

Genotype by environment interactions for grain yield in upland breeding lines of rice under direct seeded conditions across multi-environments

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Abstract

Eighteen rainfed upland breeding lines were evaluated under four environments in randomized complete block design with three replications. Data on grain yield were subjected to combined ANOVA and AMMI analysis. The AMMI model was applied, with additive effects for the 18 breeding lines of rice genotypes (G) and four seasons of testing (Environments = E), and multiplicative term for genotype $\times$ environment interaction. The AMMI statistical model has shown that more than 50% proportion of the total variation in grain yield was attributed due to genotype $\times$ environment interaction. Most of the breeding lines showed environment specificity. CR2897-11-1 and CR2881-8-1 were found to be favorable during 2011 (En. 4) and CR2908-12-5-1 and CR2899-7-1 were found to be favorable in the year 2010 (En. 3) with grain yield more than 3 t ha⁻¹.

Key words: Rice, AMMI, upland, stability

Rice is the staple food of over half the world's population. It is one of the most important food crops of India in term of area, production and consumer preference. Development and adaption of high yielding cultivars under wide range of diversified environments is one of the major goals for the plant breeders in crop improvement programme. Therefore, the present study of the genotype $\times$ environment interaction (GEI) is important in plant breeding programs because a significant GEI can seriously impair efforts in selecting superior genotypes in relation to new crop introductions and cultivar development programs leads to successful evaluation of stable genotype, which could be used

for general cultivation (Vasgas et al. 2001; Reza et al. 2007). AMMI biplot analysis is considered to be an effective tool to diagnose GEI patterns graphically. In AMMI, the additive portion is separated from interaction by analysis of variance (ANOVA). Then the Principal Component Analysis (PCA), which provides a multiplicative model, is applied to analyze the interaction effect from the additive ANOVA model. The biplot display of PCA scores plotted against each other provides visual inspection and interpretation of GEI components. Integrating biplot display and genotypic stability statistics enables genotypes to be grouped based on similarity of performance across diverse environments (Thillainathan and Fernandez 2001). The results of AMMI analysis are useful in supporting breeding program decisions such as specific and broad adaptation and selection of environment (Raza et al. 2007; Zobel et al. 1988; Gauch 2006, 2013). Therefore, the objectives of this study were to assess the extent of genotype $\times$ environment interaction for grain yield, to evaluate rice genotypes for their yield and stability and to select the rice genotypes with high grain yield for their differential responses to environments.

For this purpose, eighteen rainfed upland breeding lines (Table 1) were evaluated over years in randomized complete block design (RCBD) with three replications at Central Rice Research Institute during four consecutive years from 2008-2011. Each year was considered an environment thus the material was

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Table 1. List of upland rice genotypes along with their pedigree and mean performance for grain yield in four environments

Genotype	Pedigree	Yield (t ha ⁻¹)
CR3424-13	IR64/Addysel	2.73
CR3426-10-1	Apo/ <i>O.nivara</i> //Apo	2.81
CR2902-5	Naveen/CR143-2-2	2.65
CR2903-17-1	IR20/Dandi	3.40
CR2904-14-8	Naveen/Dandi	3.57
CR2908-12-5-1	IR20/Apo	3.36
CR2910-2-1	IR20/Dandi	3.73
CR2896-7	Naveen/CR143-2-2	3.38
CR2897-11-1	CR143-2-2/ <i>O.nivara</i> //CR143-2-2	3.65
CR2898-4-2-1	CR143-2-2/Addysel	3.76
CR2899-7-1	Lalat/Selumpikit	3.95
CR2900-3-6-1	Naveen/Selumpikit	3.85
CR2901-12-5	Lalat/Addysel	2.46
CR2902-6-1	Naveen/CR143-2-2	2.67
CR2882-6-7	Lalat/Addysel	2.20
CR2881-8-1	CR143-2-2/Swarna	3.01
CR2880-5-4	Naveen/Kalakari	2.86
CR2884-12-3-1	CR143-2-2/Addysel	3.25

evaluated in 4 environments (2008 = Env. 1, 2009 = Env. 2, 2010 = Env. 3 and 2011 = Env. 4). Each breeding line was dry direct seeded at 2-3 cm soil depth by hand plough with the seed rate of 60 kg ha⁻¹ to maintain 3-4 seeds hill⁻¹ in four rows of 4m length with 20 cm row spacing. Appropriate agronomic and cultural were undertaken in order to raise a healthy crop. At harvest, grain yields was adjusted at 12% moisture level and then converted to yield t ha⁻¹.

Grain yield data were subjected to combined ANOVA and AMMI (Thillainathan and Fernandez 2001) analysis. The SAS 9.2 (SAS Institute 2010) software was used for combined ANOVA and AMMI analysis. The combined analysis of variance showed genotype (G), environment (E) and genotype × environment interaction (GEI) were significant ($P = 0.01$) for grain yield. Genotypic, environment and their interaction effects explained 21.10%, 25.84% and 50.80% variation in the yield respectively. The significant GEI effects demonstrated that genotypes responded differently to the variation in environmental conditions. The mean grain yield of the 18 genotypes ranged from

2.20 to 3.94 t ha⁻¹ and, the highest grain yield was obtained from genotypes GEN11. The AMMI analysis of variance for grain yield (t ha⁻¹) of 18 breeding lines tested in four environments showed that 42.02% of the total sum of squares was attributed to environmental effects, only 26.44% to genotypic effects and 51.98% to genotype × environment interaction effects which were significant at $P = 0.01$ probability level. The GEI sum of squares was about 2.4 times larger than that for genotypes, which determined substantial differences in genotypic response across environments.

The presence of 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 at $P = 0.01$ probability level. This implied that the interaction of the 18 rice genotypes with four environments was predicted by the first three components of genotypes and environments.

The biplot generated through AMMI analysis (Fig. 1) showed main effects and the first principal component scores of interaction (IPCA1) of both genotypes and environments. In the biplot display, genotypes or environments that appear almost on a perpendicular line of a graph had similar mean yields and those that fall almost on a horizontal line had similar interactions (Crossa et al. 1990). Thus, the relative variability due to environments was greater than that due to genotypic differences. Genotypes or environments with large negative or positive IPCA scores have high interactions, while those with IPCA1 scores near zero (close to horizontal line) have little interaction across environments and vice versa for environments (Goucha and Zobel 1996) and are considered more stable than those further away from the line. In the biplot, genotypes CR2897-11-1, CR2881-8-1, CR2901-12-5 and CR2882-6-7 were vertically distant apart; however, they did not fall close to the horizontal line. This implies that these genotypes lack stability but had high yield potential in favorable environments.

Since, IPCA2 scores were also important (21.77% of $G \times E$ SS) in explaining genotype × environment interaction, the biplot of the first two IPCAs was also used to demonstrate the relative magnitude of the GEI for specific genotypes and environments (Fig. 2). The IPCA scores of genotypes in the AMMI analysis is an indication of stability or adaptation over environments (Goucha and Zobel 1996). The greater

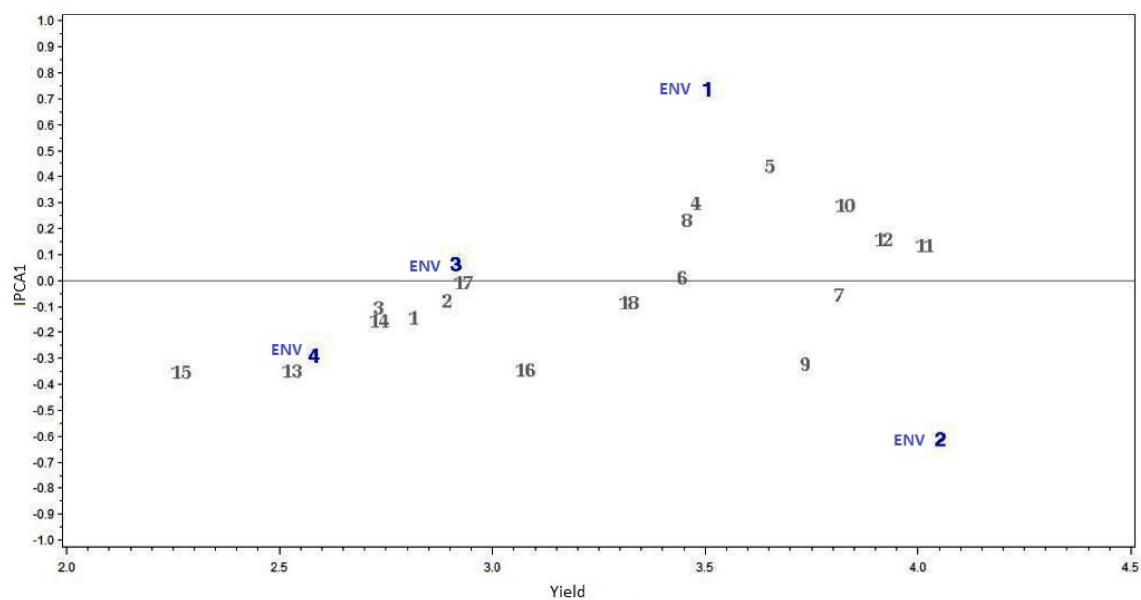


Fig. 1. AMMI biplot of 18 rice genotypes and four environments for grain yield (t ha^{-1}) using genotypic and environmental scores

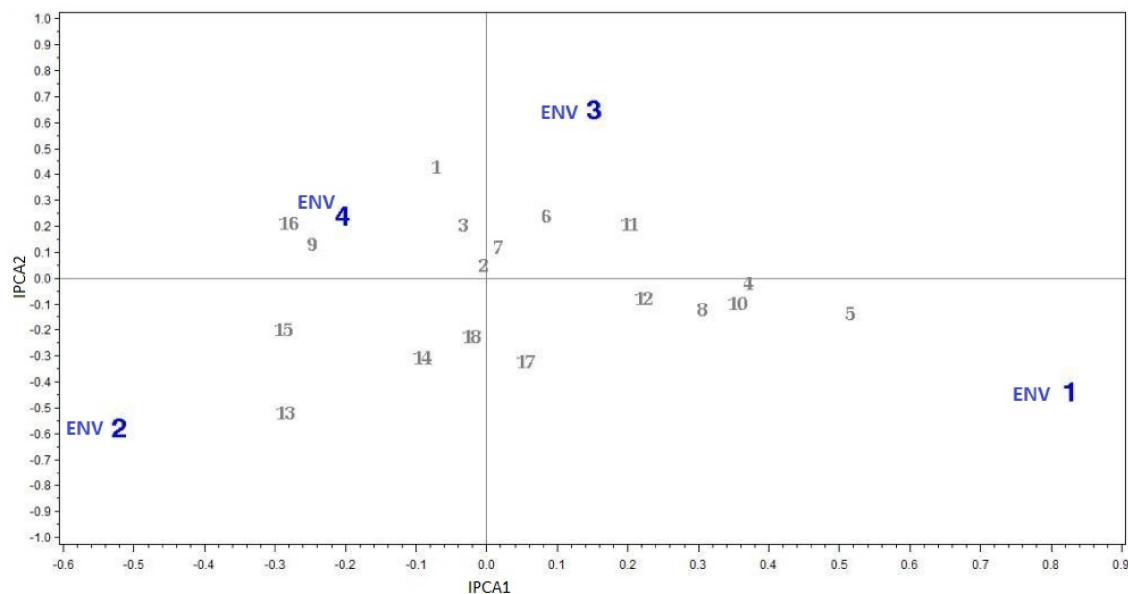


Fig. 2. Biplot of the second interaction principal component axis (IPCA2) against the first interaction principal component axis (IPCA1) scores for grain yield of 18 upland rice genotypes in four environments

the IPCA scores, the more specifically adapted is a genotype to certain environments (Sanni et al. 2009). The more the IPCA scores approximate to zero, the more stable or adapted the genotype is over all the environments sampled. The biplot of the first two IPCA shows that GEN2 is the best adapted genotype in almost all the environments. CR2897-11-1 and CR2881-8-1 were well adapted to high yielding

environment with yield more than 3 t ha^{-1} of ENV4 and GEN6 and GEN11 were well adapted to high yielding environment with grain yield more than 3 t ha^{-1} of ENV3. Considering all the environments, GEN2 was found to be nearer to IPCA1 and IPCA2 scores close to zero line. Hence, GEN2 is considered as stable genotype but with low grain yield (2.81 t ha^{-1}). The result shows that more than 50% proportion of the

total variation in grain yield was attributed to GEI. As a result, almost all of the evaluated breeding lines were affected by GEI effects. Most of the breeding lines showed environment specificity. GEN2 was found to be stable in almost all the environments with low yield (2.81 t ha^{-1}). GEN 9 and GEN 16 were found to be favorable in ENV4 and GEN6 and GEN11 were found to be favorable in ENV3 with grain yield more than 3 t ha^{-1} .

References

- Vargas M., Crossa J., Van Eeuwijk F., Sayre K. D. and Reynolds M. P. 2001. Interpreting treatment x environment interaction in agronomy trials. *Agronomy J.*, **93**: 949-960.
- Reza M., Armon M., Shabani A. and Daryaei A. 2007. Identification of stability and adaptability in advanced durum genotypes using AMMI analysis. *Asian J. Plant Sci.*, **6**(8): 1261-1268.
- Zobel R.W., Wright M. J. and Gauch H. G. 1988. Statistical analysis of yield trial. *Agron J.*, **80**: 388-393.
- Gauch H. G. 2006. Statistical analysis of yield trials by AMMI and GGE. *Crop Sci.*, **46**: 1488-1500.
- Gauch H. G. 2013. A simple protocol for AMMI analysis of yield trials. *Crop Sci.*, **53**: 1860-1869.
- Thillainathan M. and Fernandez G. C. J. 2001. SAS applications for Tai's stability analysis and AMMI model in genotype x environmental interaction (GEI) effects. *J. Hered.*, **92**(4): 367-371.
- Gauch H. G. and Zobel R. W. 1997. Identifying mega-environments and targeting genotypes. *Crop Sci.*, **37**: 311-326.
- SAS Institute 2010. SAS/STAT Version 9.2 SAS Institute, Cary, North Carolina, USA.
- Crossa J., Gauch H. G. and Zobel R. W. 1990. Additive main effects and multiplicative interaction analysis of two international maize cultivar trials. *Crop Sci.*, **30**: 493-500.
- 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, pp. 85-122.
- Sanni K. A., Ariyo O. J., Ojo D. K., Gregorio G., Somado E. A., Sanchez I., Sie M., Futakuchi K., Ogunabayo S. A., Guel R. G. and Wopereis M. C. S. 2009. Additive main effects and multiplicative interaction analysis of grain yield performance in rice genotypes across environments. *Asian J Plant Sci.*, **8**(1): 48-53.