GGE bipot analysis of genotype x environment interaction in rice (oryza sativa l.) genotypes in Bangladesh

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Materials and Methods

Introduction

Rice is an important cereal crop which is receives the most attention of specialists in plant breeding and production. However, its production is limited by the adverse environmental conditions. Therefore, Multi-environment trials (MET) are conducted to evaluate yield stability performance of genetic materials under varying environmental conditions (Delacy et al. 1996, Yan et al. 2000, Yan and Rajcan 2002). A genotype grown in different environments will frequently show significant fluctuations in yield performance. These changes are influenced by the different environmental conditions and are referred to as genotype-by-environment (GE) interaction (Allard and Bradshow, 1964, Kang 2004). But, GE interaction reduces the genetic progress in plant breeding programs through minimizing the association between phenotypic and genotypic values (Comstock and Moll 1963). Hence, GE interaction must be either exploited by selecting superior genotype for each specific target environment or avoided by selecting widely adapted and stable genotype across wide range of environments (Kaya, 2006 and Mitrovic et al. 2012). Numerous methods such as regression coefficient (Finlay and Wilkinson 1963), sum of squared deviations from regression (Eberhart and Russel 1966), stability variance (Shukla 1972), coefficient of determination (Pinthus 1973), coefficient of variability (Francis and Kannenberg 1978) and additive main effects and multiplicative interaction (AMMI) (Gauch and Zobel, 1988, Zobel et al. 1988, Gauch 1992) have been commonly used to analyze MET data to reveal patterns of GE interaction. Yan et al. (2000) proposed another methodology known as GGE-biplot for graphical display of GE interaction pattern of MET data with many advantages. A GGE biplot as a data visualization tool is able to graphically demonstrate a GE interaction pattern. It is an effective tool to identify a mega-environment, genotype evaluation based on the both yield and stability; and evaluation of test environments from a discrimination aspect. The objectives of this study were to apply a GGE biplot to evaluate the magnitude of the effect of GE interaction on grain yield of six genotypes tested across six locations, determine the best performing genotypes for selection locations, the identification of mega-environments and analysis of the ideal genotype and environment for rice production areas in Bangladesh.
Plant breeders perform multi-environment trial (MET) to evaluate new improve genotypes across test environments before a specific genotype is released a variety for production to supply growers. This investigation was done to study GE interaction for grain yield in six genetically diverse genotypes. Grain yield performances were evaluated under six different regions in Bangladesh during winter cropping season, 2012-13 using Randomized complete block design with three replication. The experiment were conducted at six districts viz. Rajshahi(E1), Comilla(E2), Bhanga(E3), Hobiganj (E4), Barisal(E5) and Kushia (E6) representing six different agro ecological zones (AEZ) of Bangladesh. A total of Six rice advanced genotypes viz. IR83140-B-11-B(G1), SAGC06,(G2) ZHONGZU14(G3),Weed tolerant rice(G4), HUA565(G5) and one check BRRI dhan28(G6) were used as experimental materials during dry season. The experiments were carried out in a randomized complete block design (RCBD) with three replications. Forty-day-old seedlings of each genotype were transplanted in 12.96 meter square. Fertilizer were applied@ 260:100:120:110:11 kg Urea, TSP, MP, Gypsum and ZnSO$_4$/ha. Nitrogen was applied in three equal splits at 15 days after transplanting (DAT), 30 DAT and 5 days before PI stage. Total amount of TSP, MP, Gypsum and ZnSO$_4$ were applied at final land preparation. Standard agronomic practices were followed and plant protection measures were taken as required following the recommendation of BRRI (BRRI, 2010).Two border rows were used to minimize the border effects. Data on grain yield was recorded from the whole plot (12m$^2$) and the yield was adjusted to 14% moisture level. The grain yield data for six(6) genotypes in Six (6) environments were subjected to combined analysis of variance (ANOVA)using statistical analysis package software Cropstat version 6.1(Cropstat, Tutorial ManualPart2,Revised April,2008) to determine the effects of environment(E), genotype(G) and their interactions. The data were graphically analyzed for interpreting GE interaction using the GGE biplot software (Yan 2001). GGE biplot methodology, which is composed of two concepts, the biplot concept (Gabriel 1971) and the GGE concept (Yan et al. 2000), was used to visually analyze the rice genotypes MET data. This methodology uses a biplot to show the factors (G and GE) that are important in genotype evaluation and that are also the sources of variation in GE interaction analysis of MET data (Yan 2001). The graphs generated based on (i) "which-won-where" pattern, (ii) ranking of genotypes on the basis of yield and stability, (iii) comparison of genotypes to an ideal genotype, (iv) relationships between testing environments based on the angles between the vectors of the environments, (v) Comparison between any two genotypes. 

**Results and Discussion**

**Combined Analysis of variance**

The results of combined ANOVA for grain yield data showed the environment (E), Genotype (G) and G x E interaction effects accounted for 23.60, 16.27 and 24.89% of the total sum of squares, respectively (Table-1). Significant differences for all sources of variation indicated the effect of environments in the GE interaction, genetic variability among the genotypes and possibility of selection for stable genotypes. As GE interaction was large, therefore, we can further proceed and estimate phenotypic stability (Farshadfar and Sutka 2003).

<table>
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<th>MS</th>
<th>%SST</th>
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<td>16.28</td>
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<td>23.6</td>
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<td>19.5</td>
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<tr>
<td>Total</td>
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**Polygon view of GGE biplot analysis of MET data**

The polygon view of a biplot is the best way to visualize the interaction patterns between genotypes and environments (Yan and Kang 2003) to show the presence or absence of cross over GE interaction which is helpful in estimating the possible existence of different mega environments (Gauch and Zobel, 1997, Yan and Rajcan, 2002, Yan and Tinker 2006).

Visualization of the "which won where" pattern of MET data is necessary for studying the possible existence of different mega environments in the target environment (Gauch and Zobel, 1997, Yan et al. 2000). Fig. 1 represents a polygon view of rice genotype MET data in this investigation. In this biplot, a polygon was formed by connecting the vertex genotypes with straight lines and the rest of the genotypes placed within the polygon. The partitioning of GE interaction through GGE biplot analysis showed that $PC1$ and $PC2$ accounted for 49.4% and 39.1% of GGE sum of squares, respectively, explaining a total of 88.5% variation. The vertex genotypes in this study were G2, G4, G3 and G6. These genotypes were the best or the poorest genotypes in some or all of the environments because they were farthest from the origin of the biplot (Yan and Kang, 2003). From the polygon view of biplot analysis of MET data, the genotypes fell in three sections and the test environments fell in two sections. The first section contains all most test environments E6, E3, E1, E5 and E2 with G2 and G4 as the best yielder. And the second section contains only one environment E4 with G3 as the poorest yielder. The other vertex genotype G6 was the poorest-yielding genotype in any environment. They were located far away from all of test locations, reflecting the fact that they yielded poorly at each location. Also, those genotypes within the polygon (for example G1 and G5 for E4) were less responsive to location than the vertex genotypes (Rahmatollah et al. 2013).
Ranking of Genotypes based on Yield and Stability performance

The estimation of yield and stability of genotypes (Figure 2) was done by using the average coordinates of the environment (AEC) methods (Yan, 2001; Yan and Hunt, 2001). The average environment is defined by the average values of PC1 and PC2 for all environments and is presented with a circle. The average ordinate environment (AOE) defined by the line which is perpendicular to the AEA (average environment axis) line and pass through the origin. This line divides the genotypes into those with higher yield than average and in to those lower yield than average. By projecting the genotypes on AEA axis, the genotypes are ranked by yield, where the yield increases in the direction of the arrow. In this study the highest yield had genotypes G2, G4, G5, G1 and the lowers had G3 and G6. Stability of the genotypes depends on their distance from the AEA abscissa. Genotypes closer to abscissa are more stable than others. In this study, the greatest stability in the high yielding group had genotypes G4, G5 and G1, while the most stable of all was G4. These results are in agreement with those obtained by Naheif (2013) in wheat.

Evaluation of genotypes relative to an ideal genotype

The genotype ranking is shown on the graph of genotype so-called “ideal” genotype (Figure 3). An ideal genotype is defined as one that is the highest yielding across test environments and it’s absolutely stable in performance (that ranks the highest in all test environments) (Yan and Kang, 2003, Farshadfar et al. 2012). Although such an “ideal” genotype may not exist in reality, it could be used as a reference for genotype evaluation (Mitrovic et al. 2012). A genotype is more desirable if it is located closer to “ideal” genotype (Kaya et al. 2006 and Mitrovic et al. 2012).
to the “ideal” genotype was G4. Ranking of other genotypes based on the ideal genotype was G2 > G5 > G1. In other words, the lower yielding genotypes (G3 and G6) were unfavorable because they are far from the ideal genotype. The relative contributions of stability and grain yield to the identification of desirable genotype found in this study by the ideal genotype procedure of the GGE biplot are similar to those found in other crop stability studies (Samonte et al. 2005, Fan et al. 2007).

**Evaluation of Environment based on Discrimination & representativeness**

The length of an environment vector is proportional to the standard deviation of cultivar means in the environment, which is a measure of the discriminating power of the environment, assuming that the experimental errors of the test environments are comparable. Therefore, among the six environments, E6 and E4 were most discriminating (informative) and E2 and E5 least discriminating (Fig. 4). Test environments that are consistently non-discriminating (non-informative) provide little information on the genotypes and, therefore, should not be used as test environments. Representativeness of Test Environments Figure 4 presents the same biplot as Fig. 2 except that an “Average-Environment Axis” [AEA, or average-tester-axis, Yan (2001)] has been added. The average environment (represented by the small circle at the end of the arrow) has the average coordinates of all test environments, and AEA is the line that passes through the average environment and the biplot origin. A test environment that has a smaller angle with the AEA is more representative of other test environments. Thus, E1 and E3 are most representative whereas E6 and E4 least representative. Test environments that are both discriminating and representative (e.g., E1) are good test environments for selecting generally adapted genotypes. Discriminating but non-representative test environments (e.g., E6 and E4) are useful for selecting specifically adapted genotypes if the target environments can be divided into mega-environments. Discriminating but non-representative test environments (e.g., E6) are useful for culling unstable genotypes if the target environment is a single mega-environment. Non-discriminating test environments (those with very short vectors, e.g., E2 and E5) are less useful because they provide little discriminating information about the genotypes.
Comparison between Two Genotypes

In a GGE biplot, two genotypes can be visually compared by connecting them with a straight line, followed by drawing a perpendicular line that passes through the biplot origin (Fig.5). This perpendicular line is the “equality line” of the two genotypes. That is, the two genotypes to be compared should be equal in all environments that are located on this line. Since the biplot distance of the line that connects the two genotypes measures the Euclidian distance between them, comparison using the method is meaningful, because the connection line is long enough. A genotype has higher values in environments that are located on its side of the equality line. Thus, G2 and G4 had higher yield in all environments except E4. The difference between two genotypes varies by environment, being proportional to the distance of the environment to the equality line. Thus, the difference between G2 and G4 was relatively large in E6 but very small in all other environments.

Conclusion

In this present study, we found that E1 and E3 two mega environments are good test environments for selecting generally adapted genotypes and G4 genotype demonstrated a high grain yield over all other genotypes as well as stability of performance across test locations and presenting a good plant material for future breeding program. Furthermore the GGE biplot procedure was an effective tool for visual interpretation of the complex GE interaction and yield stability for studies applied to plant breeding programs.

References

BRRI 2010. Adhunik dhaner chash(15th edition), Bangladesh Rice Research Institute, Gazipur- 1701, Bangladesh, p.20-50


