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AMMI Biplot Analysis for Stability of Grain Yield in Hybrid Rice (*Oryza sativa L.*)

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Abstract

Genotype x environment interaction and stability performance were investigated on grain yield with 12 rice genotypes in five environments. The ANOVA for grain yield revealed highly significant (P<0.01) for genotypes, environments and their interactions. The significant interaction indicated that the genotypes respond differently across the different environments. The mean grain yield value of genotypes averaged over environments indicated that BRRI 10A/ BRRI 10R (G3) had the highest (5.99 tha^{-1}) and BRRI dhan39 (G12) the lowest yield (3.19 tha^{-1}), respectively. In AMMI analysis, AMMI 1 biplot showed the hybrids BRRI 1A/ BRRI 827R (G1), IR58025A/ BRRI 10R(G2), BRRI 10A/BRRI 10R(G3) and BRRI hybrid dhan1(G4) have higher average mean yields with high main (additive) effects with positive IPCA1 score, but the hybrid BRRI 10A/BRRI 10R(G3) being the overall best. Hence, the genotype G3 would be considered more adapted to a wide range of environments than the rest of genotypes. Environments, such as Gazipur (E1) and Jessore (E5) could be regarded as a more stable site for high yielding hybrid rice improvement than other location for grain yield due to IPCA score near zero which had no interaction effect. In AMMI 2 biplot, Comilla (E2) and Rangpur (E4) are the most discriminating environments, while BRRI 1A/ BRRI 827R (G1) and Heera 99-5 (G9) are the most responsive genotypes.

Keywords: AMMI analysis; Stability; GEI structure; Hybrid rice

Introduction

Rice has a special significant position as a source of food providing over 75% of Asian's staple food and more than three billion of world population's meal which represents 50 to 80% of their daily calorie intake [1,2]. This population will increase to over 4.6 billion by 2050 [3] which will demand more than 50% of rice needs to be produced what is produced present to cope with the growing population [4,5]. Yields of improved inbreed rice varieties in favorable conditions have reached to a plateau or even subsequently declined in many countries including Bangladesh. It is recommended that a large number of high yielding stable hybrids with high adaption capability to diverse environments are required to accomplish specific socio-economic and agricultural needs. Hence, we need new hybrid rice because it gives 15-30% yield advantage over inbred rice. Moreover, hybrid rice has also shown 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.

Yield is a complex character which is dependent on a number of other characters and is highly influenced by many genetic factors as well as environmental fluctuations. On the other hand, the G x E interaction is an important aspect of both plant breeding program and the introduction of new crop cultivars [6-8]. The AMMI model is a hybrid model involving both additive and multiplicative components of two way data structure which enabled a breeder to get precise prediction on genotypic potentiality and environmental influences on it. AMMI uses ordinary ANOVA to analyze the main effects (additive part) and principal component analysis (PCA) to analyze the non-additive residual left over by the ANOVA [9]. The effectiveness of AMMI procedure has been clearly demonstrated by various authors using multilocation data in soybean [10], maize [11], Wheat [12-14], pearl millet [15], Okra [16], Field pea [17] and rice [18,19]. The main objectives of the present study are to identify more high yielding stable promising hybrids and to determine the areas where rice hybrids would be adapted by AMMI model. Therefore, using the AMMI analysis with biplot facility, yield data were analyzed to determine the nature and magnitude of G x E interaction effects on grain yield in diverse environments.

Materials and Methods

The experiments were conducted at five districts namely Gazipur (E1), Comilla (E2), Barisal (E3), Rangpur (E4) and Jessore (E5) representing five different agro-ecological zones (AEZ) of Bangladesh. Twelve genotypes consisting of 3 advanced lines (BRRI 1A/ BRRI 827R (G1), IR58025A/ BRRI 10R (G2) and BRRI 10A/ BRRI 10R (G3)), 6 released hybrids (BRRI hybrid dhan1(G4), Tea (G5), Mayna (G6), Richer (G7), Heera-2 (G8) and Heeta 99-5 (G9)), and 3 inbreed check varieties (BRRI dhan31 (G10), BRRI dhan33 (G11) and BRRI dhan39 (G12)) were used as experimental materials. The experiments were carried out in a randomized complete block design (RCBD), with three replications. Twenty-one-days 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 @ 150:100:70:60:10 kg/ha Urea, TSP, MP, gypsum and $ZnSO_4$, respectively. Standard agronomic practices were followed and plant protection measures were taken as required

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following the recommendation of BRRI [20]. Two border rows were used to minimize the border effects. The grain yield (tha^{-1}) data were collected at 14% moisture level. Data were collected followed by standard method as described by [21]. The grain yield data for twelve (12) genotypes in five (5) environments were subjected to AMMI analysis of variance using statistical analysis package software Cropstat version 6.1 (Cropstat, Tutorial Mannual Part 2, Revised April, 2008).

Results and Discussion

AMMI analysis of variance

The AMMI analysis of variance for grain yield (tha^{-1}) of 12 genotypes tested in five environments showed that the main effects of G and E accounted for 67.11% and 18.46% variation, respectively, and G x E interaction effects represent 13.11% of the total variation for grain yield (Table 1). The analysis revealed that variances due to environments, and G x E interactions are significant (P<0.01). 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 in harmony with the findings of [22,23]. The presence of genotype-environment interaction (GEI) was clearly demonstrated by the AMMI model, when the interaction was partitioned among the first three interaction principal component axis (IPCA) as they were significant in postdictive assessment. The IPCA1 explained 9.68% of the interaction sum of square in 14% of the interaction degree of freedom (DF). Similarly, the second and third principal component axis (IPCA 2-3) explained a further 2.02% and 1.23% of the GEI sum of squares, respectively (Table 1). This implied that the interaction of the rice genotypes with five environments was predicted by the first three components of genotypes and environments, which is in agreement with the recommendation of Sivapalan et al. [24]. However, this contradicted the findings of Gauch and Zobel [25] which recommended that the most accurate model for AMMI can be predicted using the first two IPCAs. These results indicate that the number of terms to be included in an AMMI model cannot be specified a prior without first trying AMMI predictive assessment [26]. In general, factors like type of crop, diversity of the germplasm and range of environmental conditions will affect the degree of complexity of the best predictive model [11].

Stability analysis by AMMI model

Biplot analysis is possibly the most powerful interpretive tool for AMMI models. There are two basic AMMI biplots, the AMMI 1 biplot where the main effects (genotype mean and environment mean) and IPCA1 scores for both genotypes and environments are plotted against each other. On the other hand, the second biplot is AMMI 2 biplot where scores for IPCA1 and IPCA2 are plotted (Table 2). The mean grain yield value of genotypes averaged over environments indicated

Source of Variation	**d.f**	**SS**	**MS**	**Explained SS (%)**
Genotypes (G)	11	40.498	3.682**	67.11
Environments (E)	4	11.142	2.785**	18.46
G x E Interaction (GEI)	44	7.908	0.179**	13.11
IPCA1	14	5.842	0.417**	9.68
IPCA2	12	1.220	0.102**	2.02
IPCA3	10	0.741	0.074**	1.23
Eroor	120	0.803	0.007	
Total	179	60.353		

** Significant at P<0.01

Table 1: Additive main effects and multiplicative interaction (AMMI) analysis of variance for grain yield (tha^{-1}) of 12 rice genotypes across 5 environments.

Genotypes/Environments	Gazipur (E1)	Comilla (E2)	Barisal (E3)	Rangpur (E4)	Jessore (E5)	Mean	Index	IPCA1	IPCA2
BRRI 1A/ BRRI 827R (G1)	5.10	5.04	4.41	3.37	5.13	4.61	0.57	0.852	0.421
IR58025A/ BRRI 10R (G2)	5.78	5.11	4.52	4.31	5.12	4.97	0.92	0.502	0.147
BRRI 10A/ BRRI 10R (G3)	6.47	6.05	5.86	5.67	5.41	5.99	1.95	0.293	0.254
BRRI hybrid dhan1 (G4)	5.83	4.66	4.26	4.19	5.19	4.83	0.78	0.356	0.001
Tea (G5)	4.40	3.19	2.99	3.58	3.22	3.48	-0.56	-0.008	0.670
Mayna (G6)	4.23	2.37	3.11	3.67	3.56	3.39	-0.66	-0.461	0.155
Richer (G7)	4.43	2.45	3.42	3.67	4.19	3.63	-0.41	-0.449	-0.294
Heera-2 (G8)	4.33	3.03	3.66	3.88	3.86	3.75	-0.29	-0.273	0.103
Heeta 99-5 (G9)	4.17	2.47	4.00	4.03	4.32	3.80	-0.25	-0.647	-0.460
BRRI dhan31 (G10)	4.34	3.35	3.11	2.76	4.02	3.52	-0.53	0.391	-0.239
BRRI dhan33 (G11)	4.24	2.62	3.03	3.34	3.65	3.38	-0.66	-0.193	0.049
BRRI dhan39 (G12)	3.80	2.32	3.08	3.40	3.37	3.19	-0.86	-0.358	0.033
Mean	4.76	3.56	3.79	3.82	4.30				
Index	0.72	-0.49	-0.26	-0.22	0.25				
IPCA 1	0.040	1.179	-0.234	-0.985	-0.001				
IPCA 2	0.278	0.328	-0.313	0.478	-0.771	**GM=4.05**			
SE	0.08	0.09	0.06	0.10	0.07				
CV(%)	3	4	3	5	3				
5% LSD	0.24	0.25	0.18	0.30	0.21				

Table 2: Stability parameters for grain yield (tha^{-1}) of 12 rice genotypes in 5 environments.

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that the genotypes G3 and G12 had the highest (5.99 tha^{-1}) and the lowest (3.19 tha^{-1}) yield, respectively. Different genotypes showed inconsistent performance across all environments. The environments mean grain yield ranged from 4.76 tha^{-1} for E1 to 3.56 tha^{-1} for E2 and averaged grain yield over environments and genotypes is 4.05 tha^{-1}. On the basis of environmental index value in terms of negative and positive, E2, E3 and E4 are poor, and E1 and E5 are rich environment. Within the genotypes G1, G2, G3 and G4 have higher average yields and these genotypes adapted to favorable environments, while genotypes G5 to G12 adapted to poor environments.

AMMI 1 biplot display

Biplots are graphs where aspects of both genotypes and environments are plotted on the same axes so that inter relationships can be visualized. In the AMMI 1 biplot, the usual interpretation of biplot is that the displacements along the abscissa indicate differences in main (additive) effects, whereas displacements along the ordinate indicate differences in interaction effects. Genotypes that group together have similar adaptation while environments which group together influences the genotypes in the same way [27]. The best adapted genotype can plot far from the environment. If a genotype or an environment has a IPCA1 score of nearly zero, it has small interaction effects and considered as stable. When a genotype and environment have the same sign on the PCA axis, their interaction is positive and if different, their interaction is negative. The AMMI 1 biplot expected yield clearly indicated for any genotype and environment combination can be calculated from Figure 1 following standard procedures suggested by Zobel et al. [10].

The AMMI 1 biplot gave a model fit 96.5%. This result is in agreement with the findings of Naveed et al. [28] and Gauch and Zobel [25]. 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 mid point of this axis has higher yields than those of left hand side. Consequently, 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 over all best. Hence, the hybrid (G3) was identified as specially adapted culture to the mentioned environments and these environments were considered as the wide range suitable environments for this genotype. Similar outcomes have reported by Das et al. [29], and Kulsum et al. [30]. Since, the environments E1 and E5 had positive IPCA1 score near zero and hence had small interaction effects indicating that all the genotypes performed well in these locations. Adugna et al. [31] and Anandan et al. [32] reported similar pattern of interactions. Thus these two locations were considered as the favorable environments for the genotypes G1, G2, G3 and G4. The genotype G5 showed IPCA1 score close to zero, indicating that the variety was stable and less influenced by the environments [33]. Other genotypes showed below average yield. Similarly, the genotype G10 was moderately stable across environments (low positive IPCA1 score) and below average yield. On the other hand, G8, G11 and environment, E3 had below average yield with negative IPCA1 score near zero indicating that these varieties were less influenced by the environments. Likewise, the environment E3, were found favorable environment for the genotype G11 and G8. Finally, The AMMI 1 biplot statistical model has been used to diagnose the G x E interaction pattern of grain yield of hybrid rice. The hybrids (G1), (G2), (G3) and (G4) were hardly affected by the G x E interaction and thus will perform well across a wide range of environments. Locations, such as E1 and E5 could be regarded as a good selection site for rice hybrid improvement due to stable yields.

AMMI 2 biplot display

In AMMI 2 biplot, (Figure 2) the environmental scores are joined to the origin by side lines. Sites with short spokes do not exert strong interactive forces. Those with long spokes exert strong interaction. An example of this is shown in Figure 2 where the points representing the environments E1, E2, E3, E4 and E5 are connected to the origin. The environments E1 and E3 had short spokes and they do not exert strong interactive forces. The genotypes occurring close together on the plot will tend to have similar yields in all environments, while genotypes far apart may either differ in mean yield or show a different pattern of response over the environments. Hence, the genotypes near the origin are not sensitive to environmental interaction and those distant from the origins are sensitive and have large interaction. In the present study,

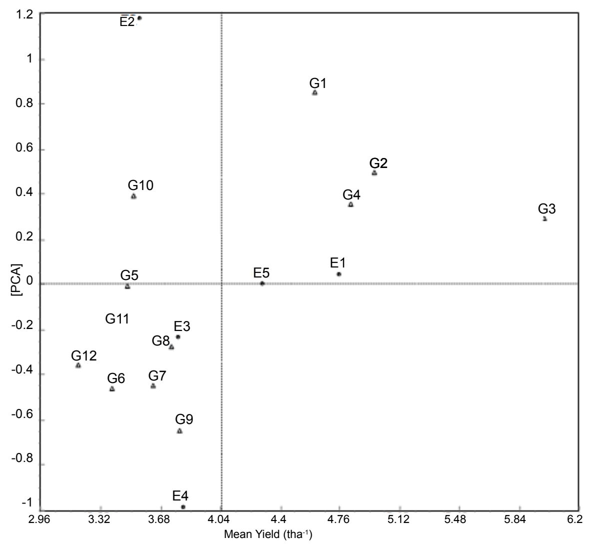

Figure 1: AMMI 1 Biplot for grain yield (tha^{-1}) of 12 rice genotypes (G) and five environments (E) using genotypic and environmental scores.

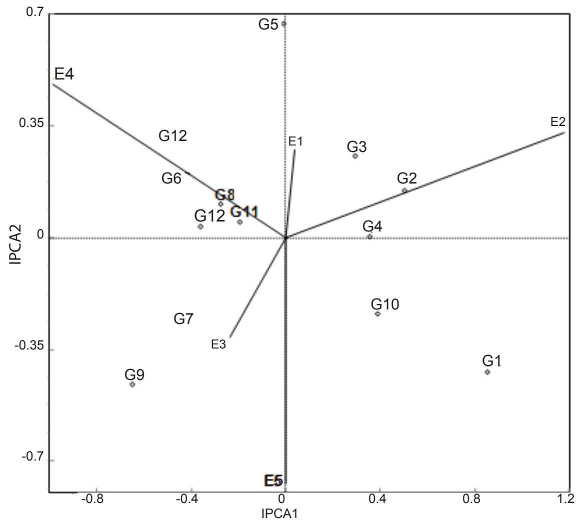

Figure 2: AMMI 2 Biplot for grain yield (tha^{-1}) showing the interaction of IPCA2 against IPCA1 scores of 12 rice genotypes (G) in five environments (E).

G1 and G9 had more responsive since they were away from the origin whereas the genotypes G8, G11, G12 and G4 were close to the origin and hence they were non sensitive to environmental interactive forces.

Conclusions

Crop yield is a complex trait that is influenced by a number of component characters along with the environment directly or indirectly. If we could develop high yielding stable hybrid rice for diverse environments, we could offer most diverse stable heterotic hybrids for the rice growers. 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. In the present study, AMMI model has shown that the largest proportion of the total variation in grain yield was attributed to environments. Here most of the genotypes showed environment specificity. The mean grain yield value of genotypes averaged over environments indicated that G3 had the highest (5.99 tha^{-1}) and G12 the lowest yield (3.19 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 x E interaction and thus would perform well across a wide range of environments.

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