Short communication

GENOTYPE BY ENVIRONMENT INTERACTION AND GRAIN YIELD STABILITY ANALYSIS FOR ADVANCED TRITICALE (*X. TRITICOSECALE* WITTMACK) GENOTYPES IN WESTERN OROMIA, ETHIOPIA

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ABSTRACT: Genotypes by environment (GXE) interactions are almost unanimously considered to be among the major factors limiting response to selection and, in general, the efficiency of breeding programs. Cognizant of this fact, 15 advanced triticale genotypes and one standard check, Dilfikir, were evaluated at Arjo, Gedo and Shambu localities in 2010 and 2011, and at Getema in 2011, to identify stable high yielding genotypes and the extent of GXE interaction. The analysis of variance using additive main effect and multiplicative interaction (AMMI) model revealed highly significant (P≤0.01) variations among environments, GXE interaction and Interaction Principal Component Analysis (IPCA-I) but insignificant variations among genotypes and the remaining IPCAs. This implies that, the tested genotypes respond differently over environments as the test environments are highly variable. Only the first IPCA-I was significant (p < 0.01) and contributed to 43.86% of the total genotype by environment interaction. It is found that genotypes TCL-70 and TCL-77 are high yielding next to TCL-76, have IPCA value closer to zero, Genotype Selection Index (GSI) of 4 each and AMMI stability value (ASV) of 0.124 and 0.087, respectively. Analysis using Eberhart and Russell model showed that genotypes TCL-70 and TCL-77 have regression coefficients closer to unity (b_i= 1.115 and 1.013) and nearly acceptable deviation from regression (s^2di = 0.297 and 0.148), respectively. However, the regression coefficients were significantly different (P≤0.05) from unity for TCL-76, TCL-67, TCL-64, TCL-60, TCL-63 and Dilfikir. Therefore, both TCL-77 and TCL-70 genotypes are proposed for possible release and are recommended for wider adaptability; the uppermost yielding genotype TCL-76, is recommended for specific environments.

Key words/phrases: *Additive main effect and multiplicative interaction (AMMI), Genotypes by environment interaction (GXE), regression coefficient, Triticale (X. Triticosecale Wittmack)*

INTRODUCTION

Triticale (X. *Triticosecale* Wittmack) is the first successful "man-made" cereal grain, and was synthesized to obtain a cereal that combines the unique grain quality of its wheat (*Triticum* ssp. AABB or AABBDD) parent with tolerant to abiotic and biotic stresses of the rye (*Secale cereale* L., RR.) parent (Ammar *et al.*, 2004). Octaploid triticale, comprising 56 chromosomes, are derived by crossing hexaploid wheat (*Triticum aestivum* L., AABBDD) and rye, while hexaploid triticale, with 42 chromosomes, are mostly complete cariotypes, partially or totally deprived from the D genome of wheat, resulting from the cross between *Triticum durum* L. (AABB) and rye (Ammar *et al.*, 2004). The largest triticale producing countries are Poland, Germany, Russia, USA, France and Brazil (Jiankang *et al*., 2003).

Under marginal conditions, where abiotic and biotic stresses are the limiting factors for grain production, triticale has consistently showed its comparative advantages over existing cultivated cereal crops. It is the combination of wheat and rye genomes that allows triticale to show characteristics of superior tolerance to low nutrient availability, drought, frost, soil acidity, aluminium and other element toxicities, salinity, waterlogged soils, high elevation, adverse climatic conditions and greater tolerance (better than wheat) to common wheat diseases (Lelley, 2006).

Exploitation of genetic variability is the most important tool in plant breeding and this has to be inferred by phenotypic expression. The consequences of the phenotypic variation depend largely on the environment. This variation is further complicated by the fact that not all genotypes react in similar ways to change in environment and no two environments are exactly the same. If relative performance of genotypes grown in different environments is different, then GXE interaction becomes a major challenging factor to crop breeding programs. A combined analysis of variance can quantify the interactions and describe the main effects but is not informative to

explain the interaction effect (Yuksel *et al.,* 2002; Asnake Worku *et al.*, 2013).

An appropriate analytical model such as the additive main effects and multiplicative interaction (AMMI) can treat both the additive main effect and multiplicative interaction component employing the analysis of variance (ANOVA) and Interaction Principal Components (IPCA), respectively (Gauch and Zobel, 1996). Furthermore, AMMI biplot analysis is considered as an effective tool to diagnose genotype by environment interaction patterns graphically (Gauch and Zobel, 1996; Thillainathan and Fernandez, 2001; Yuksel *et al.,* 2002). Grain yield performance is not the only parameter for selection as a genotype with the highest grain and would not necessarily mean stable and adaptable across location and years. Therefore, the Eberhart and Russell (1996) model and AMMI stability analysis could be the preferable tools to identify stable, high yielding and adaptable genotype (s) for wider or specific environments.

It is crucial for plant breeders to identify adaptable and stable high yielding genotypes with other desirable traits under varying environmental conditions prior to release as a variety (Ario, 1989; Flores *et al.,* 1998; Showemimo *et al.*, 2000; Mustapha *et al.*, 2001). Adaptability is the result of GXE interaction and generally falls into two classes: (1) the ability to perform at an acceptable level in a range of environments or general adaptability and (2) the ability to perform well only in desirable environments or specific adaptability (Farshadfar and Sutka, 2006). The central aims of this study were, therefore, to identify stable high yielding triticale genotypes (pipeline varieties) that could be adapted for wider and/or specific environments and make recommendations for possible release and production in the test environments and similar agro ecologies.

MATERIALS AND METHODS

Experimental design

Fifteen advanced triticale genotypes were evaluated against the standard check (Dilfikir) at Shambu (altitude 2468 masl, 9°58"N, 37°12"E), Gedo (2473 masl, 9°05"N, 37°43"E) and Arjo (2457 masl, 08⁰74"N, 36°50"E) in 2010 and 2011 and at Getema (2262 masl), all located in western Oromia, Ethiopia, during the 2011 main cropping season) in the 2011 main cropping season. The design was randomize complete block design (RCBD) and replicated four times. The plot size was 6 rows of 0.2 m spacing between rows and 2.5 m row length. Seed rate of 120 kg/ha and fertilizer rate of 100 kg/ha DAP and 100 kg/ha Urea were used. Urea

was applied in split form. Data were recorded for grain yield per plot (g).

Data analysis

Additive mean effect and multiplicative interaction model

The AMMI model equation is:
$$Y_{ger} = \mu + \alpha_g + \beta_e + \sum_n \lambda_n \gamma_{gn} \delta_{en} + \varepsilon_{ger} + \rho_{ge};$$
where, Y_{ger} is the observed yield of genotype (g) in environment (e) for replication (r);

Additive parameters: μ is the grand mean; α_g is the deviation of genotype g from the grand mean, β_e is the deviation of the environment e;

Multiplicative parameters: λ_n is the singular value for IPCA, γ_{gn} is the genotype eigenvector for axis n, and δ_{en} is the environment eigenvector; ε_{ger} is error term and ρ_{ge} is PCA residual. Accordingly, genotypes with low magnitude regardless of the sign of interaction principal component analysis scores have general or wider adaptability while genotypes with high magnitude of IPCA scores have specific adaptability.

AMMI Stability Value (ASV): ASV is the distance from the coordinate point to the origin in a two-dimensional plot of IPCA1 scores against IPCA2 scores in the AMMI model (Purchase, 1997). Because the IPCA1 score contributes more to the GXE interaction sum of squares, a weighted value is needed. This weighted value was calculated for each genotype and each environment according to the relative contribution of IPCA1 to IPCA2 to the interaction sum of squares as follows:

$$ASV = \sqrt{[(SS_{IPCA1} \div SS_{IPCA2})(IPCA1 score)]^2 + (IPCA2 score)^2}$$

where, SS_{IPCA1} / SS_{IPCA2} is the weight given to the IPCA1-value by dividing the IPCA1 sum of squares by the IPCA2 sum of squares.

The larger the ASV value, either negative or positive, the more specifically adapted a genotype is to certain environments. Smaller ASV values indicate more stable genotypes across environments (Purchase, 1997).

Genotype Selection Index (GSI): Stability is not the only parameter for selection as most stable genotypes would not necessarily give the best yield performance. Therefore, based on the rank of mean grain yield of genotypes (RY_i) across environments and rank of AMMI stability value ($RASV_i$), genotype selection index (GSI) was calculated for each genotype as:

$$GSIi = RASVi + RYi$$

A genotype with the least GSI is considered as the most stable (Farshadfar, 2008).

Eberhart and Russell regression model

The stability of yield performance for each genotype was calculated by regressing the mean grain yield of individual genotypes on environmental index and calculating the deviation from regression as suggested by Eberhart and Russell (1966) as:

$$Y_{ij} = \mu_i + b_i I_j + s^2 d_{ij};$$

where Y_{ij} is the mean performance of ith variety in j^{th} environment, μ_i is the mean of ith variety over all environments; b_i is the regression coefficient which measures the response of ith variety to varying environment; $s^2 d_{ij}$ is deviation from regression of ith variety in the jth environment, and I_j is the environmental index of jth environment.

Regression coefficient (b_i) was considered as an indication of the response of the genotype to varying environment. If the regression coefficient is not significantly different from unity ($b = 1.0$), the genotype is adapted to all environments, genotypes with $b > 1.0$ are more responsive or adapted to high yielding environments, whereas any genotype with b significantly lower than 1.0 is adapted to low yielding environments (Eberhart and Russell, 1966).

Both AMMI and Eberhart and Russel models were computed using Agrobase software (Agrobase, 2000) and the biplot analysis using MINITAB-14 (MINITAB, 2003) computer software.

RESULTS AND DISCUSSION

Additive Main Effects and Multiple Interaction (AMMI) model

A combined analysis of variance revealed highly significant (P≤0.01) variations among environments, GXE interaction and Interaction Principal Component Analysis (IPCA-1) but insignificant variations among genotypes (Table 1). This implies that, triticale genotypes respond differently over environments as the test environments are highly variable. The mean grain yield across geographic locations ranges from 2.73 ton ha⁻¹ at Gedo in 2010 to 6.64 ton ha⁻¹ at the same location in 2011 main cropping seasons (data not shown). This implies that, not only the genotypes and locations, but also variations in seasons or environmental conditions during different seasons greatly influence the grain yield performance. Similarly, grain yield obtained in different locations in 2010 was by far less than that obtained during 2011. The genotypes mean grain yield across years and environments ranges

from 4.70 ton ha⁻¹ for genotype TCL-2 to 5.95 ton ha⁻¹ for genotype TCL-76 (Table 2). In line with the present finding, statistically significant differences between environments, genotypes and GXE interaction were reported for grain yield of eight triticale lines evaluated across six environments (Dogan *et al.*, 2011).

In the present study, considerable percentage of GXE interaction (43.86%) is explained by IPCA-I followed by 20.35% and 17.06% for IPCA-II and IPCA-III, respectively. Except the first IPCA-I, the remaining five IPC axes were non- significant and contributed 56.14% of the GXE interaction (Table 1). Several authors also reported for various crops that significant and greater percentage of GXE interaction was explained by the first IPCA score (Wonde Abera and Labuschagne, 2005, on maize; Farshadfar, 2008, on bread wheat; Abeya Temesgen *et al.*, 2008, on common bean; Girma Mengistu *et al.*, 2011, on Field pea).

The most accurate model for AMMI can be predicted by using the first two PCAs (Gauch and Zobel, 1996). This suggestion was later modified such that factors like type of crop, diversity of the germplasms and range of environmental conditions affect the degree of complexity of the best predictive model and hence the number of PCAs to be used (Crossa *et al.*, 1990). In the present study, the first two IPCAS were used to portray genotype by environment interaction and placement on the biplots. Accordingly, TCL-77, TCL-70 and TCL-69 attain IPCA values (of both) relatively close to zero and hence are better stable and widely adaptable genotypes across location (Fig. 1). Genotypes with low magnitude IPAC scores have general adaptability while those with high magnitude of IPAC scores have specific adaptability (Gauch and Zobell, 1996). However, TCL-67, TCL-76, TCL-64, TCL-74, TCL-73 and the released variety Dilfikir, attained IPCA values closer to one, either for both or for IPCA-I alone (Fig. 1).

The biplot (Fig. 1) also shows the unique grain yield performance of a genotype at a specific site. For instance, triticale genotype TCL-74 gave the highest grain yield in 2010 at Arjo site (Ar1) than it did across years and locations and hence it is placed nearest the test environment Ar1 on PC axis (Fig. 1). Similarly, TCL-63 gave the highest grain yield at Gedo location during the 2011 cropping season (Gd2) than it did at other locations and years (Fig. 1). Asnake Worku *et al.* (2013) and Yuksel *et al.* (2002) reported results that are in agreement with the present study.

Table 1. Analysis of variance for grain yield using Additive Mean Effect and Multiple Interactions (AMMI) model.

Source	df	SS	MS	F-Value	Pr> F	% GXE interaction	% cumulative interaction
Environments	6	635.24	105.87	24.70	0.000		
Genotype	15	34.54	2.30	1.38	0.157		
GXE interaction	90	150.46	1.67	1.54	0.004		
IPCA 1	20	65.99	3.30	3.04	0.000	43.86	43.86
IPCA II	18	30.62	1.70	1.56	0.068	20.35	20.35
IPCA III	16	25.66	1.60	1.48	0.107	17.06	81.27
Total	447	1252.69	2.82				
Residual	315	1.09	1.09				

Table 2. Mean grain yield (GY) (ton ha^{-1}), AMMI stability value (ASV) and genotype selection index (GSI) for test genotypes and locations.

Genotype name	Mean GY (ton ha^{-1})	ASV	GSI
TCL-76	5.95	1.991	13.00
TCL-63	5.46	1.109	14.00
TCL-69	5.41	0.506	12.00
TCL-67	5.13	1.726	24.00
TCL-2	4.70	0.328	20.00
TCL-60	5.20	0.479	15.00
TCL-72	5.27	0.621	16.00
TCL-70	5.56	0.124	4.00
TCL-65	5.15	0.571	19.00
TCL-74	5.39	2.363	19.00
TCL-61	5.15	2.391	26.00
TCL-77	5.51	0.087	4.00
TCL-75	4.88	0.297	18.00
TCL-78	5.11	0.362	19.00
TCL-64	5.17	2.808	25.00
Dilfikir	5.24	24.139	24.00
Mean	**5.27**	**2.490**	**17.00**
Environment			
Shambu-2010	5.030	0.435	7.00
Shambu- 2011	5.960	0.928	8.00
Arjo-2010	4.720	2.064	7.00
Arjo-2011	5.900	0.903	8.00
Gedo-2010	5.870	0.584	7.00
Gedo-2011	6.650	0.825	5.00
Getema-2011	2.740	0.230	8.00

AMMI Stability Value (ASV) and Genotype Selection Index (GSI):

The analysis using AMMI stability value indicated that TCL-77 (0.087), TCL-70 (0.124), TCL-75 (0.297), TCL-2 (0.328) and TCL-78 (0.362) were among genotypes with lower ASV values, in order of importance. This revealed that these genotypes are relatively more stable than others. However, Dilfikir (24.139) followed by TCL-64 (2.808), were classified under the least stable genotypes (Table 2). Stability is not the only parameter for selection of high yielding genotypes as the most stable genotypes would not necessarily give the best yield performance. As such, the genotype selection index revealed that TCL-70 and TCL-77 are the best and top-ranking genotypes integrating both stability and grain yield performance parameters

followed by TCL-69 and TCL-76 (Table 2). This result is in agreement with that of IPCA biplot (Fig. 1). Therefore, all the above four genotypes could be potential candidates for variety verification as revealed using AMMI model and as observed in the actual field condition. Similar results were reported by Farshadfar (2008). Further analysis was made using the Eberhart and Russell regression model for confirmation of the result obtained by AMMI model and for proper recommendation of the genotypes.
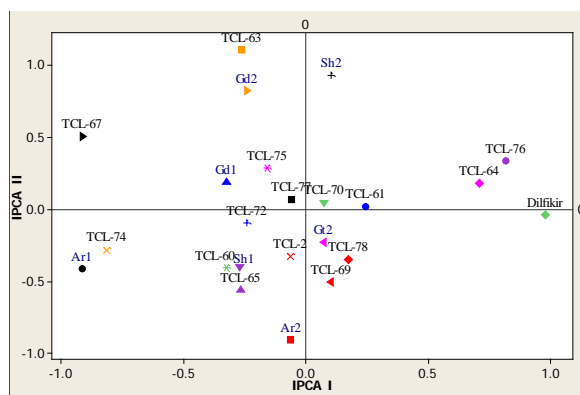

Figure 1. Biplot showing genotypes grain yield stability and preferential adaptation environment using the first two IPCAs. (Key: Ar1=Arjo site in 2010, Ar2=Arjo in 2011, Sh1=Shambu in 2010, Sh2=Shambu in 2011, Gd1=Gedo in 2010, Gd2=Gedo in 2011, Gt2=Getema in 2011)

Analysis based on Eberhart and Russel regression model

Based on the Ebrehart and Russell (1996) analysis model, pipeline genotypes TCL-70, TCL-77 and TCL-69 were the most acceptable candidates with better grain yield (5.56, 5.51 and 5.41 ton ha^{-1}), regression coefficients approaching one (1.115, 1.013 and 0.884) and quite acceptable deviation from regression (0.297, 0.148 and -0.176), respectively, implying that they are stable and widely adaptable than the other genotypes (Table 3). An

ideal genotype has the highest average grain yield, a regression coefficient (b_i) value of approximately one and a mean square deviation from regression (s^2d_i) value close to zero (Eberhart and Russell, 1966; Becker and Leon, 1988). These results are consistent with those reported by Finlay and Wilkinson (1963) and Farshadfar (2008). The regression coefficients were significantly ($P \leq 0.05$) different from unity for TCL-76, TCL-67, TCL-64, TCL-60, TCL-63 and the standard check, Dilfikir (Table 3, Fig. 2). This indicates that the above five genotypes are less stable and characterized by specific adaptability. The result obtained using Eberhart and Russell (1996) model is highly corroborated with AMMI model.

Genotype TCL-76 gave the highest grain yield (5.950 ton ha^{-1}) but the regression coefficient (b_i) was significantly ($P \leq 0.05$) higher than unity (Table 3, Fig. 2) and the deviation from regression is positive (Table 3). This implies that this genotype is highly responsive to the change in environment and hence is recommended for favourable environmental conditions with appropriate agronomic practices. Likewise, genotypes TCL-60, TCL-67 and Dilfikir gave grain yields below the average, regression coefficients (b_i) significantly ($P \leq 0.05$) different from one and squared deviations from regression (s^2d_i) higher than zero and hence are poorly adapted to all environments (Table 3). Finlay and Wilkinson (1963) and Dogan *et al.* (2011) reported results that are in agreement with those in the present study.

Table 3. Regression coefficient (b_i) and squared deviation from linearity of regression (s^2d_i) by the test genotypes revealed using Eberhart and Russell model.

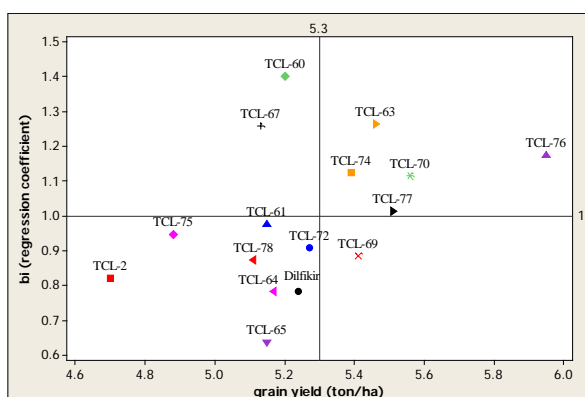| Genotype	Sum of Squares	Regression coefficient (b_i)	Squared deviation from regression (s^2d_i)	F-Ratio	Pr.>F
TCL-76	3.929	1.174*	0.464	2.442	0.034
TCL-63	3.245	1.264*	0.327	2.017	0.046
TCL-69	0.729	0.884	-0.176	0.454	0.811
TCL-67	4.038	1.259*	0.486	2.510	0.030
TCL-2	0.438	0.822	-0.234	0.272	0.928
TCL-60	1.883	1.402*	0.055	1.170	0.323
TCL-72	2.248	0.909	0.128	1.397	0.225
TCL-70	0.122	1.115	-0.297	0.076	0.996
TCL-65	0.899	0.636	-0.142	0.559	0.731
TCL-74	3.834	1.125*	0.445	2.383	0.038
TCL-61	0.483	0.976	-0.225	0.300	0.912
TCL-77	0.868	1.013	-0.148	0.539	0.746
TCL-75	1.504	0.947	-0.021	0.935	0.458
TCL-78	0.719	0.873	-0.178	0.447	0.815
TCL-64	2.430	0.783	0.164	1.511	0.186
Dilfikir	3.620	0.782*	0.402	2.250	0.049

Standard error of beta = 0.1976

Figure 2. Matrix plot of genotypes mean grain yield (ton ha^{-1}) versus regression coefficient (b_i) indicating stability and yield performance of the test genotypes. (Key: The reference lines, x-axis is at about an average grain yield of genotypes and y-axis is the regression coefficient (b_i=1) indicating genotype stability).

CONCLUSION AND RECOMMENDATION

Combined analysis of variance portrayed highly significant GXE interaction, a major challenge in the course of variety development activities. Besides, variations were significant among the test locations. Both AMMI and Eberhart and Russell models revealed that genotypes TCL-70 and TCL-77 were widely adaptable and stable high yielding, and thus are recommended for possible release with wider environmental adaptability. Genotype TCL-76 gave the highest mean grain yield, with a regression coefficient (b_i) significantly larger than unity and hence is recommended for high yielding environments. The remaining genotypes showed inconsistent performance across locations and seasons; 43.86% of the total GXE interaction was contributed by IPCA-I and the interaction was

significant (p < 0.01). A total of 81.27% GXE interaction is explained by the first three PCAs.

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