RESEARCH PAPER

AMMI analysis of genotype × environment interaction in bread wheat over rainfed and irrigated conditions

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Abstract

In order to determine stable bread wheat accessions, field experiments were conducted with 20 genotypes for 4 consecutive years under two different irrigated and rainfed conditions. The experiment was laid out in a completely randomized block design with three replications in each environment. Combined analysis of variance showed highly significant differences for the GE interaction indicating the possibility of selection for stable entries. The results of additive main effect and multiplicative interaction (AMMI) analysis revealed that 10% of total variability was justified by the GE interaction which was 2.5 times more than that of genotypes. Ordination techniques displayed high differences for the interaction principal components (IPC1, IPC2 and IPC3), exhibiting that 83% of the GE sum of squares was justified by AMMI1, AMMI2 and AMMI3, i.e. 3.77 times more than that explained by the linear regression model displaying the relative efficiency of AMMI1 model in comparison with regression model. The results of AMMI model and biplot analysis indicated 3 stable genotypes with high grain yield and general adaptability tfor both rainfed and irrigated conditions.

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Introduction

To identify wheat genotypes with wide or specific adaptation to different environments, multi-location yield trails are grown each year. These have led to emperical identification of superior cultivars, some of which have been released in several counties (Asenjo *et al.*, 2003; Basford *et al.*, 2004).

The environments now involve a wide range of photoperiods and temperatures which could cause large genotype(G) × environment(E) interactions (GEI), especially in the semi-arid areas. Large real crossover-type GEI, especially among high yielding lines invalidates recommendations to farmers of the cultivar(s) giving the highest average yield across all test environments. Quantification of GEI and understanding its physiological bases are needed to breed efficiently for superior environments (Vergas *et al.*, 2001; Thomason and Phillips, 2006). Most yield trails are used only to determine which cultivars give the highest average seed yield, and therefore merit recommendation for planting by farmers. Multilocation yield trials facilitate quantification of the environment and GEI effects. However, a fact not generally recognized is that, in addition, every yield trial by analyzing processes that determine yield can inexpensively quantify the genetic, physiological and environmental controls that result in yield differences among cultivars, seasons and locations (Tarakanovas and Rusgas, 2006).

For detailed study of underlying patterns of interactions classical analysis of variance is not effective, therefore, for a more in-depth analysis of interactions, the additive main effects and multiplicative interaction (AMMI) model has been found to be an effective tool (Zobel *et al.*, 1988). AMMI is essentially effective where the assumption of linearity of responses of genotypes to a change in environment is not fulfilled (Zobel *et al.*, 1988; Farshadfar and Sutka, 2006) which is required in stability analysis techniques (Finlay and Wilkinson, 1963; Eberhart and Russel, 1966). The AMMI model

does not require this assumption. It is a hybrid statistical model which incorporates both additive and multiplicative components of the two-way genotype-environment data structure. It separates the additive main effects from the interaction which is analyzed as a series of multiplicative components using principal component analysis and helps to indicate the interaction pattern (Farshadfar and Sutka, 2003). Complex relationships among locations or among genotypes can be adequately represented in a scatter gram (Crossa *et al.*, 1991). Plots, which show both the genotypes and the environments simultaneously are called biplots (Gabriel, 1971). The present investigation was carried out to quantify GE interaction effects on the yield and to determine stable entries within the genotypes pool used in this study.

Materials and methods

Experimental layout and genetic materials

In order to determine stability of 20 bread wheat genotypes field experiments were conducted for 4 consecutive years (2009-2012) under two different conditions (irrigated and rainfed). Therefore 8 environments were created. The experimental layout at each environment was completely randomized block design with three replications. The environments were considered as random factors while genotypes as fixed factors. Plots consisted of two 1m rows spaced 20cm apart. Average rainfall in the research station was 478mm for each year. Maximum and minimum temperature was 44°c and -27°c, respectively, and the region was semi-arid.

Statistical analysis

Combined analysis of variance, Bartlett's test for additivity on grain yield and mean comparison with Duncan's multiple range test were done using MSTAT-C and SPSS statistical softwares. The additive main effect and multiplicative interaction (AMMI) analysis was performed using the model suggested by Crossa *et al.* (1991) as:

$Y_{ij} = \mu + g_i + e_j + \sum_{n=1}^{h} \lambda_n \alpha_{ni}.\gamma_{nj} + R_{ij}$.

Where Yij is the yield of the ith genotype in the jth environment, μ is the grand mean, gi is the mean of the ith genotype minus the grand mean, ej is the mean of the jth environment minus the grand mean, λn is the square root of the eigen value of the principal component analysis (PCA) axis, αni and γnj are the principal component scores for PCA axis n of the ith genotype and jth environment, respectively and Rij is the residual. A biplot based on the singular value decomposition (SVD) of GE contains only the GE interaction and can be referred to as a GE biplot. In contrast a biplot based on the SVD of G and GE contains only G plus GE, and will be characterized as a GGE biplot (Weikai *et al.*, 2000). The GE biplot was projected for 20 genotypes tested at 8 environments. Clustering was computed for the genotype score using an agglomerate hierarchical alogarithm based on Ward's method (Farshadfar, 1998) and the result of cluster grouping for the genotype PCA score was projected in the biplot of PCA1 and PCA2, and the biplot of PCA1 and mean yield. The regression of yield for each variety on the yield means for each environment was computed and the parameters MS-REG, the contribution of each variety to the regression component of the treatment × location (TL)

interaction, and MS-TL, the contribution of each variety to interaction MS, were estimated with the IRRISTAT program.

Results and discussion

Combined analysis of variance

The results of combined analysis of variance (Table 1) showed highly significant differences for genotypes, environments and GE interaction indicating the effect of environment in the GE interaction, genetic variability and possibility of selection for stable entries. As GE interaction was significant, therefore we can further proceed and calculate phenotypic stability (Jalilnejad, 2002; Farshadfar and Sutka, 2003; Farshadfar and Sutka, 2006). As Tukey,s test of additivity was not significant, it can be concluded that the effects are additive and additivity assumption of analysis of variance is provided (Snedecor and Cochran,1989; Ortiz *et al.*, 2001). Bartlett test was significant exhibiting the heterogeneity of error variance, but as transformation of data caused missing some information and incorrect decision, hence no transformation exerted on the actual data (Hugh and Gauch, 1988).

Table 1. Combined analysis of variance for grain yield over different rainfed and irrigated conditions.

Source of variation	Degree of freedom	Mean squares
Environment(E)	7	200844**
Error1	16	688.31
Genotype(G)	19	3131.74**
G × E	133	1274.52**
Error2	304	509.67
Non-additivity	1	1724.76[ns]
Real error	*303*	505.79
Total	479	-
Bartlet·s test	-	26.13%

**: significant at 1% level of probability; ns: non-significant.

Mean comparison using Duncan's multiple rang test revealed that maximum grain yield belonged to genotypes number 20 (106.2 g) and minimum grain yield was attributed to genotype number 18 (61.43 g).

Regression analysis

The results of regression analysis (Table 2) exhibited that main effects of genotypes and GE interaction were relatively small and accounted for 4% and 10% of total sum of square (TSS), respectively. Linear GE interaction was not significant and accounted for 22% of the variability in the GE interaction.

As a general rule the usefulness of regression analysis is when 50% of the total sum of squares is accounted for by linear GE interaction (Hayward *et al.*, 1993), hence regression analysis is not useful for stability analysis of genotypes (Wade *et al.*, 1995). Nevertheless using regression analysis of Finlay and Wilkinson (1963) and Eberhart and Russell (1966), it

was concluded that genotypes number 4 and 17 have regression coefficient significantly greater than one with minimum deviation from regression indicating general adaptability for rainfed and irrigated conditions (Farshadfar, 1998; Farshadfar and Sutka, 1999).

Table 2. Regression analysis of phenotypic stability of bread wheat genotypes.

S.O.V	D.F	M.S	TSS%
Genotype(G)	19	1044.77**	4%
Environment(E)	7	6697.7**	86%
G×E	133	414.89**	10%
S.O.V	D.F	M.S	GESS%
G×E (linear)	19	631.78ns	22%
Deviation from regression	114	378.74**	78%
Total	159	-	-

AMMI model and pattern analysis

In AMMI model, principal component analysis is based on the matrix of deviation from addetivity or residual, while pattern analysis employs both classification and ordination techniques. In this respect both the results of AMMI analysis, the genotypes and environments will be grouped based on their similar responses (Gauch, 1992; Wade *et al.*, 1995; Algarswamy and Chandra, 1998).

Using ANOVA, yield sum of square was partitioned into genotype, environment and GE interaction. GE interaction was further partitioned by principal component analysis (Table 3). The results of AMMI analysis indicated that 10% of total variability was justified by GE interaction, 86% by environment and 4% by genotype. Ordination technique revealed high significant differences for IPC1, IPC2 and IPC3.

Table 3. AMMI analysis of grain yield in bread wheat genotypes over different environments.

S.O.V	D.F	M.S	TSS%
Genotype(G)	19	1044.77**	4%
Environment(E)	7	66977.7**	86%
G×E	133	414.897**	10%
S.O.V	D.F	M.S	GESS%
IPC1	25	804.94**	36.5%
IPC2	23	589.97**	24.5%
IPC3	21	584.13**	22%
Residual (noise)	64	146.38	17%
Total	159	-	-
Pooled error	320	518.60	

**: Significant at 1% probability level.

First three interaction principal components (IPC1, IPC2 and IPC3) explained 83% of variability in the GE interaction. Corrected grain yield can be obtained by AMMI1, AMMI2 and AMMI3 for each environment and used as a selection criteria in breeding programs. In general the importance of AMMI model is in reduction of the noise even if

principal components do not cover much of the GESS (Gauch and Zobel, 1989; Gauch, 1992; Jalalnejad, 2002).

Pattern analysis

Biplot analysis (Fig. 1) displayed that genotypes 10 and 12 and environments C, E and G have the

greatest effect in the GE interaction. Genotype number 12 has specific adaptation with environments G and E, while genotype number 10 has specific adaptability with environment C and genotype 8 has specific adaptation with environments A and D. The accessions 2 and 11 have negative GE interaction.
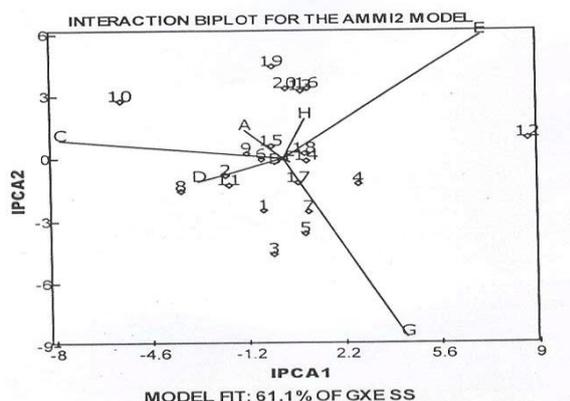

Fig. 1. Biplot analysis of GE interaction based on AMMI2 model for first two interactions principal component scores.

Genotypes toward the center of biplot have zero interaction, therefore have general adaptation with different mean grain yield. Genotypes 6, 9, 14, 15, 17 and 18 are located in this category and as the entries 6, 14 and 17 have mean yield over the grand mean, therefore they can be considered as stable with high performance.

Biplot of IPC1 and IPC2 (Fig. 1) covers 61.1% of GE interaction. The accessions 1, 3, 4, 5, 7, 8, 10, 16, 19 and 20 are located around the center of biplot indicating the variability of these entries (Manrique and Hermann, 2000). Genotypes farther from the center of biplot show specific adaptation. The genotype 12 has specific with environment E because their angle is less than 90° and their GE interaction is positive. Genotype 1, 3, 5 and 7 have positive interaction with environment G, but as the length of the vector for genotype 3 is more on the environment G, hence it has specific adaptability with environment G. The entries 2 and 11 have positive interaction with environment D and the entry 10 showed specific adaptation with environment C.

As AMMI2 has the least RMSPD (root mean square predictive difference), therefore recommendation must be based on this model (Crossa *et al.*, 1991; Wade *et al.*, 1995; Farshadfar and Sutka, 2006).

In pattern analysis genotypes are judged in grouping form and therefore save time and precision in interpretation and selection (Wade *et al* ., 1995; Alagarswamy and Chandra, 1998; Farshadfar and Sutka, 2003).

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