

Stability Analysis of Bread Wheat Genotypes for Heading Time and Grain Yield Using AMMI Model



Ahmed, A.A.¹; M.B. Tawfelis²; M.A. Sayed¹; R.E. Mahdy¹ and M.O. Mostafa²

¹Agronomy Department, Faculty of Agriculture, Assiut University, Assiut, Egypt

²Wheat Dept., Field Crops Research Institute, A.R.C., Giza, Egypt

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Abstract

Additive main effects and multiplicative interactions (AMMI) model analyses were performed to assess and quantify the magnitude of genotype by environment interaction (GEI) for number of days to heading (DH) and grain yield (GY/P) stability of sixteen promising bread wheat (*Triticum aestivum* L.) genotypes. Field experiments under recommended (N) and late (L) sowing date in newly reclaimed soil were conducted in the Agricultural Research Station at Arab-Elawamer, Assiut, Egypt for three consecutive seasons (2016/2017, 2017/2018 and 2018/2019). The combined ANOVA showed highly significant differences among genotypes and among environments for both traits, while GEI was highly significant for DH and not significant for GY/P. Results of AMMI analysis indicated that the first three AMMI (PC1, PC2 and PC3) were highly significant for DH and AMMI1 was only significant in case of GY/P. In addition, the environments showed high contributions to the total sum of squares (TSS) and explained 84.7 and 85.3% for days to heading and grain yield/plot, respectively. While, the genotypes captured 10.4 and 6.8% of the TSS for the same traits, respectively. Although that the GEI showed low contribution to the total SS, but its magnitude (7.9%) was larger than that for genotypes in case of GY/P. The AMMI stability value discriminated genotypes G3, G7, G9, G12 and G14. G3 were the most promising stable and adapted genotypes according to grain yield performance over environments.

Keywords: AMMI model, AMMI stability value, Bread Wheat, Sowing dates.

Introduction

Wheat (*Triticum spp* L.) is the main food and the first cereal crop in Egypt. It is commonly considered as strategically important crop worldwide. Egypt is the largest wheat importer in the world and consumes an extensive amount of bread (Abdelmageed *et al.* 2019).

Climate is changing; therefore, the timing of sowing is critical; sowing at the wrong time can reduce wheat yield by up to 10–30%. However, the optimal sowing time is from 5 until 25, November overall Egypt. Because the temperature in South

Egypt is very high and in North Egypt is moderate, sowing earlier or later these dates can reduce wheat yield. Moreover, the risk of aphid infestation increases (Hassanein *et al.* 2012; Abdelmageed *et al.* 2019). Furthermore, terminal heat, which is referred as increase in temperature during grain filling, is one of the important stress factors for wheat production worldwide (Hays *et al.* 2007).

The performance of a genotype in a given environment is more important for wheat cultivation and improvement (Li *et al.*, 2006). One of the main ultimate aim of wheat

breeders is producing and improvement cultivars capable of expressing their maximum potential yield and quality in diverse environments (Mladenov *et al.* 2012). However, attaining this goal is made more complicated by (GEI) genotype-environment interactions. GEI is frequent in multi-environment trials and represents differential responses of genotypes across environments. The existence of GEI complicates the identification of superior genotypes for a range of environments and calls for the evaluation of genotypes in many environments to determine their true genetic potential (Yaghotipoor and Farshadfar 2007 and Hagos and Abay 2013).

The big challenges facing the specialists in biometrical genetics is to find the perfect stability analysis of genotypes across wide range of environments. AMMI analysis is widely used as a multivariate technique for interaction investigation (Mohammadi *et al.* 2010). Furthermore, it is more effective in partitioning the sum of squares of the interaction than the linear regression technique (Nachit *et al.*, 1992 and Gauch, 1992). Also, this technique captures a large portion of the interaction sum of squares; at the same time separates main as well as interaction effects and shows that which genotype will be suitable for which environment. Purchase *et al.* (2000) developed the AMMI stability value (ASV) based on the AMMI model's IPCA1 and IPCA2 (Interaction Principal Components Axes 1 and 2, respectively) scores for each genotype. The ASV is comparable with the methods of Eberhart and Russell (1966) and Shukla (1972)

stability methods. Therefore, the AMMI model is used to interpret GEIs and the results can be displayed graphically. Subsequently, the meaningful interpretation of data will support breeding programs such as genotype stability is necessary at multi location trials (Jeberson *et al.* 2017).

The objective of the current investigation was to identify wheat genotypes with high and stable yield under recommended and late sowing conditions at the newly reclaimed soil using AMMI analysis.

Materials and Methods

Plant materials and experimental conditions

In order to determine stability of 16 bread wheat genotypes for grain yield and number of days to heading, field experiments were conducted at newly reclaimed soil in the Agricultural Research Station, Arab-Elawamer, Assiut, Egypt under two sowing dates as recommended (N) at 25th November and late (L) at 25th December (heat stress) in three consecutive seasons (*i.e.*, 2016/2017, 2017/2018 and 2018/2019). According to this, there are six environments (*i. e.*, recommended date (E1) and late sowing date (E2) in the first season; recommended date (E3) and late sowing date (E4) in the second season and recommended date (E5) and late sowing date (E6) in the third season). The names and origin of the 16 genotypes are provided in Table 1. The Meteorological data for monthly average during 2015/2016, 2016/2017 and 2017/2018 wheat growing seasons is shown in Table 2.

The experiments were carried out in a randomized complete block design (RCBD) with four replica-

tions. The experimental plots consisted of 6 rows of 4m length each. Row-to-row and plant-to-plant distances were kept at 20 cm and 5 cm, respectively at all the experiments. Data of

grain yield/plot (GY/P) and number of days to heading (DH) were taken from the middle 4 rows of each plot, leaving aside the guard rows on either side of a plot.

Table 1. Pedigree of bread wheat genotypes used in the study

Genotype	Pedigree	Origin
1	ATTILA 50Y//ATTILA/BCN/3/STAR*3/MUSK-3	ICARDA
2	KATILA-15//MNCH/3*BCN	ICARDA
3	KAUZ//ALTAR 84/AOS 3/KAUZ/3/CATBIRD-10	ICARDA
4	SERI.1B*2/3/KAUZ*2/BOW//KAUZ/4/ANGI-2	ICARDA
5	ATTILA 50Y//ATTILA/BCN/3/STAR*3/MUSK-3	ICARDA
6	FLORKWA-2/6/SAKER'S/5/RBS/ ANZA/3/KVZ/HYS//YMH/TOB /4/BOW'S/7/DAJAJ-6	ICARDA
7	HUBARA-3*2/SHOUHA-4	ICARDA
8	WHEAR / VIVITSI // WHEAR	CIMMYT
9	VEE#7/KAUZ	Sudan
10	FLORKWA-2/6/SAKER'S/5/RBS/ANZA/3/KVZ/HYS//YMH/TOB/4/BOW'S/7/DAJAJ-6	ICARDA
11	KAUZ'S/FLORKWA-1//GUMARIA-3	ICARDA
12	MEXIPAK/FLORKWA-2	ICARDA
13	MELLAL-1/OUEDZEM-1	ICARDA
14	HUBARA-3*2/SHUHA-4	ICARDA
15	OASIS/SKAUZ//4*BCN/3/2*PASTOR. CMSOYO1881T -050M-030Y-030M-030WGY-33M-0Y-0S.	Egypt
16	SW8488*2/ KUKUNA- CGSS01Y00081T-099M-099Y-099M-099B-9Y-0B-0SD.	Egypt

Statistical analysis

The data were subjected to combined ANOVA and AMMI analysis. ANOVA was used to partition genotype (G), environments (E) and GEI deviations from the grand mean. Subsequently, multiplication effect analysis (AMMI) was used to parti-

tion GE deviations into different interaction principal component axes (IPCA). The Genotype \times Environment Analysis with R software for Windows, Version 4.0 (GEA-R) (Pacheco *et al.* 2016) was used for combined ANOVA and AMMI analysis.

Table 2. Meteorological data for monthly average during 2015/2016, 2016/2017 and 2017/2018 wheat growing seasons.

Month	Periods	Average temperature °C								
		2015/2016			2016/2017			2017/2018		
		Max.	Min.	Mean	Max.	Min.	Mean	Max.	Min.	Mean
Nov.	01-10	26.78	14.72	20.4	28.17	13.94	20.6	25.4	12.33	18.37
	11-20	26.02	12.46	18.85	28.05	13.74	20.28	27.32	10.72	18.56
	21-30	26.22	12.31	19.13	24.50	10.11	16.60	22.47	9.74	15.87
Mean		26.34	13.16	19.46	26.91	12.60	19.16	25.06	10.93	17.60
Dec.	01-10	20.66	7.74	14.15	21.92	7.77	14.35	23.25	8.42	15.11
	11-20	20.28	7.32	13.39	19.66	6.17	12.54	24.13	9.53	16.22
	21-31	20.26	6.48	12.72	18.17	5.05	11.48	22.30	9.19	15.44
Mean		20.40	7.18	13.42	19.92	6.33	12.79	23.23	9.05	15.59
Jan.	01-10	19.9	6.1	12.8	17.54	3.53	10.29	20.55	7.19	13.2
	11-20	20.32	6.44	12.87	20.43	5.89	12.53	20.53	6.43	13.15
	21-31	16.85	3.05	9.71	19.95	6.38	12.90	18.81	6.06	11.88
Mean		19.02	5.20	11.79	19.31	5.27	11.91	19.96	6.56	12.74
Feb.	01-10	20.3	6.06	12.88	19.88	5.26	12.33	28.79	9.94	19.08
	11-20	27.36	9.42	18.08	18.16	5.61	11.89	22.69	11.18	16.6
	21-29	25.93	9.69	17.89	24.04	8.53	15.93	27.03	12.95	19.69
Mean		24.53	8.39	16.28	20.69	6.47	13.38	26.17	11.36	18.46
Mar.	01-10	29.13	12.5	21.21	25.41	9.84	17.46	32.30	15.20	23.80
	11-20	26.97	14.02	20.38	23.21	10.06	16.71	28.70	12.70	20.70
	21-31	27.87	12.74	20.11	27.01	12.81	20.13	30.60	14.20	22.40
Mean		27.99	13.09	20.57	25.21	10.90	18.10	30.53	14.03	22.30
Apr.	01-10	35.78	16.5	26.35	30.43	13.2	22.2	28.20	13.60	20.90
	11-20	32.87	15.78	24.49	30.81	16.24	23.17	36.70	19.10	27.90
	21-30	36.55	19.16	27.87	32.75	16.92	24.98	32.20	17.00	24.60
Mean		35.07	17.15	26.24	31.33	15.45	23.45	32.37	16.57	24.47
May.	01-10	35.38	20.12	28.03	34.99	18.77	27.16	38.10	22.30	30.20
	11-20	38.28	21.22	29.86	37.75	20.69	28.99	35.50	21.40	28.30
	21-31	34.83	18.74	27.17	36.15	20.61	28.90	39.50	23.40	31.40
Mean		36.16	20.03	28.35	36.30	20.02	28.35	37.70	22.37	29.97

AMMI Stability Value (ASV)

The AMMI stability value (ASV) as described by Purchase *et al.* (2000) was calculated as follows:

$$ASV = \sqrt{\frac{IPCA_1 SS}{IPCA_2 SS} (IPCA_1 score)^2 + (IPCA_2 score)^2}$$

Where, IPCA1 SS and IPCA2 SS are the sum of squares of IPCA₁ and IPCA₂, respectively. Smaller ASV scores indicate a more stable genotype across environments.

Genotype Selection Index (GSI)

Based on the rank of mean grain yield of genotypes (RGY_i) across environments and rank of AMMI stabil-

ity value (RASV_i), a genotype selection index (GSI) was calculated for each genotype which incorporates both mean grain yield and stability index in single criteria (GSI_i) as recommended by Farshadfar (2008) as follow:

$$GSI_i = RASV_i + RGY_i$$

Stress Tolerance index (STI)

STI for heading date and grain yield was computed as described by Farshadfar *et al.* (2001) as follows:

$$STI = (GY_N)(GY_L)/(GY_N)^2$$

Where GY_N and GY_L are grain yield/plot under recommended (N)

and late (L) sowing dates, respectively.

Results and Discussion

AMMI ANOVA

The combined analysis of variance showed highly significant differences ($p < 0.01$) among the 16 genotypes and among the six environments for days to heading (DH) and grain yield/plot (GY/P) (Table 3). The environments (the three seasons and the two sowing dates) were diverse and caused for a great variation in both traits. Recommended and late sowing dates, where the promising lines were tested, seem to be informative because of their contrasting weather conditions. Moreover, the genotype by environment interaction (GEI) was highly significant for DH and not significant for GY/P. The significant interaction of DH of the genotypes indicates that the genotypes varied across all environments. In contrast, the nonsignificant interaction refers to that some of the genotypes were stable overall environments and may have close performance.

The environments showed high contributions to the total sum of squares (TSS) and explained 84.7 and 85.3% for days to heading and grain yield/plot, respectively. On other hand, the genotypes contributed with low percentage to the TSS and cap-

tered 10.4 and 6.8% for the previous traits, respectively. Although that the GEI showed low contribution to the total SS, but its magnitude (7.9%) was larger than that for genotypes in case of grain yield/plot, indicating sizeable differences in genotypic response across environments. This advocates the possible presence of different genotype groups. Similar results were obtained by Kadhem and Baktash (2016); Jeberson *et al.* (2017).

The multiplicative variance of the sum of squares due to GEI was partitioned into six interaction principal components axes (IPCA) and a residual term. The first principal component axis (IPCA-1) of the interaction in both traits was significant and captured 56.4 and 44.9% of the interaction sum of square for DH and GY/P, respectively. Similarly, the second principal component axis (IPCA-2) explained further 28.2% and 29.3 of the GEI sum of square for DH and GY/P, respectively. The variation contributed by the first two multiplicative IPCAs were sufficient to confirm the variation revealed by GEI in both traits across environments (Gauch, 2006). The results were in corroboration with the previous research results which obtained by Verma *et al.*, 2015; Kadhem and Baktash (2016).

Table 3. AMMI analysis of variance for number of days to heading (DH) and grain yield/plot (GY/P) of 16 bread wheat genotypes across the 6 environments.

Source	DF	Days to heading		Grain yield/plot	
		MS	TSS%	MS	TSS%
ENV	5	5047.02**	84.7	10.28**	85.3
GEN	15	207.33**	10.4	0.27**	6.8
ENV*GEN	75	19.31**	4.9	0.06	7.9
PC1	19	42.98**	56.4	0.11**	44.9
PC2	17	24.06**	28.2	0.08	29.3
PC3	15	7.21*	7.5	0.05	16.0
PC4	13	4.86	4.4	0.02	6.7
PC5	11	4.67	3.5	0.01	3.1
PC6	9	0.00	0.0	0.00	0.0
Residuals	288	3.75	0.0	0.06	0.0

*, ** significant at 0.05 and 0.01 probability levels, respectively

Genotypes performance

Number of days to heading (DH)

As an average under recommended (N) and late (L) sowing dates across three seasons, the mean number of days to heading of genotypes were 99.66 and 86.29 days, respectively (Table 4). It is clear that the genotypes were earlier in heading under late sowing date than at recommended date. The genotype no.14 was the earliest ones under recommended and late sowing dates and recorded 92.83 and 82.75 days, respectively. While the genotype no. 13 showed the latest ones under recommended and late sowing dates and recorded 105.92 and 89.50 days, respectively. Consequently, the genotypes numbers 14 and 13 were the earliest and latest genotypes in heading overall environments, respectively. On other hand, mean number of days to heading overall genotypes varied from 80.94 (E6) to 105.34 (E1) days with an average of 99.66 days under recommended sowing date and 86.29 days under late sowing date. The wide range of DH among environments, indicating large variation in the response of the genotypes to heading (Table 5). The broad-sense heritability estimates

(h^2_b) of the investigated genotypes were higher in most cases under recommended sowing dates than under late date, this may reflex the size of environments variance under both conditions. The h^2_b ranged between 77.14% (E6) and 96.88% (E1). Our results in harmony with those obtained by El-Kalla *et al.* (2010); Khan *et al.* (2014); El-Basyoni (2018); El Sayed *et al.* (2018).

Grain yield/plot (GY/P)

As an average under recommended (N) and late (L) sowing dates across the three seasons, the mean grain yield/plot of genotypes were 1.82 and 1.34 kg plot⁻¹, respectively (Table 5). Grain yield/plot ranged between 1.64 and 2.28 kg/plot under recommended sowing date, while it varied from 1.04 to 1.36 kg/plot under late sowing date. The genotype no. 15 was the most yielded genotype overall environments followed by genotype no. 3, while the lowest one was the genotype no. 12. From other hand, mean grain yield/plot overall genotypes varied from 1.08 Kg (E2) to 2.08 kg/plot (E5) with an average of 1.83 kg/plot under recommended sowing date and 1.20 kg/plot under late sowing date.

The wide range of GY/P among environments, indicating large variation in the response of the genotypes to grain yield (Table 4). In contrast of DH, the broad-sense heritability estimates (h^2_b) of the investigated genotypes ranged from low (16.58%) to high (75.87%) estimates. In addition, they were higher under late sowing dates than under recommended date except in the second season, this may reflex the size of environments variance on yield trait under both conditions. The heritability in broad-sense (h^2_b) ranged between 27.21 % (E6) and 75.87% (E2). Similar findings were also obtained by Tarakanovas and Ruzgas (2006); El-Kalla *et al.* (2010); Amiri *et al.* (2013); Verma *et al.*, 2015; Kadhem and Baktash (2016); El Sayed *et al.* (2018).

AMMI Biplot Analysis

The AMMI analysis displays two basic AMMI biplots to understand the interaction between genotypes and environments. First, the AMMI 1 biplot, where the main effect (Genotype and Environment means) and IPCA-I scores are plotted against each other (Fig. 1 and 3). Second, AMMI 2 biplot, where scores of IPCA-I and IPCA-2 are plotted against each other (Fig. 2 and 4). In AMMI 1 biplot, the differences among genotypes in terms of direction and magnitude along the X-axis (trait) and Y axis (IPCA 1 scores) are important.

In the biplot display, Alberts (2004) stated that the genotypes or environments that appear almost on a perpendicular line of the graph had similar mean yields and those that fall almost on a horizontal line had similar interaction. Genotypes or envi-

ronments on the right side of the midpoint of the perpendicular line have higher values (such as grain yield) than those on the left side. The score and sign of IPCA1 reflect the magnitude of the contribution of both genotypes and environments to GEI, where scores near zero are characteristic of stability, whereas higher score considered as unstable and specifically adapted to certain environment. Also, IPCA scores took both positive and negative values. Consequently, a genotype that has large positive IPCA score with some environments most have negative interaction with some other environments. Thus, these scores presented a disproportionate genotype response which was the major source of variation for any cross-over interaction (Mohammadi *et al.* (2007); Amiri *et al.* (2013).

AMMI 1 Biplot Analysis of days to heading (DH)

According to the previous description and in contrast of grain yield trait, the characterization of each genotype to mean number of days to heading (DH) and contribution to GEI by mean of IPCA1 (Fig.1) indicates that genotypes nos.14, 15 and 2 were specifically adapted to early heading environments E2 and E6 with number of days to heading less than the average of heading days overall environments (Fig. 1). However, genotypes numbers 2, 4, 8, 14 and 15 were early heading and relatively unstable. With respect to their contribution to GEI (*i.e.* stability) the IPCA1 score, the genotypes nos. 7 and 16 were the most stable genotypes and also adapted to early heading environments (E2 and E6). On the other

hand, genotypes nos. 5, 6, 1, 12, 10, 11 and 13 were adapted to late heading environments E1 but not stable. (Fig. 1). Our results in harmony with those obtained by Verma *et al.* (2015); Elbasyoni (2018).

For DH, the best genotype needs to combine good number of days to heading and stable performance across a range of production environments. For example, the genotype no. 9 can be judged based on its stability over the environments, which combined low absolute IPCA-I score with good relatively early heading (Table 4). In addition, the environments showed much variability in both additive main effects and interactions. The environment with most early heading (E2 and E6) having high positive IPCA-I score showed differential performance of genotypes for DH (Table 4). The latest heading environment (E1) had recorded lowest but negative IPCA I score suggesting that all the genotypes poorly performed under this environment. The current results in accordance with those obtained by Verma *et al.* (2015); Elbasyoni (2018).

AMMI 2 Biplot Analysis of days to heading (DH)

When IPCA1 was plotted against IPCA2 (Fig. 2), genotype no. 9 was found to be closer or at a lesser distance from the center of the biplot when compared with other genotypes and that would be considered as most stable genotype with regard to its lesser contribution to GEI. On the contrary, genotypes nos. 13, 14 and 15 exhibited longer vectors from origin indicating the high contribution of these genotypes to GEI (*i.e.* unstable genotypes). The longer vec-

tor of environments compared to genotypes explain the higher sum of square of environments as compared to sum of squares of genotypes in the ANOVA (Table 3). The best genotypes with respect to environments E1 were nos. 6, 10 and 12. Genotypes nos. 9, 3, 2, 4 and 14 were suitable for environment E2. Whereas, genotypes nos. 8, 7, 15 and 16 were best for environments E3 and E6. Best genotypes for E4 and E5 were nos. 1, 11 and 13 (Fig. 2). Our results in harmony with those obtained by Verma *et al.* (2015); El-Basyoni (2018); Kalwar *et al.* (2018).

AMMI 1 Biplot Analysis of grain yield/plot (GY/P)

The characterization of each genotype to mean grain yield/plot (GY/P) and contribution to GEI by mean of IPCA1 (Fig.3) indicates that genotypes no. 2, 4, 5 and 11 were specifically adapted to high yielding optimum environment 1 with mean grain yield more than the average of grain yield overall environments (Fig 1). However, genotype nos. 4 and 11 were high yielding but relatively unstable. In addition, the genotype no. 5 could be considered high yielding and stable genotype according to its contribution to GEI (IPCA1 score) because it is close to the center. On the other hand, genotypes nos. 3, 10, 15 and 16 were adapted to high yielding optimum environments 3 and 5. (Fig. 3). Also, it is clear that the genotype no.15 was more stable than the genotype no. 16 under all environments. Genotypes nos. 1, 2, 6, 7, 8, 9, 13 and 14 were low yielding and adapted to late environments 2, 4 and 6. The most stable and low yielding geno-

types were genotypes nos. 7, 8 and 9 under late sowing dates.

The best genotype needs to combine good grain yield/plot and stable performance across a range of production environments. For example, the genotype no. 7 can be judged based on its stability over the environments, which combined low absolute IPCA-I score with good relative grain yield (Table 6). In addition, the environments showed much variability in both additive main effects and interactions (Table 3). The environment (E1) was the most having high positive IPCA-I score showed differential performance of genotypes for GY/P (Table 6). The lowest yielding environment (E3) had recorded lowest but negative IPCA I score suggesting that all the genotypes poorly performed under this environment. Our results in harmony with those obtained by Verma *et al.* (2015); Elbasyoni (2018); Kalwar *et al.* (2018).

AMMI 2 Biplot Analysis of grain yield/plot (GY/P)

The genotypes nos. 7, 12 and 14 were located closer or at a lesser distance from the center of the biplot when compared with other genotypes and that would be considered as most stable genotypes with regard to its lesser contribution to GEI (Fig. 4). On the contrary, genotypes nos. 1, 4, 5, 8, 11, 13 and 15 exhibited longer vectors from origin indicating the high contribution of these genotypes to GEI (i.e. unstable genotypes). The longer vector of environments compared to genotypes explain the higher sum of square of environments as compared to sum of squares of genotypes in the ANOVA (Table 3). The

best genotypes with respect to environments 1 were nos. 2, 4, 9 and 13. Genotype no. 11 had good performance under environment 2. Whereas, genotypes nos. 5 and 8 for environments 4, genotype no. 16 for environment 6 and genotype no. 6 for environment 5. While genotype no. 1 is between environment 5 and environment 6 (Fig. 2). These results are in line with the findings of Jeberson *et al.* (2017); Ali and Sayed (2019).

AMMI stability value (ASV)

A genotype with least ASV score considered as the most stable. Accordingly, genotypes nos. 9, 3, 5, 16, and 6 were the most stable and adapted genotypes for number of days to heading, while genotypes nos. 13, 14, and 15 were the most unstable. For grain yield/plot, the genotypes nos. 7, 9, 14, 12 and 3 were the most stable and adapted genotypes according to grain yield performance over environments, while genotypes nos. 11, 4, 6 and 15 were the most unstable genotypes. Genotypes nos. 3 and 9 could be considered as the most stable and adapted genotypes for days to heading and yield performance (Tables 5 and 6). These results are in line with the findings of Khan *et al.* (2014); Verma *et al.* (2015); Jeberson *et al.* (2017).

Stress Tolerance index (STI)

For days to heading, the highest stress tolerance index (Table 4) was revealed by the genotypes nos. 2 and 14 (STI = 0.89 for each) and both genotypes were early heading under both sowing dates. While the lowest STI was obtained by genotype no. 13 (STI= 0.84), indicates the instability of this genotype and it was adapted to late heading environments 1. This re-

sult is partially agreement which those obtained by AMMI analysis of days to heading (Fig. 1). For grain yield/plot, the highest stress tolerance index (Table 5) was revealed by the genotype no. 5 (STI= 0.76) and genotype no. 8 (STI = 0.74) and both genotypes were early heading under both sowing dates. While the lowest STI was obtained by genotype no. 10 (STI= 0.59), indicates the instability of this genotype and it was adapted to high yielding environment 3. These results are in accordance with the findings of Ihsan *et al.* (2016); Jahan *et al.* (2018).

Genotype Selection Index (GSI)

The least GSI is considered as the most stable with early heading.

GSI discriminated genotypes nos. 4, 9 and 16 with general adaptability and early heading across both sowing date conditions which was in partially agreement with the results of AMMI biplot analysis (Table 5). For grain yield/plot, the GSI discriminated genotypes nos. 3, 16, 2 and 7 with general adaptability and moderate to high grain yield across both sowing date conditions which was in partially agreement with the results of AMMI biplot analysis (Table 6). These results are in accordance with those obtained by Bose *et al.* (2014) and Kadhem and Baktash (2016).

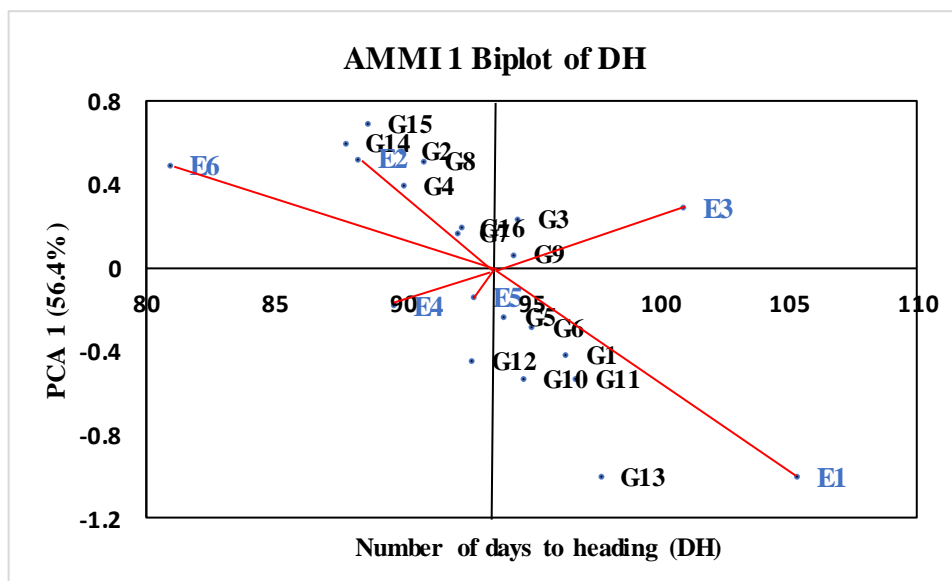


Figure 1. AMMI 1 biplot for additive effects vs. IPCA1 for number of days to heading of 16 wheat genotypes from six environments

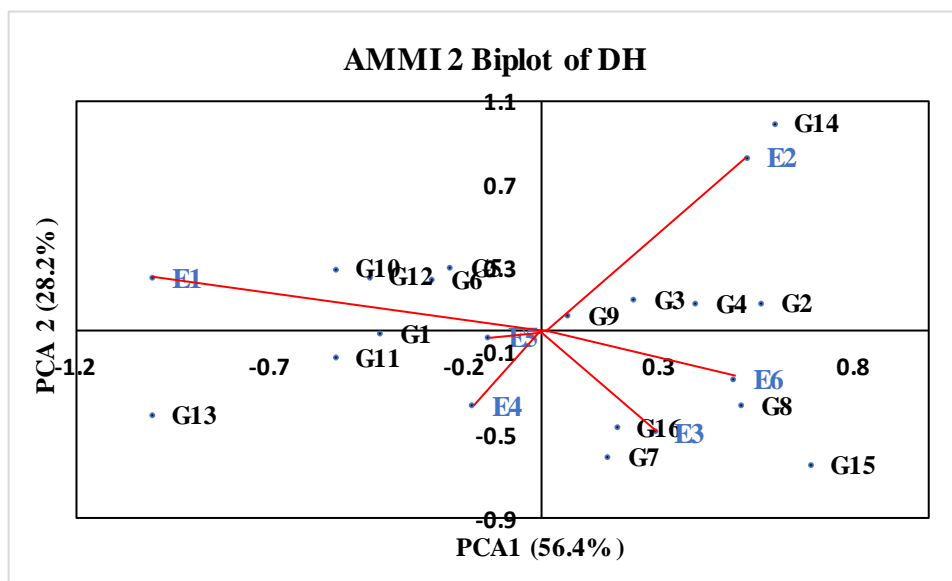


Figure 2. AMMI2 biplot for no. of days to heading showing the two main axes of interaction (IPCA1 vs. IPCA2) in wheat genotypes from six environments

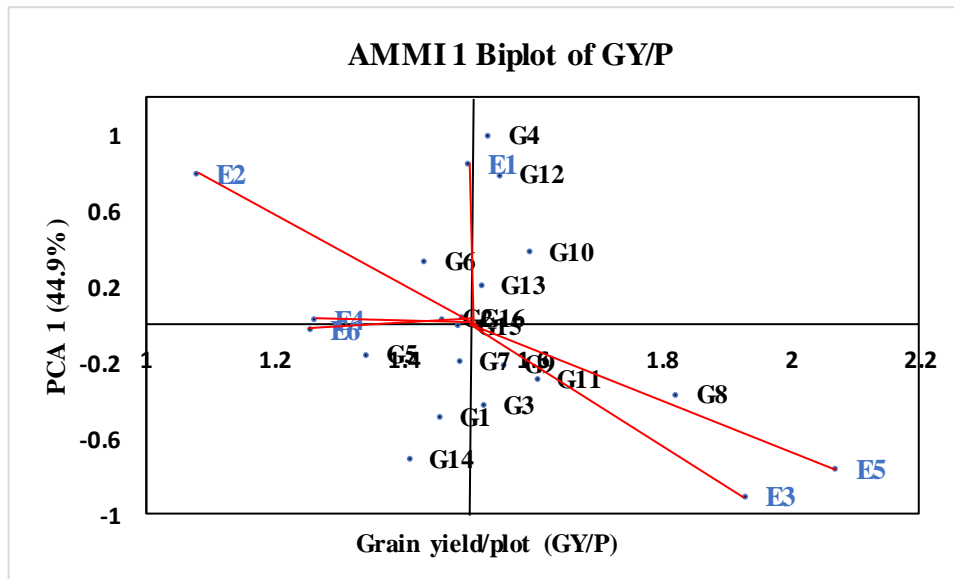


Figure 3. AMMI 1 biplot for additive effects vs. IPCA1 for grain yield/plot of 16 wheat genotypes from six environments

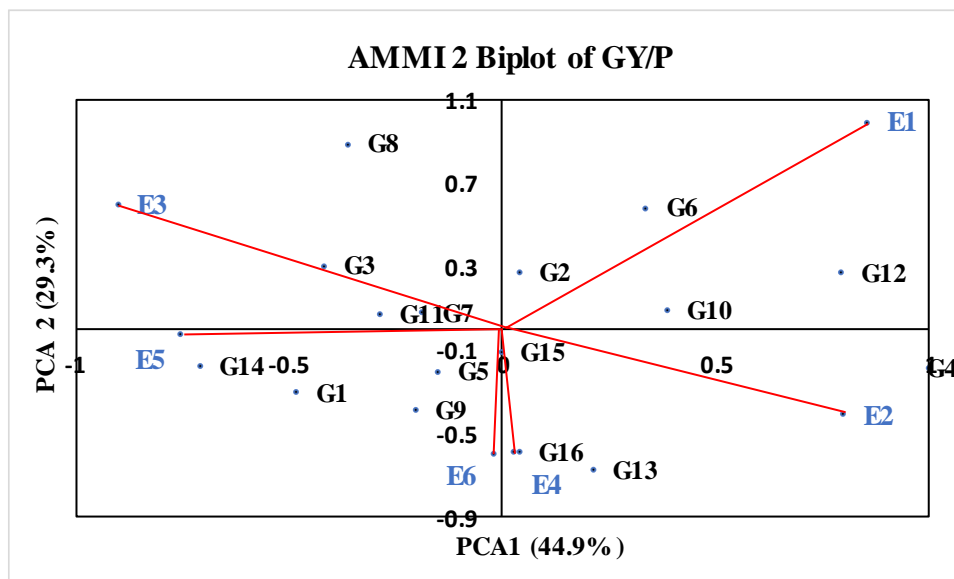


Figure 4. AMMI2 biplot for grain yield/plot showing the two main axes of interaction (IPCA1 vs. IPCA2) in wheat genotypes from six environments

Conclusion

The results of this investigation prove and confirm the importance of testing genotypes under representative environmental conditions to identify the best, stable, early and high yielding genotypes. Both traits under investigation and stability of performance should be considered simultaneously to reduce the effect of GEI and to make selection of genotypes more precise and refined. Accordingly, results of AMMI analysis indicated that the first three AMMI were highly significant for days to heading and AMMI1 was only significant in case of grain yield/plot. In addition, the environments showed high contributions to the total sum of squares (TSS) and explained 84.7 and 85.3% for days to heading and grain yield/plot, respectively. While, the genotypes captured 10.4 and 6.8% of the TSS for the same traits, respectively. Although that the GEI showed low contribution to the total SS, but its magnitude (7.9%) was larger than that for genotypes in case of grain yield/plot. The AMMI stability value discriminated genotypes nos. 3, 7, 9, 12 and 14 were the most promising stable and adapted genotypes according to grain yield performance over environments.

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تحليل الثبات لتكوين وراثية من قمح الخبز لميعاد طرد السنابل ومحصول الحبوب باستخدام نموذج التأثيرات الرئيسية المضافة والتفاعل المضاعف

عاطف أبو الوفا أحمد¹, مورييس توفيلس², محمد عبدالعزيز سيد¹, رشا عزت مهدي¹ ومصطفى عمر مصطفى²

¹قسم المحاصيل – كلية الزراعة – جامعة اسيوط – مصر

²قسم القمح – معهد بحوث المحاصيل الحقلية – مركز البحوث الزراعية – الجيزة - مصر

المخلص

أجري تحليل الثبات باستخدام نموذج التأثيرات الرئيسية المضافة والتفاعلات المضاعفة (AMMI) لتقييم وقياس التفاعل الوراثي-البيئي، لصفتي عدد الأيام حتي طرد السنابل ومحصول الحبوب لستة عشر تركيب وراثي من قمح الخبز. تكونت هذه التراكيب الوراثية من خلال برامج التهجين المختلفة في المحطات البحثية بالسيمييت CIMMYT, إكاردا ICARDA, السودان ومصر. تم تنفيذ التجربة تحت ميعاد الزراعة الموصي به وميعاد الزراعة المتأخر في تربة حديثة الأستصلاح بمحطة البحوث الزراعية في عرب العوامر، أسيوط، مصر لمدة ثلاثة مواسم متتالية (2017/2016 و 2018/2017 و 2019 / 2018). أظهر تحليل التباين المشترك وجود اختلافات معنوية بين التراكيب الوراثية وبين البيئات لكلتا الصفتين بينما كان التفاعل الوراثي – البيئي معنوياً لصفة طرد السنابل وغير معنوي لصفة محصول الحبوب. أشارت نتائج تحليل AMMI إلى أن الثلاثة مكونات الأولى من AMMI كانت عالية المعنوية لصفة طرد السنابل بينما كان المكون AMMI معنوية فقط لصفة محصول الحبوب بالإضافة إلى ذلك، ساهمة البيئات بنسبة عالية بالنسبة لمجموع مربعات الانحرافات الكلية وكانت بنسبة 84.7 و 85.3% لطرد السنابل ومحصول الحبوب، على التوالي. بينما ساهمت التراكيب الوراثية بنسب 10.4 و 6.8% من مجموع مربعات الانحرافات الكلية لنفس الصفات على التوالي. على الرغم من أن التفاعل الوراثي البيئي أظهر مساهمة منخفضة في إجمالي مجموع مربعات الانحرافات الكلية، ولكنه كان أكبر من تأثير التراكيب الوراثية في حالة محصول الحبوب. ميز تحليل الثبات بنموذج AMMI التراكيب الوراثية أرقام 3 و 7 و 9 و 12 و 14. كان التركيب الوراثي رقم 3 أكثر التراكيب الوراثية الواعدة ثباتاً وأقلماً وفقاً لأداء محصول الحبوب تحت البيئات المتعددة.