

Genotype-by-Environment interactions in Maize hybrids using GGE-biplot and AMMI model

Shahadat Hossain^{1,6}, Md Sarowar Alam^{2*}, Sadia Sabrina Alam³, Md. Bikash Sarker⁴, and Md Amraul Islam⁵

¹Plant Breeding Division, Bangladesh Agricultural Research Institute (BARI), Regional Agricultural Research Station (RARS), Hathazari, Chattogram, Bangladesh

²Plant Breeding Division, BARI, RARS, Akbarpur, Moulvibazar 3210, Bangladesh

³Plant Breeding Division, BARI, Joydebpur, Gazipur 1701, Bangladesh

⁴Plant Breeding Division, BARI, RARS, Bhurrihat, Rangpur, Bangladesh

⁵Plant Breeding Division, BARI, RARS, Jamalpur, Bangladesh

⁶Department of Arid Land Agriculture, Faculty of Meteorology, Environment and Arid Land Agriculture, King Abdulaziz University, Jeddah 21589, Saudi Arabia

*Corresponding author: asarowar04bau@bari.gov.bd

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Abstract— Evaluation of the productivity and performance of maize hybrid genotypes in variable environments is a basic demand for releasing varieties. The purpose of this research was to assess the yield, performance, and stability of maize hybrids and to identify suitable environments for maize production in Bangladesh. The maize hybrid Sunshine produced the highest yield (11.24 t ha⁻¹ to 12.85 t ha⁻¹) followed by Kaveri 60 (7.04 t ha⁻¹ to 12.72 t ha⁻¹). Genotype × environment interaction effects have influential effects on the yield of maize hybrids. The sums of squares of GGE were found as 43.96% and 24.2%, respectively, for the principal component 1 (PC1) and principal component 2 (PC2), respectively. In the biplot polygon view, there were six rays that divided the biplot into six sectors and the six environmental locations were accommodated within four sectors. Jessore was determined as the typical test environment for the country followed by Bhurrihat and Jamalpur. Ideal testing sites would provide information to identify the superior maize hybrids to minimize the expenses of the country. Considering the yield potentiality and stability, Sunshine, 9MS/S5-1×BIL-114 and, 9MS/S7-9×BIL-114 were found as the most stable and high yield producing hybrids across the six environmental conditions. Therefore, these three genotypes were identified as the best hybrids over the locations of Bangladesh.

Keywords— AMMI Model, evaluation, GGE-biplot, maize, stability

I. INTRODUCTION

Maize (*Zea mays* L.) is the best grain crop which can survive in a diversified environment around the world. Maize achieved the first rank in the world cereal production which is one of the top cash crop in the world used as the main source of food, energy and for animal and poultry feed [1]. Total 1148.48 million tons maize was produced around the world during 2019-20 [2]. Although maize is a promising cereal crop for yield improvement, but still the yield gap is very high for this crop. Global yield potential is 10.5 t/ha but the actual yield is only 5.5 t/ha [3]. Appropriate management of inputs is the key to successful maize production for sustainable environment and agricultural production [4], [5]. Input covers cultivars that can

fit to multiple environments, plant population size, soil management, intercultural operations like fertilizer application, plant protection, irrigation and drainage, and harvesting of crops [6]–[8].

Environmental conditions have a great influence on the varietal responses to variable soil and climatic conditions. Phenotypic expression of a crop is measured by the interaction between genotypes and environment. Genotype and environmental effects along with genotype-environment (GE) interaction determine the yield of maize [9]. Significant genotype × environment interactions (GE) affect the different stages of crop. Therefore, the varietal performance for a specific area may not be the same in other areas [10]. Moreover, plant growth stage and its performance are also greatly influenced by different environmental factors or stresses [11], [12]. Responding of crops to GE are variable:— some exhibit high while others express low. Thus, the analysis of GE interaction for varietal evaluation experiment is essential for the breeders. Both genotypes and environments have interactive effects on the qualitative and quantitative traits of cultivars [13]. Research findings of G × E interactions provide basic information to the plant breeders to make a good planning to identify the most adapted genotypes for the target location [14]. Adaptive genotypes are stable for yield over the testing environments. Besides, cultivars with high yield potential at a selected place may not be able to produce the same yield in an unexpected area identified to have minimum adaptation [15].

The stability analysis of varietal yield gives important information related to their performance in particular environments [16], [17]. To increase seed yield is the principal objective of maize breeding. Good understanding and skill on the genetics of seed yield assist breeders to manage the genetic advance of the variety. Genotypes, environments, and GE interaction determine the expression of polygenic characters like heterosis, yield, etc [18]–[20]. GE interaction analysis is done by Additive Main Effects and Multiplicative Interaction (AMMI) model [9], [21]. Several methods such as AMMI model, GGE biplot, Eberhart and Russell model, Finlay–

Wilkinson model, etc. are used to assess Genotype × Environment interaction [22]. GEI for field experiments, for yield, is usually determined by AMMI model. In the case of genotype evaluation for macro environment analysis and genotype evaluation, AMMI graph is comparatively less efficient than GGE biplot as it provides less information about G + GE [23]. GGE biplot can effectively evaluate the target location by analyzing the status of discriminating vs. representativeness. It cannot be possible by AMMI analysis. Better graphical illustration is possible by using multiple environments the GGE biplot model as it uses multi-location data [24]. Better understanding of the complex G × E interactions of genotypes and agronomic experiments for multilocation is easy by GGE biplot. It can effectively determine the performance of crop genotypes under multiple environmental stresses, typical varieties, large environments, and principal experimental locations. There are several research findings revealed that this model has been perfectly applied for different crop experiments [25]–[31].

Although, Bangladesh Agricultural Research Institute (BARI) has developed released few superior maize hybrids, those are now cultivated in farmers fields along with some commercial varieties but there is higher demand to develop more hybrids to fulfill the sustainable development goal, farmers interest and to fit for variable environments. In this

experiment, eighteen maize breeding hybrids including five check varieties were tested for their yield, performance, and stability in six different locations of Bangladesh during the cropping season of 2017-2018.

II. MATERIALS AND METHODS

Location

The research was conducted in six different agro-ecological environments throughout Bangladesh. The sites were (1) BARI, Gazipur with location: 23°59'19.21" N, 90°24'36.65" E, and 13.1 metres above the sea level (masl) (2) Regional Agricultural Research Station (RARS), Jamalpur with location: 24°56'6.14" N, 89°55'56.86" E; and 21.6 masl (3) RARS-Rahmatpur with location: 22°47'10.9" N; 90°17'47.1" E; and 8.1 masl (4) RARS, Jessore with location: 23°11'14.52" N, 89°11'11.99"E; and 10.4 masl (5) RARS, Hathazari with location: 22°30'06.1" N, 91°47'39.9"E; and 26.2 masl and (6) RARS, Bhurirhat with location: 25°49'20" N, 89°14'11.3"E; and 36 masl.

Weather conditions of the cropping season

Average temperature, humidity, and total precipitation data were collected for every month throughout the growing season and tabulated (Table 1). Weather data were collected from a particular meteorological stations of the respective area.

Table 1. Weather data of the maize growing season during November 2017- April 2018

Environment	Rainfall (mm),	Temperature (°C),		Relative Humidity (%)	
		Maximum	Minimum	Maximum	Minimum
Gazipur (Gaz)	315	31.45	24.96	88.50	41
Hathazari (Hat)	152	32.45	25.92	94.71	38.50
Bhurirhat (Bur)	162	30.29	23.55	95.79	49.13
Jessore (Jes)	95	31.89	25.92	95.13	43.46
Rahmatpur (Rah)	181	31.77	27.03	99.08	44.88
Jamalpur (Jam)	331	29.91	21.58	95.85	56.82

Experimental materials, treatments, and design

Thirteen maturing maize advanced breed lines, Pac-60/S6-3×CML-425, Pac-60/S6-5×CML-425, Pac-60/S6-8×BIL-114, Pac-60/S5-14×BIL-113, Pac-60/S6-18×Utn/S5-18, Pac-60/S6-20×BIL-113, Pac-60/S6-21×Utn/S5-10, 9MS/S5-1×BIL-114, 9MS/S7-2×BIL-114, 9MS/S7-9×BIL-114, 9MS/S7-10×BIL-114, 9MS/S7-12×BIL-114, 9MS/S7-18×BIL-114, and one hybrid (BHM 9) variety developed by BARI and other four commercial varieties (981, Sunshine, Pioneer, Kaveri 60) were used as checked.

Experimental layout

Randomized Complete Block Design with 3 replications was followed for the trial. Seeds were sown manually in line by hand. Seeds of each genotype were sown in two rows of 4m long plots with 60 cm and 20 cm spacing between rows and hills, respectively. Seeds were sown by mid-November 2017. One healthy seedling was kept per hill for thinning. No insecticides or pesticides were applied. N, P, K, S, Zn and B were applied @ 250, 55, 110 40, 5 and 1.5 kg/ha respectively. Two extra rows were used at the end of each replication to avoid the border effect. Weed control was done manually as and when

needed. Mature cobs were harvested from the field manually and dried under the sun and seeds were separated.

Data collection

Data on days to 50% tasseling (DT), days to 50% silking (DS), plant height (PH), ear height (EH), thousand grain weight (TGW), and grain yield (kg) were collected on a whole plot basis. Ten randomly selected plants were used for data collection. All plants in two rows were considered for plot yield and converted to yield in t/ha.

Statistical analysis

Joint analysis of variance for traits over the environments was done using plot means with PB tools statistical package. Genotype×Environment analyses for stability and grain yield performance were done with R version 3.6.2 [32]. Data were processed and analyzed using R software version 3.6.2 [32], [33] and PB tools (Version 1.4, <http://bbi.irri.org/products>) respectively.

III. RESULTS AND DISCUSSIONS

Analysis of variance

Combined analyses of variance (ANOVA) for the maize genotypes of the experiment show differences for most of the traits under the locations, especially in case of grain yield. The

ANOVA of genotypes for different traits were determined and showed significant mean squares for genotype, environment, and interaction (Table 2). The mean sum of squares for the genotypes was highly significant for all traits except yield which exposed genetic variability remaining among the genotypes. Mean sums of squares for environments were found highly significant for all traits except thousand grain weight. Significant effects of the environment indicate the differential response of genotypes over the locations. GXE interactions over the environments were influenced by soil structure and moisture. Relative magnitude of the environment was higher than the genotypic effect, recommending that environmental factors have strong effects upon genotypic expression.

The sum of squares for genotype and environment were higher than that of G × E interaction (Table 2). In this condition, the performance of grain yield is significantly controlled by genotype and environments[34]–[36]. Some groups of researchers stand their opinion against this study that the effect of genotype and environment were lower than that of GE interaction [37] while other groups reported that the genotype and effects of genotype × environment interaction was three times lower than the environmental effect [38], [39].

Table 2. Full joint ANOVA including the partitioning of the G -x-E interaction of maize hybrids over 6 locations during 2017-18

Source of variation	df	Mean sum of square					
		DT	DS	PH	EH	TGW	YPH
Genotype(G)	17	98.76**	97.28***	1068.57***	1196.98	27.67***	3580
Environments(E)	5	99.68**	242.19**	42335****	21808.6**	19.96	59213**
Interaction(G×E)	85	7.94***	8.22**	207.94***	127.15	5.09	2954.9
AMMI component-1	21	4.58	3.94	111.81	41.98	0.35	326.27
AMMI component-2	19	1.86	1.81	60.15	28.24	0.25	233.01
AMMI component-3	17	0.91	0.87	59.50	18.21	0.05	166.31
Residuals	102	4.09	4.45	93.75	73.53	4.16	2182.9

Where, DT= Days to 50% tasseling, DS= Days to 50% silking, PH= Plant height(cm), EH= Ear height(cm), TGW Thousand grains weight(g), YPH= Yield (t/ha), ***P<0.001, **P<0.01, and *P<0.05

Performance of genotypes over different environmental locations

The mean values of all variables for the genotypes were measured and significant variations were observed among these across the locations. Highly significant variations were observed for almost all characters like days to tasseling, days to silking, plant height, ear height, thousand grains weight (Table S1), and grain yield (Table 3). Stability parameters i.e, regression coefficient (bi), and mean square deviation for the

yield of the individual genotypes are presented in Table 3. In the case of Hathazari, the highest yield was found at Kaveri 60 (12.27 t/ha) followed by 981(12.24 t/ha) and Sunshine (11.81 t/ha) which were statistically identical. In the case of Gazipur, the highest yield was found from Sunshine (11.24t/ha) followed by 9MS/S7-10×BIL-114 (11.09 t/ha) and Pac-60/S6-8×BIL-114 (11.02 t/ha) which were statistically similar with each other. At Jamalpur, the highest yield was found at Kaveri 60 (12.61 t/ha) followed by Sunshine (12.03 t/ha) and 981(11.87

t/ha). In the case of Bhurirhat, the highest yield was obtained from Sunshine (12.85 t/ha) followed by Kaveri 60 (12.72 t/ha) and 981(12.36 t/ha), which were statistically similar for the yield. At the location Rahmatpur, the highest yield was found

from Sunshine (12.55 t/ha) followed by BHM 9 (11.96 t/ha), and these provided an identical amounts of yield. In the case of Jessore the highest yield was found from Sunshine (12.04 t/ha), and same yield was found from Kaveri 60 (12.04 t/ha).

Table 3. Yield performance and stability of the eighteen genotypes over environmental locations

Sl No.	Genotypic Entry and Code		Yield(t/ha)						Mean Yield (t/ha)	Coeffi- cient (bi)	Mean square deviation
			Environments								
			Hat	Gaz	Jam	Bur	Rah	Jes			
1	BHM9 (Ch-1)	G1	11.04	8.74	11.05	11.93	11.96	11.32	11.17	1.38*	0.01
2	Pac-60/S6-3×CML-425	G2	10.52	10.42	8.77	9.57	9.02	8.23	9.42	0.59*	0.03
3	Pac-60/S6-5×CML-425	G3	7.63	8.07	7.86	8.70	7.75	7.16	7.86	0.86*	0.009
4	Pac-60/S6-8×BIL-114	G4	10.47	11.02	10.98	10.41	11.15	11.56	10.93	0.66*	0.005
5	981(Ch-2)	G5	12.24	10.03	11.87	12.36	11.77	11.32	11.60	1.00*	0.09
6	Pac-60/S5-14×BIL-113	G6	10.75	7.98	8.13	8.17	10.97	8.53	9.09	1.12*	0.04
7	Pac-60/S6-18×Utn/S5-18	G7	9.97	7.10	9.50	10.24	10.54	7.24	9.10	1.20*	0.03
8	Pac-60/S6-20×BIL-113	G8	9.56	8.86	8.02	9.03	9.07	7.66	8.70	0.85*	0.02
9	Sunshine (Ch-3)	G9	11.81	11.24	12.03	12.85	12.55	12.04	12.09	0.73*	0.05
10	Pac-60/S6-21×Utn/S5-10	G10	7.45	10.69	7.32	7.31	8.35	5.88	7.83	0.97*	0.22
11	9MS/S5-1×BIL-114	G11	10.29	9.24	10.61	11.15	10.47	9.83	10.27	0.87*	0.03
12	9MS/S7-2×BIL-114	G12	10.20	9.36	8.97	10.77	10.51	10.10	9.99	0.83*	0.01
13	Pioneer (Ch-4)	G13	11.45	9.23	10.73	11.03	11.23	11.04	10.79	2.04*	0.18
14	9MS/S7-9×BIL-114	G14	11.36	10.19	11.02	11.94	10.73	11.47	11.12	1.09*	0.002
15	9MS/S7-10×BIL-114	G15	8.56	11.09	9.89	10.77	11.05	8.13	9.92	0.79*	0.06
16	9MS/S7-12×BIL-114	G16	9.46	8.19	11.72	11.80	10.51	11.01	10.45	0.89*	0.07
17	9MS/S7-18×BIL-114	G17	9.54	9.38	10.67	10.30	7.64	9.26	9.47	0.77*	0.01
18	Kaveri 60 (Ch-5)	G18	12.27	7.04	12.61	12.72	11.27	12.04	11.33	1.27*	0.18
	Level of significant		***	***	***	***	-	***			
	CV (%)		21.53	9.65	25.98	23.77	35.80	36.67			
	Lsd (0.05)		4.70	2.11	5.65	5.38	8.75	7.81			

***P<0.001, **P<0.01, and *P<0.05

Genotype×environment interaction analysis using GGE biplot analysis

The significant mean sum squares of genotype (G) × environment (E) interactions for grain yield over the six test environments showed a meaningful role to evaluate the performance of genotypes in variable locations. For the identification of accurate performance of the genotypes, GGE biplot method is best. In the graphical analysis, PC1 (horizontal axis) represented the main effect of the genotypes, while PC2 (vertical axis) specified the genotype × environment interaction (G×E). Numerical values of PC1 and PC2 were found as 43.96% and 24.2%, respectively, and these two principal components interpreted as 68.16% of the entire variation in yields (figures 1 to 6). They also revealed that the PC1 score was above zero, indicating the studied genotypes were efficient

in terms of yield potentiality [30], [40]. PC1 explained the variation among the calculated yield while PC2 illustrated the genotype stability over the environments [41], [42]. GGE biplot is a statistical tool using for identifying appropriate genotypes for an appropriate mega- environments. The GGE biplot explained the superior genotypes to the appropriate mega-environments vividly by “which-won-where pattern” of the GEI[19], [43], [44].

The GGE biplot generates an asymmetrical polygon and vertical lines from the starting point [21], [45]. These vertical lines split the biplot into several sectors. Here, in the case of this experiment, six lines (Figure. 1) split the biplot into six specific divisions but all environments covered by four of them. G6, G10, G15, G16, G17, and G18 were identified as vertex genotypes. Genotypes of vertexes were found as the most

responsive as they are remaining remote from the source [22]. However, for mega-environments cultivars of the vertex of the segment are treated as the superior [20], [46], [47]. In this experiment, only one environment (Gazipur) was found in the first mega environment and the genotypes for this environment were G2, G4, G10, and G15, suggesting that this genotype was performing best in this environment. Rahmatpur and Hathazari environments were detected in the second mega-environment and G6, G7, G8, G12, and G13 were found in these environments also performed well. The third mega-environment was covered Jessore and G1, G5, G14, and G18 were found as vertex genotypes, but the performance of these were not so good. Again, in the fourth mega-environment resided two environments which were Jamalpur and Burirhut where G9, G11, and G16 genotypes performed well. On the other hand, genotypes G3 and G17 were not suitable for any environment as these hybrids were found less adaptation ability to the research areas.

Typical environment should have the minimum two criteria for cultivating any crop. One of these is to be highly preferential to the varieties while another should be representative of aim location [48]. Exploitation of variance within the postulant varieties for used locations can be done by state of discrimination [31], [49]. Besides this, representativeness expresses the area which represents situation of other areas [9], [48]. High yielding genotypes with good stability to the environments can be easily determined from field experiments by appropriate use of GGE biplot as it was followed in this study.

9=Sunshine, 10=Pac-60/S6-21×Utn/S5-10, 11=9MS/S5-1×BIL-114, 12=9MS/S7-2×BIL-114, 13=Pioneer, 14=9MS/S7-9×BIL-114, 15=9MS/S7-10×BIL-114, 16=9MS/S7-12×BIL-114, 17=9MS/S7-18×BIL-114, and 18=Kaveri 60

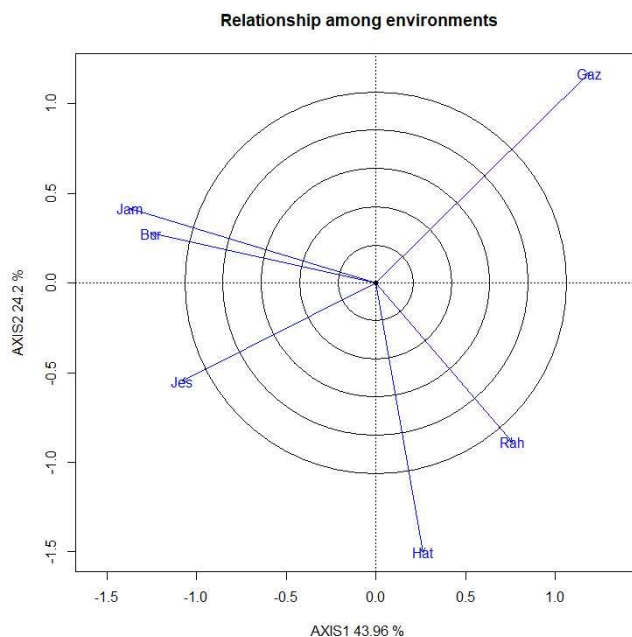


Figure. 2. Vector view of the GGE biplot showing relationships among locations. Locations: Gazipur (Gaz), Jessore (Jes), Jamalpur (Jam), Rahmatpur (Rah), Hathazari (Hat), and Bhurirhat (Bur)

Relationship among environments (test locations)

Yield of the studied maize hybrids exhibited significant variation in all environments. In GGE biplot (Figure. 2), the vector expresses the interlink relation among the environments and vectors of biplot origin to markers for the environments. Angles between the vectors of environments reveal the correlation coefficient of them [50]. The short angle bears the highest correlation to the environments [22], [51]. Near-zero correlations were found between Rahmatpur Gazipur and Rahmatpur Jessore environments. Positive correlation coefficient indicates the angle is less than 90° between the environments [50]. Positive correlations among Jamalpur, Bhurirhat, and Jessore, as well as Rahmatpur and Hathazari locations were also observed. On the other hand, a negative relationship was found between Gazipur and Jessore. From the analysis of the vector of GGE biplot, the six environments were clustered into four groups: only Gazipur constituted the first group, then Rahmatpur and Hathazari in the second group, only Jessore as the third group while as Jamalpur and Bhurirhat resided as the third group (Fig. 2). Similar trends of relationships were also recorded in several other researches[30], [47], [52].

Discriminating ability of the locations and representativeness

The capacity of an environment to make out a typical environment is called the discriminating ability of an

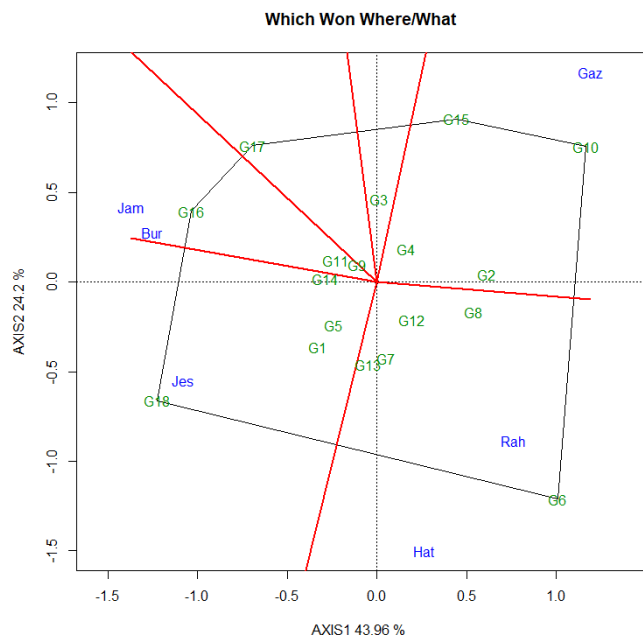


Figure. 1: “Which won where” GGE Biplot for eighteen maize genotypes. Environments: Gazipur (Gaz), Jessore (Jes), Jamalpur (Jam), Rahmatpur (rah), Hathazari (Hat), and Bhurirhat (Bur) Genotypes: 1=BHM 9, 2=Pac-60/S6-3×CML-425, 3=Pac-60/S6-5×CML-425, 4=Pac-60/S6-8×BIL-114, 5=981, 6=Pac-60/S5-14×BIL-113, 7=Pac-60/S6-18×Utn/S5-18, 8=Pac-60/S6-20×BIL-113,

environment [53]. Distances between the markers to the biplot origin determine it for the environment [54]. Representativeness is the power of a test environment to correspond to the mega-environment [53]. It is measured with the extent of the vector from the pointer of the environment to the axis of the average environment coordinate (AEC) [54]. Direction of the average environment axis (AEA) determined by the small circles and the arrow point of vector [22]. Longer vectors of environments carry more information about the genotypes than shorter vectors. Short vectors of test environments show weak correlation with those of long vectors. Therefore, the short vectors of jes, Bur, and jam environments could be determined as exclusive environments without any restriction for research. Thus, these become meaningful research environments. gaz is the most discriminative environments followed by hat for the cultivars as long-vector test environments. gaz had the largest opposite vector but creates small angles with the AEC abscissa. It means this location might be excluded for the evaluation of better hybrid maize genotypes, but it could be used to remove unstable hybrids. Moreover, close links among test environments having more or less similar information can be found in few environments. Hat was found highly discriminating because it was in long distance, but it revealed the minimum representative as it made a large angle with the AEC abscissa. rah had the short vector but the right angle to the AEC abscissa, which also indicated lower discrimination and representativeness. jes, Bur, and jam, and locations carry almost the same information of genotypes as these environments remain closely. Therefore, a potential single cross hybrid would be better for the expected yield over these areas. This view of biplot (Figure 3) sharply recommends that incase of discriminating and representativeness the environment of jes is better than hat. Therefore, another hybrid may be selected for this location. Test locations Jam and Bur were highly correlated according to their ranking. Hence, a promising intermediate hybrid is recommended to this mega-environment in this study. Jes appeared as a more representative location than Bur. Hence, jes has been branded as a typical environment followed by Bur and Jam in Bangladesh. Order of ranking the test locations according to their discriminating and representativeness were as follows: Jes, Bur, Jam, Hat, Rah., and Gaz.

Means vs. stability

Mean grain yield and its stability for all the genotypes have been visualized by GGE biplot (Figure 4). ATC abscissa on horizontal lines based on mean performance over the environments determined the rank and order of hybrids. This figure of AEC is the observation of the GGE biplot. The perpendicular line splits genotypes into below-average means and above-average means. Projections of their markers on the average tester axis numerated the mean yield of varieties. Just in the center of the horizontal line indicates the varietal stability. Longer length of the vector indicates less stability. Therefore, G18 was the highest yielding followed by G1, G5, G14, G13, G11, G7, G9 while hybrid G10 was the lowest yielding. Genotypes having the shortest vector from the AEA

are the most stable. Thus, among the tested hybrid maize, genotypes G14, G2, G9, and G11 are more stable, whereas genotype G6 is the most unstable. Although, the genotype G1 identified as a stable genotype but it had below average yield, suggesting it may not be a good variety. Again, genotype G18 was the highest yielding but with lower stability. Therefore, genotypes G14, G11, and G9 in a were more favorable genotypes based on both mean yield and stability aspects.

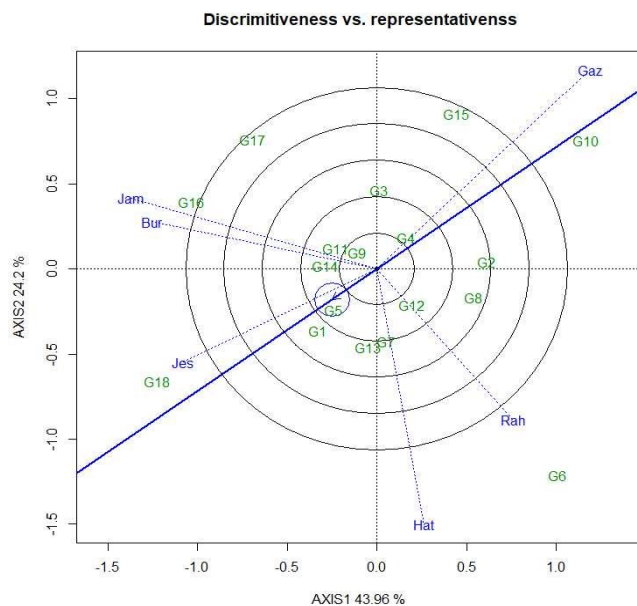


Figure 3. The discriminating ability and representativeness of the test locations. Locations: Gazipur (Gaz), Jessore (Jes), Jamalpur (Jam), Rahmatpur (rah), Hathazari (Hat), and Bhurirhat (Bur)

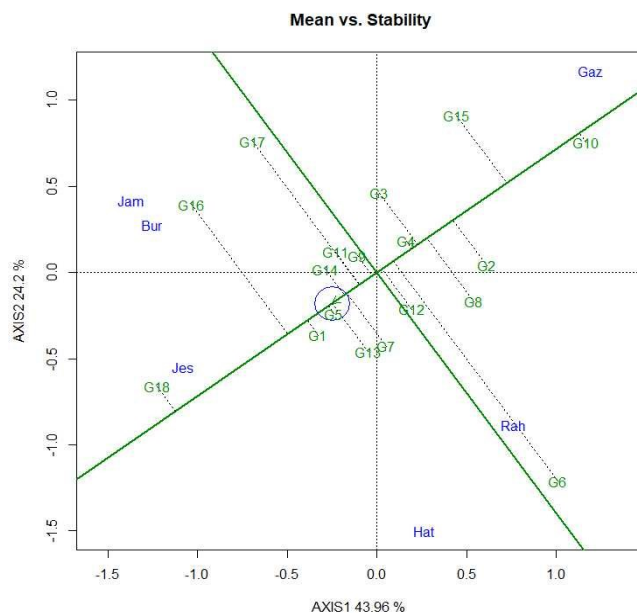


Figure 4. Means vs stability biplots of 18 hybrids lines including 5 checks were assessed at six locations in Bangladesh. Locations: Gazipur (Gaz), Jessore (Jes), Jamalpur (Jam), Rahmatpur (rah), Hathazari (Hat), and Bhurirhat (Bur).

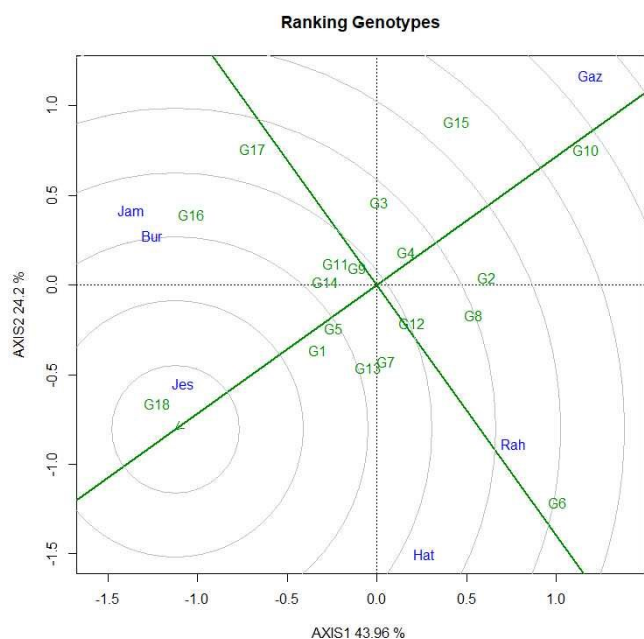


Figure 5: The average environment coordination (AEC) view for ranking genotypes in comparison to an ideal genotype (the center of the concentric circle)

Ranking of the maize hybrid genotypes to determine an ideal genotype

In the GGE biplot analysis, an ideal genotype is characterized as to have both high mean yield and high stability (Yan and Tinker 2006). From this point of view, the origin and average point of the genotypes are interlinked and continues to both sides [30]. The ideal genotype resided at the center of the concentric circles (Figure 5). In the present research, the genotypic ranking was represented by comparing with the ideal genotype. The best genotype was identified as that which were closer to the position of the ideal genotype. Here, the entries G18, G1, G5, G13, and G14 were close to the ideal genotype, which were considered as ideal genotypes considering the yield potential and stability in comparison with other studied hybrid maize genotypes.

Location ranking to determine an ideal environment for all genotypes

The ranking of the ideal environment for a certain genotype (s) represented by the GGE biplot discrimination and representativeness, where the center of the concentric circles of the polygon showed the ideal test environment. An Ideal test environment is a point on the AEA in the positive direction (“most representative”) with the longest environment vector from the biplot origin in the GGE biplot[22]. An ideal test environment is both the most discriminating (informative) and the most representative of the target environment[52]. In our research, Jessore is the closest to the ideal environment point, therefore, it was the best, whereas Gazipur and Rahmatpur were in the farthest from the ideal environment. Thus, these two environments were the worst for the selection of genotypes to be adapted to the country.

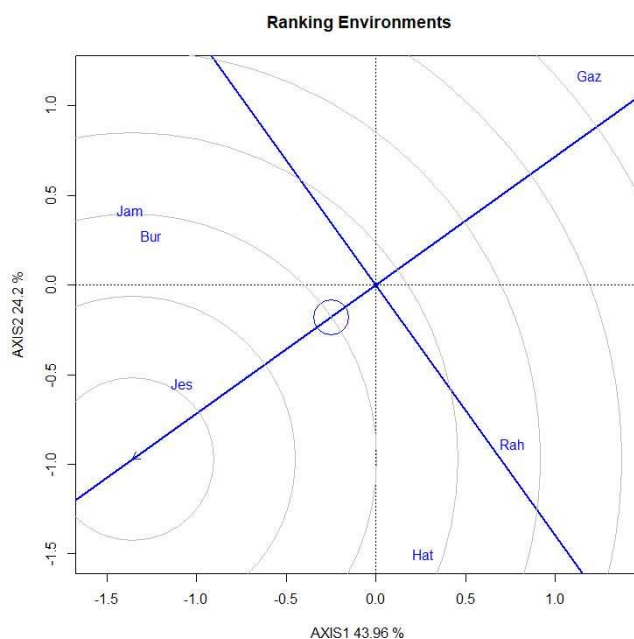


Figure 6: Environment ranking to determine an ideal environment for all maize hybrid genotypes during 2017-2018

IV. CONCLUSION

$G \times E$ interactions controlled the ranking of the genotypes over the locations and evaluated some genotypes were better for some locations than others. The performance of the tested maize hybrid genotypes was significantly influenced by the six environmental locations. Among the environments, Jessore was found as the best of the studied genotypes and Gazipur was the most unfavorable one. Considering the mean yield, G18(Kaveri 60) was the best performer, whereas the G10(Pac-60/S6-21×Utn/S5-10) was the lowest yielding. Again, G14 (9MS/S7-9×BIL-114) was the most stable, while the G6 (Pac-60/S5-14×BIL-113) was the most unstable one. However, considering the mean yield and stability, G9(Sunshine), G11(9MS/S5-1×BIL-114), and G14(9MS/S7-9×BIL-114) were selected for all locations.

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CONFLICT OF INTERESTS

The authors declare that they have no conflict of interest.

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