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Identification of Stability and Adaptability in Advanced Durum Genotypes Using AMMI Analysis

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Abstract: This study was undertaken to determine the yield performance of 15 improved durum wheat genotypes selected from Iran/ICARDA joint project in 12 environments during 2004-06 in Iran. Our results showed that contributions to treatment main-effects were: genotype (2.85%), environment (61.59%) and GE (14.86%). Analysis of the interaction revealed decreasing magnitude of contributions to the GE sum of squares in the order: Interaction Principal Component Axis 1 (IPCA1) = 28.2%, IPCA2 = 25.04%, IPCA3 = 18.98% and IPCA4 = 8.52%. In this study the IPCA scores presented a disproportionate genotype response, which was the major source of variation for crossover GE interaction. GE interaction patterns revealed by AMMI biplot analysis indicated that the durum wheat genotypes are narrowly adapted. No genotype has superior performance in all environments. The genotype Mrb3/Mna-1 was the best at combining yield stability and productivity. The genotypes 12A-Mar8081 and 14A-Mar8081 had the most stability but low yielding. Mna-1/Rfm-7 had the highest yield performance and relative widely adapted to across environments.

Key words: Durum wheat, GE interaction, AMMI analysis, biplot, stability

INTRODUCTION

Multi Environment Trials (METs) are important in plant breeding and agronomy for studying yield stability and predicting yield performance of genotypes in across environments. The differential response of genotypes to environmental changes is a Genotype by Environment (GE) interaction (Vargas *et al.*, 2001). Understanding of the causes of GE interaction can be used to establish breeding objectives, identify ideal test conditions and formulate recommendations for areas of optimal genotype adaptation (Yan and Hunt, 2001). The term GE interaction commonly refers to yield variation that cannot be explained by the genotype main effect (G) and the environment main Effect (E). For genotype evaluation, however, both G and GE must be considered simultaneously. Using a environments regression model (SREG), Yan *et al.* (2000) combined G and GE, denoted as G+GE or GGE and repartitioned this into noncrossover GE interaction and crossover GE interaction. The term GE interaction will be hereafter used to denote this combination. Understanding the causes of noncrossover and crossover GE interaction would help develop an understanding of the genotypic characteristics that contribute to a superior genotype and the environmental factors that can be manipulated to facilitate selection for such genotypes (Yan *et al.*, 2000). Numerous methods

have been used for an understanding of the causes of GE interaction (van Eeuwijk *et al.*, 1996). These methods can be categorized into two major strategies. The first strategy involves factorial regression analysis of the GE matrix (i.e., the yield matrix after the environment and genotype main effects are removed) against environmental factors, genotypic traits, or combinations thereof (Baril *et al.*, 1995). The second strategy is associated with the use of the Additive Main Effects and Multiplicative Interaction (AMMI) model in MET data analysis.

The AMMI model is a hybrid analysis that incorporates both the additive and multiplicative components of the two-way data structure. AMMI is the only model that distinguishes clearly between the main and interaction effects and this is usually desirable in order to make reliable yield estimations (Gauch, 1992). AMMI biplot analysis is considered to be an effective tool to diagnose GE interaction patterns graphically. The AMMI modeled describes the GE interaction in more than one dimension and it offers better opportunities for studding and interpreting GE interaction than analysis of variance (ANOVA) and regression of the mean (Vargas *et al.*, 2001). In AMMI, the additive, portion is separated from interaction by ANOVA. Then the Interaction Principle Components Analysis (IPCA), which provides a multiplicative model, is applied to analyze the interaction effect from the additive ANOVA model. The

biplot display of IPCA scores plotted against each other provides visual inspection and interpretation of the GE interactions. Integrating biplot display and genotypic stability statistics enables genotypes to be grouped based on similarity of performance across diverse environments (Thillainathan and Fernandez, 2001).

Concerning the use of AMMI in METs data analysis, which partitions the GE interaction matrix into individual genotypic and environmental scores, an example was provided by Zobel *et al.* (1988), who studied the GE interaction of a soybean MET. Other examples were provided by Annicchiarico and Perenzin (1994), Yan *et al.* (2000), Vargas *et al.* (2001), Yan and Hunt (2001), Kaya *et al.* (2002), Lafitte and Courtois (2002), Brancourt-Hulmel and Lecomte (2003) and Tarakanovas and Ruzgas (2006). Among multivariate methods, AMMI analysis is widely used for GE interaction investigation. This method has been shown to be effective because it captures a large portion of the GE interaction sum of square, it clearly separates main and interaction effects that present agricultural researchers which different kinds of opportunities and the model often provides agronomically meaningful interpretation of the data (Ebdon and Gauch, 2002). The results of AMMI analysis are useful in supporting breeding program decisions such as specific adaptation and selection of environment (Gauch and Zobel, 1996). Usually, the results of AMMI analysis shown in common graphs are called biplot. The biplot shows both the genotypes and the environments value and relationship using singulars vectors technique (Tarakanovas and Ruzgas, 2006).

This study was undertaken to interpret GE interaction obtained by AMMI analysis of yield performances of 15 durum wheat genotypes over 12 environments, visually assess how to vary yield performances across environments based on the biplot and group the genotypes having similar response pattern across environments.

MATERIALS AND METHODS

Statistical methods: GE interaction for grain yield was first analyzed according to a classical multiplicative model or AMMI (Gollob, 1968; Mandel, 1971; Gauch, 1992; Brancourt-Hulmel and Lecomte, 2003) with three multiplicative terms. It is written as follows:

$$E[Y_{ge}] = \mu + \alpha_g + \beta_e + \lambda_1 \gamma_{g1} \delta_{e1} + \lambda_2 \gamma_{g2} \delta_{e2} + \lambda_3 \gamma_{g3} \delta_{e3}$$

Where:

$E[Y_{ge}]$ = Expectation of performance

Y_{ge} = Genotype g grown in environment e

μ = General mean

α_g = Genotype main effect

β_e = Environment main effect; each of the multiplicative term has the same structure

λ_1 = Size

γ_{g1} = Normalized genotype vector of the genotype scores or sensitivities

δ_{e1} = Normalized environmental vector of the scores describing the environments, all assigned to the first term.

The parameters of the second and third terms follow the same definition. For each genotype, interaction was described in terms of ecovalence (von Wricke, 1962) and the interaction pattern with genotype scores provided by the AMMI model.

Biplot derived by plotting the genotypes and environments markers (scores) of the first two multiplicative terms of the AMMI model are also useful for summarizing GE interaction patterns (Vargas *et al.*, 2001).

Other statistics methods: Purchase *et al.* (2000) developed one test based on the AMMI model's IPCA1 and IPCA2 values for each genotype and each environment. They called it the AMMI Stability Value (ASV). This ASV is in effect the distance from the coordinate point to the origin in a two dimensional scatter gram of IPCA1 scores against IPCA2 scores.

Because the IPCA1 score contributes more to the GE interaction sum of squares (SS), a weighted value is needed. This weight is calculated for each genotype ($ASV_{(G)}$) and environment ($ASV_{(E)}$) according to the relative contribution of IPCA1 to IPCA2 to the interaction SS as following.

$$ASV_{(G)} = \sqrt{\left[\frac{SSIPCA1}{SSIPCA2} (GIPCA1score) \right]^2 + (GIPCA2score)^2}$$

$$ASV_{(E)} = \sqrt{\left[\frac{SSIPCA1}{SSIPCA2} (EIPCA1score) \right]^2 + (EIPCA2score)^2}$$

Where:

$$\frac{SSIPCA1}{SSIPCA2}$$

is the weight given to the IPCA1 value by dividing the IPCA1 sum of squares by the IPCA2 sum of squares. GIPCA1 and GIPCA2 scores are the IPCA1 and IPCA2 scores for the specific genotype. EIPCA1 and EIPCA2 scores are the IPCA1 and IPCA2 scores for the specific environment.

Fox *et al.* (1990) suggested three parameters for general adaptability. The proportion of environments at

Table 1: Code, cropping season, names and origin of genotypes, status of rainfall+ irrigation for each environment

Env	Cropping season	Location	Code of Env	Rainfall+SI †	Code of genotypes	Genotype	Origin
1	2003-04	Kermanshah	A	Rainfed (597.1 mm)	G1	Omgencil-3	ICARDA
2	2003-04	Kermanshah	B	SI (597.1+50 mm)	G2	Omrabi-5	ICARDA
3	2003-04	Ilam	C	Rainfed (590 mm)	G3	Syrian-4	ICARDA
4	2003-04	Ilam	D	SI (590+0 mm)	G4	Mrb3/Mna-1	ICARDA
5	2004-05	Kermanshah	E	Rainfed (431.5 mm)	G5	Waha	ICARDA
6	2004-05	Kermanshah	F	SI (431.5+50 mm)	G6	Mna-1/Rfm-7	ICARDA
7	2004-05	Ilam	G	Rainfed (552 mm)	G7	9A-Kor8081	Iran
8	2004-05	Ilam	H	SI (552+50 mm)	G8	12A-Mar8081	Iran
9	2005-06	Kermanshah	I	Rainfed (514.3 mm)	G9	14A-Mar8081	Iran
10	2005-06	Kermanshah	J	SI (514.3+0 mm)	G10	15A-Mar8081	Iran
11	2005-06	Ilam	K	Rainfed (570 mm)	G11	18A-Mar8081	Iran
12	2005-06	Ilam	L	SI (570+50 mm)	G12	19A-Mar8081	Iran
					G13	20A-Mar8081	Iran
					G14	Zardak (Durum wheat local check)	Iran
					G15	Sardari (Bread wheat national check)	Iran

†: SI is supplemental irrigation

which the genotypes occurred in the top, middle and bottom third of the ranks was computed to form the parameters of TOP, MID and LOW, respectively. A genotype that occurred mostly in the top third (high value of TOP) was considered as widely adapted genotype.

Data source: This study was carried out with 13 improved durum wheat genotypes in 12 environments (year-location combinations during 2004-2006) including six rain-fed environments and six supplemental irrigation (50 mm at flowering stage) environments undertaken at dryland agricultural research stations of Sararood (Kermanshah province, Iran) and Zanjireh (Ilam province, Iran). Of 13 genotypes, six were from the international durum wheat improvement program based on Iran/ICARDA joint project and seven from the national durum wheat improvement program. Also two genotypes Zardak (durum wheat) and Sardari (bread wheat) that are typically grown by Iranian farmers were considered as national check in this study (Table 1). Experimental layout was a randomized complete blocks design with three replications in each environment. Sowing was done by an experimental drill in 1.2×6 m plots, consisting of six rows with 20 cm between the rows. Seeding rate was 350 seeds m⁻² for each location. Fertilizer application was 41 N kg ha⁻¹ and 46 P₂O₅ kg ha⁻¹ at planting. Yield (kg ha⁻¹) was obtained by converting the grain yields obtained from plots to hectares. A combined ANOVA and AMMI analysis on the values of grain yield was processed using the program IRRISTAT.

RESULTS

AMMI analysis: The AMMI analysis of variance (Additive main effects) showed significant effects for genotype, environment and GE interaction (Table 2). These results showed that 61.59% of the total sum of squares (SS) was attributable to environment effects, only

2.85 and 14.86% to genotype and GE interaction effects, respectively. A large of SS for environments indicated that the environments were diverse, with large differences among environmental means causing most of the variation in grain yield. The magnitude of the GE interaction SS was 5.2 times larger than that for genotypes, indicating that there were sustainable differences in genotypic response across environment.

Results from AMMI analysis (Multiplicative effect) also showed that the first Interaction Principle Component Axis (IPCA1) captured 28.2% of the interaction SS in 15.58% of the interaction Degrees of Freedom (df). Similarity the IPCA2 and IPCA3 explained a further 27.86 and 18.98% of the GE interaction SS, respectively. Furthermore, IPCA1 and IPCA2 had SS greater than that of genotypes. The mean squares for IPCA1 and IPCA2 were significant (p<0.01) and cumulatively contributed to 53.24% of the total GE interaction. Therefore, the post-dictive evaluation using an F-test at p = 0.01 suggested that two IPCA1 and IPCA2 were significant for the model with 46 df. In total, AMMI2 model contained 91.23% of the treatment SS, while the residual contained only 9.6%. The treatment and block SS combined make up 81.8% of the total SS, with only 37.7% of the total df, while the error term's SS make up 18.6% of the total SS, while containing 62.3% of the total df. These results indicate that the AMMI model fits the data well and justifies the use of AMMI2.

IPCA's represent noncrossover and crossover GE interaction: IPCA's scores of genotypes and environments took both positive and negative values (Table 3, 4). Consequently, a genotype that has large positive IPCA score with some environments must have large negative interactions with some other environments. Thus, these scores presented a disproportionate genotype response (Yan and Hunt, 2001), which was the major source of variation for any crossover GE interaction.

Table 2: Additive main effects and multiplicative interactions analysis of variance for grain yield of the 15 genotypes in 12 environments

Source	df	SS	MS	F	Explained (%)
Total	539	332281147	616477	-	-
Treatment	179	263488660	1472004	8.18**	79.29
Genotypes	14	9457645	675546	3.75**	2.85
Environments	11	204637631	18603421	53.62**	61.59
Interactions (GxE)	154	49393384	320736	1.78**	14.86
IPCA1	24	13930366	580432	3.23**	28.20
IPCA2	22	12367005	562137	3.12**	25.04
IPCA3	20	9374946	468747	2.60**	18.98
IPCA4	18	4207834	233769	1.30 ^{ns}	8.52
Residuals	70	9513233	135903	0.76 ^{ns}	19.26
Block	24	8327278	346970	1.93**	2.51
Error 336	60465209	179956	-	18.20	

The block source of variation refers to blocks within environments, ** and ^{ns} are significant at 1% level and non-significant, respectively

Table 3: Mean yield and the first two IPCAs scores, AMMI Stability Value (ASV) parameter and parameters of TOP, MID and LOW and for 15 genotypes in 12 environments

Genotype	Mean yield	GIPCA1 [†]	GIPCA2	ASV [‡]	TOP [¶]	MID [¶]	LOW [¶]
G1	2874	-0.65	-15.59	15.61	25	33	42
G2	2948	10.11	3.63	11.95	25	42	33
G3	3131	-8.94	-5.49	11.47	50	25	25
G4	3122	3.76	2.67	5.01	42	58	0
G5	3093	7.01	-20.28	21.76	50	17	33
G6	3255	22.61	6.23	26.22	83	0	17
G7	2927	-16.21	16.92	24.89	33	25	42
G8	2732	1.96	3.79	4.39	0	17	83
G9	2932	-2.31	1.35	2.93	25	50	25
G10	3121	16.17	22.66	29.07	42	33	25
G11	2937	-20.46	1.18	23.08	42	17	42
G12	2853	-10.24	5.77	12.90	8	50	42
G13	3070	13.84	-15.82	22.21	33	42	25
G14	2892	-5.96	5.46	8.65	8	42	50
G15	3020	-10.69	-12.49	17.35	33	50	17

†: GIPCA is genotypic IPCA scores, ‡: ASV is genotypic AMMI stability value parameter by Purchase *et al.* (2000b), ¶: TOP, MID and LOW are parameters by Fox *et al.* (1990)

Table 4: Environments ranked on EIPCA1 scores; including the first four recommended genotypes for each environment based on AMMI2 estimates and environmental ASV parameter

Environment	Mean	EIPCA1 [†] score	EIPCA2 score	AMMI2 genotype recommendations				ASV [‡]
				1st	2nd	3rd	4th	
C	1688	23.90	-6.58	G13	G6	G10	G5	27.71
D	3462	14.85	-20.22	G6	G3	G5	G4	26.24
G	2548	10.31	5.41	G10	G6	G2	G4	12.81
K	2968	7.90	31.65	G10	G6	G13	G4	32.88
F	3381	5.42	3.23	G10	G6	G7	G2	6.91
E	2780	2.35	-4.90	G6	G3	G5	G4	5.57
B	3131	-0.42	-5.33	G5	G13	G3	G6	5.35
A	1994	-0.79	-4.36	G3	G5	G6	G4	4.45
J	3809	-8.83	16.03	G6	G7	G11	G10	18.87
L	3387	-11.17	-1.06	G3	G15	G11	G5	12.63
I	3270	-19.59	-14.40	G15	G14	G7	G11	26.35
H	3549	-23.92	0.53	G6	G11	G15	G3	26.95
Dominant genotype				G6	G6	-	G4	

†: EIPCA is environmental IPCA scores, ‡: ASV is environmental AMMI Stability Value parameter of Purchase *et al.* (2000)

This disproportionate genotype response is referred to as crossover GE interaction for convenience. Diversely, scores with the same sign or near zero represent a noncrossover GE interaction or a proportionate genotype response.

Explaining the behavior of the most interactive genotypes: The analysis of genotypes and environments

parameters resulting from AMMI, because this parameters help to describe the behavior of genotypes. Genotypes near to origin show little interaction, while genotypes distance from it represent the most interactive genotypes (Fig. 1). Genotypes G6, G10, G13, G7, G11 and G15 were the most interactive, while G4, G8 and G9 were the least interactive. Out of six most interactive genotypes, G6 and G10 had the most similar interaction pattern. G10

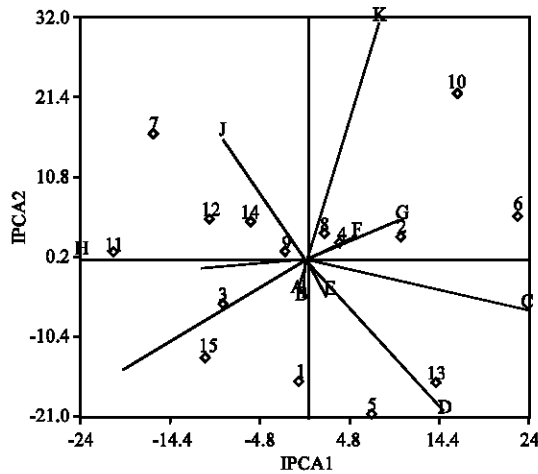


Fig. 1: AMMI2 biplot of 15 genotypes (Numbers) and 12 environments (Letters) for grain yield using genotypic and environmental scores

showed positive interaction effect at the environments F, G and K. G6 showed positive interaction effects at C, D, F, G and K. G13 showed positive interaction effects at D environment (Fig. 1, Table 3). In the experiments under consideration, not only G4 had positive interaction in environments with high yield, but also had the lowest interaction in across environments. It had higher grain yield than grand mean in all environments (Table 3, Fig. 1).

According to AMMI Stability Value (ASV), genotypes G9, followed by G8 and G4 were stable and undesirable genotypes regarding to this parameter were G10, G6, G7, G11 and G5, respectively. G6 had the highest yield mean across environments and according to TOP parameter was considered as widely adapted genotype (TOP = 83%) (Table 3).

Test of environments: The results of AMMI analysis showed that 61.59% of the total Sum of Squares (SS) was attributable to environment effects. A large of SS for environments indicated that the environments were diverse, with large differences among environmental means causing most of the variation in grain yield (Table 2). Also, to help interpret AMMI results from the environmental viewpoint, the correlations between the environments were computed. Correlations of genotypes yield among environments varied widely. The correlations were varied from -0.60 to 0.77 ($p < 0.01$) (Data not shown). The largest yield were recorded in environments with supplemental irrigation (B, D, F, H, J and L). The environments F, K and G were close to each other in the AMMI2 biplot indicating similar discrimination of genotypes (Fig. 1, Table 4). Similarity, environments C and

D grouped together. The environments K, C, D, I and H differed from all other environments in interaction with genotypes. Environmental IPCAs scores close to zero are characteristic of environments which contribute little to the interaction, that is, they are stable. In this study the environments of A, B, E and F were stable and had the least interaction with genotypes. These results were taken by ASV parameter too (Table 4).

Biplot: The AMMI biplot was generated using genotypic and environmental scores of the first two IPCAs (Fig. 1). In this case, biplot has four sections, depending upon signs of the genotypic and environmental scores. In the figure 1, the environments fell into four sections: with respected to all three environments F, K and G, G10 and G6 were the best, respectively. Also G6 has the highest yield among the genotypes in the environments D, E, J and H. For the environments of C and D the genotypes of G13, G5 were the best (Fig. 1). Genotypes located near the plot origin were less responsive than the vertex genotypes. Genotype G6 gave the highest average yield (largest IPCA1 score) but was relatively stable in across environments, due to the fact that it does not give very small absolute IPCA2 score. In contrast the non adapted genotypes of G8 and G9 yielded low at all environments, as indicated by their small IPCA1 (low yielding) and small IPCA2 (high stable). G3 and G4 had high yield ($G6 > G3 > G4$) and relatively high stable ($G4 > G3 > G6$), in this fact due to relatively small IPCA1 and IPCA2 scores G3 and G4 in comparison with G6. The biplot shows not only the average yield of a genotype (IPCA1), but also how it is achieved. That is, the biplot also shows the yield of a genotype at individual environments. For example genotype G6 had the highest average yield because it yielded at environments B, G, I and J and yielded above average at all other environments.

Genotype recommendations: In this study we want to make genotype recommendations based on the genotypes used. Accordingly a good estimate of genotype performance for specific environments can be made. In Table 4 the first four genotype recommendations based on estimated yield are shown for each environment. From this table it can be seen that firstly, G6 is prominent in the top four environments (D, E, J and H) followed by G3 being the genotype of choice in environments of A and L. G10 is the preferred genotype for the environments F, G and K and G13 for C. Lastly G15 was adapted to the environment I.

According to Fox *et al.* (1990) parameter, a genotype usually found in the top third of entries across environments can be considered relatively well adapted.

Thus, G6 was adapted because it ranked in the top third of genotype in a high percentage of environments (high top value, 83%) and was followed by G3 (50%) and G5 (50%). The undesirable genotypes in this method were G8, G12 and G14 (Table 3).

Table 3 and 4 give valuable information regarding genotypes performance and adaptation. From Table 3, becomes evident that G6 was the first recommendation in four out of 12 times, second in four out of 12 times, third in one out 12 times and fourth in one out of 12 times, being in the top four recommendations 10 out of 12 times. No other genotype matches the performance of G6. The both G10 and G3 were in the top four recommendations 5 out of 12 times.

DISCUSSION

There are two strategies for developing genotypes with low G x E interactions. The first is sub-division or stratification of a heterogeneous area into smaller, more homogeneous sub-regions, with breeding programs aimed at developing genotypes for specific sub-regions. However, even with this refinement, the level of interaction can remain high, because breeding area does not reduce the interaction of genotypes with locations and years. The second strategy for reducing G×E interaction involves selecting genotypes with better stability across a wide range of environments in order to better predict behaviour (Eberhart and Russell, 1966; Tai, 1971). Various methods use G×E interaction to facilitate genotype characterization and as a selection index together with the mean yield of the genotypes.

Numerous methods have been used for an understanding of the causes of G×E interaction (van Eeuwijk *et al.*, 1996). One of them is Additive Main Effects and Multiplicative Interaction (AMMI) model in MET data analysis. The AMMI modeled describes the GE interaction in more than one dimension and it offers better opportunities for studding and interpreting GE interaction than analysis of variance (ANOVA) and regression of the mean (Vargas *et al.*, 2001). In AMMI, the additive, portion is separated from interaction by ANOVA. Then the Interaction Principle Components Analysis (IPCA), which provides a multiplicative model, is applied to analyze the interaction effect from the additive ANOVA model. The biplot display of IPCA scores plotted against each other provides visual inspection and interpretation of the GE interactions. Integrating biplot display and genotypic stability statistics enables genotypes to be grouped based on similarity of performance across diverse environments (Thillainathan and Fernandez, 2001).

In this study the results of AMMI analysis indicated that the AMMI model fits the data well and justifies the use of AMMI2. This made it possible to construct the biplot and calculate genotypes and environments effects (Gauch and Zobel, 1996; Vargas and Crossa, 2000; Yan and Hunt, 2001; Kaya *et al.*, 2002). The Interaction Principal Component Axes (IPCA) scores of a genotype in the AMMI analysis indicate the stability of a genotype across environments. The closer the IPCA scores to zero, the more stable the genotypes are across their testing environments (Carbonell *et al.*, 2004). In this study, G6 gave the highest average yield (largest IPCA1 score) but was relatively stable over the environments. In contrast the non adapted genotypes of G8 and G9 yielded low at all environments, as indicated by their small IPCA1 (low yielding) and small IPCA2 (high stable). G3 and G4 had high yield and relatively high stable, in this fact due to small IPCA2 scores G3 and G4.

The most accurate model for AMMI can be predicted by using the first two IPCAs (Gauch and Zobel, 1996; Yan and Hunt, 2001; Kaya *et al.*, 2002). Conversely, Sivapalan *et al.* (2000) recommended a predictive AMMI model with the first four IPCAs. These results indicate that the number of the terms to include in an AMMI model cannot specify a prior without first trying AMMI predictive assessment. In general, factors like type of crop, diversity of the germplasm and range of environmental conditions will affect the degree of complexity of the best predictive model (Crossa *et al.*, 1990).

However, the prediction assessment indicated that AMMI with only two interaction principal component axes was the best predictive model (Zobel *et al.*, 1988). Further interaction principal component axes captured mostly noise and therefore did not help to predict validation observations. In this study, the interaction of the 15 genotypes with 12 environments was best predicted by the first two principal components of genotypes and environments.

AMMI Stability Value (ASV) is in effect the distance from the coordinate point to the origin in a two dimensional scattergram of IPCA1 scores against IPCA2 scores (Purchase *et al.*, 2000). Stability in itself should however not be the only parameter for selection, as the most stable genotype wouldn't necessarily gives the best yield performance. As example, consider G9, which has the lowest ASV. If G9 was selected as genotype of choice because of its stability, a mean yield 2932 kg ha⁻¹ would have been reached (Table 3). This is no real improvement on the grand mean of 2994 kg ha⁻¹. Referring to Table 4, G9 was not recommended according to AMMI2 in first

four recommendations across environments. This performance does not match that of a genotype like G4, with reasonably good ASV ($ASV = 5.01$) and good average yield (3122 kg ha^{-1}). If G4 was planted in all 12 environments, an increase in average yields from 2994 to 3122 kg ha^{-1} would be achieved. Only at three environments the average yield of G4 was below grand mean of environments. G3 is another genotype with higher mean yield than G4 ($3131 > 3122 \text{ kg ha}^{-1}$) but its ASV higher than G4 ($11.47 > 5.01$).

Genotypes evaluation must be conducted in multiple locations for multiple years to fully sample the target environment (Cooper *et al.*, 1997). Genotype in the presence of unpredictable GE interaction is a perennial problem in plant breeding (Bramel-Cox, 1996). To select for superior genotypes, it seems that there is no easier way other than to test widely (Troyer, 1996) and select for both average yield and stability (Lin and Binns, 1994; Kang, 1997).

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