Research Article

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Evaluation of yield stability of seven barley (*Hordeum vulgare* L.) genotypes in multiple environments using GGE biplot and AMMI model

Abstract: Evaluation of genotypes under multiple environments is the prerequisite for the development of stable and superior genotypes for sustainable barley production and a changing climate. GGE (G, genotype and GE, genotype (G) by environment (E), interaction) biplot and the AMMI (The Additive Main effects and Multiplicative Interaction) model are the effective methods to find out the genotype(s) which are stable and suitable to cultivate in specific or multiple environments. The experiment was conducted to analyze the performance of seven barley genotypes for selecting stable and superior genotypes across three different environmental conditions of Bangladesh (i.e., at the Bangladesh Agricultural Research Institute (BARI), Gazipur; at the Regional Agricultural Research Station (RARS), BARI, Jamalpur and at the RARS, BARI Ishurdi). All genotypes in three locations were arranged in a randomized complete block design (RCBD) with three replications. After two years observation, it was found that all genotypes across the location were found highly significant (p≤0.01), due to the variation of environments, genotypic variability and their interaction. The first two principle component axes (PC1 and PC2) of site regression model were significant (P≤0.01) and cumulatively contributed to 89.65% of the total GE interaction. In the polygon view of biplot, there were five rays which divided the biplot into five sectors, and all three locations fell into two of these five sections. Location Jamalpur fell into sector 1, whereas Ishurdi and Gazipur fell into sector 2. Among the locations, Ishurdi was found the best for all genotypes, where Gazipur and Jamalpur were found unfavourable. Among the genotypes, 'E7' performed

the best for the average grain yield (GY) followed by 'E3', 'E2' and 'E4', whereas 'E1' had lowest average GY for all locations. The highest yield in environment Jamalpur was obtained by the genotype 'E2', on the other hand genotype 'E7' produced the highest GY in locations of Ishurdi and Gazipur. Considering yield stability, genotypes 'E3', 'E4' and 'E1' were found to be more stable, whereas genotype 'E2' was the most unstable over all locations. Genotypes 'E7' and 'E3' were found to be close to the ideal genotype position, in the case of the maximum GY and yield stability across the locations as compared to other genotypes and recommended for commercial cultivation for Bangladesh including South-Asia.

Abbreviation

AMMI, The Additive Main effects and Multiplicative Interaction; AEZ, Agroecological Zone; ANOVA, Analysis of variance; BARI, Bangladesh Agricultural Research Institute; GGE, the genotype main effect (G) and the genotype × environment interaction (G × E); GY, Grain yield; PCA, principal component analysis; PC1 and PC2; principle component axes; RARS, Regional Agricultural Research Station; RCBD, Randomized Complete Design.

1 Introduction

Among the cereals, barley is the firstborn domesticated food-cereal across the globe (Wang et al. 2015). In Bangladesh, barley is a minor cereal crop and mostly grown in the northern part of the country during rabi season. However, due to the lack of improved variety, this crop is not widely accepted by farmers as compared to other cereals. Therefore, it is necessary to develop varieties having high yield and desired characteristics.

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In this regard, a multi-location yield trial is an essential tool for variety adaptation because of the presence of genotype and environment interactions. Genotype x environment interaction is considered to be a feasible method for plant breeders and agronomists to study the genotype effect and the interaction between genotype and environment simultaneously.

The GGE biplot analysis (i.e., the genotype main effect (G) and the genotype × environment interaction (G×E) (Frutos et al. 2014; Hossain et al. 2018) is a useful tool for plant breeders and geneticists to find out the maximum yield and stable genotypes across the multiple locations; as well as to find out the most favourable location for a specific genotype through acquiring a graphical form (Gabriel 1971; Yan and Kang 2002; Koutis et al. 2012). The stability obtained by this method is widely used to characterize a genotype, performing a relatively stable yield and not even affected by altering the environmental conditions (Kiliç 2014). In all of the barley improvement activities and research, GEI (genotype × environment interaction) is of major importance as well as for other crops (Voltas et al. 2002). The stability methods can be categorized as parametric (univariate and multivariate) and non-parametric stability measures. Univariate and nonparametric stability statistics cannot generate an accurate picture of the complete response pattern, due to the multivariate nature of the genotype's response under different environments (Kılıç 2014).

Hence, the AMMI model with multivariate statistics is better than the univariate stability methods to explain GEI (Kılıç 2014). To interpret GEI, the AMMI model provides multivariate analytical parameters (Ebdon and Gauch 2002). The AMMI model is considered as the main component to provide accurate yield estimation while main effects and interaction are both equally important (Zobel et al. 1998). Combining of ANOVA and principal component analysis (PCA) into a joint method is possible by AMMI model. The vital characteristic of this analysis is that the adjustment is accomplished by information from other locations to perfect the estimates within a given locations (Sadeghi et al. 2011). It eliminates residual or noise deviation from GEI (Crossa et al. 1990). It has no explicit experimental design requirements, except for a two-way data structure (Zobel et al. 1988). The usefulness of the AMMI model has been used widely by many scientists for a long time (Zobel et al. 1988; Yan and Rajcan 2002; Kaya et al. 2002; Mahalingam et al. 2006; Rodriguez et al. 2007; Bantayehu 2009; Ilker et al. 2009; Banik et al. 2010;

Muhe and Assefa 2010; Mandry et al. 2012). Therefore, the major objectives of the study are to figure out the acclimatization of barley genotypes using the AMMI model to assess the significance of the GE interaction of yield, identify the mega-environments, determine the best performing genotype in each mega-environment, and to discuss the implication of the GE interaction to barley breeding.

2 Materials and Methods

2.1 Location

The present study was carried out in three multiple environments of Bangladesh: (i) at the Bangladesh Agricultural Research Institute (BARI-Gazipur, geographical position: 23°59'19.21" N, 90°24'36.65" E; 13.1 masl) under the agro-ecological zone 28 (AEZ–28) (i.e., Modhupur Tract); (ii) at the Regional Agricultural Research Station (RARS-Jamalpur, geographical position: 24°56'6.14" N, 89°55'56.86" E; 21.6 masl), under the AEZ–9 (i.e., Old Brahmaputra Floodplain) and (iii) at the RARS-Ishurdi, geographical position: 24.03° N; 89.05° E; 16 masl, under the AEZ-11 (i.e., High Ganges River Floodplain) (FRG 2012).

2.2 Environmental condition during growing season

Meteorological data on weekly average maximum, minimum and mean temperatures and total rainfall were documented during crop growth stage and presented in Figure 1. For recording the meteorological data, particularly the weekly average maximum, minimum and mean temperature, HOBO U12 family data loggers was set in all three locations of BARI-Gazipur, RARS-Jamalpur and Ishordi during crop season; where raingauge was used to calibrate the total rainfall.

2.3 Experimental materials, treatments and design

Seven barley genotypes were used as experimental materials. All genotypes in three locations were arranged in a randomized complete block design (RCBD) with three replications. Detaileddescriptions for all barley genotypes with their pedigree are presented in Table 1.
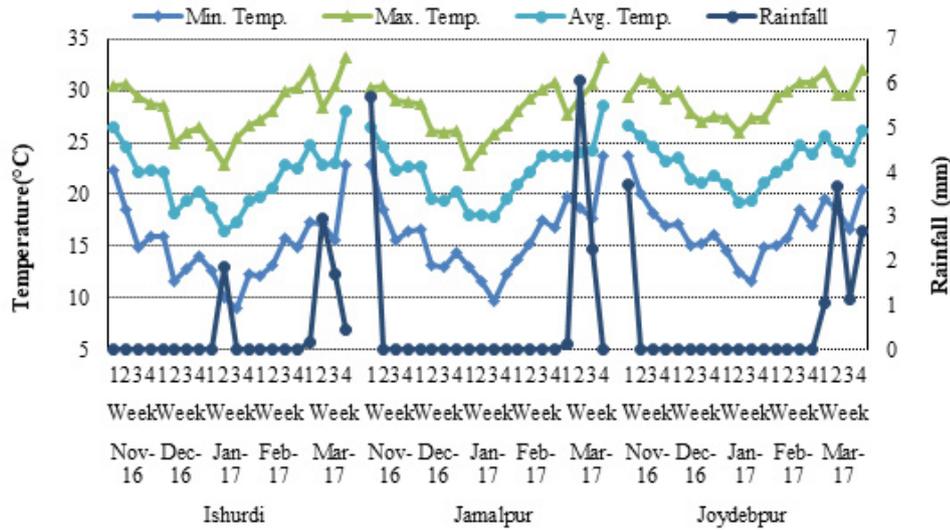
Figure 1: Meteorological condition during (2016-2017) crop growth stages in three locations

Table 1: Seven barley genotypes and their pedigree, evaluated under different environments

Entry		Cross/pedigree
E1		INBYT-HI/15
E2	BHL-15	IBON/96-163×Karan-19
E3	BHL-25	BHL14×BB-5
E4	BHL-26	BB-7×BB-5
E5	BHL-27	BHL-15×BB-4
E6	F_6	BHL-10×BB-1
E7	BB-7	E-21 MRA×Karan-351

2.4 Field experiment

Seeds of all barley genotypes at the rate of 200 seeds m^{-2} were sown on early November in both years. Seeds were sown in line by hand, where row to row distance was 25 cm. Each plot consisted of ten rows with 5 m long rows. Before sowing, 500 liters of water were applied in each plot for proper and uniform germination. For proper growth and development, four irrigations were done in all three locations (i.e., first irrigation was applied at tilling stage, second was at stem elongation, third at flowering, and fourth irrigation was applied at grain filling stages). Weeds were controlled manually by hand.

2.5 Data collection

In each plot with an area of 3 m long, 10 middle rows were harvested at full maturity to avoid border effects. Then sample crops were bundled and tagged separately and

dried in bright sunshine. After that, they were manually threshed separately on a threshing floor. Data on GY was adjusted at 12 % moisture (according to Hellevang 1995):

$$Y(M_2) = \frac{100 - M_1}{100 - M_2} \times Y(M_1)$$

where, Y (M_2), grain weight at 14% moisture; Y (M_1), grain weight at actual moisture %; M_1, actual moisture % and M_2, expected moisture %.

2.6 GGE Biplot and AMMI Model

2.6.1 GGE biplot analysis

The GGE biplot analysis (i.e., the genotype main effect (G) and the genotype × environment interaction (G×E) (Frutos et al. 2014; Hossain et al. 2018) is a useful tool for plant breeders and geneticists to find out the maximum yield and stable genotypes across multiple locations; as well as to find out the best favourable location for a specific genotype through acquiring a graphical form (Gabriel 1971; Yan and Kang 2002; Koutis et al. 2012).

2.6.2 AMMI Model

Duarte and Vencovsky (1999) first proposed the AMMI (The Additive Main effects and Multiplicative Interaction) analyses. The AMMI model is the most effective method to find out the genotype(s) which are stable and suitable to cultivate in a specific or multiple environments (Zobel

et at. 1988). Thus, the mean response of the genotype i in environment j (Yij) is modeled by: Yij = μ + gi +aj +∑λkyikαjk +ρij + eij.

According to Eberhart and Russel (1966), regression coefficient (bi), deviation from regression (S²di) and the stability parameters were also estimated through the AMMI model.

2.7 Statistical Analysis

Before the GGE biplot and the AMMI model analysis, data on GY for all genotypes across locations were examined by R package (version 2.15.3) at the 5% level of significance (R Core Team 2013).

Ethical approval: The conducted research is not related to either human or animal use.

3 Results and Discussion

3.1 Agro-ecological condition during crop stage

Soils under AEZ-28 were found to be weakly acidic, AEZ-9 were strongly acidic, and AEZ-11 were found to be neutral, respectively, while organic matter and total nitrogen were found low across all three AEZs. Phosphorus (P) in AEZ-9 was found to be high, but in AEZ-28 and AEZ-11 was very low. Potassium (K) and three essential micronutrients such as S, B and Zn concentration in soils were below the critical levels.

In both growing seasons, the climatic conditions, particularly temperature and rainfall of all three locations (AEZs), were found to be different during the crop growth stage. While the monthly average maximum temperature varied from 25 to 35°C, and the monthly average minimum temperature was varied from 10-11°C (Figure 1). Similarly, total rainfall was also varied during the crop growth stage.

3.2 Mean grain yield (t ha⁻¹) of seven barley genotypes tested across three environments

To find out the maximum yield and stable genotypes across the three locations; as well as to find out the best favourable location for a specific genotype the GGE biplot analysis was used to acquire a graphical form (Table 2). Results revealed that there were significant (p ≤ 0.001) variations for genotype, environment and also for genotype × environment interaction (Table 2). The percentages of total sums of squares considered for genotype, environment and GE interactions were treated as a determinative of variation imposed on barley grain yield. The biplot analysis of the variance of barley grain yield of seven genotypes examined in three environments exhibited that 49.50% was environmental effect whereas 26.24% was genotypic effect and 24.26% was GE interaction effect (Table 2). From this result, the effect of environment was expected to be high because the environment was responsible for 49.50% of the total variation for grain yield. Therefore, tested locations in this experiment were diverse for the barley grain yield and a large part of variation in barley grain yield might have resulted from change in environment. The result was in agreement with Kendal (2016) where he found a high environmental effect by GGE biplot analysis of barley grain yield using four cultivars in eight environments. It was reported that high environmental effects were found in wheat (80%) and soybean (59%) (Yan and Kang 2002). Several other researchers also found high environmental effects in different crops such as wheat and oilseeds (Brar et al. 2010; Mohammadi and Amir 2011; Letta et al. 2008;

Table 2: Combined analysis of variance of grain yield of barley genotype examined in three locations

SOV	Df	Sum Square	Mean Square	F value	Pr(>F)	% GE
Environment (E)	2	487.96	243.981	229.1073	2.159e-06 ***	49.50
Rep(E)	6	6.39	1.065	0.2287	0.9646326	
Genotype (G)	6	258.70	43.117	9.2597	3.778e-06 ***	26.24
G×E	12	239.20	19.933	4.2808	0.0003361 ***	24.26
Residuals	36	167.63	4.656			
PC1	7	151.59986	21.65712	4.65	0.0009***	
PC2	5	87.60014	17.52003	3.76	0.0077**	

Df = Degrees of freedom; GE = genotype by environment interaction; *, **, and *** indicate at the levels of 5%, 1% and 0.1%, respectively

Dash and Pandey 2009; Sing et al. 2009).

Grain yield for all genotypes were significantly varied in three locations. Genotype 'E7' gave the highest yield in locations Gazipur and Ishurdi, whereas genotype 'E2' gave the highest yield for Jamalpur. Generally, the highest yield in all environmental conditions was obtained by the genotype 'E7' and the lowest was obtained from genotype 'E1' (Table 3). In case of the tested locations, the environmental condition of Gazipur was found to be better than the other two locations.

3.3 Environmental specific genotype ranking

A polygon view was produced by using the GGE biplot analysis to show which genotype better in which environment for grain yield of barley. A graphical analysis (Figure 2 to 5) was generated by GGE biplot analysis to find out the maximum yield and stable genotypes across three locations; as well as to find out the best favourable location for a specific genotype. In the graphical analysis, PC1 (the horizontal axis) symbolizes the main effect of genotype,

Table 3: Mean grain yield (t ha⁻¹) of seven barley genotypes tested across three environments

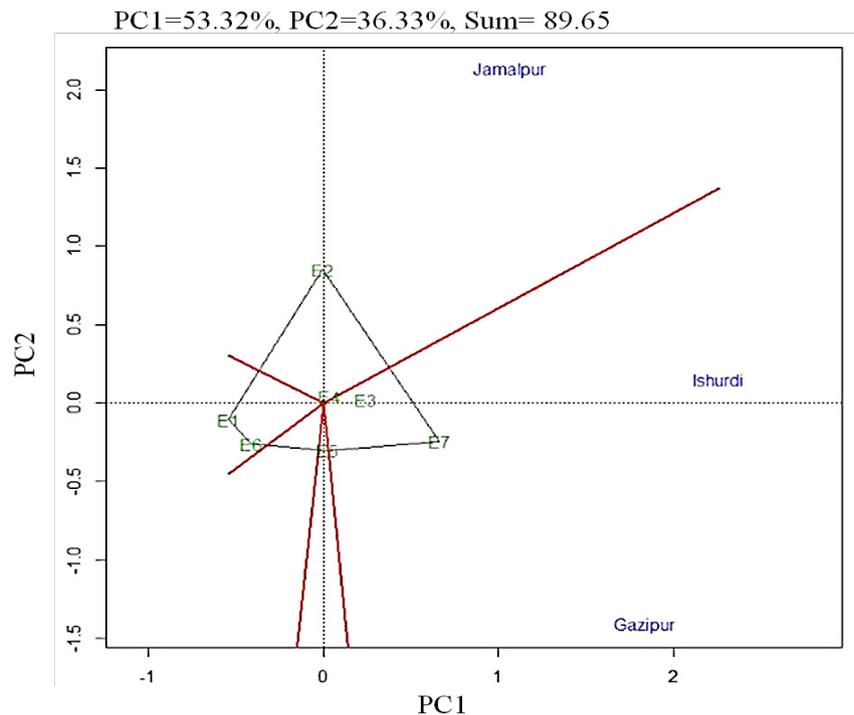| Genotypes	Locations			
	Gazipur	Ishurdi	Jamalpur	Mean
E1	7.93	3.63	1.3	4.29
E2	7.87	7.87	7.87	7.87
E3	11.07	10.3	4.2	8.52
E4	9.47	10.1	3.2	7.59
E5	12.47	4.83	3.13	6.81
E6	9.2	4.1	1.1	4.8
E7	13	15.47	3.53	10.67
Mean	10.14	8.04	3.48	

Figure 2: Polygon view of the GGE biplot to show which genotype better in which environment for grain yield of barley

while the PC2 (vertical axis) specifies the genotype × environment interaction (G×E) (Figure 2 to 5). These charts represent 89.65% of the total data variance with 53.32% and 36.33% of total variance for PC1 and PC2, respectively. Arshadi et al. (2018) revealed that the performance of different genotypes and their interaction with multiple environments may be obtained by the factors PC1 and PC2, by using GGE biplot analysis. They also stated that the PC1 score was above zero, indicating testing genotypes were efficient regarding yield potentiality (Arshadi et al. 2018).

In the GGE biplot analysis, a polygon view is used to identify better genotypes in specific environment by a
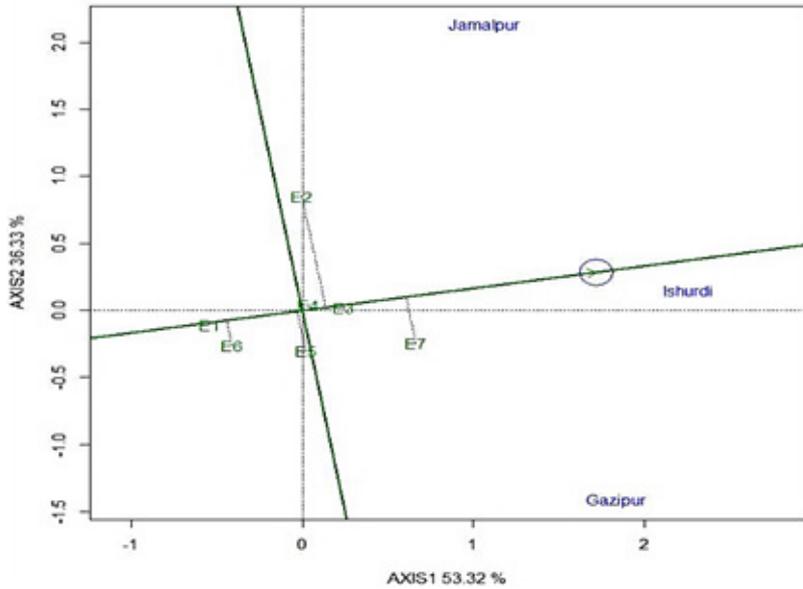

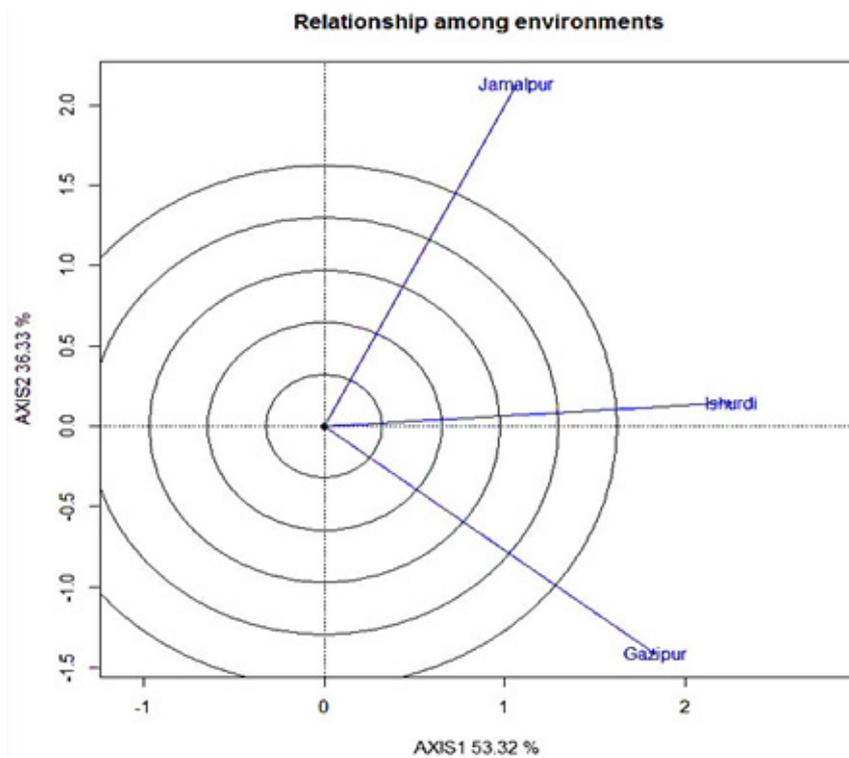**Figure 3:** Mean performance and stability of seven genotypes and specific genotype by environment interactions

Figure 4: Vector view of GGE biplot analysis for relationship among three locations
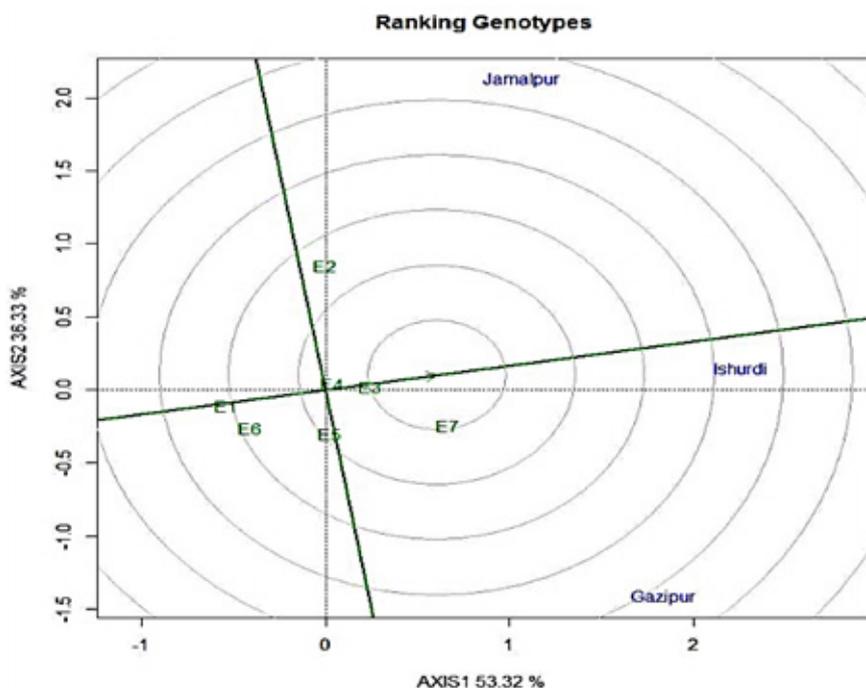
Figure 5: The average-environment coordination (AEC) view to rank genotypes relative to an ideal genotype (the center of the concentric circles)
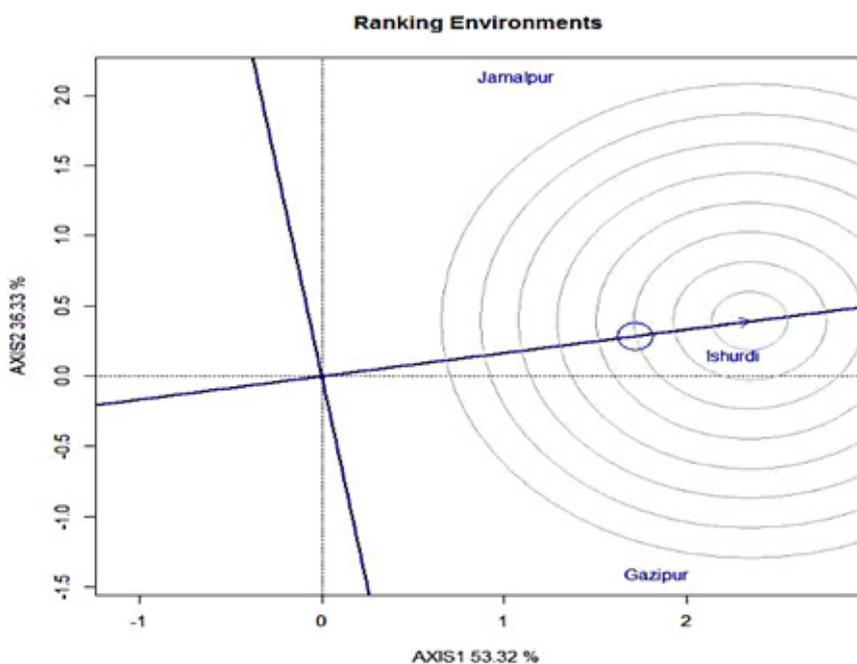

Figure 6: The discrimination and representativeness view of the GGE biplot to rank test environments relative to an ideal test environment (represented by center of the concentric circles)

"which wins where" structure. The polygon is formed by connecting the furthest genotypes from the biplot origin after then lines are drawn perpendicular to the sides of the polygon so they pass through the origin. These perpendicular lines divide the biplot into some sectors. According to the polygon view of GGE biplot shown in Figure 2, the vertex genotypes of the polygon are the most favorable genotypes for a particular environment (Ding et al. 2007; Yan 2002; Hossain et al. 2018). In this Biplot, five perpendicular lines divide the biplot into five sectors and the locations fell into two of them. Location Jamalpur fell into sector 1 with the most favorable genotype 'E2' whereas

Ishurdi and Gazipur fell into second sector with the most favorable genotype 'E7'. The rest vertex genotypes 'E1', 'E5' and 'E6' were the poorest yielding (Figure 2).

3.4 Mean yield performance and yield stability across the multiple environments

Mean yield performance and yield stability in the biplot diagram for all seven barley genotypes are shown in Figure 3. In the biplot diagram, the line passing through the biplot origin and the average of the first and second principal components of environments from lower left to upper right is called average environment axis (AEA) with an arrow indicating the positive end of the axis (Ding et al. 2007; Arshadi et al. 2018). Where the line passing through the biplot origin and is perpendicular to the average environment axis is called the stability of genotypes. The mean yield performance of all genotypes is estimated by the projections of their markers to the average environment axis. Genotypes with higher positive values on the average environment axis have the highest yield. Therefore, tested genotypes were divided into two groups (a) genotypes with above average yield and (b) genotypes with below average yield. Thus genotype 'E7' had the highest average grain yield followed by 'E3', 'E2' and 'E4', whereas 'E1' had the lowest average grain yield for all locations (Figure 3). Genotypes having the shortest vector from the average environment axis are the most stable. Thus, among tested genotypes 'E3', 'E4' and 'E1' are more stable whereas genotype 'E2' is the most unstable. Although, the genotype 'E1' falls into the stable group of genotypes but it showed below average yield suggesting it may not be a good variety. Therefore, indicated genotypes 'E3' and 'E4' in Figure 3 were more favorable genotypes based on both mean yield and stability aspects.

3.5 GGE biplot analysis for relationship among three locations through Vector

Results of the interrelationships among tested three locations are shown in Figure 4. In GGE biplot analysis, interrelationships among environments are evaluated by a vector view of environments. Connections of test environments and biplot origin are called environment vectors. The angle between two environment vectors shows relationship of them. The cosine of the angle between the vectors of two environments estimates the correlation of the respective environments (Yan and Tinker 2006; Kendal 2016).

The distance between two environments measures their dissimilarity in discriminating the genotypes (Yan and Tinker 2006). A strong crossover of GE is indicated by the presence of a wide obtuse angle among test environments (Yan and Tinker 2006). Here the largest angle is slightly larger than 90° between Gazipur and Jamalpur indicating that the GE is moderately large. Positive and negative correlations occurred when the vector angle of two environments is less than 90° and greater than 90° whereas a right vector angle shows no relationship between two environments (Yan and Tinker 2006). According to this interpretation, Gazipur-Ishurdi and Ishurdi-Jamalpur are positively correlated whereas Gazipur-Jamalpur is negatively correlated (Figure 4).

3.6 Genotypes ranking to find out an ideal genotype (the center of the concentric circles)

In the GGE biplot analysis, an ideal genotype is a virtual genotype which should have both high mean yield and high stability (Yan and Tinker 2006). In this purpose, origin and average point of genotypes are connected and continues to both ends (Arshadi et al. 2018). The position of the ideal genotype is at the center of the concentric circles (Figure 5). In our study, ranking of genotypes was shown by the comparison with the ideal genotype. The best genotype is a genotype which is closer to the ideal genotype position. Thus, genotype 'E7' and 'E3' which were close to the ideal genotype position, were considered as ideal genotypes in our study in terms of yield capacity and stability compared to other genotypes.

3.7 Locations raking to find out an ideal environment for all genotypes

The discrimination and representativeness of the GGE biplot generally shows the ranking of an ideal test environment for a specific genotype or over all genotypes through representing by center of the concentric circles in a polygon view. In GGE biplot, an Ideal test environment is a point on the average environment axis (AEA) in the positive direction ("most representative") with the longest environment vector from the biplot origin (Yan and Tinker 2006). An ideal test environment is with both the most discriminating (informative) and also most representative of the target environment. Figure 6 shows an "ideal test environment", which is the center of the concentric circles. Ishurdi is the closest to the ideal environment point,

therefore, it was the best, whereas Gazipur and Jamalpur were the poorest for selecting genotypes adapted to the whole region.

4 Conclusions and recommendation

In conclusion, the performance of tested barley genotypes were influenced significantly by all three locations. Among the locations, Ishurdi was found to be the best for all genotypes, where Gazipur and Jamalpur were found unfavourable. Among the genotypes, 'E7' had the highest average grain yield followed by 'E3', 'E2' and 'E4', whereas 'E1' had lowest average grain yield for all locations. Considering yield stability, genotypes 'E3', 'E4' and 'E1' were found more stable, whereas genotype 'E2' was the most unstable. Genotypes 'E7' and 'E3' were found closely to the ideal genotype position and considered as ideal genotypes in terms of yield capacity and stability as compared to other genotypes.

Conflicts of interest: The authors declare no conflicts of interest.

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