Genotype × Environment Interaction and Yield Stability Analysis in Hybrid Rice (*Oryza sativa* L.) By AMMI Biplot

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ABSTRACT

Assessing the adaptability and stability of promising rice genotypes is one of the important steps for accurate evaluation. This study determined the genotype × environment interaction (GEI) and stability performance of 12 promising rice genotypes in four environments during 2009 Aman season. The experiment used randomized complete block design with three replications. Yield stability and adaptability of yield performance were analyzed by combined analysis and additive main effects and multiplicative interaction (AMMI) model. The environment, genotype main effects, and the GEI were all highly significant (P<0.001). The study indicated that the tested genotypes, such as BRRHA G1 (5.47 tha^{-1}), G2 (5.68 tha^{-1}), G3 (6.29 tha^{-1}) and G4 (5.27 tha^{-1}) had higher average yields, which indicated these genotypes adapted to favourable environments (E1 and E3). Whereas the environment, E3 could be regarded as a more stable site for high yielding hybrid rice improvement than the other locations. Based on AMMI biplot analysis, genotypes BRRI1A/BRRI827R (G1), IR58025A/BRRI10R (G2), BRRI 10A/BRRI 10R (G3) and BRRI hybrid dhan1 (G4) have higher average mean yields with high main (additive) effects and positive IPCA1 score, among them BRRI 10A/BRRI10R (G3) being the overall best. Locations E1 and E3 could be regarded as a good selection site for rice hybrid improvement due to stable yields.

Key words: G × E interaction, stability, AMMI analysis, hybrid rice.

INTRODUCTION

Hybrid rice is a modern technology which gives 15-30% yield advantage over inbreeds rice. It is obviously proved that hybrids show better performance under adverse conditions like drought and saline conditions. If we can develop high yielding stable hybrid rice adopted on diverse environments, we can find most diverse stable heterotic hybrid combinations to increase food production for increasing world population. But grain yield depends on genotype, environment and management practices and their interaction with each other (Messina *et al.*, 2009). Under the same management conditions, variation in grain yield is principally explained by the effects of genotype and environment (Dingkuhn *et al.*, 2006). So information of genotype × environment interaction leads to successful evaluation of stable genotype, which could be used for general cultivation.

The level of performance of any character is a result of the genotype (G) of the cultivar, the environment in which it is grown (E), and the interaction between G and E (GEI). Interactionbetween these two explanatory variables gives insight for identifying genotype suitable for specific environments. The environmental effect is typically a large contributor to total variation (Blanche *et al.*, 2009). Moreover, G x E interactions greatly affect the phenotype of a variety, so the stability analysis is required to characterize the performance of varieties in different environments, to help plant breeders in selecting desirable varieties. Sreedhar *et al.* (2011), evaluated 60 hybrid rice cultivars for yield and its component stability across three different agro-climatic zones, and also found that stability in single plant yield was due to plasticity and stability in yield components. Mosavi (2013) observed significant yield differences among rice genotypes, environment and genotype by environment interaction.

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Various statistical procedures have been proposed to find out the stability of new cultivars. One of the most frequently used stability measures is based on a regression model (Yates and Cochran 1938). The additive main effects and multiplicative interaction (AMMI) model has found more use recently since it incorporates both the classical additive main effects model for G x E interaction and the multiplicative components into an integrated least square analysis and thus becomes more effective in selection of stable genotypes (Crossa et al., 1991; McLaren and Chaudhary, 1994; Ariyo, 1998; De Cauwer and Ortiz, 1998; Haji and Hunt, 1999; Ariyo and Ayo-Vaughan, 2000; Taye et al., 2000; Yan and Hunt, 2001). The effectiveness of AMMI procedure has been clearly demonstrated by various authors using multilocation data in soybean (Zobel et al., 1998), maize (Crossa et al., 1990), Wheat (Crossa et al.,1991; Haji and Hunt,1999; Yan and Hunt, 2001; Tarakanvos and Ruzgas, 2006), Pear millet (Shinde et al., 2002), Okra (Ariyo and Ayo-Vaughan 2000), Field pea (Taye et al., 2000) and Rice (Zavel-Garcia et al., 1992; Das et al., 2009; Sewagegne Tariku et al., 2013; Nassir, A.L. 2013; Islam et al., 2014). The present experiment was aimed to identify high yielding stable promising hybrids and to determining the variations about locations by AMMI model.

MATERIALS AND METHODS

Experimental design and plant materials

The experiments were conducted at four districts (environments) namely Gazipur (E1), Jamalpur (E2), Bhanga (E3) and Rajshahi (E4) representing four different agro-ecological zones (AEZ) of Bangladesh during T. Aman season 2009. Twelve genotypes consisting of three advanced lines (BRRI1A/BRRI827R (G1), IR58025A/BRRI10R (G2) and BRRI 10A/BRRI10R (G3), six released hybrids (BRRI hybrid dhan1 (G4), Tea (G5), Mayna (G6), Richer (G7), Heera-2 (G8) and Heeta 99-5 (G9) and three inbreed check varieties (BRRI dhan31 (G10), BRRI dhan33 (G11) and BRRI dhan39 (G12)) were used. The experiments were carried using the randomized complete block design (RCBD), with three replications. Twenty-one-day-old seedlings were transplanted in 20 square meter plot using single seedling per hill at a spacing of 20 cm × 15 cm. Fertilizers were applied at 150:100:70:60:10 kg ha^{-1} of urea, TSP, MP, gypsum and $ZnSO_4$ respectively. Standard agronomic practices were followed and plant protection measures were taken as required following the recommendation of *Adhunik dhaner chash*, BRRI (2009). Two border rows were maintained to minimize the border effects. The grain yield (t ha^{-1}) data were collected at 14% moisture level. Data were collected followed by standard method as described by Yoshida et al. (1976).

Statistical analysis

The combined analysis of variance was proceeded to look at G × E and stability of the genotypes across all environments. The AMMI model, which combines standard analysis of variance with PC analysis (Zobel et al., 1988), was used to investigate of G × E interaction. In AMMI model the contribution of each genotype and each environment to the GEI is assessed by use of the biplot graph display in which yield means are plotted against the scores of the IPCA1 (Zobel et al.,1988).
The AMMI model is:

$$Y_{ge} = \mu + \alpha_g + \beta_e + \sum_{n=1}^{N} \lambda n \gamma_{gn} \delta_{en} + \rho_{ge}$$

Where, Y_{ge} = yield of the genotype (g) in the environment (e); μ = grand mean; α_g = genotype mean deviation; β_e = environment mean deviation; N = No. of IPCAs (Interaction Principal Component Axis) retained in the model; λn = singular value for IPCA axis **n;** γ_{gn} = genotype eigenvector values for IPCA axis **n;** δ_{en} = environment eigenvector values for IPCA axis **n and** ρ_{ge} = the residuals.

Biplot analysis

Biplot analysis is the most powerful interpretive tool of AMMI models. Biplots are

graphs where aspects of both genotypes and environments are plotted on the same axis so the inter-relationships can be visualised. There are two basic AMMI biplots, the AMMI1 biplot where the main effects (genotype mean and environments) are plotted against each other and the AMMI2 biplot where scores for IPCA 1 and IPCA 2 are plotted.

RESULTS AND DISCUSSION

Combined analysis of variance

Table 1 presents the combined analysis of variance. Genotype (G), environment (E) and genotype × environment interaction (GEI) were highly significant (P<0.001) for grain yield. The factors explained showed that rice grain yield was affected by genotype (48.61%), environment (19.98%) and their interaction (20.65%). In general, a wide genetic diversity for maximum traits existed in the rice materials used in this study and this may be due to their diverse origins. The effects of G and E as shown in their highly significant mean square

(MS) for maximum traits reflected genotypic differences towards adaptation to different environments. Thus the highly significant G × E effects suggest that the genotypes may be selected for adaptation to specific environments. This is in harmony with the findings of Aina*et al*. (2009) and XuFei-fei *et al.* (2014) in G × E interaction effects of cassava genotypes. The significant genotype × environment interaction effects demonstrated that genotypes responded differently to the variation in environmental conditions of locations. This is indicative of the necessity of testing rice varieties at multiple locations. This also attests to the difficulties encountered by breeders in selecting new varieties for release. The large sum of squares for genotypes indicated that the genotypes were diverse, with large differences among genotypic means causing most of the variation in grain yield, which is harmony with the findings of Misra *et al.* (2009) and Fentie *et al.* (2013) in rice production.

Table 1. Combined analysis of variance of grain yield for 12 rice genotypes evaluated at four environments

Source	df	SS	MS	Explained SS (%)
Genotype (G)	11	66.529	6.048***	48.61
Environment (E)	3	27.359	9.119***	19.98
G x E interaction(GEI)	33	28.262	0.856***	20.65
Error	96	14.721	0.153	
Total	143	136.871	0.957	

***indicates significance at P<0.001 probability level; df=degree of freedom; SS=Sum of squares; MS=Mean of squares.

AMMI analysis of variance

The AMMI analysis of variance for hybrid rice grain yield (t ha^{-1}) of 12 genotypes tested in four environments showed that 19.98% of the total sum of squares was attributed to environmental effects, only 48.61% to genotypic effects and 20.65% to genotype × environment interaction effects (Table 2). The genotypes sum of squares was about approximately 2.5 times larger than that for environments and genotype × environment interaction, which determined substantial differences in genotypes. The

presence of GEI was clearly demonstrated by the AMMI model, when the interaction was portioned among the first three interaction principal component axis (IPCA), as they were significant P< 0.001 in a postdictive assessment. These imply that the interaction of the 12 rice genotypes with four environments was predicted by the first three components of genotypes and environments, which is in agreement with the recommendation of Sivapalan *et al.* (2000).

Table 2. Additive main effects and multiplicative interaction (AMMI) analysis of variance for grain yield (tha⁻¹) of 12 rice genotypes across four environments

Source	df	SS	MS	Explained SS (%)
Genotype (G)	11	22.176	2.016***	48.61
Environment (E)	3	9.119	3.039***	19.98
G × E interaction(GEI)	33	9.421	0.285***	20.65
IPCA1	13	5.628	0.433***	12.34
IPCA2	11	2.605	0.237***	5.71
IPCA3	9	1.187	0.132**	2.60
Error	96	4.906	0.051	
Total	143	45.623	0.319	

** and *** indicate significances at the P<0.01 and P<0.001 respectively.

Stability analysis by AMMI model

The mean grain yield value of 12 rice genotypes averaged over four environments presented in Table 3, which showed that the genotypes G3 and G12 had the highest (6.29 tha⁻¹) and the lowest (3.84 tha⁻¹) productivity, respectively. Different genotypes showed inconsistent performance across all the environments. The genotype G3 (6.29) was the top performers, while G1 (5.47 tha⁻¹), G2 (5.68 tha⁻¹) and G4 (5.27 tha⁻¹) were moderate and G5 (4.62 tha⁻¹) to G12 (3.84 tha⁻¹) were the poorest yielders.

Among environments, the mean grain yield ranged from 5.28 to 4.33 tha⁻¹ and average grain yield over environments and genotypes was 4.81 tha⁻¹. On the other hand, the genotypes G1, G2, G3 and G4 had higher average yields with positive index values, which indicated these genotypes adapted to favorable environments, while genotypes G5 to G12 adapted in poor environments. On the basis of environmental index value in terms of negative and positive, E2 and E4 were poor and E1 and E3 were rich environment.

Table 3. Stability analysis for grain yield (t ha⁻¹) of 12 rice genotypes in four environments

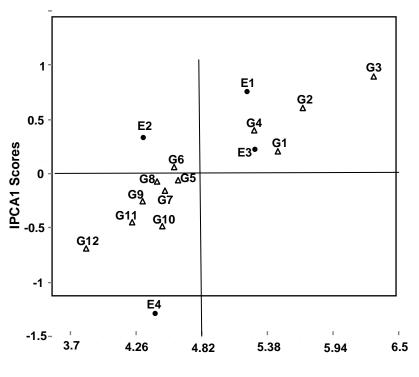| Genotype/Environment	Gazipur (E1)	Jamalpur (E2)	Bhanga (E3)	Rajshahi (E4)	Genotype mean	Index	IPCA1	IPCA2
BRRI 1A/ BRRI 827R (G1)	5.60	5.50	6.10	4.70	5.47	0.66	0.21	-0.41
IR58025A/BRRI10R(G2)	6.65	5.42	6.08	4.57	5.68	0.87	0.60	0.16
BRRI10A/BRRI10R(G3)	7.76	5.66	6.87	4.87	6.29	1.31	0.89	.37
BRRI hybrid dhan4(G4)	6.16	4.77	5.70	4.43	5.27	0.46	0.40	0.21
Tea (G5)	4.48	4.03	5.83	4.13	4.62	-0.19	-0.06	-0.65
Mayna (G6)	4.45	4.49	5.45	3.93	4.58	-0.23	0.07	-0.62
Richer (G7)	5.09	3.94	4.58	4.43	4.51	-0.30	-0.16	0.37
Heera-2 (G8)	4.53	4.03	5.12	4.07	4.44	-0.37	-0.07	-0.29
Heera-995(G9)	4.67	3.97	4.29	4.33	4.32	-0.50	-0.26	0.26
BRRI dhan31 (G10)	4.75	3.89	4.52	4.80	4.49	-0.32	-0.48	0.29
BRRI dhan33(G11)	4.40	3.67	4.36	4.47	4.23	-0.59	-0.45	0.17
BRRI dhan39 (G12)	3.99	2.54	4.42	4.40	3.84	-0.97	-0.69	0.16
Environment mean	5.21	4.33	5.28	4.43	GM=4.81			
Index	0.40	-0.49	0.47	-0.38				
IPCA1	0.75	0.32	0.22	-1.29				
IPCA2	0.88	-0.37	-0.79	0.28				
SE	0.08	0.04	0.27	0.23				
CV (%)	5.31	4.41	9.82	10.86				
5% LSD	0.47	0.32	0.88	0.81				

AMMI 1 biplot display

The AMMI 1 biplot gave a model fit 90.7% (Fig. 1). Among the hybrids, (G1), (G2), (G3) and (G4) were generally exhibited high yield with high main (additive) effects showing positive IPCA1 score, but the hybrid (G3) being the overall best. Hence, the hybrid (G3) was identified as specially adapted to the environments E1 and E3 and these two

environments were considered as the wide range suitable environments for this genotype. Genotype G6 showed positive IPCA1 score while genotypes G5 and G8 showed negative IPCA1 score with below average yield and IPCA1 score near zero. Other genotypes showed below average yield and negative IPCA1 score.

Fig. 1. AMMI 1 biplot for grain yield (tha^{-1}) of 12 rice genotypes (G) and four environments (E) using genotypic and environmental IPCA scores.

On the other hand, the environments E1 had large positive IPCA1 score with high mean value while E3 showed small positive IPCA1 score near zero with high mean value. Environment, E2 had relatively small positive IPCA1 scores and E4 had large negative IPCA1 scores. In the AMMI 1 biplot, the genotypes that group together (i.e G1, G2, G3 and G4) have similar adaptation while environments, which group together influences the genotypes in the same way (Kempton R A, 1984). Genotypes and environments on the same parallel line, relative or ordinate have similar yields and a genotype or environment on the right side of the midpoint of this axis has higher yields than those of left hand side. Although, the genotypes G1, G2, and G4 were considered as the favourable environments for E1 and E3. Similar outcomes have reported by Das *et al*. (2010) and Kulsum*et al*. (2013). The genotype G6 showed positive IPCA1 score and genotypes G5 and G8 were showed negative IPCA1 score with below average yield and IPCA1 score near zero indicating that these varieties were stable and less influenced by the environments (Yau S K, 1995). Other genotypes showed below average yield and negative IPCA1 score. On the other hand, the environments E1 have large positive IPCA1 score with high mean value and E3 showed small positive IPCA1 score near zero with high mean value and hence had small interaction effects indicating that all the genotypes performed well in these locations. The environment, E4 has large negative IPCA1 scores, which interact positively with genotypes having negative IPCA1 scores and negatively with the genotypes that having positive IPCA1 scores. Environment, E2 has relatively small positive IPCA1 scores,

suggesting that it had little interaction with genotypes. Similar findings and interpretation have been made by Adugna *et al*. (2007); Anandan *et al*. (2010) and Islam *et al*. (2014). Finally, the AMMI 1 biplot statistical model has been used to diagnose the G × E interaction pattern of grain yield of hybrid rice. The hybrids (G1), (G2), (G3) and (G4) were hardly affected by the G × E interaction and thus will perform well across a wide range of environments. Locations, such as E1 and E3 could be regarded as a good selection site for rice hybrid improvement due to stable yields.

AMMI 2 biplot display

In Figure 2, the environments fell into three sections. Among the environments E2 and E3 had short spokes and they do not exert strong interactive forces but the environments E4 and E1 had long spokes and hence represent the most discriminating environments. In AMMI 2 biplot, the genotypes, G3 and G12 were more responsive since they are more distant from the origin where - as the best genotype is G3 with respect to the best enhancing environment E1. On the other hand, the genotypes G1, G5, G6, G7, G8 and G9 were close to the origin and hence were less sensitive to environmental interactive forces. Similar result was reported by Anandan *et al*. (2009); Crossa, (1990) and Kempton R A, (1984).
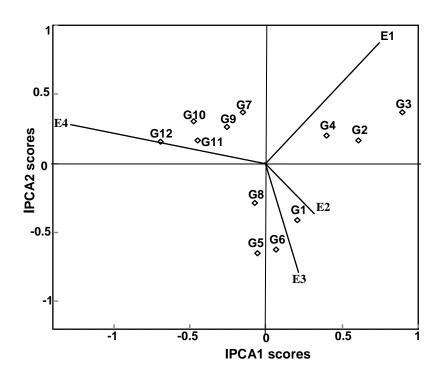

Fig. 2. AMMI 2 biplot for grain yield (tha^{-1}) showing the interaction of IPCA2 against IPCA1 scores of 12 rice genotypes (G) in four environments (E).

CONCLUSIONS

AMMI statistical model could be a great tool to select the most suitable and stable high yielding hybrids for specific as well as for diverse environments. As a result, almost all of the evaluated genotypes were affected by the genotype × environment interaction effects, so that no genotype had superior performance in all environments. Thus the highly significant G × E effects suggest that genotypes may be

selected for adaptation to specific environments. In the present study, the mean grain yield value of genotypes averaged over environments indicated that G3 had the highest (6.29 tha^{-1}) and G12 the lowest yield (3.84 tha^{-1}), respectively. It is noted that the variety G3 showed higher grain yield than all other varieties over all the environments. The genotypes (G1), (G2), (G3) and (G4) were hardly affected by the G × E interaction and thus would perform well across a wide range

of environments. Most of the genotypes showed environment specificity. The biplots also indicated the stability levels of the cultivars and the environment. AMMI biplots are necessary in describing the test sites and the genotype performance across tests sites. In this study, the AMMI biplot model classified the testing environments into three sections. Accordingly, four of the tested genotypes (G1, G2, G3 and G4) were found to be the best for environments E1 and E3 and five genotypes (G7, G9, G10, G11 and G12) were most adapted to environment E4, while the other two genotypes (G5 and G8) were not found best to any of the testing environments.

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