GGE Biplot Analysis of Genotype x Environment Interaction in Basmati Rice (*Oryza sativa* L.)

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**A B S T R A C T**

Nature and magnitude of genotype x environment interaction (GEI) was studied among 12 Basmati rice genotypes across four environments viz., normal transplanting, late transplanting, system of rice intensification (SRI) and direct seeded rice (DSR) during *Kharif 2016* using GGE biplot analysis. Genotype x management interaction followed by environment was found to be the major source of variation and the first two principal components (PCs) of GGE biplot accounted for more than 70% of variation for yield. As per AMMI analysis, discriminating ability of E2 and E3 was found to be closest to the ideal environment and G5 and G10 are top performing in E2 and E3 and G6 and G8 are better performing in E4 and E1 respectively while, stability mean of genotypes revealed that G4 is most stable cultivar and G8, G9 and G6 are the most unstable cultivars. ‘Which-won-where’ analysis revealed two mega environments (ME) among the test locations, with ME1 represented by 2 locations E2 and E3 with G10 as winning genotype and ME2 with 2 locations E1 and E4 with G6 as another winning genotype.

**Keywords**

GGE biplot, G x E interaction, Basmati.

**Introduction**

Rice (*Oryza sativa* L.) is one of the most important cereals, providing the caloric needs of millions of people daily. In India, during *Kharif 2016* it was cultivated over an area 44.0 m ha with production and productivity of 108.8 m tones and 2.47 tones/ha respectively (Anonymous, 2016). In J & K state rice was cultivated over an area of 271.49 thousand hectare with production and productivity of 5567 thousand quintals and 21.51 quintals hectare⁻¹, respectively (Anonymous, 2014). In Jammu region of J&K state Basmati rice commands a premium place being cultivated on an area of 62.25 thousand hectares and has great export potential to augment the income of the farmers. In present scenario of global warming water has become limiting factor and water resources both surface and underground are shrinking. In such a situation alternative methods that are more water efficient and less labour intensive needs to be explored so as to enable farmers to produce more at less cost. Stability of genotype across environments is a pre requisite for recommending varieties and various statistical models like Analysis of variance (ANOVA), Principle component analysis (PCA) and Linear regression have been suggested over time to understand the complex GEI. Genotype (G) main effect plus GE interaction
(GGE) biplot analysis is a robust method to visualize and interpret multi environment data graphically as well and its utility in understanding GEI has been demonstrated in many crops including rice. In the present study an attempt has been made to have an insight into the nature and magnitude of GEI among 12 basmati rice genotypes across four environments using GGE biplot analysis. In addition efforts were also made to identify Mega environments within the test locations.

**Materials and Methods**

The present investigation was carried on during *Kharif* 2016 at experimental area of Division of Plant Breeding and Genetics SKUAST-Jammu in which 12 locally adapted as well as improved basmati cultivars (Table 1) were evaluated across four environments designated as E₁ (Normal transplanting), E₂ (Late transplanting), E₃ (System of rice intensification) and E₄ (Direct seeded). The experiment was conducted in Randomized Block Design (RBD) with three replications having a plot size of 2 m² in each replication each environment. Standard crop management practices as applicable were followed in all the four environments. Yield data was recorded at physiological maturity and plot data harvested was converted to kg ha⁻¹ using the plot size as factor.

**Data analysis**

The data so generated was analyzed using R studio software. GEI was analyzed by the use of biplot graph in which the yield means are plotted against the scores of first principal component of interaction (IPCA1). Similarly, data was analysed for discriminativeness vs representativeness ranking of environments and ranking of genotypes relative to ideal environment and ranking of environment based on ideal genotype was also performed. Mega-environments and winning genotypes in given set of environments was identified by using option ‘which-won-where’.

**Results and Discussion**

The presence of GEI was clearly demonstrated by AMMI model and the interaction was portioned among the first two interaction principal component axis (IPCA), as 65.56% and 20.08% respectively (Table 2); while the cumulative variance was 85.64% for PCAI and PCAII thereby, demonstrating that genotypes may be selected for adaptation to specific environments. These results are in harmony with the findings of Aina *et al.*, (2009) and XuFei-fei *et al.*, (2014) in G x E interactions effects. The environmental variance was also found to be significant which indicates that the environments under study were different from each other.

The model was additive and the results of AMMI analysis were represented in the form of graphs called biplots (Gauch and Zobel, 1996). Further Gauch (1988) recommended that the most accurate model for AMMI can be predicted by using first two principal component analysis. Admassu *et al.*, (2008), in accordance with Zobel *et al.*, (1988), proposed that two interaction principal component axes for the AMMI model were sufficient for a predictive model. Thus, the interaction of 12 rice genotypes with four environments was predicted by the first two components of genotypes and environments (Sivapalan *et al.*, 2000).

Stable genotypes were identified by graphical representation (GGE biplot) which uses genotype and G x E components and identifies G x E interaction pattern of multi-environment data and clearly shows which variety performs best in which environment (Lakew *et al.*, 2014). Vijaykumar *et al.*, (2001) detailed that these biplots help in visual interpretation of GE patterns and
identify genotypes or environment that exhibit low, medium or high interaction effects.

**Identification of stable genotypes with highest mean performance**

In GGE biplot the complex GEI are partitioned in different principal components (PCs) and the data obtained are presented graphically against PCs. GGE biplots captured 85.64% of the variation via PC1 (65.56%) and PC2 (20.08%). Figure 1 depicts the GGE biplot abridgment mean performance and stability of different genotypes. The stability of genotype is analyzed by the absolute length of the projection of a genotype. The greater the absolute length of projection of a genotype, the less stable it is. Thus, G6, G7, G4 and G9 were the best performing genotype followed by G2, G3 and others. G10 was observed as most unstable genotype. The genotype, G7 was closest to the ‘ideal genotype’ followed by G9, G6 and G4, which is denoted by small circle at the center of concentric rings in Figure 2. An ‘ideal genotype’ is stable performer across environments.

**Table.1** Details of genotypes used in study

| S. No. | Genotype         | Code | S. No. | Genotype         | Code |
|--------|------------------|------|--------|------------------|------|
| 1      | Basmati 370      | G1   | 7      | Pusa Basmati 1121| G7   |
| 2      | Basmati 564      | G2   | 8      | Pusa 1401        | G8   |
| 3      | Saanwal Basmati  | G3   | 9      | Pusa Basmati 1509| G9   |
| 4      | Ranbir Basmati   | G4   | 10     | Pusa Basmati 1   | G10  |
| 5      | Jammu Basmati 129| G5   | 11     | CSR 30           | G11  |
| 6      | Pusa Sugandh 2   | G6   | 12     | Pusa 1460        | G12  |

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

| Source of variation       | df  | MS       | Variation explained (%) |
|---------------------------|-----|----------|-------------------------|
| Environment (E)           | 3   | 74.40**  |                         |
| Genotype (G)              | 11  | 7.47*    |                         |
| G X E interaction         | 33  | 1.94*    | 85.64                   |
| IPCA1                     | 13  | 3.24**   | 65.56                   |
| IPCA2                     | 11  | 1.17*    | 20.08                   |
| Error                     | 94  | 0.09     |                         |
| Total                     | 143 | 3.03     |                         |

* and ** indicate significances at the P<0.01 and P<0.001 respectively.
Fig.1 GGE Biplot of combined analysis for yield: Mean vs. Stability of genotypes

Fig.2 Ranking of genotypes relative to an ideal genotype

Fig.3 GGE biplot analysis

Fig.4 Ranking of environments based on discriminating ability and representatives

Fig.5 GGE biplot combined analysis: ‘Which-won-where’
Combined GGE biplot analysis of genotypes

In Figure 3, genotypes G9, G4 and G2 were close or at origin and therefore found more stable. Genotypes G4, G9, G7, G2, G3, G12 and G5 showed positive interaction with E1, E2 and E4 whereas, others genotypes G1, G10, G8 and including G9, G6 and G7 showed positive interaction with E3.

Environment evaluation

Angles between environment vectors in biplots indicate their relationship as the cosine of the vector angles is indicative of their correlation. Acute angle between two environment vectors indicates positive correlation while an obtuse angle indicates negative correlation and right angle suggests no relation. Environments show complex relationship among themselves. The ‘ideal environment’ is denoted by a small circle at the center of the concentric rings.

The maximum discriminating ability and representativeness with highest vector length indicates an ‘ideal environment’. E2 with E4 and E1 with E2 and E3 having acute angles (Fig. 4) were positively correlated with ideal environment. Environments generating similar information may be removed from multi-location testing as they will provide similar results. This will help in optimum allocation of limited resources during multi-location trials. Obtuse angled vectors show negative correlation with ideal environment for instance E4 with E3 and E2 with E4. Discrimination ability of the environments was measured by the length of the environment vectors and the testing environment could be ranked from top to bottom as E3>E1>E2>E4. E2 and E4 were found to be closest to the ideal environment and E3 was considered as an “ideal environment”.

“Which-won-where” and mega environment identification

‘Which-won-where’ analysis involving GEI, mega-environment differentiation, specific adaptation of genotypes etc. are graphically addressed (Fig. 5). Genotypes located on the vertices of the polygon performed either the best or the poorest in one or more environments (Yan and Kang 2003). In the current study ‘Which-won-where’ biplots gave rise to a pentagon with five genotypes, G3, G5, G7, G10 and G11 at vertices. The equality lines divided the biplot into five sectors effectively. Four testing environments were spread within the biplot, three in one and one in other sector. Testing environment could be partitioned into mega-environment (ME). Three out of five sectors had no single environment and hence it did not reflect any separate ME and could be merged into nearest MEs. First ME (ME1) was represented by E1, E2 and E4 with G7 as winning genotype and second ME (ME2) was composed of E3 with G10 as another winning genotype. Thus, this study established the effectiveness of GGE biplot analysis in identifying stable and superior genotypes. Similar findings and interpretation have been made by Adugna et al., (2007); Anandan et al., (2010) and Islam et al., (2014). Several authors used AMMI to evaluate multi-environment experiments to distinguish the effects of the genotype and the environment and then assess the G x E interaction in a reduced dimensional space with minimum error (Kandus et al., 2010).

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