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Short communication

GENOTYPE-BY-ENVIRONMENT INTERACTION AND GRAIN YIELD STABILITY OF BREAD WHEAT

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ABSTRACT: The objective of this paper is to identify stable and high yielding varieties among 20 Ethiopian Bread wheat (*Triticum aestivum* L.) genotypes on the basis of experiments conducted during the 2007 and 2008 growing seasons. The additive main effects and multiplicative interaction (AMMI) model has been used to estimate G×E interaction and also to identify stable genotypes in environments. Combined ANOVA of G×E indicated the presence of significant interactions, as well as significant differences between genotypes and environments. According to AMMI, model genotypes G11, G10, G5 and G12 are found stable. In graphical display of the biplot, Adet is categorized under high yielding wheat environment as compared to the three relatively low yielding categorized environments (Holeta, Kulumsa and Sinana).

Key words/phrases: AMMI model, ANOVA, Genotype-by-Environment Interaction, main effects, stability

INTRODUCTION

Ethiopia is the largest producer of wheat in sub-Saharan Africa. Wheat farming occupies about 1.8 million hectares and ranks fourth in area and second in productivity among cereals grown in Ethiopia. (CSA, 2012). Bread and durum wheat are the major types of wheat grown in the country. Bread wheat is of recent introduction; durum wheat is indigenous to Ethiopia which is considered as the secondary centre of diversity for tetraploid wheat'.

Wheat genotypes are generally evaluated in multi-environment trials (MET) to test their performance across environments and to select the best genotypes for specific environments. There are two major approaches to study genotype-by-environment interactions (GEI) and determining the adaptation of genotypes (Hühn, 1996). The most common approach is parametric analyses, which are based on statistical assumptions about the distribution of genotypic, environmental and GEI effects.

Multivariate statistical methods are appropriate for analyzing two-way layouts of genotypes and environments in multi-environment trials. The additive main effect and multiplicative interaction (AMMI) (Zobel *et al.*, 1988), shifted multiplicative model (Cornelius *et al.*, 1992), site regression biplot (Yan *et al.*, 2000) are the most common multivariate statistical methods used for investigation of the G×E interaction and yield stability analyses. Stability analysis is only relevant if GEI is present (Hussain *et al.*, 2000).

The aim of this study was to identify suitable genotypes using additive main effect and multiplicative interaction (AMMI) (Zobel *et al.*, 1988; Zubair and Ghafoor, 2001).

METHODLOGY

Materials

The data being considered here are obtained from trials conducted by the Ethiopian Institute of Agricultural Research (EIAR). Twenty bread wheat hybrids were selected by EIAR and these were evaluated over a period of two years from 2007 to 2008 in four locations namely, Adet, Holeta, Kulumsa and Sinana under irrigated condition. The experimental layout was a randomized complete block design (RCBD) with four replications. Planting method was on 30 cm apart at a seed rate of about 120 kg/ha. Plots were managed conventionally and followed the established local practices but usually the plot areas ranged from 10 to 15m^2. The whole plot was harvested to estimate grain yields and to reduce border effects; data were recorded from the two central rows of each plot. Grain yields are expressed in kg/ha at 12.5 moisture content.

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The locations were different in soil type, altitude, mean annual temperature and rainfall and were considered as individual environments. Also, the growing season had different rainfall patterns. Therefore, locations in each year were considered as different environments. Hence, an environment is defined here as a location-year combination. Consequently, combinations of seasons (Year 1 and Year 2) and four locations were treated as eight environments (E1-E8).

Statistical methods

Analysis of variance

We considered the linear model with additive main effects and multiplicative interactions (AMMI) for analyzing the data of multi-environment yield trials and to estimate additive main effects. The linear model for the analysis of variance (ANOVA) is

$$Y_{ijk} = \mu + G_i + E_j + GE_{ij} + B_{jk} + e_{ijk}$$

where,

i=1,2,…,l, j=1,2,…,m, l=1,2,…,k,

Y_{ijk}, G_i, E_j, GE_{ij}, B_{jk} and e_{ijk} have their usual meaning.

Additive main effects and multiplicative interaction method (AMMI)

The model equation is:

$$Y_{ijk} = \mu + G_i + E_j + \sum_{n=1}^{N} \lambda_n \alpha_{in} \gamma_{jn} + e_{ijk}$$

where,

Y_{ijk}, G_i and E_j have their usual meaning.

μ is the grand mean;

λ_n is the eigenvalue of the principal component analysis (PCA) axis n;

α_{in} and γ_{jn} are the genotype and environment principal component scores for axis n;

N is the number of principal components retained in the model.

There are at most min($l-1$, $m-1$) axes, but usually the number of axes N retained in the model is smaller, thereby producing a reduced model denoted AMMI1 or AMMI2 retaining 1 or 2 Interaction Principal Component Axis (IPCA), and so on.

The AMMI stability value (ASV)

In order to rank genotypes in terms of stability, the following measure was proposed by Purchase (1997):

$$AMMI\ Stability\ Value\ (ASV) = \sqrt{\left[\frac{IPCA1\ Sum\ of\ Squares}{IPCA2\ Sum\ of\ Squares}(IPCA1\ score)\right]^2 + [IPCA2\ score]^2}$$

RESULTS AND DISCUSSION

Combined analysis of variance

G×E interaction analysis

The statistical analyses were done using the software's SAS for combined ANOVA and GenStat Discovery, Edition 4 for AMMI analysis. The usual diagnostics such as plots-including a normal probability plot and histogram of residuals, plot of residual versus fitted values, plot of residuals versus level of regress or variable etc. were employed. Examination of these diagnostics did not reveal any serious violations of the model assumptions. For testing homogeneity of residual variance, the Bartlett's test has been applied. The test result showed that the eight error variances are homogenous. A combined analysis of variance (ANOVA) was performed to the original yield data.

Analysis of variance and estimation of variance components

The relative performance of genotypes based on the mean grain yield (kg ha^{-1}) environments are ranked and presented in Table 1.

Table 1. Mean grain yield (kg/ha) of 20 bread wheat genotypes over 8 test environments.

Genotype	Code of genotype	Mean grain yield	Rank
K6290Bulk	G1	3853.23	1
K6295-4A	G2	3570.28	6
ET-13.A2	G3	3673.42	3
ET12.D4	G4	3593.33	4
KKBB	G5	3186.36	15
Mitikie(HAR-1709)	G6	3329.14	12
Wabe(HAR-710)	G7	3313.60	13
Kubsa(HAR-1685)	G8	3513.09	7
Galama(HAR-604)	G9	3456.28	9
Abola(HAR-1522)	G10	3048.72	16
Magal(HAR-1595)	G11	3034.36	18
Tusie(HAR-1407)	G12	3030.58	19
Tura(HAR-1407)	G13	3454.74	10
Katar(HAR-1899)	G14	3273.31	14
Shinna(HAR-1868)	G15	3577.59	5
HAR-407	G16	3438.62	11
HAR-416	G17	3465.84	8
Gara	G18	3048.49	17
Batu	G19	3759.88	2
K6106-9	G20	2759.81	20

The combined analysis of variance (ANOVA) is given in Table 2. The combined analysis of variance across locations and years showed highly significant differences among locations (L),year (Y) and genotypes (G) and their interaction (L×Y, G×L, G×L×Y). However, the interaction G×Y was not significant.

Table 2. Combined ANOVA for yield and the percentage sum of squares of the 20 hybrids tested at 8 environments over a period of two years (2007 and 2008).

Source	DF	Sum of Squares	%SS	Mean Square	F Value	Pr > F
Env(E)	7	999543941.9	77.9	142791991.7	439.17	<.0001
Location (L)	3	623756478.2		207918826.1	639.47	<.0001
Year (Y)	1	5160646.2		5160646.2	15.87	<.0001
L×Y	3	370626817.5		123542272.5	379.96	<.0001
Reps(env)	24	14149904.6	1.1	589579.4	1.81	0.0112
Genotype(G)	19	48459603.8	3.78	2550505.5	7.84	<.0001
Env*genotype	133	72644063.7		546196.0	1.68	<.0001
G×L	57	35364200.2		620424.6	1.91	0.0002
G×Y	19	8002038.5		421159.9	1.30	0.1808
G×L×Y	57	29277825.0		513646.1	1.58	0.0064
Error	456	148264845	11.56	325142		
Corrected Total	639	1283062422				

From Table 2. we see that location contributed the major share (48.61%) of variability followed by location × year interaction (28.89%). The interaction G×L was significant and accounted for 2.76% of the total variability and 48.68% of the G×E interaction.

The restricted maximum likelihood (REML) estimates of variance components for environment, genotype and genotype × environment interaction with % are shown in Table 3.

Table 3. Estimates of variance components for grain yield, genotypes and their interactions.

Variance Component	Estimate	% variance component
Var(env) $\hat{\sigma}^2_e$	1774767.5	
Var(rep(env)) $\hat{\sigma}^2_{R/E}$	13221.9	
Var(genotype) $\hat{\sigma}^2_g$	62634.7	14.14
Var(env*genotype) $\hat{\sigma}^2_{G\times E}$	55263.4	12.47
Var(Error) $\hat{\sigma}^2_e$	325142.1	73.39

The GEI is highly significant (p<0.01) accounting for 5.66% of the sum of squares. When a significant G×E interaction is present, the effects of genotype and environment are non-additive. Hence, such multi-location trial data along with a highly significant G×E interaction requires stability analysis.

Additive main effects and multiplicative interaction (AMMI) model

The results of the combined analyses of variance (ANOVA) of the 20 wheat genotype evaluated over two years (2007 and 2008) and across four locations based on AMMI model are presented in Table 4.

The ANOVA indicated highly significant differences (p < 0.01) for environments, genotype and genotype × environment interaction. The F-test was highly significant (p < 0.01) for the first two IPCA axes and significant (p < 0.05) for the third IPCA.

Table 4. Analysis of variance (ANOVA) based on the AMMI model for grain yield (kg ha^{-1}) for the two years (2007-2008).

Source	df	SS	MS	F	prob	Total variation explained (%)	G × E explained (%)	Cumulative (%)
Total	639	1283062539	2007923	-	-			
Treatments	159	1120647854	7048100	21.68	0.00000			
Genotypes	19	48459604	2550505	7.84	0.00000	3.78		
Environments	7	999544204	142792029	242.19	0.00000	77.90		
Reps within Env. (Block)	24	14149905	589579	1.81	0.01117			
Interactions G × E	133	72644046	546196	1.68	0.00005	5.66		
IPCA 1	25	23438053	937522	2.88	0.00001**		32.26	32.26
IPCA 2	23	17702491	769674	2.37	0.00042**		24.37	56.63
IPCA 3	21	12908381	614685	1.89	0.01023*		17.77	74.4
IPCA 4	19	9872819	519622	1.60	0.05258		13.59	87.99
IPCA 5	17	5677587	333976	1.03	0.42656		7.816	95.81
IPCA 6	15	1998751	133250	0.41	0.97632		2.751	98.56
Residuals	13	1045965	80459	0.25	0.99690			
Error	456	148264780	325142	-	-			

**P < 0.05, ** P < 0.01; IPCA= Interaction principal component axis*
Grand mean = 3369.032 R-squared= 0.8745 C.V. =17.245%

The total variation explained, ranged from 3.78% for genotype, 77.90% for environment and 5.66% for G×E. The high percentage of environment is an indication that the major factor that influences yield performance of wheat in Ethiopia is environment. Out of the total eight IPCA, the three IPCA axes explained 74.4% of the G×E interaction. The first IPCA captured 32.26% of the total interaction sum of squares with 19 degrees of freedom. The second IPCA explained 24.37% of the interaction sum of squares with 17 degrees of freedom (Table 5).

In Figure 1, the IPCA1 scores for both the genotype and the environments are plotted against mean yield for the genotype and the environment, respectively.

The high yielding environments classified according to the AMMI 1 model are E1, E4 and E5 and the low yielding environments areE2, E3,E6,E7 and E8 (Table 6). Therefore, Adet is categorized under high yielding wheat environment compared with the three relatively low yielding environments (Holeta, Kulumsa and Sinana). It is further noted that E1 (Adet in 2007) was the most favourable season and E6 (Holeta in 2008) was less favourable among the eight environments (Fig. 1) The genotypes categorized under favourable environments with above-average means areG1, G3, G8, G13, G15, G16,G17 and G19; G3 is found to be more stable. Genotypes grouped under low yielding environments are G5, G6 and G20.

Table 5. IPCA1, IPCA2 scores and graph ID for the 20 wheat genotypes on mean yield.

Genotype	Genotype mean	IPCA 1	IPCA 2
G1	3853	7.21379	9.49195
G2	3570	-14.23447	13.78071
G3	3673	0.40226	2.60547
G4	3593	-14.40887	7.65245
G5	3186	-2.74489	3.19634
G6	3329	-11.43273	4.89232
G7	3314	1.21947	10.05481
G8	3513	8.85011	18.08441
G9	3456	-12.86274	-9.03752
G10	3049	6.09173	-0.67620
G11	3034	1.41815	-3.62202
G12	3031	1.19780	-4.23959
G13	3455	2.95747	-1.90659
G14	3273	1.20037	7.13527
G15	3578	6.49709	-5.02418
G16	3439	24.85984	-20.08422
G17	3466	6.97929	5.84181
G18	3048	3.05275	-12.80126
G19	3760	10.22350	-3.17157
G20	2760	-26.47995	-22.17241

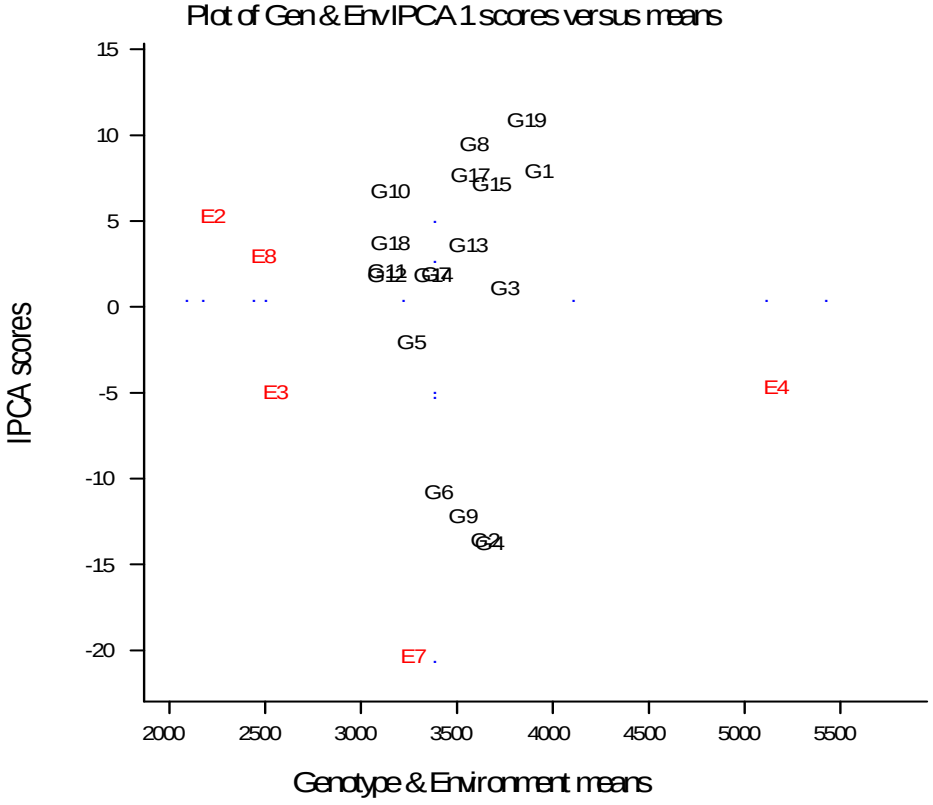

Figure 1. AMMI 1 biplot for grain yield of wheat genotypes showing means of genotypes and environments plotted against their IPCA1 scores (genotype/environment in place of others with similar means are not shown).

Table 6. The IPCA1, IPCA2 scores and the graph ID for the eight environments on environmental mean yield.

Environment	Environmental mean	IPCA 1	IPCA 2
E1	4091	32.34405	9.25409
E2	2160	4.62382	-21.47754
E3	2488	-5.59216	-11.42495
E4	5096	-5.33133	24.19281
E5	5409	16.57043	10.02760
E6	2076	-23.93305	-2.51294
E7	3207	-20.99327	14.70052
E8	2425	2.31150	-22.75959

The AMMI 2 biplot generated using the first two principal component scores showed a clear association between genotype and environment (Fig. 2). The biplot showed that E1 was the most discriminating environment for the genotypes. However, due to its high IPCA score, genotype variability in this environment may not exactly reflect the average genotype performance across environments**.**

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The AMMI stability value (ASV)

According to the ASV ranking the most stable genotypes are G3, G11 and G13 (Table 7). However, G1 and G19, which have the highest, mean yield (first and second) ranked twelfth and thirteenth for the ASV. The most unstable genotypes according to the ASV are G20, G16 and G2.

The AMMI 2 biplot indicated that the wheat genotypes G20 and G16 are the unstable genotype. Genotype G3, G5, G13, G11 and G12 were positioned closer to the origin of the biplot indicating their stability in performance across environments. G9 was more adapted to low yielding environment.

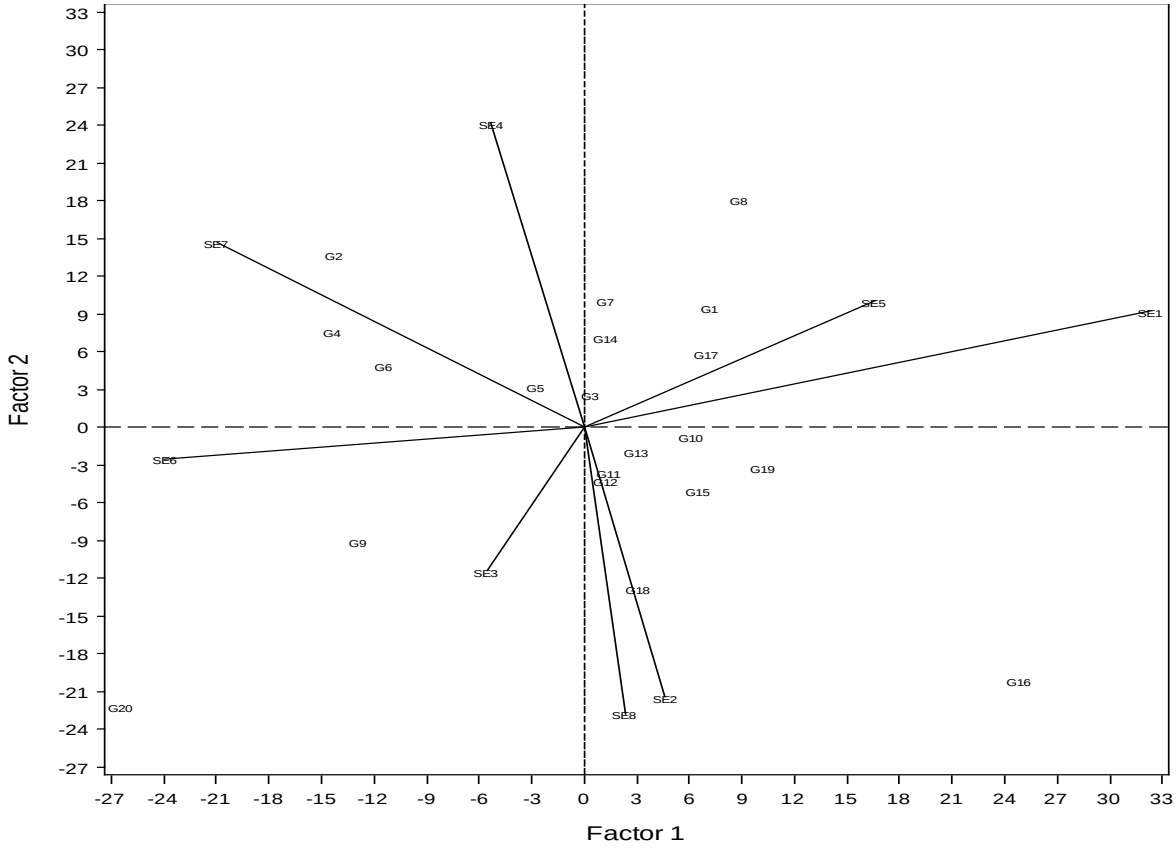

Figure 2. AMMI 2 biplot for grain yield of wheat genotypes showing the plotting of IPCA1 and IPCA2 of genotypes and environments with vectors. The angle and the projection of the vectors indicate the association among the environments.

Table 7. AMMI stability value (ASV) and ranking with the IPCA 1 & 2 scores for the 20 bread wheat varieties.

Genotype	Environmental mean	Rank	IPCA1	IPCA2	ASV	Rank
G1	3853.23	1	7.21379	9.49195	13.46549	12
G2	3570.28	6	-14.23447	13.78071	23.34727	18
G3	3673.42	3	0.40226	2.60547	2.659347	1
G4	3593.33	4	-14.40887	7.65245	20.55489	16
G5	3186.36	15	-2.74489	3.19634	4.839855	5
G6	3329.14	12	-11.43273	4.89232	15.90788	14
G7	3313.60	13	1.21947	10.05481	10.18362	9
G8	3513.09	7	8.85011	18.08441	21.54869	17
G9	3456.28	9	-12.86274	-9.03752	19.27967	15
G10	3048.72	16	6.09173	-0.67620	8.093731	7
G11	3034.36	18	1.41815	-3.62202	4.079769	2
G12	3030.58	19	1.19780	-4.23959	4.526494	4
G13	3454.74	10	2.95747	-1.90659	4.355187	3
G14	3273.31	14	1.20037	7.13527	7.310124	6
G15	3577.59	5	6.49709	-5.02418	9.961879	8
G16	3438.62	11	24.85984	-20.08422	38.55815	19
G17	3465.84	8	6.97929	5.84181	10.93228	10
G18	3048.49	17	3.05275	-12.80126	13.42418	11
G19	3759.88	2	10.22350	-3.17157	13.90249	13
G20	2759.81	20	-26.47995	-22.17241	41.48224	20

CONCLUSION

Twenty bread wheat genotypes were evaluated for grain yield in mid altitude areas of Ethiopia, in a period of two farming seasons in 2007 and 2008 across four locations.

All of the REML variance components are highly significant, indicating that factors such as rainfall, temperature, and disease incidence could result in conditions unique to each year-location combination and that the genotypes respond differently to these conditions.

The analysis of variance of the AMMI model identified highly significant differences between genotypes and environments. The first three interaction principal component axes (IPCA) of the AMMI model together accounted for 74.4% of the G×E interaction sum of squares for grain yield. The first three IPCA axes were highly significant and hence, the AMMI-3 model was used as the best fit for the bread wheat data. Genotype G11, G10, G5 and G12 are stable compared with the other genotypes. Genotypes G16, G3, G20 and G1 were unstable according to AMMI. On the basis of the biplots, Adet was categorized as high yielding wheat environment compared to the three categorized under low yielding environments (Holeta, Kulumsa and Sinana). It is noted that among the eight environments 2007 was the favourable season for Adet (E1) and 2008 was the least favourable for Holeta (E6).

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