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Parametric model based assessment of genotype×environment interactions for grain yield in durum wheat under irrigation

K.F. Solomon*, H.A. Smit, E. Malan, W.J. Du Toit

Agricultural Research Council, Small Grain Institute, Private Bag X29, Bethlehem 9700, South Africa.
*Corresponding authors. E-mail: S_kebede2001@yahoo.com

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Abstract

The objectives of this study were to assess the genotype (G) by environment (E) interaction of grain yield of durum wheat(*Triticum durum* Desf.) based on parametric models, additive main effects and multiplicative interaction (AMMI) and joint linear regression models; and compare the relative efficiency of the two models in explaining the GE effects**.** Twenty-three genotypes were evaluated across 12 environments (location-year combinations) in 2003 and 2004. Combined analysis of variance showed that the environment (E) accounted for a high percentage of sums of squares (remaining after removing the sums of squares due to error and replications). The genotypic variability of grain yield among genotypes was small. The best genotype 6 (DBSP02/8) out yielded the check by 0.24 ton/ha. Based on full AMMI model analysis, AMMI-1 was found to explain up to 94% of the main and interaction effects, and AMMI-2 was found to fully capture target percentage sums of squares in the GE interaction pattern. The biplot based on the first bilinear AMMI model terms indicated that genotype 7 (DBSP02/9) and genotype 19 (DBSP03/16) could be suited for cultivation across the test environments. However, no genotype had superior performance in all environments. Reitrivier normal planting date in 2003 (E403) was the most favorable environment for yield, whereas, Upington in 2003 (E603) was the least favorable one. Model comparison criteria showed that AMMI model was superior to joint regression model in terms of its predictive accuracy and efficiency of explaining the pattern of GE sum of squares. It was concluded that AMMI biplot clearly facilitate identification of mega-environments and cultivars for specific recommendations. The differential response of genotypes observed in this study reaffirms the necessity of multi location evaluations to identify superior and stable genotypes. However, trends in specific adaptation could be detected using the which-won-where pattern of the AMMI analysis, and site-specific breeding may be exploited when feasible.

Keywords: AMMI; Durum wheat; Genotype by environment interaction; Joint regression; Yield.

Introduction

Various statistical models have been developed to quantify GE interactions and identify relatively stable genotypes across different locations and years. Parametric model based joint linear regression analysis is among the most widely used methods to identify superior

cultivars, and include the method proposed by Eberhart and Russell (1966). This method employs variance of regression deviations (σ^2_{di}) to measure a cultivar's stability and the linear regression coefficient (β_i) to measure a cultivar's adaptability. Although regression is widely applied, the fact that mean of cultivars in each environment is taken as a measure of environmental index and is used as an independent variable in the regression may be considered as a serious limitation because there cannot be independence among variables, particularly, when the number of genotypes is less than 15 (Crossa, 1990). Moreover, the variation of the estimates of the regression coefficient is usually so small that classification of the genotype for stability and adaptability is difficult (Yue et al., 1997). The additive main effects and multiplicative interaction (AMMI) model that combines analysis of variance and principal component analyses has been reported to be more effective than the conventional two way fixed effects model with interactions because it achieves the following: (1) parsimony, because the model contains relatively few degrees of freedom for the interactions. (2) effectiveness, because the model contains most of the interactions sum of squares (SS) that is rich in pattern leaving residual that is rich in noise with most of the degrees of freedom but small SS, thereby affording greater predictive accuracy and statistical efficiency (Guach and Zobel, 1997). AMMI model provides a biplot graph useful for delineating stable genotypes and mega-environments (homogeneous sub-regions) (Guach and Zobel, 1997). The importance of GE interactions in national cultivar evaluation and breeding programs have been demonstrated in almost all major crops, including durum wheat (Tesemma et al., 1998; Akcura et al., 2005).

Durum wheat production in South Africa is relatively small compared to the bread wheat. Wheat and local industries depend heavily on import of durum wheat. However, with the increasing trend for durum wheat consumptions, identification of the genotypes that are specifically adapted to the growing conditions and production practices of durum wheat growing regions of South Africa are vital. Therefore, Small Grain Institute (SGI) is conducting durum wheat genotypes evaluation across different localities under irrigation. These production areas are usually diverse in terms of agro-climatic variables. They are believed to represent the major durum wheat production areas of South Africa under irrigation. Tremendous variability in terms of adaptation to these localities and stability of genotypes has been noted (Solomon et al., 2007). However, there has been little study to verify the extent and pattern of environment and GE effects on the yield of durum wheat genotypes. Information gained from this assessment should facilitate the design of a testing strategy to assist in selecting widely adapted superior genotypes for irrigation areas of South Africa.

The objectives of the present study were therefore to evaluate the GE interactions for grain yield of durum wheat genotypes, and to compare the relative efficiency of joint regression and AMMI models in describing the pattern of GE effects.

Materials and Methods

Twenty-two elite lines and one local check variety were evaluated across five locations representing the major durum wheat growing irrigation areas of South Africa. The genotypes used in this experiment represent wide range of phenotypic variation for straw strength, height, adaptation, lodging and disease tolerance as well as quality characteristics. Kronos (Unknown) is the commercial cultivar currently under production with relatively short growth period and high yield potential. DBSP00/1 (unknown) has good yield

potential; DBSP00/2(unknown) was selected for its good yield potentials and high gluten. Both genotypes were originated from 2000 South Africa durum wheat eliteyield trial. DBSP02/6 (PORRON_4 / YUAN_1), DBSP02/7 (SKEST // HUI/TUB / 3 / SILVER), DBSP02/8 (SN_TURK_MI83-84375 / NIGRIS_5 // TANTLO_1) and DBSP02/9 (STOT//ALTAR_84 /ALD) were selected from 32nd International Durum Yield Nursery (32IDUYN) for their high yield potentials and good agronomic characteristics. DBSP02/10(TILO_1/LOTUS_4),DBSP02/11 (DIPPER_2 / BUSHEN_3) andDBSP02 /13 (SOOTY_9 / 2*TARRO_1) were selected for their good yield potentials and strong straw from 31st Durum Yield Trial (31DUYT). DBSP02/11 and DBSP02/13 have high gluten. DBSP02/19 (CADO / BOOMER_33) and DBSP02/22 (DUKEM_5/MUSK_1//KKV5) were selected from 33rd International Durum Yield Nursery (33IDUYN) for their good agronomic characteristics and yield potentials. DBSP03/02 (OSSL-1/4/MRBSH /3/RABI //GS / CR/5/KRS/HCN), DBSP03/03 (QUADALETE//ERP/MAL/3/ UNK/4 /GBCH-2), DBSP03/04 (STJ3//BCR/LKS4) were selected from Durum Yield Trial- Mediterranean Areas (DYT-MTA) for their good yield and adaptation. DBSP03/10 (GALLI_1 /BOOMER_20), DBSP03/11 (GREEN_14 // YAV_10 / AUK), DBSP03/12 (PLATA_1 / SNM // PLATA_9), DBSP03/16 (RASCON_21 /KNAR_3// PLATA_8), DBSP03/17 (RASCON_37 / 2*TARRO_2), DBSP03/18 (SN TURK MI83-84 375/NIGRIS_5//TANTLO_1), DBSP03/19 (PLATA_1/ SNM // PLATA_9) and DBSP03/20 (TOPDY_18 / FOCHA_1 // ALTAR 84) were selected from 31nd Durum Yield Trial (32DUYT). They were all selected for good yield potential and tolerance to lodging. DBSP03/12, DBSP03/16 and DBSP03/18 also have high gluten.

The 23 genotypes were evaluated across five locations (Figure 1); Loskop (Mpumalanga province) represents warm irrigation areas where plants grow relatively faster. All the other locations, Upington, Marydale, Prieska and Reit rivier are found in Northern Cape province. Except for Upington, all of these locations represent cooler irrigation areas where crops require relatively longer growth period to mature.

The description of the study locations is given in Table 1. In all the test localities (Figure 1), yield trials were performed for two years (2003 and 2004, identified by 03 and 04) in RCBD with three replications. The following location and year combinations were defined as environments. Namely, Loskop (E104 and E103), Marydale (E204 and E203), Prieska (E304 and E303), Reitrivier normal planting date (E404 and E403), Reit rivier late planting date (E504 and E503), and Upington (E604 and E603). Experimental plots were 5.1m^2 with six rows each with 5m long and 0.17m inter row spacing. Plot yield was converted to t ha^{-1} and used for the analyses.

Table 1. Characteristics of the testing locations.

		Temperature °C					Coordinate	
Locality	Rainfall (mm)	[a]Min.	[b]Ave.	[c]Max.	Altitude (m.a.s.l)	Soil texture	Latitude (°S)	Longitude (°E)
Marydale	313	8	14	22	1100	Clay loam	29.2	22.1
Upington	234	11	20	29	793	Sandy loam	28.5	21.2
Prieska	178	9	18	25	931	Clay	29.6	22.4
Reitrivier	361	10	18	25	1121	Sandy	29.1	24.6
Loskop	307	12	20	29	956	Cay loam	25.2	29.4

[a]Min. represents the mean minimum annual temperature, [b]Ave. represents the mean annual temperature and [c]Max. Represents the mean maximum annual temperature. Rainfall is the total annual precipitation.

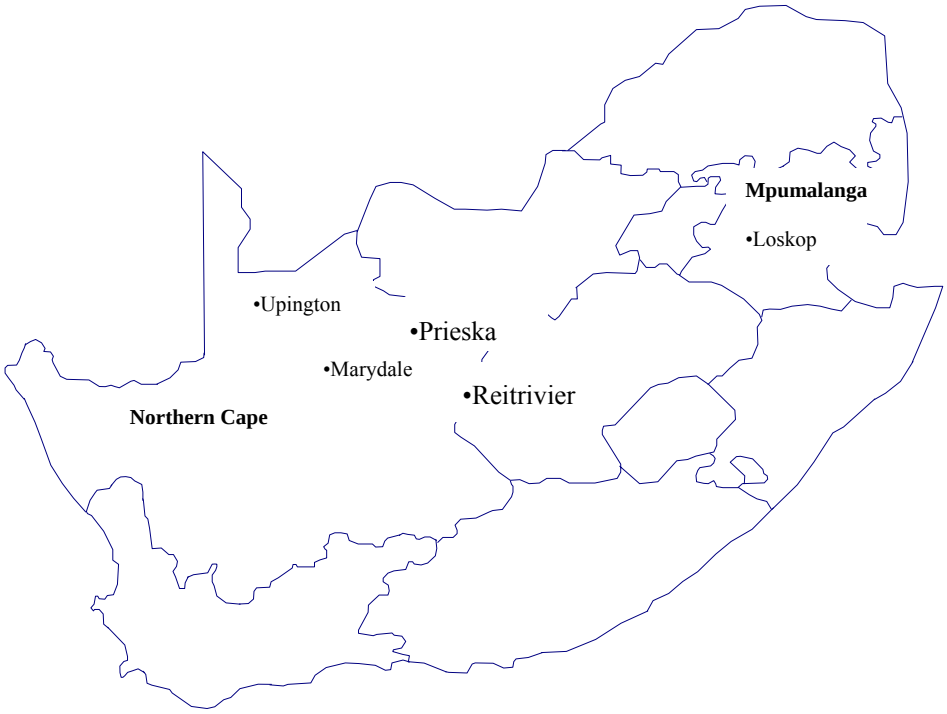

Figure 1. Geographical location of the testing sites in the Republic of South Africa.

Yield of the genotypes was first compared by analysis of variance in each environment separately. In the combined analysis of variance, effects of replication and environment were considered random, while genotype effect was fixed. The analysis was performed according to Hussien et al. (2000) using PROC GLM procedures (SAS, 1999). Biplots were produced using SAS GPLOT procedures (Burgueno et al., 2001).

Numerical stability parameters were estimated using joint linear regression based on Eberhart and Russell (1966) model. Heterogeneity of genotype regressions in the joint regression analysis was tested on deviations from regressions, and significance of deviations from regression was tested on pooled error (residual). Similarity of among test environments and genotypes based on main effects and GE interaction effects were evaluated using AMMI model (SAS, 1999). Interactive principal components (IPCAs) significance in the AMMI analysis (Hussien et al., 2000) was tested by F_R test as recommended by Piepho (1995). Following the approach by Guach and Zobel (1997), relevant portion of GE was computed to avoid spurious interpretation of statistical results. Based on this procedure, factoring the errors from uncontrolled variation ("noise") out of the total GE sums of squares is important because most of the noise appears in the interaction, since the interaction contains a majority of the treatment *df* (Gauch and Zobel, 1997). Proportion of "noise" sums of squares, "real structure" sums of squares, and target relevant variation percentage were calculated as described by Gauch and Zobel (1997).

The "noise" sums of squares is estimated by multiplying MS error x df (GE). Factoring the "noise" sums of squares out of the GE sums of squares gives "real structure" sums of squares [SS GE-SS noise]. Thus, the total relevant variation within the total treatment sums of squares [SS (Genotype)+ SS (GE)] is calculated by the addition of SS (genotype) + SS ("real structure"). Hence, the target percentage of the relevant variation explained by IPCA in the AMMI analysis should be equal to the ratio of (SS relevant / SS treatment). Variance component of genotype×environment interaction (σ^2_{ge}) in joint linear regression and AMMI models were estimated as described by Annicchiarico (2002). *F*-test was used to test whether the variances were significantly different from zero or not according to Annicchiarico (2002). Ratios of % GE interaction sum of squares and % GE degree of freedom were computed for model parameters according to Brancourt-Humel et al. (1997). In Both AMMI and joint regression models, computations were carried out based on the GE and its components sum of squares and degree of freedoms. Association between stability parameters, AMMI principal components and yield were estimated based on simple correlation analysis.

Results and discussion

Significant genotypic and environmental effects on the grain yield variability were evident both from the joint linear regression and AMMI models analyses. The environment (E) accounted for a high percentage of sums of squares (89.6%) remaining after removing the sums of squares due to error and replications. The genotype (G) and the GE interactions accounted for relatively smaller proportions, 2.1 and 8.2%, respectively (Table 2). In multi-environmental trial (MET), environment explains 80% or higher of the total yield variation (Yan, 2002). More pronounced influence of environment on the grain yield compared to the genotype or the GE interaction effects has been documented in many crops, wheat (Tesemma et al., 1998; Kaya et al., 2003; Akcura et al., 2005). This is particularly true when the trials are composed of more uniform elite materials (Guach and Zobel, 1997). The effect of GE interaction was highly significant ($P<0.01$) (Table 2). This interaction showed that the genotypes responded differently relative to each other to the changing environment. Analysis of genotype by environment interaction is vital for breeders in order to design the dissemination strategies for new varieties. It is important to identify cultivars with specific and general adaptation. Precise recommendation of lines for general and specific adaptation requires clear understanding of the real pattern of genotype by environment interaction. Thus, GE sum of squares was partitioned into "noise" and "real structure" following the procedure by Gauch and Zobel (1997). This computation ignores irrelevant environmental effects and much interaction noise while focusing mainly on the relevant genotype and real interaction effects (Gauch and Zobel, 1997; Campbell and Jones, 2005). GE interaction contained 48.9% noise and 51.09% real structure, with the relevant (target) variation being 6.3% of the treatment sums of squares. Analysis based on AMMI full model showed that the first five principal components were significant (Table 2).

The genotype main effect and the first two IPCAs of the GE interaction components accounted for 6.2% of the treatment sums of squares. This was almost equal to the target percentage of the treatment sums of squares explained (6.3%). Hence, the two IPCAs represented the practical level variation that can be exploited. Thus, biplot was constructed

Table 2. Partitioning of the sum of squares (SS) and mean squares (MS) from the AMMI analysis of 23 durum wheat genotypes yield performance evaluated across 12 environments.

Source	DF	SS[a]	MS	% Treatment SS
Treatment	275	4610.787	16.766**	
Environments (E)	11	4133.196	375.745**	89.64
Reps within E	24	92.438	3.8520	
Genotype (G)	22	98.107	4.459**	2.13
G × E	242	379.484	1.568**	8.23
IPCA 1	32	103.17(27.19)	3.224**	2.24
IPCA 2	30	84.263(22.2)	2.809**	1.83
IPCA 3	28	61.95(16.32)	2.212**	1.34
IPCA 4	26	39.959(10.53)	1.537**	0.87
IPCA 5	24	29.279(7.72)	1.22*	0.64
IPCA 6	22	18.798(4.95)	0.8540	0.41
IPCA 7	20	15.635(4.12)	0.7820	0.34
IPCA 8	18	11.557(3.05)	0.6420	0.25
IPCA 9	16	8.596(2.27)	0.5370	0.19
IPCA10	14	3.782(1.00)	0.2700	0.08
IPCA11	12	2.496(0.66)	0.2080	0.05
Residual	528	404.847	0.7670	
Total	827	5108.072		

[a] Numbers in brackets are percentage of GE explained by interactive principal components (IPCA). DF=degree of freedom.
* and ** are significant at P<0.05 and 0.01, respectively.

based on AMMI2 (IPCA1 and IPCA2) scores to display which-won-where patterns of the genotypes (Figure 2A). Visualization of the which–won–where pattern of multiple environmental trials (MET) data is important for further partitioning of a region into mega-environments (Gauch and Zobel, 1997; Yan et al., 2000; 2001). The polygon view of a genotype and GE interaction biplot explicitly displays the which-won-where pattern, and hence is a concise summary of the GE pattern of a MET data set (Yan, 2002) (Figure 2A). The polygon in the figure is formed by connecting the markers of the genotypes that are further away from the biplot origin such that all other genotypes are contained in the polygon. In this study, a polygon with four sides was formed. The rays that are perpendicular to the sides of the polygon or their extension were identified in capital letters, A, B, C and D. These rays partitioned the biplot into four sections (Figure 2A). In the GE biplot, the vertex genotype for each section had the highest yield in all environments that fell in the sector (Yan et al., 2000; Yan, 2002). For example, five environments; E404, E303, E204, E504 and E304 fell into the sector delineated by ray-A and B.

These environments represent cooler irrigation areas, and showed similar interaction effects with the genotypes that fell in the section, suggesting they may represent a mega-environment. The vertex genotype for this section was 1 (check variety), suggesting it was

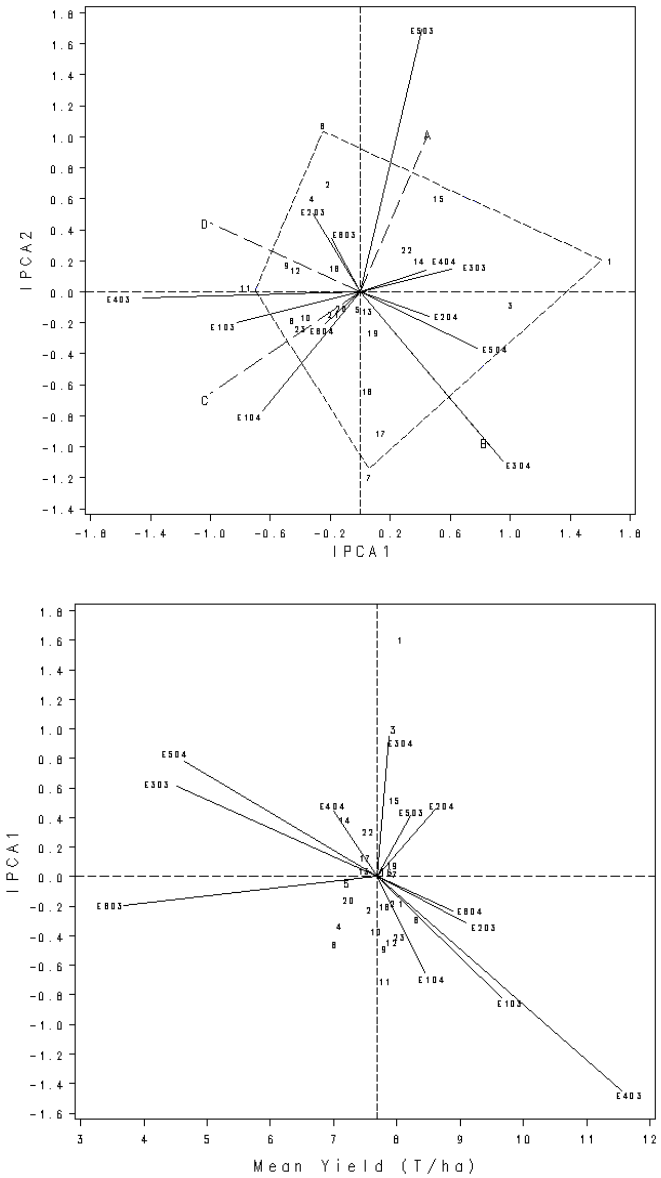

Figure 2. AMMI biplot for (A) the first two IPCAs to show the which-won-where pattern and (B) IPCA1 *vs* mean yield, to show genotype performance in relation to stability of 23 durum wheat genotypes evaluated across 12 environments. Number in the plots represents genotypes (See Table 2 for names). Environment is designated as "E", and location is represented in number (1-6) followed by 03 or 04 to indicate year.

the best yielding genotype in all of these environments. Similarly, E604 and E104 fell in the sector demarcated by ray B and C. These two environments represent warmer irrigation areas, and hence possibly similar agro ecology. However, classification of the environments was not consistent over the years, thus defining them, as mega-environment would be inconclusive. The winner genotype in this sector was genotype 7. In the sector delineated by ray C and D, E103 and E403 were identified. The vertex genotype in this section was genotype 11 that gave the highest yield in E103 and E403. Ray D and A identified a section that contained three environments; E203, E603 and E503. In terms of geographical proximity, these environments are closely located. However, E203 and E503 represent cooler irrigation areas while E603 represents warm irrigation areas. Moreover, the grouping of these environments appears to be due year or planting date effects rather than homogeneity of the environments. The vertex genotype in this sector was genotype 6, suggesting it was the winner in these environments. The vertex genotype performance in each sector in Figure 2A corresponds to the maximum yield in each test environment (Table 3). Table 3 shows that the genetic variability for yield in this study was small. Across environments, only genotype 6 (DBSP 02/8) gave the best yield, surpassing the check (genotype 1) by 0.24 ton/ha. However, no genotype showed consistent performance across all environments (Table 3). This suggests, in the final stage of elite lines evaluation, emphasis is shifted to the evaluation of adaptation rather than yield *per se* selection.

To visualize the genotypes performance in relation to stability, mean performance was plotted against IPCA1 (Figure 2B). The biplot based on AMMI-1 model captures the genotype SS of 98.107 and the environment SS of (4133.196), and the IPCA1 captures 103.17 of the interaction SS of 379.484. Thus, it is very informative since it explains 94 % of the treatment SS. Genotypes located near the biplot origin was less responsive than the vertex genotypes (Yan, 2002). Genotype 7, 13, 16, 17 and 19 were located near to the center of the origin, suggesting they had the maximum stability. Genotype 7 and 19 had mean performance higher than the average throughout the test environments suggesting they had a very good general adaptation. Genotype 8, 4 and 14 were the least stable genotypes and also with very poor yield performance (Figure 2B and Table 3). However, genotype 14 could be specifically adapted to environment, E404 (Figure 2B). The genotypes with higher yield were genotypes 1, 6, 21 and 23 (Table 3). However, the genotype 1 was unstable due to high absolute IPCA1 scores, along the ordinate (Figure 2B). Genotypes 9, 11 and 12 had mean yield close to the average (Table 3). However, these genotypes had high absolute IPCA1 scores (Figure 2B) suggesting they had poor general adaptation. They had, however, good specific adaptations to E103 and E104 (Table 3). The most discriminating environments were indicated by the longest distance from the origin (E403, E603, E504, and E303) (Figure 2B). Year differences were very high for some localities, such as, Reitrivier normal planting date (E403 and E404) and Upington (E603 and E604) (Figure 2B). This underlines the importance of evaluating multi-location yield trials over different seasons. Mean genotype performance across environments was correlated neither to IPCA1 (r=0.18; P>0.05) nor to IPCA2 (r=–0.05; P>0.05). However, environment mean performance was correlated significantly to both IPCA1 and IPCA2 (r= –0.61; P<0.05).

Table 3. Mean grain yield (t ha^{-1}) of 23 durum wheat genotypes in 12 environments (combination of year and location).

Genotype	Code	E104	E204	E304	E404	E504	E604	E103	E203	E303	E403	E503	E603	Mean
KRONOS	1	7.6	†9.7	9.5	8.1	6.2	8.8	8.6	9.0	5.9	9.6	9.6	3.8	8.03
DBSP00/1	2	7.9	8.3	6.8	6.9	4.1	8.7	9.6	9.4	4.4	11.7	9.2	3.8	7.57
DBSP00/2	3	8.1	9.3	9.2	7.7	5.7	8.9	9.1	9.0	5.4	10.4	8.8	3.7	7.94
DBSP02/6	4	7.6	7.8	6.3	6.3	3.6	8.2	9.2	8.9	3.8	11.4	8.5	3.4	7.08
DBSP02/7	5	8.0	8.1	7.5	6.5	4.2	8.4	9.2	8.5	4.0	11.1	7.5	3.1	7.18
DBSP02/8	6	8.4	8.9	7.1	7.6	4.7	9.3	10.2	10.3	5.1	12.5	10.5	4.7	8.28
DBSP02/9	7	9.6	9.1	9.5	7.2	5.4	9.4	10.1	8.8	4.7	11.8	6.6	3.6	7.98
DBSP02/10	8	8.2	7.8	7.0	6.1	3.7	8.4	9.4	8.5	3.6	11.6	7.1	3.0	7.03
DBSP02/11	9	8.8	8.5	7.4	6.9	4.3	9.1	10.1	9.4	4.4	12.4	8.4	3.9	7.80
DBSP02/13	10	8.8	8.4	7.7	6.8	4.4	9.0	10.0	9.1	4.3	12.1	7.8	3.7	7.68
DBSP02/19	11	9.0	8.4	7.3	6.8	4.2	9.2	10.3	9.4	4.2	12.7	8.1	3.9	7.79
DBSP02/22	12	8.9	8.6	7.5	7.0	4.5	9.2	10.2	9.5	4.5	12.4	8.5	4.0	7.90
DBSP03/02	13	8.3	8.4	7.8	6.8	4.5	8.7	9.4	8.8	4.3	11.3	7.8	3.4	7.46
DBSP03/03	14	7.5	8.2	7.5	6.7	4.4	8.2	8.8	8.6	4.3	10.5	8.2	3.2	7.18
DBSP03/04	15	7.9	9.0	8.0	7.6	5.1	8.9	9.4	9.5	5.2	11.1	9.7	4.0	7.95
DBSP03/10	16	8.9	8.7	8.6	6.9	4.9	9.0	9.8	8.8	4.5	11.6	7.2	3.5	7.70
DBSP03/11	17	8.9	8.6	8.8	6.7	4.9	8.8	9.5	8.4	4.3	11.2	6.5	3.1	7.48
DBSP03/12	18	8.7	8.7	7.8	7.2	4.7	9.1	10.0	9.5	4.7	12.0	8.7	4.0	7.93
DBSP03/16	19	8.8	8.9	8.5	7.2	5.0	9.2	9.9	9.2	4.8	11.7	8.1	3.8	7.93
DBSP03/17	20	8.2	8.1	7.4	6.5	4.1	8.5	9.4	8.6	4.0	11.3	7.5	3.2	7.23
DBSP03/18	21	9.0	8.9	8.2	7.2	4.9	9.3	10.1	9.4	4.7	12.1	8.2	4.0	8.00
DBSP03/19	22	7.9	8.6	7.7	7.0	4.6	8.6	9.2	9.0	4.6	11.0	8.7	3.6	7.54
DBSP03/20	23	9.2	8.8	8.1	7.1	4.8	9.4	10.3	9.5	4.6	12.5	8.0	4.0	8.03
Mean		8.4	8.6	7.9	7.0	4.6	8.9	9.6	9.1	4.5	11.6	8.2	3.7	7.68
Max†		9.6	9.7	9.5	8.1	6.2	9.4	10.3	10.3	5.9	12.7	10.5	4.7	

† Underlined values are the maximum yield at each test environment.

Partitioning the GE interaction into linear (GE linear) and non-linear (deviation from regression) in the joint regression analysis (Table 4) showed that both components were significant ($P<0.01$). A larger proportion of GE sums of squares (86%) were accounted for by the deviation from regression. Only small portions of GE sums of squares (14%) were accounted for by heterogeneity of regressions (Table 4). This was small compared to some studies, for example Ortiz et al. (2001) reported heterogeneity of regressions to account for 23%. However, for consideration of regression coefficient as stability parameter, heterogeneity of regression should explain more than 35% (Annicchiarico, 1997; Annicchiarico et al., 2006). This suggested that the joint regression analysis offered an incomplete explanation of the GE interaction for grain yield in this study. Nevertheless, a significant heterogeneity of regressions (genotype × environment linear comparison) indicated that the stability parameter, β, estimated by a linear response to a change in environment was not consistent among genotypes. The significance of the mean squares due to pooled deviations from regressions showed that the performance of some genotypes were not stable over environments. This highlighted the need to assess response of genotype to environmental changes using both a linear regression coefficient, (β) and deviations from the regression (δ_{di}). According to Eberhart and Russell (1966), genotypes

are grouped according to the size of their regression coefficients, less than, equal to, or greater than one, and according to the size of the deviation from the regression (equal to or different from zero). Genotypes with regression coefficient greater than one would be more adapted to favorable environments, and those with regression coefficients less than one would be adapted to unfavorable growth conditions, and those with regression coefficients equal to one would have an average adaptation to all environments. Genotypes with deviations from regression equal to zero would have highly predictive behavior, where as with regression deviations greater than zero, they would have low predictability.

Genotype 1 (check variety) had a high mean yield and a regression coefficient, which was significantly lower than one (Table 5), thus characterizing it as genotype probably adapted to unfavorable environmental conditions. However, deviation significantly different from zero coupled to the lowest coefficient of determination (R^2=72%) (Table 5), indicate that this genotype could be less predictable. However, genotypes, 9, 11, 12, 18, 19, 21 and 23 showed yield performances above average, regression coefficients close to unity, and deviation not significantly different from zero. These genotypes had also high coefficients of determination (Table 5). Therefore, they had an average capacity for adaptation to all the environments and were highly predictable. These kinds of genotypes could be considered ideal cultivars, since they maintained good performance in environments with low yield (Eberhart and Russell, 1966). The yield performance of genotypes 4, 5, 8, 14 and 20 were below the average (Table 5). Theses genotypes had regression coefficients equal to one. Thus, these genotypes could be stable, but with less response to environmental changes. The high coefficients of determination and deviations variance close to zero for these genotypes imply that these genotypes had relatively good predictability (Table 5). Finlay and Wilkinson (1963), Perkins and Jinks (1968) reported that linear response of a genotype is associated with mean performance. In our study however, neither the regression coefficient (r=0.20) nor the deviations mean square (r=0.29) was associated to mean yield performance (P>0.05). This agrees with the findings of similar studies in sorghum (Haussmann et al., 2000). Eberhart and Russell (1966) also emphasized that both the regression coefficients and the deviations need to be considered in assessing stability and their responses were independent from each other.

Table 4. Partitioning of GE into linear and nonlinear component from joint linear regression analysis of 23 durum wheat genotypes yield performance evaluated across 12 environments.

Source	DF	SS[a]	MS
Genotype (G)	22	32.702	1.486**
Environment (E)+GE	253	1504.227	5.946**
E(linear)	1	1377.732	1377.732**
GE (Linear)	22	17.888(14.25)	0.813*
Pooled deviation from Regression	230	108.606(85.75)	0.472**
Residual	552	165.762	0.300
Total	827	1536.929	

[a]Number in brackets are percentage of GE explained by linear regression and deviations from regression. DF=degree of freedom, SS=sum of squares, MS=mean squares.
* and ** are significant at P<0.05 and 0.01, respectively.

Table 5. Mean yield across environments and stability parameters of Eberhart and Russell (1966) model for 23 durum wheat genotypes evaluated across 12 environments.

			Yield	Stability parameter	
Name	Code	t ha^{-1}	β	δ_{di}	R^2 (%)
KRONOS	1	8.03	0.65**	0.71**	72
DBSP00/1	2	7.56	1.03	0.45**	90
DBSP00/2	3	7.95	0.83	0.38*	86
DBSP02/6	4	7.09	1	0.19	92
DBSP02/7	5	7.19	0.94	-0.06	96
DBSP02/8	6	8.27	1.13	0.59**	89
DBSP02/9	7	7.97	1.06	0.48**	90
DBSP02/10	8	7.01	1	0.31	91
DBSP02/11	9	7.79	1.16	0.13	95
DBSP02/13	10	7.66	0.99	0.26*	91
DBSP02/19	11	7.79	1.08	0.19	93
DBSP02/22	12	7.91	1.1	-0.17	98
DBSP03/02	13	7.48	0.93	-0.07	96
DBSP03/03	14	7.17	0.86	-0.18	97
DBSP03/04	15	7.95	0.96	0.27*	91
DBSP03/10	16	7.71	1.11	0.09	95
DBSP03/11	17	7.48	0.99	0.34*	90
DBSP03/12	18	7.91	1.1	0.06	95
DBSP03/16	19	7.92	0.99	-0.04	96
DBSP03/17	20	7.24	1	0.16	93
DBSP03/18	21	7.99	1.04	0.00	96
DBSP03/19	22	7.53	0.91	-0.11	96
DBSP03/20	23	8.03	1.17	-0.03	97
	Mean	7.68	1.00		
	Stderr	0.073	0.088		

β = linear regression coefficient. $\delta_{di=}$ deviation from regression
* and ** are significant at P<0.05 and 0.01, respectively.

In order to compare the efficiency of the two models, model comparison criteria were computed (Table 6). The amount of GE variation explained by heterogeneity of regression in the joint linear regression analysis model (R^2=14%) was lower than that of the variation explained in both IPCA 1 and 2 of AMMI model (R^2=27 and 22 %, respectively). The AMMI2 (IPCA1 and IPCA2) explained (R^2=49%), which was more than three time higher than the amount explained due to heterogeneity of regression in the joint linear regression analysis model. The estimated variance components of the GE interaction (σ^2ge) were significantly (*P*<0.01) different from zero in all cases (Table 6). However, the relative size of variance represented in the GE interaction by AMMI model was larger than the joint linear regression model. IPCA1 had GE variance that was almost five times bigger than the heterogeneity of regression. AMMI2 represented almost nine times larger variance compared to the heterogeneity of regression in the joint analysis model. Annicchiarico, et al. (2006) pointed out that mean squares and degree of freedom are related to the predictive ability of the model. This is because they take into account accuracy (i.e., the amount of GE interaction sum of squares), and parsimony (i.e., the amount of degree of freedom) of the model. Examining the ratio of % GE SS to % GE DF revealed further evidence to the

Table 6. Model comparison criteria computed from joint regression and AMMI models parameters for 23 durum wheat genotypes evaluated across 12 environments.

Parameter	R^2 (%)	σ^2_{ge}	%GE SS/%GE DF
Joint Regression			
Heterogeneity	14.25	0.128**	1.63
Deviation	85.75	0.043**	0.93
AMMI			
IPCA1	27.19	0.614**	2.06
IPCA2	22.20	0.510**	14.16
AMMI2	49.39	1.124**	7.91

σ^2_{ge} = variance of GE. ** indicates that the value is significantly (P<0.01) different from zero

superiority of the AMMI model in terms of its predictive ability. Based on this criterion, IPCA1 showed a ratio higher than of the heterogeneity of regression (Table 6). AMMI2 showed a ratio, which was almost five times larger than the heterogeneity of the regression in the joint regression analysis model. The superiority of AMMI model over joint regression model has already been reported in various crops (Annicchiarico, 1997; Brancourt-Hulmel et al., 1997; Annicchiarico, 2002; Annicchiarico and Piano, 2005; Annicchiarico et al., 2006).

Conclusions

The joint regression analysis based on Eberhart and Russell (1966) model provided an incomplete explanation to the GE interaction patterns. Comparison of the joint regression model with AMMI based on the different efficiency measurement criteria confirmed that AMMI model was superior to the joint regression model. Moreover, AMMI provided adequate explanation to the relevant pattern of variation in the treatment sum of squares and GE interactions. Detailed information was generated based on AMMI biplot analysis. The extent of variability among genotypes in relation to their target environment was evident. The biplot showed how a particular genotype that fell in a particular sector attained the observed performances. Moreover, clear stratification of environments was evident, which could possibly represent mega- environments. The association between the regression coefficient and the IPCA1 was strong (r= -0.88; $P< 0.01$). Moreover, neither the Eberhart and Russell (1966) stability parameters nor the IPCAs were related to mean yield performance. However, for practical cultivars recommendation purposes AMMI based analysis of genotype by environment interactions assessments should be powerful tool because it can easily discern which-won-where pattern. Moreover, in national variety trials where a number of diverse localities are included identification of environments with similar patterns (mega-environments) would be possible.

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References

Akcura, M., Kaya, Y., Taner, S., 2005. Genotype-environment interaction and phenotypic stability analysis for grain yield of durum wheat in the Central Anatolian Region. Turk. J. Agri. 29, 369-375.

Annicchiarico, P., 1997. Joint regression vs AMMI analysis of genotype-environment interactions for cereals in Italy. Euphytica 94, 53-62.

Annicchiarico, P., 2002. Genotype X environment interactions: Challenges and opportunities for plant breeding and cultivar recommendations. FAO plant production and protection paper No. 174. FAO, Rome.

Annicchiarico, P., Piano, E., 2005. Use of artificial environments to reproduce and exploit genotype X location interaction for Lucerne in northern Italy. Theor. Appl. Genet. 110, 219-227.

Annicchiarico, P., Russi, L., Piano, E., Veronesi, F., 2006. Cultivar adaptation across Italian locations in four Turf grass species. Crop Sci. 46, 264-272.

Brancourt-Hulmel, M., Biarnès-Dumoulin, V., Denis, J.B., 1997. Guiding marks on stability and genotype-environment interaction analyses in plant breeding. Agronomie 17, 219-246.

Burgueno, J., Crossa, J., Vargas, M., 2001. SAS programs for graphing GE and GGE biplots. Biometrics and Statistics Unit, CIMMYT.

Campbell, B.T., Jones, M.A., 2005. Assessment of genotype X environment interactions for yield and fiber quality in cotton performance trials. Euphytica 144, 69-78.

Crossa, J., 1990. Statistical analysis of multilocation trials. Adv. Agron. 44, 55-85.

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

Finlay, K.W., Wilkinson, G.N., 1963. The analysis of adaptation of plant breeding programme. Aust. J. Agric. Res.14, 742-754.

Gauch, J.H.G., Zobel, R.W., 1997. Identifying mega-environments and targeting genotypes. Crop Sci. 37, 311-326.

Haussmann, B.I.G., Obilana, A.B., Ayiecho, P.O., Blum, A., Schipprack, W., Geiger, H.H., 2000. Yield and Yield stability of four population types of grain sorghum in a semi-arid area of Kenya. Crop Sci. 40, 319-329.

Hussien, M.A., Bjornstad, A., Astveit, A.H., 2000. SASG X ESTAB: A SAS program for computing genotype x environment stability statistics. Agron. J. 92, 454-459.

Kaya, Y., Taner, S., Ceri, S., 2003. Nonparametric stability analysis of yield performances in oats (*Avena sativa* L.) genotypes across environments. Asian J. Plant Sci. 2, 286-289.

Ortiz, R., Wagoire, W.W., Hill, J., Chandra, S., Madsen, S., Stølen, O., 2001. Heritability of and correlations among genotype-by-environment stability statistics for grain yield in bread wheat. Theor. Appl. Genet. 103, 469-474.

Perkins, J.M., Jinks, J.L., 1968. Environmental and genotype-environmental components of variability. III. Multiple lines and crosses. Heredity 2, 339–356.

SAS institute. 1999. SAS/STAT user's guide. 8 Version. SAS Institute Inc. Cary, NC.

Solomon, K.F., Smit, H.A., Malan, E., Du Toit, W.J., 2007. Comparison study using rank based nonparametric stability statistics of durum wheat. World J. Agric. Sci. 3, 444-450.

Tesemma, T., Tsegaye, S., Belay, G., Bechere, E., Mitiku, D., 1998. Stability of performance of tetraploid wheat landraces in Ethiopian highland. Euphytica 102, 301-308.

Yan, W., 2002. Singular-value partitioning in biplot analysis of multienvironment trial data. Agron. J. 94, 990-996.

Yan, W., Cornelius, P.L., Crossa, J., Hunt, L.A., 2001. Two types of GGE biplots for analyzing multi-environment trial data. Crop Sci. 41, 656-663.

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

Yue, G.L., Roozeboom, K.L., Schapaughjr, W.T., Liang, G.H., 1997. Evaluation of soybean cultivars using parametric and nonparametric stability estimates. Plant Breed. 116, 271-275.