPUR	HAT	JML				
1. CML 330× CML 332(G1)	10.44	8.31	8.84	7.09	8.08	8.55	-1.60	3.75	0.48
2. CML 330× CML 322(G2)	10.50	8.86	11.17	9.61	10.97	10.22	0.07	1.25	0.46
3. CML 330× CML 311(G3)	10.68	10.99	10.21	7.58	9.93	9.88	-0.28	2.62	0.90
4. CML 330× CML 331(G4)	10.85	8.99	10.34	8.94	10.73	9.97	-0.18	2.26	0.10
5. CML 330× CML 518(G5)	11.79	8.92	11.33	10.83	9.84	10.54	0.39	1.90	0.73
6. CML 330× CML 383(G6)	9.31	10.29	10.74	9.70	9.47	9.90	-0.25	0.66	0.16
7. CML 332× CML 322(G7)	10.20	10.08	9.66	8.83	9.67	9.69	-0.47	1.26	0.41
8. CML 332× CML 311(G8)	11.33	10.58	10.17	9.81	9.50	10.28	0.12	1.69	0.29
9. CML 332×CML 331(G9)	6.84	6.67	7.00	8.89	5.15	6.91	-3.24	1.59	1.44
10. CML 332×CML 518(G10)	11.27	10.55	11.54	11.34	11.71	11.28	1.13	0.13	0.32
11. CML 332×CML 383(G11)	11.55	11.72	10.93	7.90	10.80	10.58	0.42	3.14	1.27
12. CML 322×CML 311(G12)	10.22	10.65	10.50	8.62	10.04	9.91	-0.25	1.25	0.06
13. CML 322×CML 331(G13)	10.92	9.30	9.61	9.37	10.26	9.89	-0.26	1.91	0.44
14. CML 322×CML 518(G14)	12.00	11.63	11.58	11.54	12.00	11.75	1.60	0.91	0.14
15. CML 322×CML 383(G15)	8.90	9.95	10.72	10.72	11.23	10.30	0.15	2.09	0.08
16. CML 311×CML 331(G16)	11.58	11.70	10.69	11.67	11.88	11.51	1.35	0.93	0.29
17. CML 311×CML 518(G17)	11.30	10.17	10.06	9.74	10.67	10.39	0.23	1.76	0.50
18. CML 311×CML 383(G18)	10.56	8.52	9.26	10.52	9.10	9.59	-0.56	0.80	0.43
19. CML 331×CML 518(G19)	10.24	10.20	10.48	9.52	10.78	10.24	0.09	0.58	0.34
20. CML 331×CML 383(G20)	11.86	11.04	11.11	11.83	11.30	11.43	1.27	0.08	0.44
21. CML 518×CML 383(G21)	11.41	10.60	9.54	10.18	10.86	10.52	0.36	1.36	0.17
22.BHM 12(G22)	11.74	11.19	10.02	11.79	10.23	10.99	0.84	0.26	0.34
23.BHM 13(G23)	11.81	10.84	9.70	10.93	10.69	10.79	0.64	1.16	0.00
24.BHM 14(G24)	8.86	8.55	9.39	7.97	7.74	8.50	-1.65	0.96	0.11
E.mean	10.67	10.01	10.18	9.79	10.11	**10.16**	-	-	-
E.index (I_j)	0.51	-0.15	0.02	-0.37	-0.05	-	-	-	-
LSD (0.05)	1.22	1.17	1.24	0.76	0.93	-	-	-	-

*BSL=Barishal; JSR=Jashore; DPUR=Dinajpur; HAT=Hathazari; JML=Jamalpur

For the identification of suitable or better performing hybrids in each location "Which-Won-Where" function of GGE biplot can be used. Data derived from the multivariate models of genotypes/varieties/hybrids and tested environments, GEI pattern can be identified effectively by plotting concurrently in one figure i.e GGE biplot polygon (Yan et al., 2001). Dehghani et al. (2009) also used GGE biplot method to pick out best maize genotypes for target sites. Fig. 1. displayed GGE biplot that showing the performance of twenty-four hybrids over five environments. The principal component Axis 1 interpreted 69.73% genotype main effects, while second principal component Axis 2 elucidated 15.36 % G×E interaction and thus the GGE biplot demonstrated 85.09% of the total variation of grain yield. Fig. 1 showed a polygon that was formed by integrating different points, located apart from the centre, where on the vertexes some of the testing hybrids were positioned, while rests of the hybrids were inside the polygon. The genotypes placed in the vertex in their sector represent the high yielding genotypes in the area that fell inside the specific area (Yan et al., 2000; Makumbi et al., 2005). Those hybrids were considered to be the most responsive due to their position on the vertex because they had an extended distance from the origin of the biplot. Yan and Rajcan (2002) explained that responsive hybrids were either the best or the poorest at one or every environment. It is apparently set out which genotype won in which environments, thus supporting the documentation of mega-environment (Yan et al., 2000; Dimitrios et al., 2008). Other researchers (Sabaghnia et al., 2008; Choukan, 2011; Shiri, 2013) have also cited this method.

The vertex genotypes in this Fig. 1 were G1 (CML 330× CML 332), G9 (CML 332×CML 331), G11 (CML 332×CML 383), G14 (CML 322×CML 518) and G20 (CML 331×CML 383) that were the most responsive one can be visually determined. The biplot was divided into seven sectors by seven rays and for each sector the highest yielding genotypes were identified. Similar results were noticed by Bhartiya et al. (2017) and Ramos et al. (2017). They marked that the GGE biplot obtained for soybean genotypes for seed yield was divided into six or eight sectors. In this study, out of seven sectors tested environments fall in two of them. The vertex genotype for sector which encompassed environments Barishal, Jashore, Jamalpur and Dinajpur was G14 (CML 322×CML 518) and for sector content environment Hathazari was G20 (CML 331×CML 383), indicating that these genotypes were the winning genotypes for that environments. In this case GE can be exploited by recommending specific genotype to specific locations (Yan et al., 2007). Other corner genotypes, G9 (CML 332×CML 331) was the poorest yielding among the tested genotypes and the location of this genotypes reflecting the fact that as this was poor yielded at each location so this was located far away from all of tested locations. Ahmed et al. (2020) also found hybrids ‘G4’, ‘G9’ and ‘G6’positioned at the pick of the GGE biplot polygon, but they had low GY in all the tested environments.

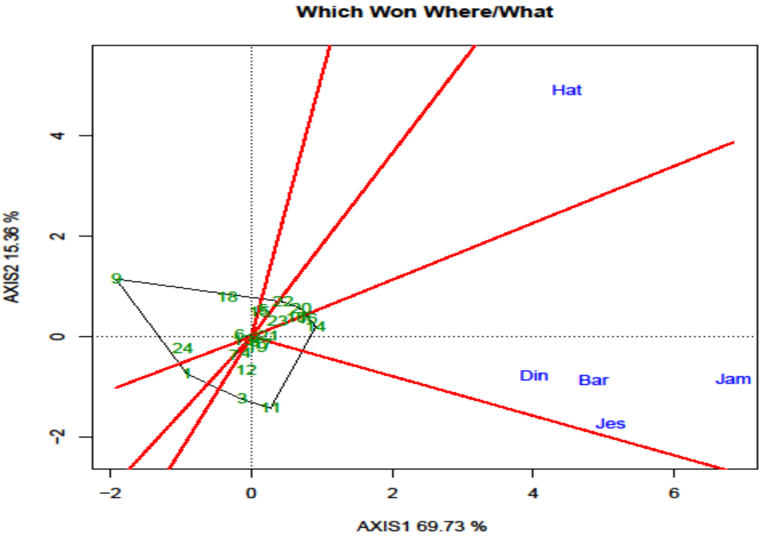

Figure 1. Polygon view of genotype + genotype × environment interaction biplot displaying performance of genotypes in each location.

In this GGE biplot method testing hybrids were compared with hypothetically determined ideal genotype (Fig. 2). The ideal genotype has maximum grain yield mean value and higher stability (PCA scores near zero) in that it will not exhibit any G×E interaction (Yan & Kang, 2003; Sharma et al., 2010; Akcura et al., 2011). According to Kaya et al. (2006), an ideal genotype is explained by having the maximum vector length of the high-yielding potential genotypes and with the lowest GEI that is presented by an arrow pointing to it. A genotype is considered best if it is located nearest to the center with an average higher grain yield and stability. Thus, keeping the ideal genotype as the center, a concentric circle has been drawn to assist in the visualization of the distance between all tested genotypes and the ideal/best genotype. In Fig. 2, G14 (CML 322×CML 518) was located at the center of concentric circles and was affirmed as an ideal genotype with maximum grain yield and higher yield stability. Whereas G16 (CML 311×CML 331), G10 (CML 332×CML 518), and G20 (CML 331×CML 383) were adjacent to the best genotype ‘G14’, also pointed out as better hybrids. However, CML 332×CML 331(G9) would not be regarded as a higher grain yielding and yield stable genotype due to having distance from genotype G14 (CML 322×CML 518). Similar findings related to our research were mentioned by Zhang et al. (2006) and Bhartiya et al. (2017). The genotype E14, E16, E10 and E20 could be utilized as a reference for evaluation of genotypes (Kaya et al., 2006) and these could be encompassed for further assessment in both selection of early and later stages (Mitrovic et al., 2012).

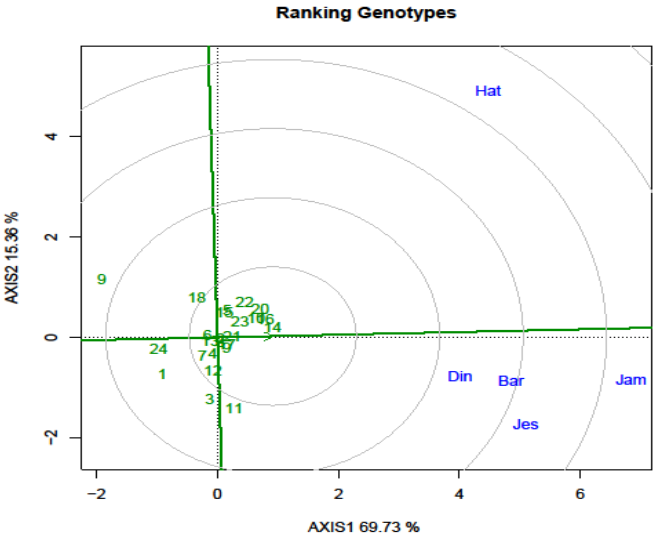

Figure 2. GGE-biplot based on genotype and environment focused scaling for comparison of the genotypes with the ideal genotype.

The indication of the stability of a genotype over locations/environments is interaction principal component analyses (IPCA) scores in the AMMI analysis. A Genotype or environment is regarded as stable genotype having IPCA1 scores nearly zero and has no interaction effect. Positive interaction of genotype or environment is reflected by the identical sign on the PCA axis, while negative interaction depicted by dissimilar sign. From the biplot, environments are distributed from low yielding genotypes and environment in quadrants I (top left) and IV (bottom left) to the High yielding genotypes (G) and favorable environment (E) in quadrants II (top right) and III (bottom right) (Fig. 3). In the present study it was observed that G14 (CML 322×CML 518), G16 (CML 311×CML 331), G10 (CML 332×CML 518), G20 (CML 331×CML 383), G22 (BHM 12) and G23 (BHM 13) were high yielding hybrids. G9 (CML 332×CML 331), G24 (BHM 14) and G1 (CML 330×CML 332) were low yielding and rest of hybrids are average yielding. Genotypes belonging to low-yielding environments are indicated at the lower left quadrant of the biplot. Among the entries, G14 (CML 322×CML 518), G2 (CML 330×CML 322), G24 (BHM 14) were more stable due to smaller IPCA1 score that was near to zero. G21 (CML 518×CML 383), G17 (CML 311×CML 518), G19 (CML 331×CML 518) and G8 (CML 332× CML 311) were average yielding and nearly stable but G11 (CML 332×CML 383) and G3 (CML 330×CML 311) were unstable. Ahmed et al. (2020) and Matin et al. (2017) also made similar findings using AMMI model.

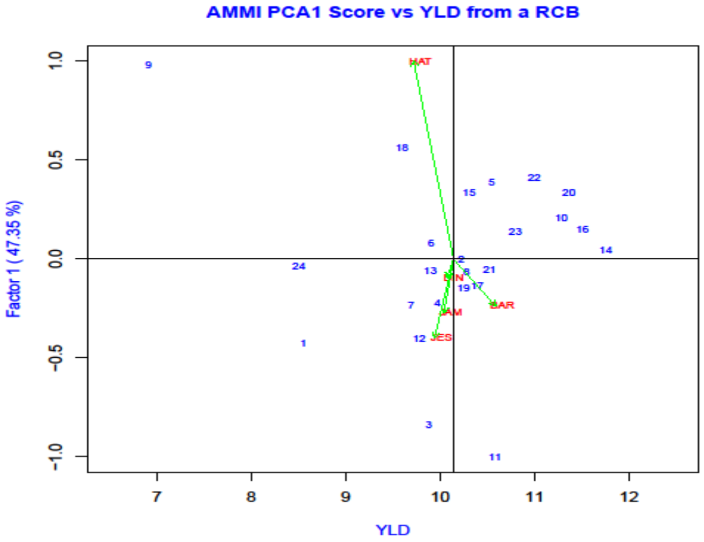

Figure 3. First AMMI interaction (IPCA1) biplot for yield (t/ha) of twenty-four maize hybrids and five environments using G × E scores

Since IPCA2 scores also have a notable part in describing the GEI; the IPCA1 scores were set against the IPCA2 scores for more exploration of adaptation. With the first two principal component scores the AMMI 2 biplot generated a distinct relationship between genotypes and environments (Fig. 4). Interaction level is indicated by the length of sidelines. The longer sideline implies strong interaction, while the shorter sideline denotes weak interaction. The biplot conveyed that with the long spoke, the environments of Hathazari exert strong interaction. The AMMI 2 biplot also specified the relationship among the genotypes. According to Fig. 4 the hybrids G11 (CML 332×CML 383), G22 (BHM-12), G9 (CML 332×CML 331), G3 (CML 330×CML 311) and G15 (CML 322×CML 383) were unstable due to their dispersed position from the other hybrids in the biplot. G24 (BHM-14), G16 (CML 311×CML 331), G13 (CML 322×CML 331), G17 (CML 311×CML 518) and G14 (CML 322×CML 518) were located adjacent to the biplot's origin which indicated their stability in performance over environments when plotting the IPCA1 and IPCA2 scores**.** Ahmed et al. (2020) stated that genotypes near to the origin will have equivalent grain yield in all locations, while distant genotypes will response diversely in mean yield and over environments.

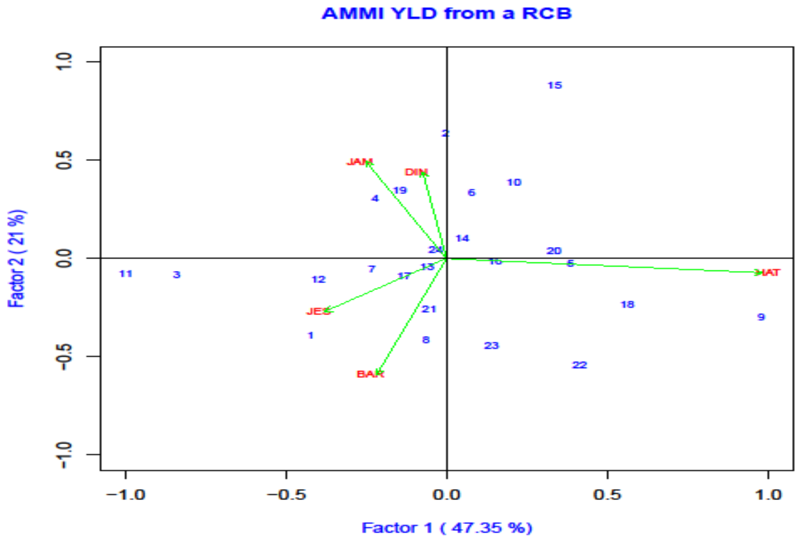

Figure 4. AMMI biplot 2 for grain yield (t/ha) displaying the relationship of IPCA against IPCA 1 scores of twenty-four maize hybrids grown in five environments

CONCLUSION

The present study revealed that the maize grain yield was greatly influenced by genotype × environment interaction that was followed by genotypic (G) and environment (E) effects, respectively. In the present investigations, phenotypic index, stability parameters, GGE, and AMMI were utilized to measure the stability of hybrids among the five tested locations in Bangladesh. Among the tested materials, G14 (CML 322×CML 518), G16 (CML 311×CML 331), G20 (CML 331×CML 383) and G10 (CML 332×CML 518) produced highest yield than check BHM-12 and BHM-14. Considering overall performance on yield, yield contributing characters and stability, G14 (CML 322×CML 518) and G16 (CML 311×CML 331) were found superior by providing information about GEI and stability as supportive addition.

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LITERATURE CITED

Abay, F. and A. Bjornstad. 2009. Specific adaptation of barley varieties in different locations in Ethiopia. Euphytica.167: 181-195.

Agahi, K., J. Ahmadi, H.A. Oghan, M.H. Fotokian and S.F. Orang. 2020. Analysis of genotype × environment interaction for seed yield in spring oilseed rape using the AMMI model. Crop. Breed. Appl. Biotechnol. 20(1): e26502012.

Ahmed, A., A. Hossain, M. Amiruzzaman, M.A. Alam, M. Farooq, A.E. Sabagh and A. Kizilgeci. 2020. Evaluating short stature and high yielding maize hybrids in multiple environments using GGE biplot and AMMI models. Turk. J. Field Crops. 25(2): 216-226.

Ahmed, M., M.A. Mian and M.A. Chowdhury. 2011. Correlation study in maize. J. Agric. Res.16: 399-405.

Akçura, M., S. Taner & Y. Kaya. 2011. Evaluation of bread wheat genotypes under irrigated multi-environment conditions using GGE biplot analyses. Agriculture. 98(1): 35-40.

BBS. 2021. Bangladesh Bureau of Statistics, Year book of Agricultural Statistics (33rd Series), Ministry of Planning, Government of the People's Republic of Bangladesh, Dhaka.

Bhartiya, A., J.P. Aditya, P. Singh, J.P. Purwar and A. Aga. 2017. AMMI and GGE biplot analysis of multi-environment yield trial of soybean in North Western Himalayan state Uttarakhand of India. Legume Research. 40(2): 306-312.

Carson, M.L., M.M. Goodman and S.M. Williamson. 2002. Variation in aggressiveness among isolates of *Cercospora* from maize as a potential cause of genotype-environment interaction in gray leaf spot trials. Plant Dis. 86: 1089-1093.

Choukan, R. 2011. Genotype, environment and genotype × environment interaction effects on the performance of maize (*Zea mays* L.) inbred lines. C. B. Journal. 1(2): 97-103.

Crossa, J., P.L. Cornelius and W. Yan. 2002. Biplots of linear-bilinear models for studying crossover genotype × environment interaction. Crop Sci. 42: 619-633.

Dehghani, H., N. Sabaghnia and M. Moghaddam, 2009. Interpretation of genotype-by-environment interaction for late maize hybrids grain yield using a biplot method. Turkish J. Agric. and Forest. 33:139-148.

Dimitrios, B., G. Christos, R. Jesus and B. Eva. 2008. Separation of cotton cultivar testing sites based on representativeness and discriminating ability using GGE Biplots. Agron. J. 100: 1230-1236.

Eberhart, S.A. and W.A. Russell. 1966. Stability parameters for comparing varieties. Crop Sci. 6: 36-40.

Gauch, H.G. 1988. Model selection and validation for yield trials with interaction. Biometrics. 44:705-715.

Gauch, H.G. 2013. A simple protocol for AMMI analysis of yield trials. Crop. Sci. 53:1860-1869.

Hassan, A.A., M. Abdikadir, M. Hasan, A.K. Azad and M. Hasanuzzaman. 2018. Genetic variability and diversity studies in maize (*Zea mays* L.*)* inbred lines. IOSR Journal of Agriculture and Veterinary Science.11(11): 69-76.

Gulati, A., J. Dixon and J.M. Dixon. 2008. Maize in Asia: changing markets and incentives. Contributors: International Maize and Wheat Improvement Center, International Food Policy Research Institute, International Fund for Agricultural Development. Academic Foundation, pp.489.

Hongyu, K., M. García-Peña, L.B. De Araújo and C.T.D.S. Dias. 2014. Statistical analysis of yield trials by AMMI analysis of genotype × environment interaction. Biom. Lett. 51. 89-102.

Hossain, A., M.A.H.S. Jahan, J. Timsina, A. Jaime, T. Silva, M.G. Mahboob and M. Farhad, 2018. Biplot yield analysis of heat-tolerant spring wheat genotypes (*Triticum aestivum* L.) in multiple growing environments. Open Agriculture. 3(1): 404-413.

Ilker, E., M. Kocaturk, A. Kadiroglu, M. Altinbas, A. Yildirim, G. Ozturk and H. Yildiz. 2018. Stability analyses for double cropping in soybean [(*Glycine max* L.) Merr]. Turk. J. Field Crops. 23(2): 80-84.

Islam, M.R. and S. Hoshain. 2022. A brief review on the present status, problems and prospects of maize production in Bangladesh. Research in Agriculture Livestock and Fisheries. 9(2):89–96.

Katsenios, N.P., D. Leonidakis, G. Katsaros, I. Kakabouki, D. Vlachakis and A. Efthimiadou. 2021. Effect of genotype environment interaction on yield of maize hybrids in Greece using AMMI analysis. *Agronomy.11:*479.

Kaundal R. and B.K. Sharma. 2006. Genotype × environment interaction and stability analysis for yield and other quantitative traits in maize (*Zea mays* L.) under rainfed and high rainfall valley areas of the sub mountain. Res Crops 7(1): 171-180.

Kaya, Y., M. Akcura and S. Taner. 2006. GGE-biplot analysis of multi-environment yield trials in bread wheat. Turk. J. Agric. For. 30: 325-337.

Kizilgeci, F., O. Albayrak and M. Yildirim. 2019. Evaluation of thirteen durum wheat (*Triticium durum* Desf.) genotypes suitable for multiple environments using GGE biplot analysis. Fresenius Environmental Bulletin.28(9): 6873- 6882.

Li, W. Z.H. Yan, Y.M. Wei, X.J. Lan and Y.L. Zheng. 2006. Evaluation of genotype × environment interactions in Chinese spring wheat by the AMMI model, correlation and path analysis. J. Agron. Crop. Sci. 192: 221–227.

Lu'Quez, J.E., L.A.N. Aguirrezabal, M.E. Aguero and Pereyra, V.R. 2002. Stability and adaptability of cultivars in non-balanced yield trials. comparison of methods for selecting 'high oleic' sunflower hybrids for grain yield and quality. J. Agron. Crop. Sci.188:225–234.

Mafouasson, H.N.A., V. Gracen, M.A. Yeboah, G. Ntsomboh-Ntsefong, L.N. Tandzi and C.S. Mutengwa. 2018. Genotype-by-environment interaction and yield stability of maize single cross hybrids developed from tropical inbred lines. Agronomy.8: 62.

Makumbi, D. 2005. Phenotypic and genotypic characterization of white maize inbreds, hybrids and synthetics under stress and non-stress environments. PhD dissertation Submitted to the Office of Graduate Studies of Texas A and M University.

Matin, M. Q. I., G. M. Rasul, A. K. M. A. Islam, M. A. K. Mian, J. U. Ahmed & M. Amiruzzaman. 2017. Stability analysis for yield and yield contributing characters in hybrid maize (*Zea mays* L.). African Journal of Agricultural Research. 12(37): 2795-2806.

Menkir, A., & M. A. Adepoju, 2005. Registration of 20 Tropical mid-altitude maize line sources with resistance to gray leaf spot. Crop Sci. 45: 803-804.

Mitrovic, B., D. Stanisavljevi, S. Treski, M. Stojakovic, M. Ivanovic, G. Bekavac and M. Rajkovic. 2012. Evaluation of experimental Maize hybrids tested in multi-location trials using AMMI and GGE biplot analysis. Turkish J. of Field Crops, 17(1): 35-40.

Mohammadi, R., R. Haghparast, A. Amri and S. Ceccarelli. 2010. Yield stability of rainfed durum wheat and GGE biplot analysis of multi-environment trials. Crop Past. Sci. 61: 92-101.

Nzuve, F., S. Githiri, D. M. Mukunya and J. Gethi. 2013. Analysis of genotype × environment interaction for grain yield in maize hybrids. Journal of Agricultural Science. 5(11): 75-85.

Rahman, H., Durreshawar, S, Ali, F. Iftikhar, I.H. Khalil, S.M.A. Shah and H. Ahmad. 2010. Stability analysis of maize hybrids across north west of Pakistan. Pak. J. Bot. 42(2): 1083-1091.

Ramos, Jr E.U., R.L. Brogin, V.P.C. Godinho, F.J.E. Botelho, F.D. Tardin and P.E. Teodoro. 2017. Identification of soybean genotypes with high stability for the Brazilian macro-region 402 via biplot analysis. Genetics and Molecular Research 16(3): 1-10.

Sabaghnia, N., H. Dehghani and S.H. Sabaghpour. 2008. Graphic analysis of genotype by environment interaction for lentil yield in Iran. Agron. J. 100:760–764.

Sharma, R. C., A. I. Morgounov, H. J. Braun, B. Akin, M. Keser, D. Bedoshvili and M. Ginkel. 2010. Identifying high yielding stable winter wheat genotypes for irrigated environments in Central and West Asia. Euphytica. 171:53-64.

Shiferaw, B., B. Prasanna, J. Hellin and M. Banziger. 2011. Crops that feed the world. 6. Past successes and future challenges to the role played by maize in global food security. Food Security. 3: 307–327.

Shiri, M. 2013. Grain yield stability analysis of maize (*Zea mays* L.) hybrids in different drought stress conditions using GGE biplot analysis. Crop Breeding Journal. 3(2):107-112.

Silveira, D.A., L.F. Pricinotto, M. Nardino, C.A. Bahry, C.E.C. Prete and L. Cruz. 2016. Determination of the adaptability and stability of soybean cultivars in different locations and at different sowing times in Paraná state using the AMMI and Eberhart and Russel methods. Ciências Agrárias Londrina. 3.7(6): 3973-3982.

Sousa, L.B., O.T. Hamawaki, A.P.O. Nogueira, R.O. Batista, V.M. Oliveira and R.L. Hamawaki. Evaluation of soybean lines and environmental stratification using the AMMI, GGE biplot, and factor analysis methods. 2015. Genetics and Molecular Research.14 (4): 12660-12674.

Yan, W., M.S. Kang., B. Ma, S. Woods and P.L. Cornelius. 2007. GGE (genotype and genotype by environment interaction) biplot vs. AMMI (additive main effects and multiplicative interaction) analysis of genotype-by-environment data.Crop Sci. 47:643–653.

Yan, W. and M.S. Kang. 2003. GGE biplot analysis: A graphical tool for breeders, geneticists, and agronomists. CRC Press, Boca Raton, FL, USA.

Yan, W. and I. Rajcan. 2002. Biplot analysis of test sites and trait relations of soybean in Ontario. Crop Sci. 42**:**11-20.

Yan, W., P.L. Cornelius, J. Crossa and L.A. Hunt. 2001. Two types of GGE biplots for analyzing multi-environment trial data. Crop Sci. 41: 656-663.

Yan, W., L.A. Hunt, Q. Sheng and Z. Szlavnics. 2000. Cultivar evaluation and mega-environment investigations based on the GGE biplot. Crop Sci. 40: 597-605.

Zhang, M., M.S. Kang, P.F. Reese Jr and H.L. Bhardwaj. 2006. Soybean cultivar evaluation via GGE biplot analysis. Journal of New Seeds 7(4): 37-50.