

Grain yield stability analysis using AMMI and GGE biplot models in different breeding zones of Bangladesh

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Abstract

During the 2018-2019 Boro season (dry season), 70 rice genotypes were examined with alpha lattice experimental design with the goal of measuring grain yield stability analysis. Results indicated that AMMI analysis explained 100% of the G×E variance, while captured 81.74% variance. Based on the GGE and AMMI analysis, the most stable and high yielding genotype was identified G41 followed by G22, G26, G58, G24 and G61. The AMMI 1 biplot analysis revealed that the first primary component of interaction (IPC1) factor was responsible for 64.2 % variation due to G × E interaction. On other hand, the second primary component (PC2) factor accounted for 35.8% variation of the G × E interaction. These two-primary component (PC1 and PC2), all together accounted for 100% variation of the G × E interaction. The contribution of G68 was highest to the interaction followed by G70, G58, G42, G61, G45, G38, G14, G33, G60, G53, and G9. Best environment analysis indicated that the ranking was Rajshahi < Gazipur < Cumilla. GGE biplot analysis accounted for 81.74% variation comprising two principal components PC1 and PC2 with 45.62% and 36.12% variations respectively. Rajshahi was more stable than Gazipur. Based on environment analysis genotypes, G22, G26, G58, and G44 can be recommended as best stable genotypes that breeding zone. However, the genotype G61 was identified adapted to Cumilla breeding zone.

Introduction

Rice belongs to the genus *Oryza* is the staple food for the one-third population of the world. Its productivity improvement is one of the main pillars of food security, particularly for Asia and Africa (Suela et al., 2019). It is a good source of calorie (one fifth) and protein (15%) (Rashid et al., 2017). In rice breeding, there is a conflict of interest in most of the breeding program between enhancement of yield potential and breeding for other desirable agronomic traits and biotic and abiotic stress related traits., Therefore, the main objectives of rice breeding is to reduce the losses of yield in unfavorable environment due to lack of sufficient tolerance and increase the yield in the favorable environment. In present situation, the area for rice production is gradually reducing due to industrialization and extension of urban area in Bangladesh. Arable land is decreasing but the population continues to grow. A lot of land for rice cultivation is being converted to non-rice purposes. The yield performance also become fixed on a national average of 4.5 t/ha (BRRI, 2018). Besides, rice breeding is threatened by manmade occurrences hence, breeders should be ready to fight to any kind of stresses that is the outcome of uncertainty. New variety development is now a challenging and resource intensive effort. The biotic stresses (fungal, bacterial, viral and insect pests) for tropical wetland rice and abiotic stresses (drought and flooding) for non-irrigated rice negatively affect production (Khush and Virk, 2005). Hence, rice breeders must develop new varieties with higher yield and stability over multiple environments or location specific varieties.

In Bangladesh, new varieties with higher yield and stability that are resistant to biotic and abiotic stresses can be identified through multi-location yield trial. Multi-location yield trial permits breeders to identify location specific superior genotypes by evaluating the comparative performance of genotypes over different locations (Lakew et al., 2017). Genotypes tested over multiple environments have significant

variations in yield because of the presence of different biotic and abiotic stresses, differences in soil fertility and unexpected rainfall (Kaya, 2006). Genotype by environment interaction (GEI) refers to the differential response of genotypes towards different locations. The genetic advancement is reduced by GE interaction in plant breeding program through decreasing the relationship between phenotypic and genotypic values. By selecting location specific superior genotypes, GE interaction can be exploited. Moreover, GE interaction can be avoided by choosing widely adapted and stable genotypes over different locations (Lakew et al., 2017). There are two widely used approaches of grain yield stability analysis for multi-location trial data such as, AMMI (Gauch et al., 2008) and (GGE-Biplot) (Yan, 2002).

The AMMI model is a popular approach to study GE interaction. Main effects of the environment and genotype with principal components analysis of GE interactions are combined through AMMI ANOVA (Sharifi et al., 2017). The GGE biplot is also a noble approach for studying GE interaction because it permits selecting genotypes with higher yield and stability in various mega-environments. The GGE biplots permit several kinds of analysis for genotypes and environments, i.e. finding out the superior genotype for every environment, stable genotype across different environments, representative environment, and discriminating influence of every environment (Donoso-Nanculao et al., 2016). Hence, the present study was conducted to assess the performance and stability of IRRI developed breeding lines for recommending the farmers wider or specific cultivation in different breeding zones of Bangladesh.

Materials And Methods

Experimental Sites and Climate

The research work was conducted at three different breeding zones of Bangladesh e.g. Rajshahi (BRRRI regional station), Cumilla (BRRRI regional station) and Gazipur (ACI-Mawna) during boro season in 2018-19. Geographically Rajshahi is located within Barind Tract in mid-western Bangladesh (24°22'26"N latitude and 88°36'04"E longitude) with the altitude of 23 m from the sea level (<https://en.wikipedia.org>). Cumilla is located at 23°27'N latitude and 91°12'E longitudes with the altitude of 17 m from the sea level (<https://dateandtime.info>). Gazipur is located within Madhupur Tract (23°53' to 24°20'N latitude and 90°09' to 90°42'E longitude) with the elevation of 34 m (Simu *et al.*, 2018). The maximum and minimum mean temperature recorded are about 35.3°C and 11°C for Rajshahi, 33.3°C and 13.1°C for Cumilla, 34.5°C and 14.9°C for Gazipur respectively (BBS, 2018a). The annual rainfall observed is about 1,463 mm for Rajshahi; 3,179 mm for Cumilla and 2,892 mm for Gazipur (BBS, 2018b).

Experimental Materials and Design

A total of 70 breeding lines including eight check varieties were used for this experiment. Three out of eight checks were BRRRI varieties (BRRRI dhan28, BRRRI dhan67 and BRRRI dhan81) and five IRRI check varieties (IRRI 104, IRRI154, IRRI156, IRRI174 and IRRI181). All these breeding lines were developed through rapid generation advance (RGA) using single seed descent (SSD) method. Total 70 breeding lines were used as experimental materials (Table 1). The experiment was conducted using alpha lattice design

with row and column orientation in two replications.. Total number of plots for replicated materials was 140 including eight standard check varieties for comparing the performance of the selected breeding lines. The plot (27 hills × 5 rows) was transplanted with spacing 20 cm × 20 cm, and 2-3 seedlings per hill..

Statistical Analysis

Statistical analysis was done for estimating the stability analysis by using the R software. Grain yield stability analysis was done by using AMMI and GGE (Genotype × Environment interaction). There are two methods in the AMMI model: ANOVA and singular value decomposition, the additive main effects of genotypes (g_i), environments (e_j) and the multiplicative interaction effect (ge)_{ij} (Hongyu, 2014). Hence, the equation of the model for the i th genotype in the j th environment in r blocks is:

$$Y_{ijr} = \mu + g_i + e_j + b_r(e_j) + \sum_{k=1}^n \lambda_k \alpha_{ik} \gamma_{jk} + \rho_{ij} + \varepsilon_{ij}$$

Where, Y_{ijr} = performance of i th genotype in j th environment for r th replication, μ = grand mean, g_i = main effects of genotype as deviations from μ , e_j = main effects of environment as deviations from μ , λ_k = singular value for the Interaction Principal Component (IPC) axis k , α_{ik} = IPC scores of genotype for axis k , γ_{jk} = IPC scores of environment for axis k , $b_r(e_j)$ = effects of the block (r) within the environment j , r = blocks number, ρ_{ij} = residual having all multiplicative terms not comprised in the model (1); n = axes number or principal components (PC) taken by the model and ε_{ijr} = experimental error, supposed independent with similar distribution, $\varepsilon_{ij} \sim N(0, \sigma^2 / r)$.

GGE biplot approach was used to evaluate multi-environmental trials (MET) data of the rice genotypes comprising two conceptions i.e. the biplot and GGE conception. The graphs were made depending on (i) The GGE biplot polygon view for identifying the best genotypes and their mega environments by using 'which-won-where' pattern, (ii) Genotypes ranking of based on the performance of yield and stability, (iii) Genotypes assessment comparing to a standard genotype, (iv) Environment assessment and (v) Contrast between two genotypes (Akter *et al.*, 2015). Yan and Kang (2002) described the statistical theory of GGE approach in details. The equation for environment centered matrix, the data were subjected to singular value decomposition (SVD) by estimating each element of the matrix using the following equation:

$$Y_{ij} = \mu + \beta_j + \sum_{k=1}^k \lambda_k \gamma_{ik} \delta_{jk}$$

Where, Y_{ij} = performance of i th genotype in j th environment, μ = grand mean, β_j = main effects of environment, k = principal components (PC) number needed for suitable illustration of GGE, λ_k = particular value of k th PC (PC_k) and γ_{ik} = i th genotypic scores for PC_k and δ_{jk} = j th environmental scores for PC_k .

Results And Discussions

Yield Performance of Breeding Lines

The grain yield performance of 70 genotypes for every environment were separately demonstrated in Table 1. Mean yield performances were listed with respective genotypic code (G1 - G70) across the environments. In Cumilla, G61 (7.41 t/ha) was the highest yielder followed by G58, G38, G29, G17, G41 etc. G68 (3.3 t/ha) was the lowest yielder and followed by G33, G60, G70, G53 etc. In Gazipur, G41 (7.6 t/ha) was the highest yielder followed by G24, G42, G22, G32, G1 etc. G70 (3.4 t/ha) was the lowest yielder and followed by G2, G13, G17, G25 etc. In Rajshahi, G9 (7.08 t/ha) was the highest yielder followed by G9, G19, G50, G12, G26, G44, G24 etc. G47 (4.32 t/ha) was the lowest yielder genotype and followed by G11, G13, G14, G33, G45, G27 etc. (Table 1). These genotypes were suitable for specific environment by considering only the grain yield performance excluding G × E interaction.

Table 1. Yield (t/ha) performance of 70 genotypes across three breeding zones

Genotypes	C	G	R	M	Genotypes	C	G	R	M
IR 107971-B-B RGA-B RGA-20 (G1)	5.10	6.69	5.63	5.81	IR 107971-B-B RGA-B RGA-14 (G36)	6.19	5.82	5.56	5.86
IR 104006:4-15-B RGA-B RGA-30 (G2)	5.18	4.00	5.35	4.84	IR 103310-B-B RGA-B RGA-13 (G37)	5.87	5.53	6.08	5.83
IR 107982-B-B RGA-B RGA-164 (G3)	5.87	4.92	5.28	5.35	IR 107971-B-B RGA-B RGA-11 (G38)	7.13	4.74	5.10	5.66
IR 107982-B-B RGA-B RGA-105 (G4)	6.56	4.93	5.53	5.67	IR 108000-B-B-B-B-34 (G39)	6.29	5.38	6.22	5.96
IR 106457-B-B RGA-B RGA-335 (G5)	5.94	6.10	5.47	5.84	IR 108000-B-B-B-B-27 (G40)	6.06	5.01	5.12	5.39
IR 107995-B-B RGA-B RGA-441 (G6)	6.50	6.04	5.92	6.15	IR 103309-B-B RGA-B RGA-347 (G41)	6.95	7.63	6.18	6.92
IR 107976-B-B RGA-B RGA-175 (G7)	5.83	6.10	6.32	6.08	IR 106436-B-B RGA-B RGA-B RGA-275 (G42)	5.63	6.97	4.90	5.83
IR 107976-B-B RGA-B RGA-154 (G8)	5.42	6.31	5.99	5.90	IR 103757-B-B RGA-B RGA-B RGA-104 (G43)	5.32	5.97	5.53	5.61
IR 106449-B-B RGA-B RGA-B RGA-118 (G9)	5.80	6.45	7.08	6.44	IR 107989-B-B RGA-B RGA-153 (G44)	6.21	5.88	6.39	6.16
IR 100707-B-B RGA-B RGA-B RGA-224 (G10)	5.34	4.86	5.83	5.34	IR 107971-B-B RGA-B RGA-140 (G45)	6.92	5.21	4.67	5.60
IR 107995-B-B RGA-B RGA-487 (G11)	5.51	4.94	4.43	4.96	IR 103297-B-B-B-B-B-60 (G46)	5.86	5.63	5.40	5.63
IR 106449-B-B RGA-B RGA-B RGA-103 (G12)	6.49	5.81	6.50	6.27	IR 100707-B-B RGA-B RGA-B RGA-149 (G47)	5.56	5.57	4.32	5.15
IR 106449-B-B RGA-B RGA-B RGA-127 (G13)	5.45	4.24	4.56	4.75	IR 103314-B-B RGA-B RGA-171 (G48)	5.44	5.89	5.27	5.53
IR 107995-B-B RGA-B RGA-56 (G14)	5.64	6.38	4.64	5.55	IR 107982-B-B RGA-B RGA-108 (G49)	6.63	4.50	5.21	5.44
IR 100821-B-B RGA-B RGA-B RGA-32 (G15)	6.14	4.48	5.60	5.41	IR 107982-B-B RGA-B RGA-149 (G50)	5.71	5.52	6.51	5.91
IR 100707-B-B RGA-B RGA-B RGA-134 (G16)	6.01	6.54	5.26	5.94	IR 103757-B-B RGA-B RGA-B RGA-18 (G51)	6.61	5.44	5.91	5.98
IR 106449-B-B RGA-B RGA-B RGA-122 (G17)	7.01	4.32	5.41	5.58	IR 103314-B-B RGA-B RGA-182 (G52)	5.74	6.69	6.31	6.25
IR 107989-B-B RGA-B RGA-2 (G18)	6.33	5.89	5.42	5.88	IR 99129-B RGA-B RGA-213 (G53)	5.00	4.63	5.82	5.15
IR 107982-B-B RGA-B RGA-152 (G19)	6.06	6.25	6.83	6.38	IR 99129-B RGA-B RGA-138 (G54)	6.24	4.55	4.95	5.25
IR 103292-B-B-B-B-B-14 (G20)	5.68	6.46	5.38	5.84	IR 106436-B-B RGA-B RGA-B RGA-182 (G55)	6.51	5.81	5.19	5.84
IR 106457-B-B RGA-B RGA-336 (G21)	6.67	4.97	5.58	5.74	IR 106449-B-B RGA-B RGA-B RGA-288 (G56)	5.25	6.49	5.59	5.78
IR 100821-B-B RGA-B RGA-B RGA-50 (G22)	6.80	6.84	6.17	6.60	IR 107976-B-B RGA-B RGA-152 (G57)	6.47	5.79	5.85	6.04
IR 108000-B-B-B-B-16 (G23)	5.20	6.54	5.82	5.85	IR 106436-B-B RGA-B RGA-B RGA-132 (G58)	7.25	6.65	5.16	6.35
IR 107976-B-B RGA-B RGA-254 (G24)	5.59	7.07	6.35	6.34	IR 100707-B-B RGA-B RGA-B RGA-172 (G59)	5.66	6.67	5.65	5.99
IR 108000-B-B-B-B-31 (G25)	6.84	4.48	5.38	5.57	IR 107971-B-B RGA-B RGA-15 (G60)	4.50	5.71	5.87	5.36
IR 107995-B-B RGA-B RGA-	6.90	6.01	6.45	6.45	IR 107982-B-B RGA-B	7.41	6.27	5.22	6.30

14 (G26)					RGA-162 (G61)				
IR 100707-B-B RGA-B RGA-B RGA-185 (G27)	5.57	5.89	4.88	5.45	IR 107989-B-B RGA-B RGA-141 (G62)	6.11	5.74	5.86	5.90
IR 103718-B-B RGA-B RGA-B RGA-B RGA-137 (G28)	6.10	5.12	5.70	5.64	IRRI 156 (G63)	5.68	5.41	5.63	5.57
IR 108000-B-B-B-B-33 (G29)	7.12	5.76	5.54	6.14	IRRI 174 (G64)	5.72	4.77	5.09	5.19
IR 107989-B-B RGA-B RGA-124 (G30)	6.45	5.74	5.07	5.75	IRRI 154 (G65)	5.11	6.24	5.61	5.65
IR 108000-B-B-B-B-30 (G31)	5.63	6.30	5.89	5.94	IRRI 104 (G66)	5.48	5.99	5.07	5.51
IR 103310-B-B RGA-B RGA-201 (G32)	5.43	6.70	5.88	6.00	IRRI 181 (G67)	6.19	5.32	6.28	5.93
IR 103757-B-B RGA-B RGA-B RGA-102 (G33)	3.57	6.05	4.66	4.76	BRRI dhan28 (G68)	3.30	4.53	6.33	4.72
IR 107995-B-B-B-B-4 (G34)	5.54	6.01	6.07	5.87	BRRI dhan67 (G69)	6.25	4.98	6.04	5.75
IR 107995-B-B RGA-B RGA-485 (G35)	5.29	6.09	5.79	5.72	BRRI dhan81 (G70)	4.92	3.44	5.51	4.62

Notes: Cumilla (C), Gazipur (G), Rajshahi (R), Mean (M).

AMMI Analysis of Variance (ANOVA)

AMMI analysis of variance of 70 genotypes was tested over three environments (Table 2). The higher value of sum of squares for genotype represented that the genotypes showed more variances in the level of mean performances. The lower value of sum of squares for environment represented that the genotypes showed less variances in the level of mean performances.

Table 2. AMMI analysis of variance for yield performance of 70 genotypes across three environments

Sources of variation	DF	Sum sq	Mean sq	F value	Pr (>F)
Environment	2	6.727	3.363	1.796	0.307
Replication	3	5.618	1.873	2.703	0.047 *
Genotype	69	86.550	1.254	1.810	0.0001 ***
Environment × Genotype	138	132.311	0.959	1.384	0.017 *
Residuals	207	143.448	0.693		

Significant codes: '***' 0.001 '**' 0.01 '*' 0.05

The magnitude of sum of squares for environment × genotype was higher representing that the response of genotypes was different across environments. The variances of genotype were significant at 0.1 % level of significance. The variances of environment × genotype and replication were significant at 5 % level of significance.

AMMI 1 Biplot Analysis

The first primary component of interaction (IPC1) factor was responsible for 64.2 % variation due to $G \times E$ interaction. A biplot between mean yield performance and primary component of interaction (IPC1) of 70 genotypes (replicated) across three environments was shown in Fig. 1. High mean yield and lower IPCA1 scores (near zero) should be the characteristics of an ideal genotype. The similar characteristics are suggested for an ideal environment. The genotypes possessing lower AMMI1 value or IPCA1 scores are stable across environments. A genotype having both lower AMMI1 value and high yield potential is more desirable. These genotypes have the potential to give stable performance. G41 (IR 103309-B-B RGA-B RGA-347) was the highest yielder (6.92 t/ha) and followed by G22 (6.6 t/ha), G26 (6.45 t/ha), G9 (6.44 t/ha), G19 (6.38 t/ha), G58 (6.35 t/ha), G24 (6.34 t/ha) etc. On the other hand, G70 (BRRI dhan81) was the lowest yielder (4.62 t/ha) and followed by G68 (4.72 t/ha), G13 (4.75 t/ha), G33 (4.76 t/ha), G2 (4.84 t/ha), G11 (4.96 t/ha), G53 (5.15 t/ha), G47 (5.15 t/ha) etc. G22 (6.6 t/ha) was best considering AMMI1 value and yield performance. G5, G10, G14, G27, G30, G46, G47, G50, G53, G55, G63, G67 etc. all were more stable genotypes due to their lower IPCA1 scores (near 0) (Table 1, Fig. 1). The genotypes close to a particular environment are more suitable for that respective environment than others. G35, G65, G43, G27 etc. were more suitable for Rajshahi.

AMMI 2 Biplot Analysis

$G \times E$ interaction patterns can be demonstrated through biplot by using the AMMI method that displays the genotypes and environments concurrently. The genotypes location in the biplot far from the origin contribute comparatively more to the $G \times E$ interaction than those lying very close to origin or in the center of the origin (Mukherjee *et al.*, 2013). The second primary component (PC2) factor accounted for 35.8% variation of the $G \times E$ interaction. These two-primary component (PC1 and PC2), all together accounted for 100% variation of the $G \times E$ interaction. The contribution of G68 was highest to the interaction. G70, G58, G42, G61, G45, G38, G14, G33, G60, G53, G9 had comparably more contribution than other genotypes to the interaction (Fig. 2).

On the other hand, the genotypes were in the center of the biplot or very near to the center representing stable performance across environments. Based on the positive or negative signs of the scores of the first two primary components (PC1 and PC2), the biplot represented four sectors. Positive PCA1 and PC2 scores by sector1, positive PCA1 and negative PCA2 scores by sector2, negative PCA1 and PCA2 scores by sector3 and negative PC1 and positive PC2 scores by sector4 were represented. The genotypes were distributed in these four sectors and environments were in three sectors. There was no environment in sector1, Cumilla in sector2, Gazipur in sector3 and Rajshahi in sector4. The ranking of environments based on mean yield performance was Rajshahi < Gazipur < Cumilla.

The genotypes located in the sector2 were relatively higher yielder and followed by sector1, sector 3, sector4. Not only the $G \times E$ interaction but also the 'which win where' pattern was displayed by AMMI2 biplot. The genotypes located far from the center were unstable across the environments. Lower value of PC1 scores indicated the lower interaction value and less variation. The genotypes having PC1 scores less than 0 reacted positively to the environments which had PC1 scores less than 0 but reacted

negatively to the environments which had PC1 scores more than 0. G33 (IR 107995-B-B-B-4) having PC1 scores less than 0 reacted positively to Gazipur having PC1 scores less than 0 but reacted negatively to Cumilla. So, the interaction was positive for Gazipur and that genotype was more adaptive to the respective environment (Gazipur). The similar stability analysis was done through AMMI by Islam *et al.* (2015).

GGE Biplot Analysis

Environment can severely affect the genotypic performance (Islam *et al.*, 2015). The length of the environment vectors can be visualized by the concentric circles of the GGE biplot. It is the measures of the ability of discrimination of the environment and proportional to the standard deviation within the respective environment (Negash *et al.*, 2013). Ideal environments and stable genotypes locating on the concentric circles can be selected (Yan, 2002). Most desirable environment can be identified by observing the location, very near to the center circle or an ideal environment (Rad *et al.*, 2013). GGE biplot analysis for grain yield of 70 genotypes over three breeding zones were conducted. It accounted for 81.74% variation due to $G \times E$ interaction comprising two principal components (PC1 and PC2) 45.62% and 36.12% respectively. The ranking of environments was done for selecting suitable environment for high yield potential and adaptability (Fig. 3). There was no environment in the center of the circle and so, there was no ideal environment. The distance from the center of circle was lower for Gazipur and followed by Rajshahi and Cumilla. Therefore, Gazipur was more suitable than others. By considering lower PC scoring, Rajshahi was more stable environment than others. These three environments were located on the two sectors. Gazipur and Rajshahi were in same sector whereas Cumilla was in another sector. So, Gazipur and Rajshahi showed similarity in performances. Highest mean yield performance and stability (PC scores close to 0) are the characteristics of an ideal genotype. The ideal genotype can perform with highest performance without the $G \times E$ interaction and so called most adaptable genotype (Akcura *et al.*, 2011). It is expected that the best genotype should have high yield and stable performance across all environments. But such genotypes are hardly found. Hence, genotypes are evaluated by their high yielding performance with relatively stable over environments (Yan and Tinker, 2006). The ranking of 70 replicated genotype was done by using the phenomena that the genotype having highest mean yield performance and stability across environments. G41 locating in the center of the circle represented that highest mean yield performance and stability than the rest genotypes. It was the ideal genotype. G22, G58, G26, G61, G29, G24 etc. were more suitable genotype locating very near to the ideal genotype or around the center of the circle for yield and stability (Fig. 4).

Moreover, G70, G68, G33, G60, G2, G13, G53, G11 etc. were located far from the ideal genotype and so, they were low yielder and unstable genotypes. These are not suitable for further crop improvement program. The genotypes having less PC scores were stable across the environments. Most of the genotypes (e.g. G24, G7, G32 etc.) were more suitable for Rajshahi. No genotypes were found specifically suitable for Gazipur and Cumilla (Fig. 4). 'Which-won-where' and GEI ($G \times E$ interaction) pattern of grain yield trial of multiple environment were represented by the polygon derived from GGE-biplot. The polygon was made by joining the genotypes that were located far from the origin and the rest genotypes falling

within the polygon. Erect lines were drawn from the origin to the side of polygon and extended beyond the polygon. Thus, seven lines divided the biplot into eight sectors and two environments (Rajshahi and Gazipur) fell into same sector. Cumilla was in another sector (Fig. 5). The vertex genotype of each sector represented best performer of the particular environment. From those eight sectors, two mega environments were selected. The first mega environment comprising two environments (Rajshahi and Gazipur) with G41 as the highest yielder genotype in those environment. Rajshahi was more stable whereas Gazipur was unstable environment. The performance of G22, G26, G58, G44 etc. were better in the specific environment than others.

The second mega environment, Cumilla was located in another sector with G61 as highest yielder genotype in that environment. G29 was also a good yielder than others in the particular environment. But Cumilla was an unstable environment. The rest sectors with the vertex genotype e.g. G38, G17, G70, G68, G33 had no environment. Those genotypes were not highest yielder at any environment. However, the genotypes within the polygon locating very near to the origin were less responsive to the environment than the vertex genotypes. The similar analysis was done for stability analysis through GGE biplot for 'Which-won-where' by Islam *et al.* (2015).

Conclusion And Recommendation

The findings showed that the GE interaction effect, as well as the surroundings and genotypes, influenced rice genotype yield performance. Grain yield is a complicated trait that is influenced by a number of individual traits as well as the environment, either directly or indirectly. The AMMI and GGE statistical models could be a useful tool for identifying the most suited and stable high yielding genotypes for distinct and different environments. The AMMI model revealed that genotypes and environments accounted for the majority of the total variation in grain yield in the current study. GGE bi-plot analysis also enabled for the visualization of the winning genotype in each sector as well as the identification of genotypes with high yield and stability. The genotypes G41, G22, G26, G58, G24, and G61 were found as the most stable and high yielding genotypes, as evidenced by AMMI and GGE bi-plots. These genotypes could be recommended for cultivation at Bangladesh's testing sites and similar breeding zones. G61 was specifically tailored to Cumilla and recommended for production in Cumilla and other breeding zones with similar conditions, among the potential genotypes.

Declarations

Conflicts of Interest

The authors declare that there are no conflicts of interest regarding the publication of this paper.

Author Contributions

The study was conceived and designed by all the authors. Marium Khatun conducted the experiments, analyzed the data and wrote the paper. All authors contributed to manuscript revision. All authors

approved the final version of the manuscript.

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Figures

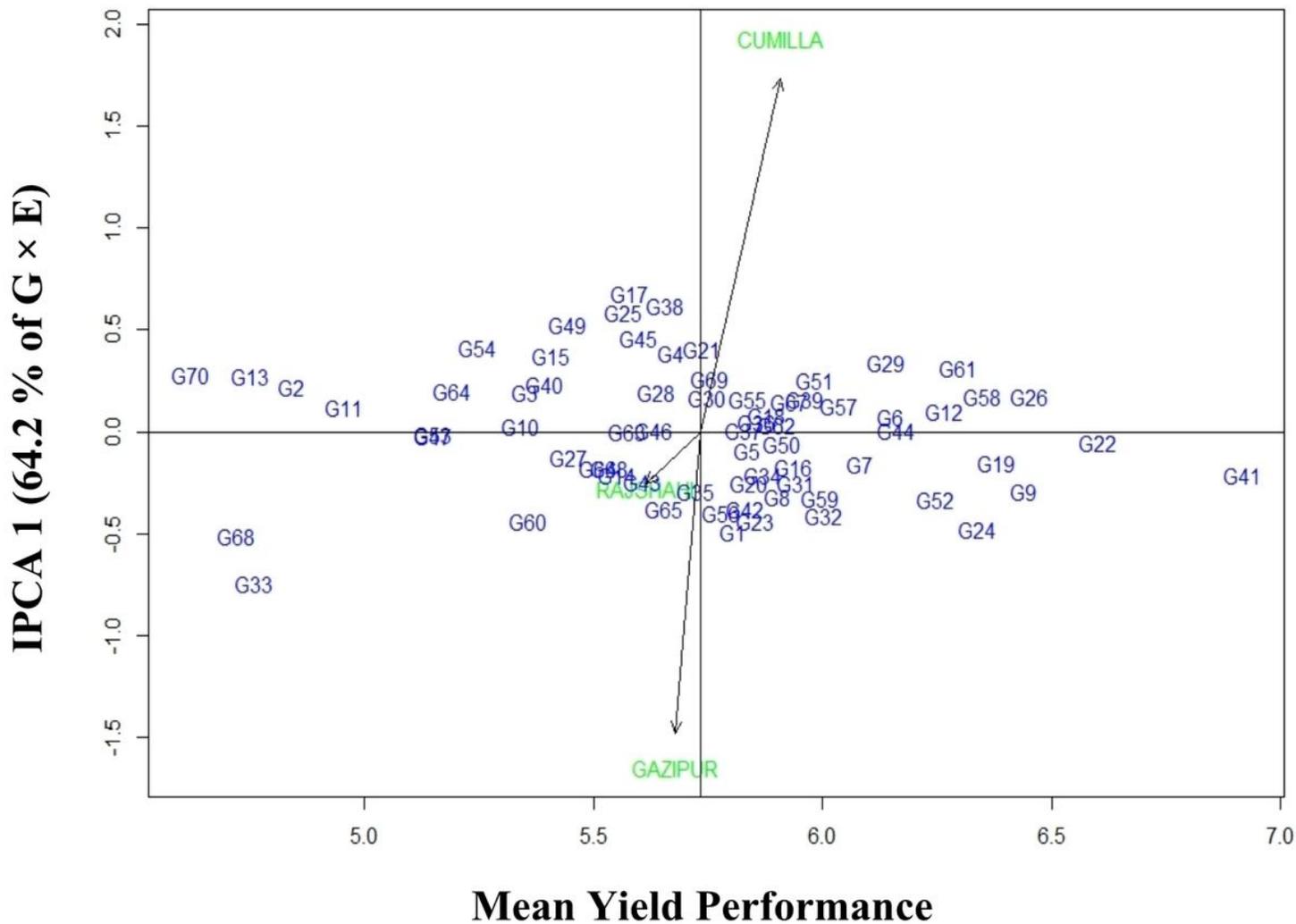


Figure 1

AMMI 1 biplot displaying mean yield performance versus primary component of interaction (IPC 1) of 70 genotypes (replicated) across three environments. Genotypic codes (G1 - G70) were used for representation of genotypes by blue font and environments by green font.

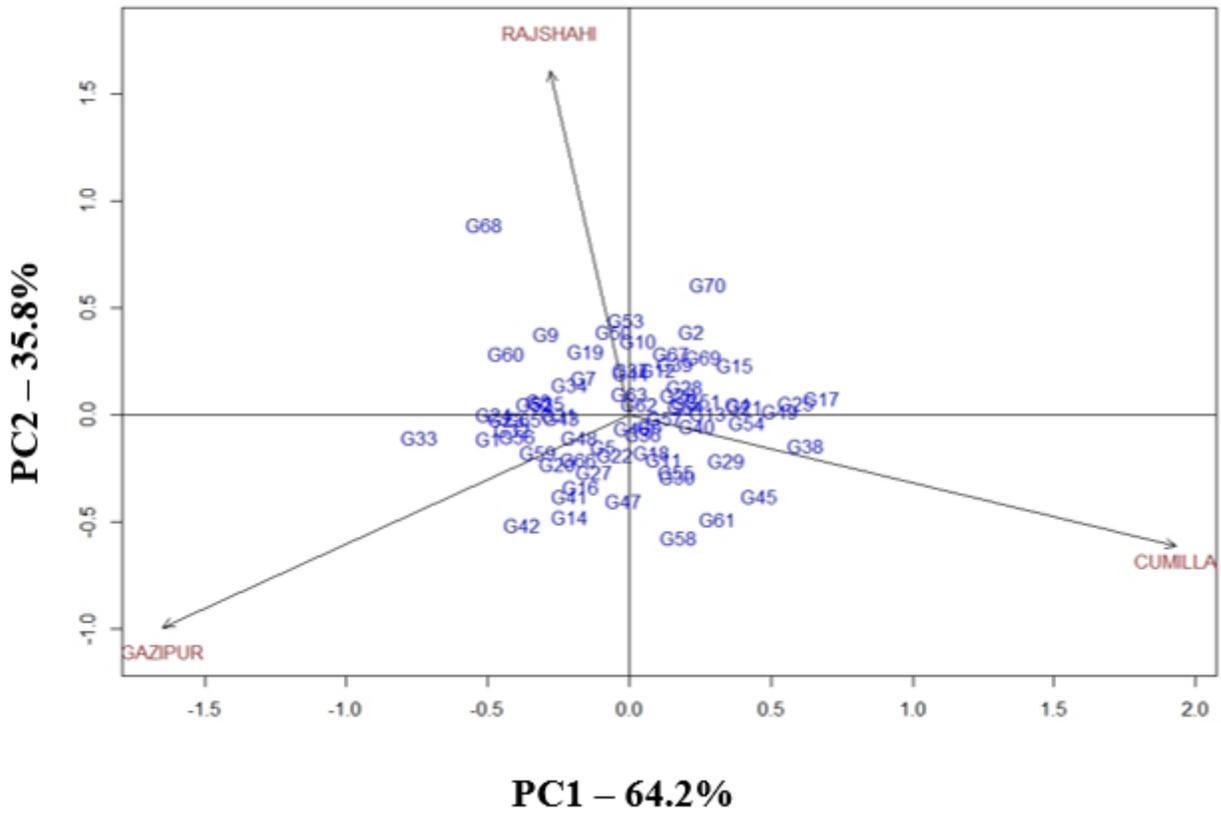


Figure 2

AMMI 2 biplot displaying primary component (PC1) versus secondary component (PC2) of 70 genotypes (replicated) across three environments for G × E interaction. Genotypic codes (G1 - G70) were used for representation of genotypes by blue font and environments in the peak point of the arrow.

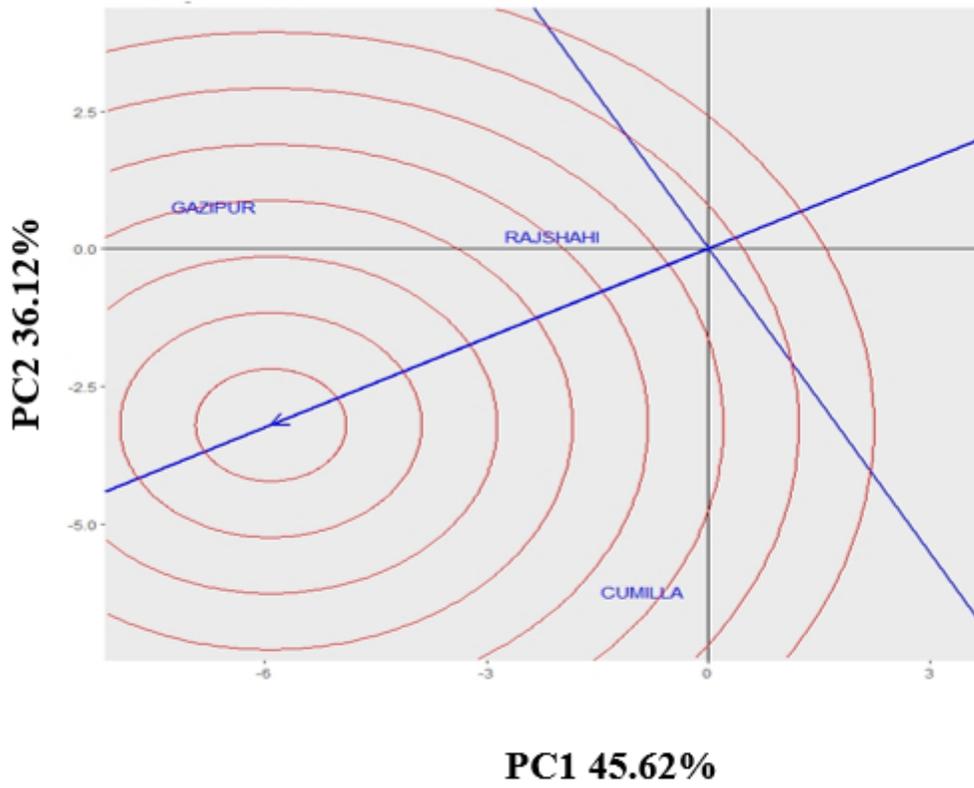


Figure 3

GGE biplot for ranking environments for high yield potential and stability. Environments were represented by blue font.

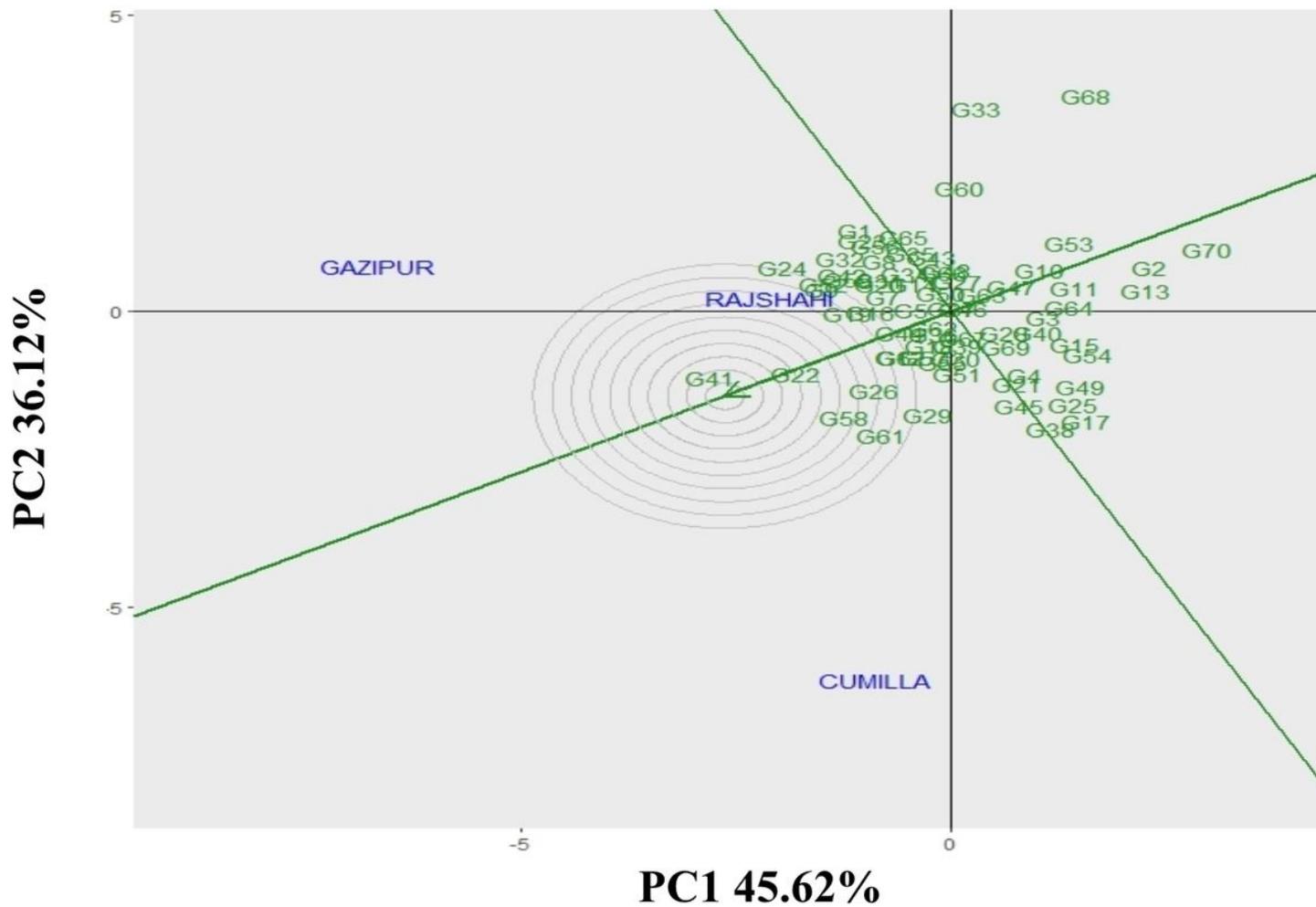


Figure 4

GGE biplot for ranking genotypes based on the yield performance and stability. Genotypic codes (G1 - G70) were used for representation of genotypes by green font and environments by blue font.

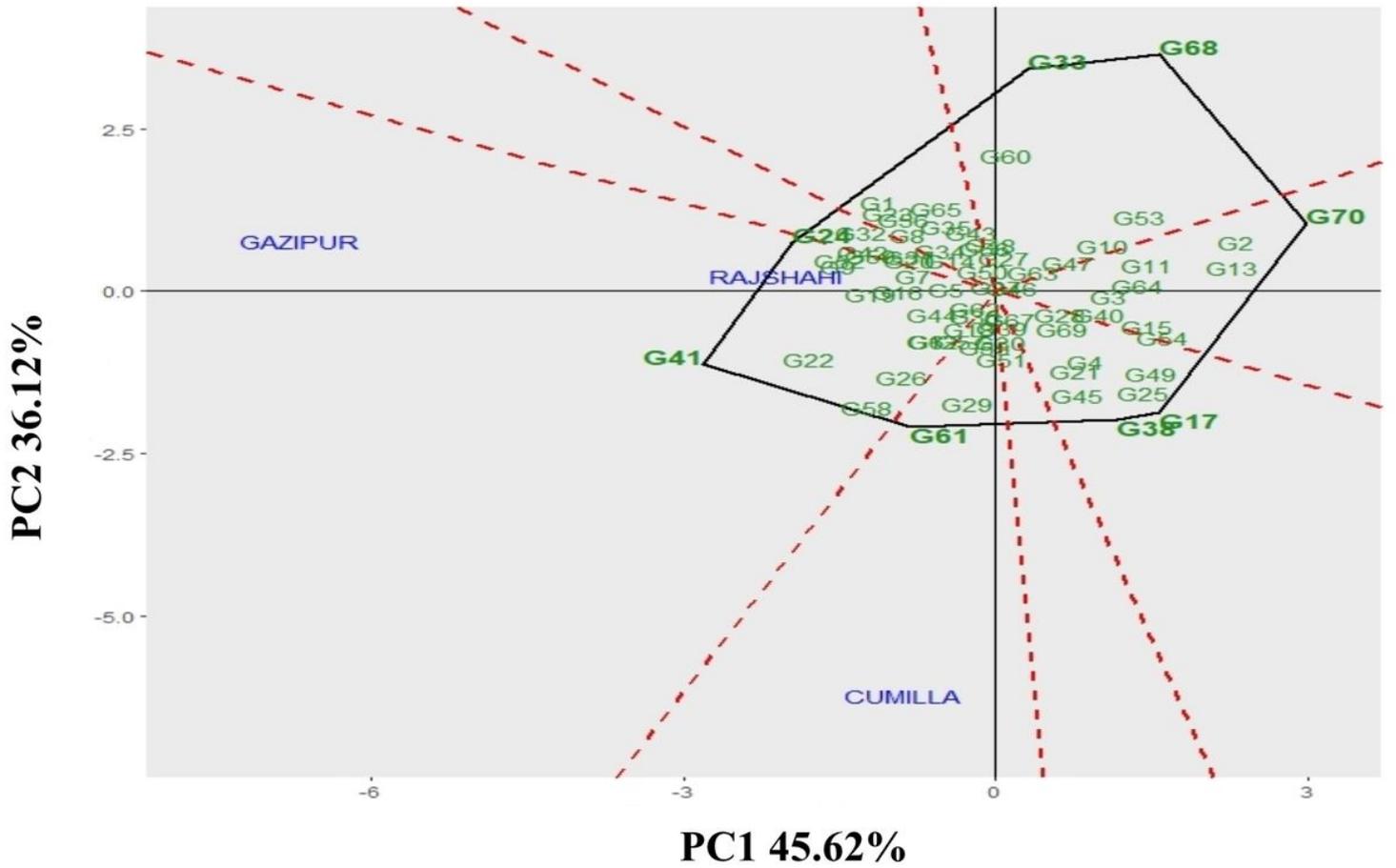


Figure 5

The polygon of GGE biplot for 'Which-won-where' and GEI ($G \times E$ interaction) pattern based on symmetrical scaling. Genotypic codes (G1 - G70) were used for representation of genotypes by green font and environments by blue font.