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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 E_2 and E_3 was found to be closest to the ideal environment and G_5 and G_{10} are top performing in E_2 and E_3 and G_6 and G_8 are better performing in E_4 and E_1 respectively while, stability mean of genotypes revealed that G_4 is most stable cultivar and G_8, G_9 and G_6 are the most unstable cultivars. 'Which-won-where' analysis revealed two mega environments (ME) among the test locations, with ME1 represented by 2 locations E_2 and E_3 with G_{10} as winning genotype and ME2 with 2 locations E_1 and E_4 with G_8 as another winning genotype.

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 o 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 E_1 (Normal transplanting), E_2 (Late transplanting), E_3 (System of rice intensification) and E_4 (Direct seeded). The experiment was conducted in Randomized Block Design (RBD) with three replications having a plot size of 2 m^2 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 discrimitiveness *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, G_6, G_7, G_4 and G_9 were the best performing genotype followed by G_2, G_3 and others. G_{10} was observed as most unstable genotype. The genotype, G_7 was closest to the 'ideal genotype' followed by G_9, G_6 and G_4, 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	G_1	7	Pusa Basmati 1121	G_7
2	Basmati 564	G_2	8	Pusa 1401	G_8
3	Saanwal Basmati	G_3	9	Pusa Basmati 1509	G_9
4	Ranbir Basmati	G_4	10	Pusa Basmati 1	G_{10}
5	Jammu Basmati 129	G_5	11	CSR 30	G_{11}
6	Pusa Sugandh 2	G_6	12	Pusa 1460	G_{12}

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	

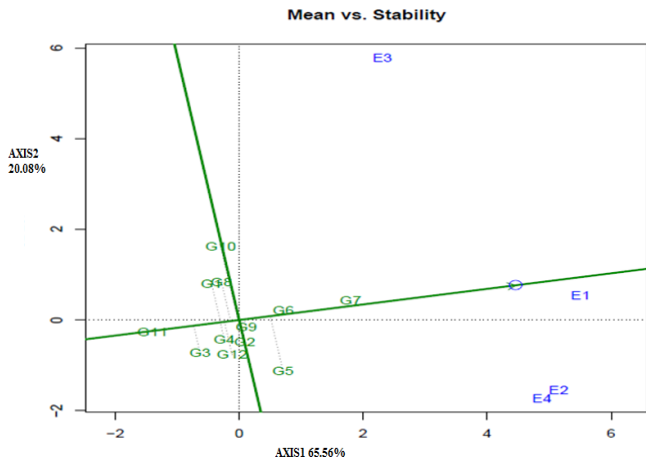* and ** indicate significances at the $P<0.01$ and $P<0.001$ respectively.

Fig.1 GGE Biplot of combined analysis for yield: Mean vs. Stability of genotypes
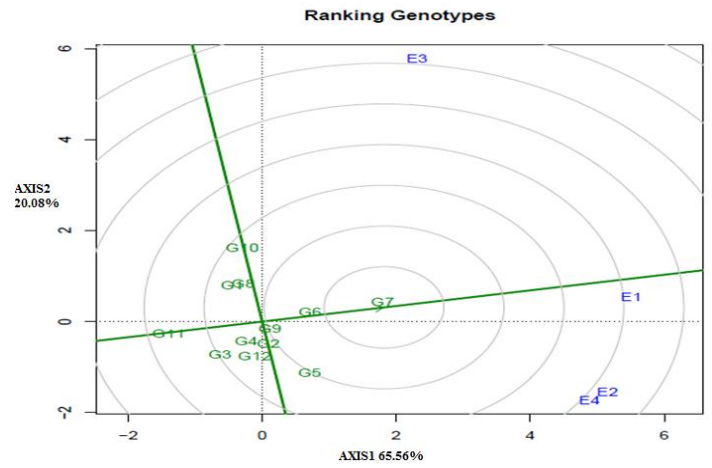

Fig.2 Ranking of genotypes relative to an ideal genotype
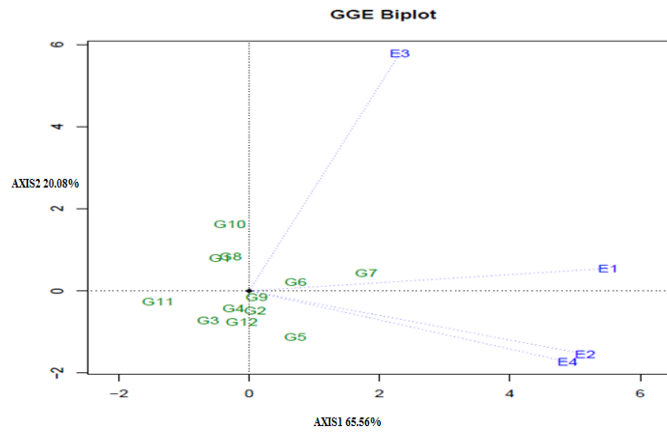

Fig.3 GGE biplot analysis
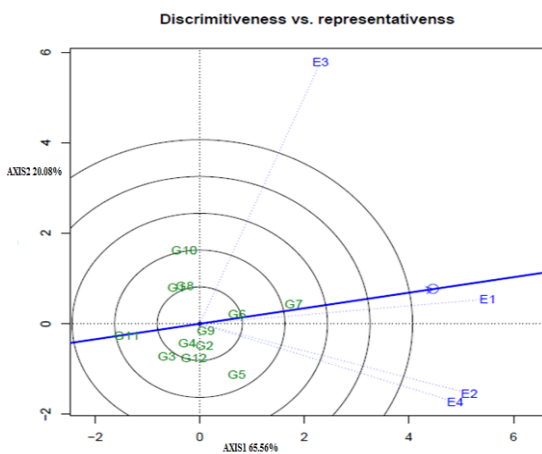

Fig.4 Ranking of environments based on discriminating ability and representatives
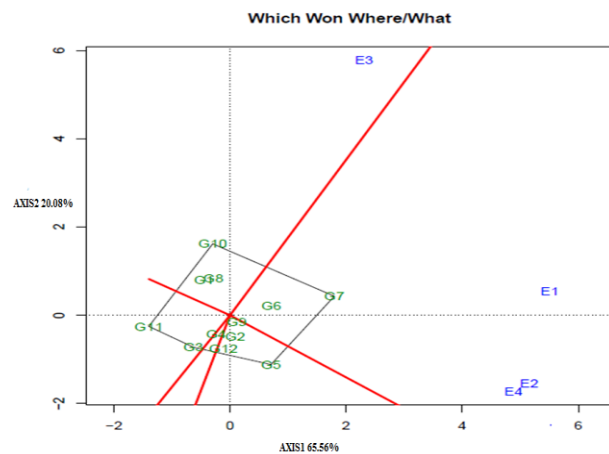

Fig.5 GGE biplot combined analysis: 'Which-won-where'

Combined GGE biplot analysis of genotypes

In Figure 3, genotypes G_9, G_4 and G_2 were close or at origin and therefore found more stable. Genotypes G_4, G_9, G_7, G_2, G_3, G_{12} and G_5 showed positive interaction with E_1, E_2 and E_4 whereas, others genotypes G_1, G_{10}, G_8 and including G_9, G_6 and G_7 showed positive interaction with E_3.

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'. E_2 with E_4 and E_1 with E_2 and E_3 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 E_4 with E_3 and E_2 with E_4. 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 $E_3 > E_1 > E_2 > E_4$. E_2 and E_4 were found to be closest to the ideal environment and E_3 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, G_3, G_5, G_7, G_{10} and G_{11} 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 E_1, E_2 and E_4 with G_7 as winning genotype and second ME (ME2) was composed of E_3 with G_{10} 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).

References

Admassu, S., Nigussie, M. and Zelleke, H. 2008. Genotype x environment interaction and stability analysis for grain yield (*Zea mays* L.) in Ethiopia. *Asian J. Plant Sci*, 7: 163-169.

Adugna, A. 2007. Assessment of yield stability in sorghum. *African Crop Sci. J*, 15: 83-92.

Aina, O. O., Dixon, A. G. O., llona, P. and Akinrinde, E. A. 2009. G × E interaction effects on yield and yield components of cassava (landraces and improved) genotypes in the savanna regions of Nigeria. *African J of Biotech*, 8: 4933-4945.

Anandan, A., Eswaran, R., Sabesan, T. and Prakash, M. 2009. Additive main effects and multiplicative interactions analysis of yield performances in rice genotypes under coastal saline environments. *Advances in Biological Research*, 3: 43-48.

Anonymous, 2014. Digest of Statistics. Directorate of Economics and Statistics, Govt of Jammu & Kashmir.

Anonymous, 2016. Agricultural Statistics at a Glance. Directorate of Economics and Statistics, Ministry of Agriculture, Govt of India.

Gauch, H. G. 1988. Model selection and validation for yield trials with interaction. *Biometrics,* 44: 705-715

Gauch, H. G. and Zobel, R. W. 1996. AMMI analysis of yield trials. In: Genotype-by-Environment Interaction, Kang MS and HG Gauch (Eds.). Boca Raton CRE CRC, New York, USA, 85-122.

Islam, M. R., Anisuzzaman. H, Khatun. H, Sharma. N, Islam. M. Z., Akter. A., and Biswas S. Partha. 2014. AMMI Analysis of yield Performance and stability of Rice genotypes across different Haor areas. *Eco friendly Agriculture Journal*, 7: 20-24.

Kandus, M., Almorza, D., Boggio, R. R. and Salerno, J. C. 2010. Statistical methods for evaluating the genotype-environment interaction in maize (*Zea mays* L.). *Phy. Yld*, 39-46.

Lakew, T., Tariku, S., Alem, T. and Bitew, M. 2014. Agronomic performances and stability analysis of upland rice genotypes in North West Ethiopia. *International Journal of Scientific and Research*, 4: 1-9.

Sivapalan, S., Brien, L. O., Ferrana, G. O., Hollamby, G. L., Barelay, I. and Martin, P. J. 2000. An adaptation analysis of Australian and CIMMYT/ICARDA wheat germplasm in Australian production environments. *Australian Journal of Agricultural Research*, 51: 903-915.

Vijayakumar, C. H. M., Ahmed, M. I., Viraktamath, B. C., Balakrishnan, R. and Ramesha, M. S. 2001. Genotype x Environment interaction effects on yield of rice hybrids in India. *Indian Journal of Genetics and Plant Breeding*, 61: 98-100.

XuFei-fei, TANG Fu-fu, SHAO Ya-fang, CHEN Ya-ling, TONG Chuan, BAO Jing-song. 2014. Genotype × environment interaction for agronomic traits of rice revealed by association mapping. *Rice Science,* 21: 133-141.

Yan, W., Kang, M. S. 2003. GGE biplot analysis: a graphical tool for breeders, geneticists and agronomists CRC Press, Boca Raton, FL.

Zobel, R. W., Wright, M. J., Gauch, H. G. 1988. Statistical analysis of a yield trial. *Agron. J,* 80: 388-393.