Indian J. Genet., 76(2): 202-204 (2016)
DOI: 10.5958/0975-6906.2016.00033.X

Short Communication

AMMI, GGE biplots and regression analysis to comprehend the G x E interaction in multi-environment barley trials

Vishnu Kumar*, A. S. Kharub, R. P. S. Verma[1] and Ajay Verma

ICAR-Indian Institute of Wheat and Barley Research, Karnal 132 001 Haryana; [1]ICARDA, Rabat, Morocco

(Received: October 2015; Revised: February 2016; Accepted: April 2016)

Abstract

The present study was carried out to ascertain the stable genotypes, environments discrimination and genotype by environment crossovers using different stability models. In AMMI ANOVA, genotype x location interaction implied substantial variation (17.61%) and IPCA1 and IPCA2 altogether captured 65.72% of the interaction mean squares, whereas, in GGE model, PC1 and PC2 captured 36.34 % and 15.74 % variation, respectively. Four genotypes *viz*., BH987, DWRB126, DWRB128 and RD2891and two checks, namely, DWRUB52 and DWRB92 were found stable as per GGE AEC view and AMMI biplot. The genotypes, DWRB126 and RD2891 and check DWRB92 were also observed as consistent performers by regression model. The test environments at Bawal, Navgaon and Hisar were observed representative with better discriminating ability. GGE biplot model was found suitable for polygon, AEC view and test environments evaluation.

Key words: AMMI, GGE, regression, stability, barley

Barley is one of the first domesticated cereals, which globally contributes 5.5-6 and 11-12 per cent of fine and coarse cereals, respectively. Barley is used for food, feed and malt purposes and it also possess good medicinal value due to the presence of high β-glucan and antioxidant properties (Kumar et al. 2014). Genotype by environment interaction (GEI) invariably misleads to researchers and distorts the estimation of genetic parameters *viz*., variances, heritability and correlation (Dehghani et al. 2006). Based on earlier studies conducted in multi-environment trials (MET), different stability models have been proposed. These parametric, non-parametric and multivariate stability models have been further categorized with main focus on grain yield only, both yield and stability and stability only (Alwala et al. 2010; Flores et al. 1998). The Eberhart and Russell (1966) model has been classified in group III by Flores et al. (1998) as it more delineates the stability based on mean, regression coefficient and deviation from the regression. Additive main effects and multiplicative interaction (AMMI) and genotype + genotype by environment interaction (GGE) are popular methods based on singular value decomposition (SVD) and biplot concept (Gauch et al. 2008). GGE is environment-centered principal components (PC) model, while AMMI is doubly-centered PC model (Gauch 2006). During last decade, the AMMI and GGE models were debated for applicability, capturing G + GE, test environment evaluation, units of absicca and ordinates (Gauch et al. 2008; Yan et al. 2007). Therefore, the present study was undertaken with 19 barley genotypes grown at nine diverse production conditions to assess the genotype by environment crossovers, identify stable genotypes and to identify discriminating representative environments vis-a-vis to study of outputs of different methods applied here for G x E analysis.

During *rabi*, 2013-14, multi-environment trials (MET) were conducted at 9 diverse locations namely, Bawal (E1), Durgapura (E2), Navgaon (E3), Hisar (E4), Ludhiana (E5), Bhatinda (E6), Mathura (E7), Karnal (E8) and Modipuram (E9). The experimental material comprised of 19 barley genotypes *viz*., BH987 (G1), BH989 (G2), KB1354 (G3), RD2891 (G4), RD2893 (G5),

---

*Corresponding author's e-mail: vishnupbg@gmail.com

Published by the Indian Society of Genetics & Plant Breeding, F2, First Floor, NASC Complex, PB#11312, IARI, New Delhi 110 012
Online management by indianjournals.com

DWRB122 (G6), KB1363 (G7), KB1349 (G8), DWRB123 (G9), DWRB126 (G10), DWRB124 (G11), RD2894 (G12), BH902 (G13), DWRB128 (G14), DWRUB52 (G15), DWRB92 (G16), DWRB127 (G17), RD2892 (G18) and BH988 (G19). Out of these genotypes, 16 were advance experimental strains and three were the commercial cultivars *i.e.*, BH902, DWRUB52 and DWRB92. The experiments were laid out in randomized complete block design (RCBD) in four replications having 6-row plots with row to row spacing of 18 cm and row length of 5 m. All the standard package and practices were adopted to raise the good crop. The GGE and AMMI biplots were generated using Gen Stat 17.1 and Eberhart and Russell (1966) regression analysis was performed using SPAR.

The highest mean grain yield over the locations was recorded by the check DWRUB52 (56.89 q/ha.) followed by the genotypes DWRB128 (56.83 q/ha.), DWRB123 (55.48 q/ha.) and RD2894 (55.02 q/ha.). The mean grain yield across the locations was depicted as 51.75 q/ha ranging from 35.78 (Karnal) to 86.04 (Mathura) q/ha. In AMMI ANOVA location effect contributed maximum part of the variation (76.51%) followed by genotype x location interaction (17.61%) and genotypic variation (5.88%) (Table 1). Both IPCA1 and IPCA2 were found significant (p<.001) and accounted for 48.46 and 17.26 % of the interaction mean squares, respectively. The genotypes viz., BH987, RD2891, RD2893, DWRB123 and DWRB126 exhibited IPCA2 scores closer to zero and the environments Durgapura, Navgaon, Hisar and Mathura showed high IPCA1 scores. The genotypes KB1363 (0.81), KB1349 (0.88), RD2892 (1.41), DWRB128 (2.12), DWRB92 (2.37), BH988 (2.48), DWRB126 (2.59) etc. had considerably low AMMI stability value (ASV) with general adaptation across the locations. Four genotypes viz. BH987, DWRB126, DWRB128 and RD2891 and the checks, DWRUB52 and DWRB92 were observed with high additive main effects and low interaction effects. While, the environments Hisar, Bhatinda and Mathura etc. were found representative with high interaction effects.

Table 1. Analysis of variance and initial two PC scores of AMMI model

Source	d.f.	SS	MS	F Pr.	%SS
Total	683	180742	265		
Treatments	170	170995	1006	<0.001	94.61
Genotypes	18	10049	558	<0.001	5.88
Environments	8	130830	16354	<0.001	76.51
Block	27	630	23	0.1877	
Interactions	144	30116	209	<0.001	17.61
IPCA 1	25	14593	584	<0.001	48.46
IPCA 2	23	5197	226	<0.001	17.26
Residuals	96	10325	108	<0.001	
Error	486	9118	19		

In GGE biplot, PC1 and PC2 captured 36.34 and 15.74 % variation, respectively and accounted for total of 52.08 % variation. The vertex genotypes were observed as DWRB123, DWRB124, DWRB128 and RD2894. Equality line between genotypes, DWRB124 and DWRB128 indicated that DWRB128 was better performer at E3 (Navgaon), E4 (Hisar), E7 (Mathura) and E9 (Modipuram), while DWRB124 won at E5 (Ludhiana) (Fig. 1). Nine environments were classified into four sectors and exhibited four different mega environments. The environments E1 (Bawal), E3 (Navgaon) and E4 (Hisar) were contained in same group, while environment E5 (Ludhiana) created separate mega environment. In AEC (Average Environment Coordination) view the genotypes in order of DWRB128>DWRB92>DWRB126>DWRUB52>RD2891>BH987 were observed with high values on absicca and low interaction for ordinate values. The desired genotypes had the high *per se* and stable

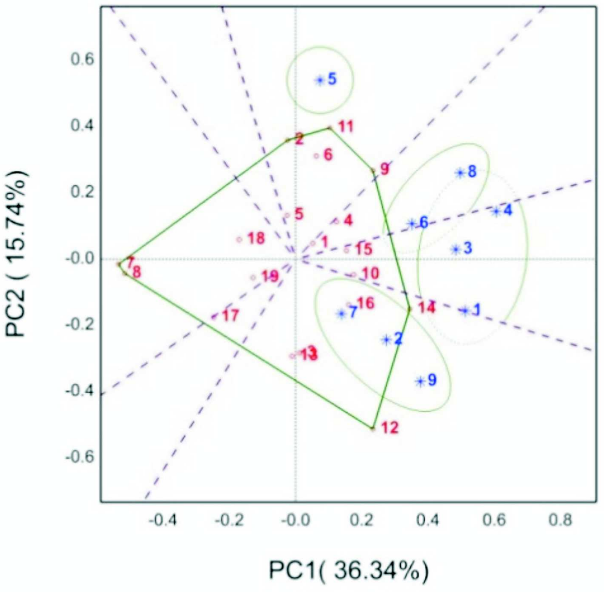

Fig. 1. Which won where pattern in GGE model

performance in different environments (Kumar et al. 2014). The environments, Bawal, Navgaon and Hisar were observed as potential environments for discriminating ability and representativeness. Yan et al. (2000) also emphasized that the environments with long vectors and less cosines are more discriminating and representative for consideration in future studies.

In regression analysis, the genotypes, viz., RD2891 (μ=53.91 q/ha, b=0.76 and S^2d_i=6.41), DWRB126 (μ=53.08 q/ha, b=0.86 and S^2d_i=8.67) and check DWRB92 (μ=53.99 q/ha, b=1.17 and S^2d_i=16.17) showed high mean grain yield accompanied with regression coefficient near to unity and exhibited low deviation from the regression. Whereas, the genotypes, namely, BH987, DWRB123, DWRB124, DWRB128 and check DWRUB52 depicted high mean and were found suitable for favourable environments. Identification of promising high yielding stable genotypes over the varying environments coupled with biotic/abiotic stresses resistance or quality traits is main aim of plant breeders. Several studies (Asfaw et al. 2009; Alwala et al. 2010; Flores et al. 1998; Rad et al. 2013) for stability analysis conducted earlier, either using Eberhart and Russell joint regression analysis or based on visual graphical tools *i.e.*, AMMI and GGE biplots showed more or less similar results. In regression model, the genotypes, namely, DWRB126 and RD2891 and check DWRB92 exhibited stable performance, while no information for which won where and mega environments could be generated. The Eberhart and Russell model is widely adapted but invariably assumption of linear response of genotypes to environments and inclusion of large number of genotypes and environments may not fulfill the requirements to draw fruitful interferences some-times (Flores et al. 1998).

On the other hand in visual graphical, ANOVA and principal component based AMMI model was quite useful for the identification of relative contribution of treatments (g+l+gl), genotypes, environments and interactions towards total variation in AMMI ANOVA. GGE biplot method is environment centered SVD model and graphically addresses important issues of crossover genotype by environment interaction, mega-environment differentiation, specific adaptation, mean vs. stability view etc. (Yan et al. 2007). The genotypes, BH987, RD2891, DWRB126 and DWRB128 and checks, DWRUB52 and DWRB92 were observed as stable with high mean grain yield, in AMMI and GGE model. Therefore, the environments at Bawal, Navgaon and Hisar were discriminating and representative for genotypic evaluation. GGE model was found suitable for polygon view and better visualization of biplots, while accommodating more number of genotypes and environments.

Acknowledgements

The authors are grateful to all the barley cooperating centres for the conduction of experiments and data recording. The help extended by Dr. Murari Singh, Senior Biometrician ICARDA is duly acknowledged.

References

Alwala S., Kwolek T., McPherson M., Pellow J. and Meyer D. 2010. A comprehensive comparison between Eberhart and Russell joint regression and GGE biplot analyses to identify stable and high yielding maize hybrids. Field Crop Res., **119**: 225-230.

Asfaw A., Alemayehu F., Gurum F. and Atnaf M. 2009. AMMI and SREG GGE biplot analysis for matching varieties onto soybean production environments in Ethiopia. Sci. Res and Ess., **4**: 1322-1330.

Dehghani H., Ebadi A. and Yousefi A. 2006. Biplot analysis of genotype by environment interaction for barley yield in Iran. Agron. J., **98**: 388-393.

Eberhart S. A. and Russell W. A. 1966. Stability parameters for comparing varieties. Crop Sci., **6**: 36-40.

Flores F., Moreno M. T. and Cubero J. I. 1998. A comparison of univariate and multivariate methods to analyze G×E interaction. Field Crop Res., **56**: 271-286.

Gauch H. G. 2006. Statistical analysis of yield trials by AMMI and GGE. Crop Sci., **46**: 1488-1500.

Gauch H. G., Piepho H. P. and Annicchiarico P. 2008. Statistical analysis of yield trials by AMMI and GGE: Further considerations. Crop Sci., **48**: 866-889.

Kumar V., Rathore A., Kharub A. S., Kumar D. and Sharma I. 2014. GGE biplot analysis of multi-locational yield trials and identification of representative environments for barley (*Hordeum vulgare* L.) in India. Res. on Crops, **15:** 871-875.

Rad M. N., Kadir M. A., Rafii M. Y., Jaafar H. Z., Naghavi M. R. and Ahmadi F. 2013. Genotype× environment interaction by AMMI and GGE biplot analysis in three consecutive generations of wheat (*Triticum aestivum*) under normal and drought stress conditions. Aust. J. Crop Sci., **7**: 956-961.

Yan W., Hunt L. A., Sheng Q. and Sulavnics Z. 2000. Cultivar evaluation and mega-environment investigation based on the GGE biplot. Crop Sci., **40**: 597-605.

Yan W., Kang M. S., Ma B., Woods S. and Cornelius P. L. 2007. GGE biplot vs. AMMI analysis of genotype-by-environment data. Crop Sci., **47**: 643-653.