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Uni and Multivariate Methods to Estimate Stability of some Bread Wheat Genotypes

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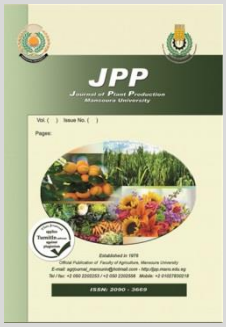

ABSTRACT

Fifteen bread wheat genotypes included twelve lines and three cultivars were evaluated during the two seasons of 2021/2022 and 2022/2023 under two nitrogen fertilization levels and three sowing dates at the farm of experiments of Faculty of Agriculture, Minia University, El-Minia, Egypt. Joint regression analysis of variance indicated that all mean squares of environments, genotypes, G x E interaction and E + (G x E interaction) were highly significant for all studied traits, indicating, genotypes considerably interacted with the different environments. For grain yield fed^{-1}, five genotypes; lines 2, 13, 14, 24 and Giza 168 were considered stable where mean grain yield exceeded the grand mean, moreover, bi and S^2di of them were insignificant from unit and zero, respectively. Line 13 recorded low ecovalence Wi% and CV%, confirming it was stable across the environments. Additive main effects and multiplicative interaction analysis showed highly significant differences among environments, genotypes and G x E interaction for all the studied traits. By genotype selection index, it could be discriminated L13, L14, L34 and Giza 168 as stable genotypes with high grain yield across environments, confirming the results of regression and deviation from regression.

***Keywords*:** regression, ecovalence, selection, stable.

INTRODUCTION

Wheat is one of the essential strategic cereal crops all over the world since it is a staple food for human. Wheat is the most staple food grain crop in the Egyptian people diet and the main source of protein and calories for a large section of the society. Where wheat present in many products as bread, baked goods, pasta, cakes, cracks. In addition to direct human feeding, its straw is used in livestock feeding. Wheat has become the most important crop all over the world because of its wide adaptation to various environmental conditions due to its great genetic diversity and its economic and strategic nature (Mondal *et al.* 2016).

Throughout recent years, many approaches have been made towards raising the yield capacity of wheat, which achieved annual production of 9.8 million tons, while local consumption needs amounted by 20.6 million tons (USDA, 2023).

Owing to reduce cultivatable area and watering supply, an increase of productivity per unit land area appears to be the mainly possible alternate of lessening the wheat production gap. This can be achieved by introducing high yielding cultivars and improving agricultural practices. Such improved cultivars must tolerate the detrimental environments and be stable in broad spectrum of environments.

The genotype x environment interaction has led to the difficulty of recommending the cultivation of cultivars in all regions. Therefore, G x E interaction must be studied before recommending the introduction of new high-yielding cultivars with high stability. Therefore, the G x E interaction effect must be studied to evaluate the new lines that make up the varieties. Therefore, determining and understanding G x E interaction is very important for any plant breeding program.

The genotype stability over different environments is tested by G x E interaction. Stability of genotype is achieved for high mean performance of genotype with low degree of volatility in mean performance, when tested over diverse environments.

Many parametric methods have been developed and successfully utilized by plant breeders to determine the genotypes stability. There are two groups of parametric methods are: univariate and multivariate. Univariate methods include the regression method between mean performance and environmental index (Eberhart and Russell, 1966), the coefficient of variation among all environments (Francis and Kannenberg, 1978) and Ecovalence (Wi) is the contribution genotype in G x E interaction (Wricke, 1962). The multivariate methods as additive main effects and multiplicative interaction method (AMMI) (Gauch, 1992).

Farshadfar (2008) developed a method of the genotype selection index (GSI) incorporate both ranking mean trait (RT) and ranking AMMI stability value (RASV) in a single criteria. A low value of GSI refer to a stable genotype with high mean trait. Heidari *et al.* (2017) illustrated that parameters of AMMI stability are suitable for identifying stable genotypes and that the parameter of GSI can determine high-yielding genotypes in wheat breeding programs. The present study aimed at measuring stability of some bread wheat genotypes using uni and multivariate methods.

MATERIALS AND METHODS

Fifteen bread wheat genotypes were included twelve lines developed by Associate Prof. Dr. Hassan M. Fouad, Agronomy. Dept., Fac. Agric., Minia Univ. and three cultivars (Table 1) were evaluated during the two seasons of 2021/2022

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and 2022/2023 under two nitrogen fertilization levels, 37.5 and 75 Kg. N/fed, and three sowing dates, 25th Oct., 20th Nov. and 15th Dec. at the experimental farm (28.11°N-30.75°E) of Fac. Agric., Minia Univ., EL-Minia, Egypt. All genotypes were evaluated in 12 environments as shown in (Table 2).

The experimental design was a randomized complete blocks design (RCBD) with 3 replications for each environment. The plot size was five rows, 3 m in length, and 0.2 m in width. Seeding rate was 60 kg/fed. Grains were sown by hand drill 5 cm. apart. Other recommended agricultural practices were applied for wheat production throughout the growing season. Data were taken on 2 m middle of plot area on the following traits: number of spikes plot^{-1} (NS P^{-1}), number of grains spike^{-1} (NG S^{-1}), 1000 grain weight in g. (TGW), and grain yield feddan^{-1}in ardab (GY F^{-1}). Metrological analysis of weather prevailing the two growing seasons are shown in Fig. 1.

Table 1. Name and pedigree of the twelve lines and three Egyptian bread wheat cultivars.

No.	Name	Pedigree
1	L2	Giza168/Sids4
2	L4	
3	L8	
4	L13	
5	L14	
6	L15	
7	L17	
8	L20	
9	L23	
10	L24	
11	L31	
12	L34	
13	Misr 2	SKAUZ/BAV 92
14	Giza 168	MIL/Buc//Seri CM93046-8M-04-0M-2Y-0B
15	Gemmeiza 12	OTUS/3/SARA/THB//VEE

Table 2. Layout of the twelve environments used in this study.

Environ.	E1	E2	E3	E4	E5	E6	E7	E8	E9	E10	E11	E12
Season	2021/2022						2022/2023					
Sowing dates	25th Oct.		20th Nov.		15th Dec.		25th Oct.		20th Nov.		15th Dec.	
Nitrogen fertilizer (kg)	37.5	75	37.5	75	37.5	75	37.5	75	37.5	75	37.5	75

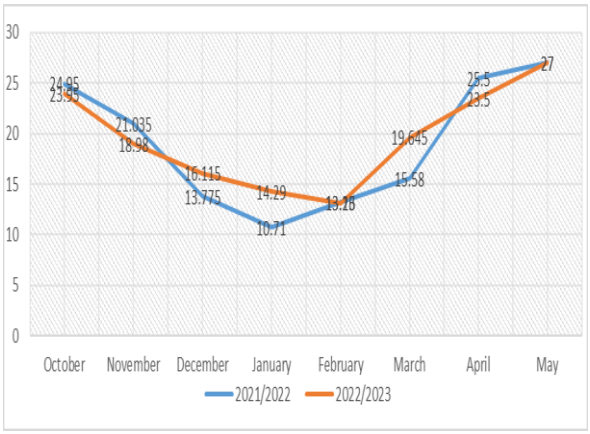


Fig. 1. Mean air temperature (C°) during 2021/2022 and 2022/2023 planting seasons at Minia conditions.

Statistical analysis:

The combined analysis and comparison environments mean using revised least significant difference (RLSD) were analyzed according to Gomez and Gomez (1984).

Stability mean performance across environments was estimated according following different methods: Regression coefficient bi and deviation from regression S^2di were done by Eberhart and Russel (1966). Ecovalence (Wi) is the contribution of genotype in the G x E interaction (Wricke, 1962). Coefficient of variability (CV%) of Francis and Kannenberg (1978). The additive main effects and multiplicative interaction method (AMMI) was computed as proposed by Gauch (1992).

The AMMI model was used to investigate G x E interaction using the following equation:

$$Y_{ij} = \mu + g_i + e_j + \sum_1^n \lambda_n \gamma_{in} \delta_{jn} + \rho_{ij}$$

where:

(i = 1, 2…….15: j = 1, 2…….12), Y_{ij} = The performance of the ith genotype in the jth environment, μ= The grand mean, g = Additive effect of the ith genotype (genotype mean deviation from the grand mean), e = Additive effect of the jth environment (environment mean deviation from the grand mean), n is the number of principal components retained in the model, λ_n= Eigen value of the interaction PCA (IPCA) axis n, γ_{in} and δ_{jn} = Eigenvectors of the genotype and environment for axis n and ρ_{ij} = error.

In addition, IPCA axes were statistically tested using Gollob's (1968) F-test procedure. The first two components were used to obtain an AMMI bi-plot (Burgueno *et al.*, 2001), which is used to interpret the AMMI model by relating genotypic means to the first IPCA by enabling the visual presentation of the G x E interaction estimate. The GEA-R software was used for AMMI analysis according to Angela *et al.* (2015).

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

$$ASV = \sqrt{\left(\frac{SS\ IPCA1}{SS\ IPCA2} IPCA1\ score\right)^2 + (IPCA2\ score)^2}$$

Where, IPCA1, IPCA2 = interaction principal component analysis 1 and 2, SS IPCA1, SS IPCA2= sum of square of IPCA 1 and 2.

Farshadfar, 2008 proposed a method of genotype selection index (GSI) incorporate both mean treat and stability index based on the rank of each of mean performance of genotypes (RY_i) over environments and AMMI stability value ($RASV_i$) where,

$$GSI_i = RASV_i + RY_i$$

RESULTS AND DISCUSSION

Analysis of variance

Pooled analysis of variance in Table 3 showed highly significant differences among the twelve environments (two seasons, three sowing dates and two N fertilizer doses), fifteen genotypes and their interaction for all the studied traits. These results indicated present environmental different as a result of wide difference in climatic conditions during two seasons, three sowing dates and the effect of two N fertilizer doses. Moreover, genetic diversity among the studied genotypes and its response to different environmental conditions. Significance of G x E interaction is referring to inconsistence of genotypes in response to changing environments due to G x E interaction. Because of there is a significant difference due to variance of G x E interaction, measuring of stability a genotypes could be done. Similar results were reported by Fouad (2019), Wardofa and Ararsa (2020), Naheed (2021) and

Khare *et al.* (2024). Partitioning of the sum of squares for different sources of variation showed high percent contribution was attributed to environment by 39.25, 52.08, 58.66 and 61.22% for NS, NG, TGW and GY, respectively followed by 37.60, 30.9 and 16.02% of genotypes for NS, NG and GY, respectively then 18.99, 12.30 and 15.30% of G x E interaction for NS, NG and GY, respectively. While 22.35% of variations caused by G x E interaction then 6.69% of variation effects caused by genotypes for TGW. Mut *et al.* (2010) and Belete *et al.* (2024) found highly significant of effects for genotypes, environments and their interaction for TGW and grain yield. Out of the total sum squares 48.4, 28.0 and 23.6% for TGW (Mut *et al.*, 2010) and 77.6%, 3.87% and 10.57% for grain yield (Belete *et al.*, 2024) accounted for the effect of environment, genotype and G x E interaction, respectively.

Table 3. Analysis of variance of pooled data for all the studied traits of 15 bread wheat genotypes tested across 12 environments

S.O.V.		Environments	Rep/Env	Genotypes	G x E	Error
Trait	d.f.	11	24	14	154	336
NS	MS	739153.76**	3419.75	556401.35**	25547.29**	2318.80
	%SS	39.25	0.40	37.60	18.99	3.76
NG	MS	6118.07**	17.91	2851.58**	103.19**	16.89
	%SS	52.08	0.33	30.90	12.30	4.39
TGW	MS	3007.49**	22.90	269.51**	81.85**	19.01
	%SS	58.66	0.97	6.69	22.35	11.32
GY	MS	875.95**	3.03	180.07**	15.64**	3.28
	%SS	61.22	0.46	16.02	15.30	7.01

**** Significant at 0.01 level of probability.**

Mean performance of bread wheat genotypes

For the genotypes, line 15 recorded the highest values for each of number of spikes plot^{-1} (848.98 spikes) and grain yield feddan^{-1} (18.87 ardab), while line 8 gave the lowest values for the same traits (395.04 and 10.16, respectively) (Table 6). For number of grains spike^{-1}, line 20 gave highest grains by (70.22), while line 17 gave lowest gains spike^{-1} (33.15). For thousand grain weight the contrast trend was observed for the same 2 lines, where line 20 recoded lowest TGW by 37.94 g. and line 17 recorded highest TGW 47.58 g. (Table 7). This may be due to increase and compact of number of grains resulted in decrease grain weight. Acreche and Slafer (2006) reported that the average weight of wheat grain reduced with increasing number of grains due for each other.

For the environments, the highest values for all traits were achieved in the favorable environments (E4 and E10) by growing in the recommended date of 25th Nov. using 75 kg N compared to the unfavorable environments (E5 and E11) by growing in late date 15th Dec. using 37.5 kg N (Tables 4). With exception sowing in early date 25th Oct. using 37.5 kg N in 1st season (E1) gave the lowest number of grains spike^{-1} 33.40 grains (Table 5), this may be due to adverse effect of the cold on pollen grains during anthesis stage. The lowest TGW was found in E 5 and E11 (late sowing using low N) by 35.54 and 33.99 g., respectively. Hamam *et al*. (2015) found that the normal sowing date increased grain yield.

The lower grains spike^{-1} in all genotype was observed under heat stress, it may be due to the high temperature during the reproductive phase which can cause pollen sterility and adverse effect of floral organs (Prasad *et al*., 2008). Chakrabarti *et al.* (2011) found that reducing grain yield as a result of low temperature effect during wheat reproductive stage that causes pollen grains sterility. Bishwas *et al*. (2021) observed heat stress caused speeds up the rate of grain filling and shortens the filling period, consequently reduction in each of weigh, size and number of grains and quality losses.

Table 4. Means of the traits of the 15 bread wheat genotypes under the 12 different environments.

Env.\Traits	NS P^{-1}	NG S^{-1}	TGW	GY Fed^{-1}
E1	539.58	33.40	38.82	11.69
E2	623.16	39.70	41.12	14.09
E3	707.11	56.18	53.12	18.16
E4	846.64	60.93	54.95	22.19
E5	481.21	34.04	35.54	8.89
E6	588.05	39.37	39.53	13.43
E7	562.54	35.14	36.93	11.45
E8	648.20	37.88	41.06	13.70
E9	742.14	57.27	53.33	17.35
E10	862.94	63.96	56.63	21.94
E11	492.26	34.15	33.99	9.30
E12	554.85	39.27	43.96	13.68
Mean	637.39	44.27	44.08	14.66
RLSD 5%	82.57	6.81	7.23	3.00

Stability analysis

Regression analysis:

Linear regression analysis of variance Table 5 indicated that genotypes (G), environments (E) and the G × E interaction mean squares were highly significant for all the studied traits. The results that the 15 genotypes considerably interacted with the 12 environments. Abd El-Rady and Koubisy (2017) and Fouad (2019) revealed that E + G × E interaction mean squares were highly significant for all the studied traits, revealing that genotypes considerably interacted with the different environments.

In fact, sum squares of E + G x E interaction linear for each trait is consist of the three parts; Environments linear ss, G × E linear ss and pooled deviation ss. Environments ss is completely included by sum squares of E (linear) which it's mean square was significant (P≥0.01) for all traits, indicating present high differences among environments and their remarkably influences would be reflected on the traits.

Also, the partition of G x E ss of the traits into its two components; 1- sum squares of regression (G × E linear ss) and sum squares of deviation from regression (pooled deviations), confirmed that G × E (linear) ss was significant

(P≥0.01) for all traits except TGW, indicating there were genetic differences among bread wheat genotypes for their regression on the environmental index. Therefore, it could be involved the stability analysis by Eberhart and Russell (1966). High significant pooled deviation mean square for all traits except TGW, indicating the genotype differed considerably with respect to their stability for these traits. Patel *et al.* (2014) found that significant mean square for linear G x E interaction and non-linear G x E interaction (pooled deviation) however greater in magnitude of linear component. Which revealed that there were genetic differences among genotypes for their regression on the different environment, and performance of genotypes would be predicted for an individual environment.

Table 5. Analysis of variance for stability of fifteen bread wheat genotypes under twelve environments for all the studied traits .

S.V.	d.f.	NS	NG	TGW	GY
Genotypes (G)	14	185467.12**	950.53**	89.84**	60.02**
Environments (E)	11	246384.59**	2039.36**	1002.49**	291.98**
G x E	154	8515.77**	34.39**	27.28**	5.21**
E + (G x E)	165	24373.69**	168.06**	92.29**	24.33**
Envi. (linear)	1	2710230.46**	22432.94**	11027.46**	3211.83**
G x E (linear)	14	24904.256**	179.47**	37.87	11.55**
Pooled Dev.	150	6418.46**	18.57**	24.48	4.27**
Error	336	2318.80	16.89	19.01	3.28

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

Stability parameters:

Eberhart and Russel (1966) defined the desired variety with that of a high mean performance ($\bar{x}$), unit regression coefficient (b = 1) and deviation from regression as smaller as possible ($s^2d = 0$) .

Considering the three criteria of the ideal cultivar recognized by Eberhart and Russel (1966). Four genotypes lines 13, 14, 15 and Misr 2 gave mean number of spikes plot^{-1} higher than the grand mean and exhibited insignificant from unit and zero for bi and S^2di, respectively.

Regression coefficient bi of lines 14 and 15 lower than 1 so it is considered adapted to unfavorable conditions while the two remained genotypes were considered adapted to favorable environments where it's bi higher than 1. Line 15 recorded the lowest parameter of ecovalence Wi% and CV%, indicating it is less fluctuation across environments (Table 6).

Table 6. Means and stability parameters for the studied traits of the 15 genotypes across the 12 environments.

	Number of spikes plot^{-1}					Number of grains spike^{-1}				
	Mean	**bi**	**S^2di**	**CV%**	**Wi%**	**Mean**	**bi**	**S^2di**	**CV%**	**Wi%**
L2	655.04	0.93	9517.91*	23.36	7.92	42.93	1.17	2.46	32.35	2.32
L4	582.72	0.74	4321.04	20.04	4.81	39.83	0.73*	5.75	22.98	4.13
L8	395.04	0.30**	2212.83	16.34	9.08	42.39	0.97	8.38	28.04	2.67
L13	709.46	1.28	7126.87	25.98	7.08	44.69	1.00	3.36	26.89	1.70
L14	752.59	0.89	6977.94	18.83	6.07	37.75	0.73*	7.19	24.27	4.49
L15	848.98	0.91	433.21	14.35	1.02	43.48	1.53**	1.03	41.35	9.12
L17	805.09	1.61**	9168.48	28.20	12.69	33.15	0.78	0.96	28.32	2.64
L20	459.35	0.47*	3690.39	19.09	7.27	70.22	1.92**	44.2*	33.28	33.27
L23	491.44	1.27	2272.17	34.74	3.31	55.50	1.24	8.00	26.81	4.20
L24	585.14	0.74	6631.06	21.37	6.60	44.62	0.70*	6.42	19.70	4.84
L31	615.27	0.79	7713.95	21.74	7.10	36.15	0.68*	3.08	23.35	4.49
L34	635.98	1.05	2347.78	22.78	2.42	48.91	0.78	37.59*	22.66	9.48
Misr 2	665.48	1.19	3149.95	24.64	3.50	41.38	1.01	25.81	31.37	5.94
Giza 168	714.32	1.29	10953.65*	27.25	10.08	39.69	0.94	33.88*	31.35	7.58
Gemmeiza 12	644.96	1.55*	8165.59	33.91	11.06	43.42	0.82	5.90	23.15	3.13
Mean	637.39					44.27				
	1000 grain weight					Grain yield fed^{-1}				
	Mean	bi	S^2di	CV%	Wi%	Mean	bi	S^2di	CV%	Wi%
L2	45.73	0.99	29.24	21.70	8.47	15.45	1.21	2.70	36.46	5.85
L4	44.25	1.06*	13.81	21.86	4.86	13.05	0.67*	0.17	24.04	4.50
L8	46.80	1.42*	28.24	27.57	11.33	10.16	0.61*	1.81	30.80	7.75
L13	41.32	0.96	7.79	20.82	3.40	16.05	0.94	1.27	27.47	3.03
L14	46.30	1.28	22.15	25.19	8.19	15.28	0.95	3.18	30.31	5.39
L15	40.36	0.85	4.76	18.99	3.02	18.87	1.34*	11.99*	36.19	19.31
L17	47.58	0.90	5.40	16.99	2.95	16.18	1.30*	3.31	37.68	7.97
L20	37.94	1.00	21.27	25.22	6.57	12.82	0.81	2.09	30.72	4.99
L23	41.48	0.67	42.36	20.74	13.53	11.92	1.07	0.51	40.74	2.12
L24	44.79	1.17	9.91	23.03	4.38	14.88	0.90	3.87	30.34	6.44
L31	44.09	0.69	16.98	16.56	7.20	13.76	0.78	6.35	31.35	10.57
L34	46.32	1.32	15.79	25.25	7.07	17.99	1.33*	2.57	34.12	7.44
Misr 2	43.88	0.83	13.58	18.29	5.23	13.62	0.92	3.19	33.00	5.53
Giza 168	46.55	1.08	26.97	22.30	8.03	15.23	1.06	3.61	33.46	5.94
Gemmeiza 12	43.86	0.77	13.85	17.29	5.77	14.57	1.13	1.07	35.65	3.17
Mean	44.08					14.66				

With respect to number of grains spike^{-1} (Table 6), two lines 13 and 23 gave mean performance higher than the grand mean and exhibited insignificant from unit and zero for bi and S^2di, respectively. The first line 13 was suitable for both favorable and unfavorable environments where it's bi nearly equal to 1, while the line 23 was adapted to unfavorable conditions because it's bi>1. Line 13 recorded low ecovalence Wi%.

For 1000 grain weight (Table 6), all genotypes except lines 4, 8, 13, 15, 20, 23 and Misr 2 were considered stable where it recorded TGW higher than grand mean in addition bi and S^2di were insignificant from unit and zero, respectively. Lines 14, 24 and 34 and Giza 168 gave bi > 1 consequently adapted for favorable environments while the five lines 17, 23, 31 and Gemmeiza 12 were considered adapted for unfavorable conditions where bi < 1. Line 17 gave low values for each of others stability parameters ecovalence Wi% and CV%.

Regarding grain yield fed^{-1} (Table 6), five genotypes lines 2, 13, 14, 24 and Giza 168; were considered stable where achieved three cases of stable genotype i.e. mean grain yield ranged from 14.88 ardab fed^{-1} for line 24 to 16.05 ardab fed^{-1} for line 13 exceeded the grand mean 14.66 ardab fed^{-1}. Moreover, bi and S^2di of them were insignificant from unit and zero, respectively. Line 2 gave bi higher than unity so it was considered adapted for favorable conditions. While the three genotypes; lines 13, 14 and Giza 168 showed bi nearly equal to one so considered adapted for all studied environments. Also, line 13 recorded low ecovalence Wi% and CV%, confirming it was stable across the environments. Belete *et al.* (2024) found that bread wheat variety ETBW9089 exhibited the lowest value for each of the Wricke ecovalence and coefficient of variation for grain yield confirming high stability and less fluctuations across the studied environments.

Additive Main effect and Multiplicative Interaction AMMI analysis:

AMMI analysis combines between the two analyses: analysis of variance and multiplication effect analysis. Briefly, analysis of variance is used to partition variance into three components: deviations each of G, E and G x E interaction from the grand mean. AMMI analysis used to partition deviations G x E interaction into different interaction principal component axes (IPCA), which can be tested for significance by ANOVA. AMMI analysis showed highly significant difference of E, G and G x E interaction for all traits (Table 7). Gupta *et al.* (2023) and Omrani *et al.* (2022) found that variance analysis in AMMI method showed significant (P≥0.01) difference for the effect of G and the G x E interaction.

Partitioning the sum of squares showed that high % contribution was due to environment by 40.95, 54.66, 66.89 and 66.16% for NS, NG, TGW and GY, respectively followed by 39.23, 32.43 and 17.31% of genotypes for NS, NG and GY, respectively then 19.82, 12.91 and 16.53% of G x E interaction for NS, NG and GY, respectively. While 25.49% of variations caused by G x E interaction then 7.63% of variation effects caused by genotypes for TGW (Table 7). These results were in simultaneous with those obtained by pooled analysis of variance. Kizilgeci *et al.* (2019) revealed that AMMI analysis showed significant variance of G, E and G x E interaction and the major sum of squares were significantly affected by E, G and GxE interaction by 85.47, 8.51 and 6.07%, respectively. Singh *et al.* (2019) reported the AMMI analysis of variance showed that 73.77, 5.99 and 20.23% of the total ss was attributable to environmental, genotypic and GxE effects, respectively for grain yield.

Analysis of AMMI showed that sum of square 1st interaction principle component axis IPCA1 explained 28.85, 57.46, 38.07 and 36.40%, while IPCA2 explained 21.04, 18.94, 20.25 and 17.70% from the GxE interaction sum of square for NS, NG, TGW and GY, respectively. Hence their means squares were highly significant. The remained IPCAs explained the other interaction effects. The two IPCAs (IPCA1+IPCA2) explained majority of GxE interaction sum of squares by 49.89, 76.40, 58.32 and 54.10% for NS, NG, TGW and GY, respectively (Table 7). Khare *et al.* (2024) found 68.9, 78.2 and 68.9% of the GxE interaction across normal sown, late sown and across two environments, respectively were explained to the first two IPCAs for grain yield. Kizilgeci *et al.* (2019) revealed that the complete GxE interaction was distributed to 62.56% of 1st principal component (PCA1) and the 37.44% of second PCA2. Mohammadi *et al.* (2018) revealed that AMMI analysis showed that 84.3% of total variation due to the environment while 14.09% was for the genotype effect for grain yield. The IPCA1 explained 77.5% of GxE interaction ss, indicating high contribution of the IPCA1 to the total GxE interaction.

Table 7. Additive Main effect and Multiplicative Interaction (AMMI) analysis of variance for the studied traits of bread wheat genotypes over the environments.

		Number of spikes $plot^{-1}$		Number of grains $spike^{-1}$	
	d.f.	MS	SS %	MS	SS %
Environments	11	739152.99**	40.95	6117.96**	54.66
Genotypes	14	556401.74**	39.23	2851.59**	32.43
GE	154	25547.33**	19.82	103.19**	12.91
IPCA1	24	47294.65**	28.85	380.52**	57.46
IPCA2	22	37625.84**	21.04	136.82**	18.94
IPCA3	20	36102.43**	18.35	77.45**	9.75
IPCA4	18	29301.28**	13.41	45.72**	5.18
IPCA5	16	15736.72**	6.39	30.97	3.12
IPCA6	14	12773.29**	4.55	18.07	1.59
IPCA7	12	11350.34**	3.46	19.03	1.44
IPCA8	10	9735.80**	2.47	19.17	1.21
IPCA9	8	5601.90	1.14	13.77	0.69
IPCA10	6	1532.44	0.23	11.35	0.43
IPCA11	4	947.65	0.10	7.69	0.19
IPCA12	2	0.00	0.00	0.00	0.00
Residuals	360	2392.20	0.00	16.96	0.00
		1000 grain weight		Grain yield fed^{-1}	
	d.f.	MS	SS %	MS	SS %
Environments	11	3007.25**	66.89	875.97**	66.16
Genotypes	14	269.51**	7.63	180.06**	17.31
GE	154	81.85**	25.49	15.64**	16.53
IPCA1	24	199.92**	38.07	36.53**	36.40
IPCA2	22	116.02**	20.25	19.38**	17.70
IPCA3	20	105.82**	16.79	15.96**	13.25
IPCA4	18	65.08**	9.29	14.78**	11.05
IPCA5	16	42.39**	5.38	11.97**	7.95
IPCA6	14	41.52**	4.61	11.08**	6.44
IPCA7	12	26.81*	2.55	6.33*	3.15
IPCA8	10	19.84366	1.57	4.32	1.79
IPCA9	8	16.61	1.05	3.46	1.15
IPCA10	6	5.69	0.27	3.32	0.83
IPCA11	4	4.79	0.15	1.66	0.28
IPCA12	2	0.00	0.00	0.00	0.00
Residuals	360	19.27	0.00	3.27	0.00

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

Farshadfar (2008) developed a method of the genotype selection index (GSI) incorporate both ranking mean trait (RT) and ranking AMMI stability value (RASV) in a single criteria. A low value of GSI refers to a stable genotype with high mean trait. GSI discriminated L14, L15,

L34 and Misr 2 for NS P^{-1}, L2, L8, L13, L23, Misr 2 and Gemmeiza 12 for NG S^{-1}, L4, L14, L17, L31 and L34 for TGW and L13, L14, L34 and Giza 168 for grain yield were high general adaptability and mean of these traits across environments (Table 8), meaning agreement with the results of method of regression and deviation from regression (Table 6). Belete *et al.* (2024) found that bread wheat variety ETBW9089 was stable and recommended for high scale production based on both Eberhart and Russel (1966) and AMMI stability model analyses.

Table 8. First and second IPCAs, mean, AMMI stability values (ASV) and genotype selection index (GSI) of the studied traits in wheat genotypes over 12 environments.

	Number of spikes plot^{-1}							Number of grains spike^{-1}						
	Mean	**R**	**IPCA1**	**IPCA2**	**ASV**	**R**	**GSI**	**Mean**	**R**	**IPCA1**	**IPCA2**	**ASV**	**R**	**GSI**
L2	655.04	7	-0.15	0.50	0.54	5	12	42.93	8	0.22	0.17	0.69	6	14
L4	582.72	12	0.41	0.59	0.82	9	21	39.83	11	-0.25	0.04	0.76	8	19
L8	395.04	15	0.99	-0.09	1.36	13	28	42.39	9	0.02	0.23	0.25	2	11
L13	709.46	5	-0.33	-0.90	1.00	10	15	44.69	4	0.03	0.21	0.23	1	5
L14	752.59	3	0.02	0.60	0.60	7	10	37.75	13	-0.25	0.21	0.80	9	22
L15	848.98	1	0.15	-0.18	0.28	2	3	43.48	6	0.43	-0.33	1.34	14	20
L17	805.09	2	-1.00	-0.13	1.38	14	16	33.15	15	-0.15	0.09	0.46	3	18
L20	459.35	14	0.86	-0.07	1.18	12	26	70.22	1	1.00	0.13	3.04	15	16
L23	491.44	13	-0.34	-0.04	0.47	4	17	55.50	2	0.27	-0.07	0.82	11	13
L24	585.14	11	0.44	-0.23	0.65	8	19	44.62	5	-0.29	-0.04	0.89	13	18
L31	615.27	10	0.36	0.32	0.59	6	16	36.15	14	-0.25	0.21	0.80	10	24
L34	635.98	9	-0.09	0.07	0.14	1	10	48.91	3	-0.26	0.35	0.86	12	15
Misr 2	665.48	6	-0.21	-0.33	0.44	3	9	41.38	10	-0.13	-0.50	0.63	4	14
Giza 168	714.32	4	-0.25	-0.95	1.01	11	15	39.69	12	-0.16	-0.48	0.68	5	17
Gemmeiza 12	644.96	8	-0.88	0.85	1.48	15	23	43.42	7	-0.22	-0.24	0.72	7	14
	1000 grain weight							Grain yield fed^{-1}						
	Mean	R	IPCA1	IPCA2	ASV	R	GSI	Mean	R	IPCA1	IPCA2	ASV	R	GSI
L2	45.73	6	0.78	0.17	1.48	13	19	15.45	5	0.33	-0.05	0.69	10	15
L4	44.25	8	0.12	-0.49	0.54	2	10	13.05	12	-0.09	-0.38	0.43	5	17
L8	46.80	2	-0.79	0.65	1.62	14	16	10.16	15	-0.09	-0.63	0.66	9	24
L13	41.32	13	-0.43	-0.16	0.82	7	20	16.05	4	-0.04	0.02	0.08	1	5
L14	46.30	5	-0.22	0.81	0.91	9	14	15.28	6	-0.10	-0.28	0.35	4	10
L15	40.36	14	-0.11	0.40	0.45	1	15	18.87	1	1.00	0.16	2.06	15	16
L17	47.58	1	0.37	-0.07	0.71	3	4	16.18	3	0.08	0.77	0.79	11	14
L20	37.94	15	-0.41	-0.62	0.99	10	25	12.82	13	-0.43	0.04	0.89	12	25
L23	41.48	12	-1.00	-0.34	1.91	15	27	11.92	14	0.10	0.02	0.21	2	16
L24	44.79	7	-0.44	0.08	0.84	8	15	14.88	8	-0.52	0.32	1.12	13	21
L31	44.09	9	0.37	0.33	0.77	4	13	13.76	10	-0.74	0.25	1.54	14	24
L34	46.32	4	0.37	0.37	0.79	5	9	17.99	2	0.26	0.21	0.58	8	10
Misr 2	43.88	10	0.66	-0.37	1.29	11	21	13.62	11	-0.13	-0.16	0.32	3	14
Giza 168	46.55	3	0.74	0.06	1.40	12	15	15.23	7	0.13	-0.35	0.45	6	13
Gemmeiza 12	43.86	11	-0.01	-0.81	0.81	6	17	14.57	9	0.23	0.05	0.48	7	16

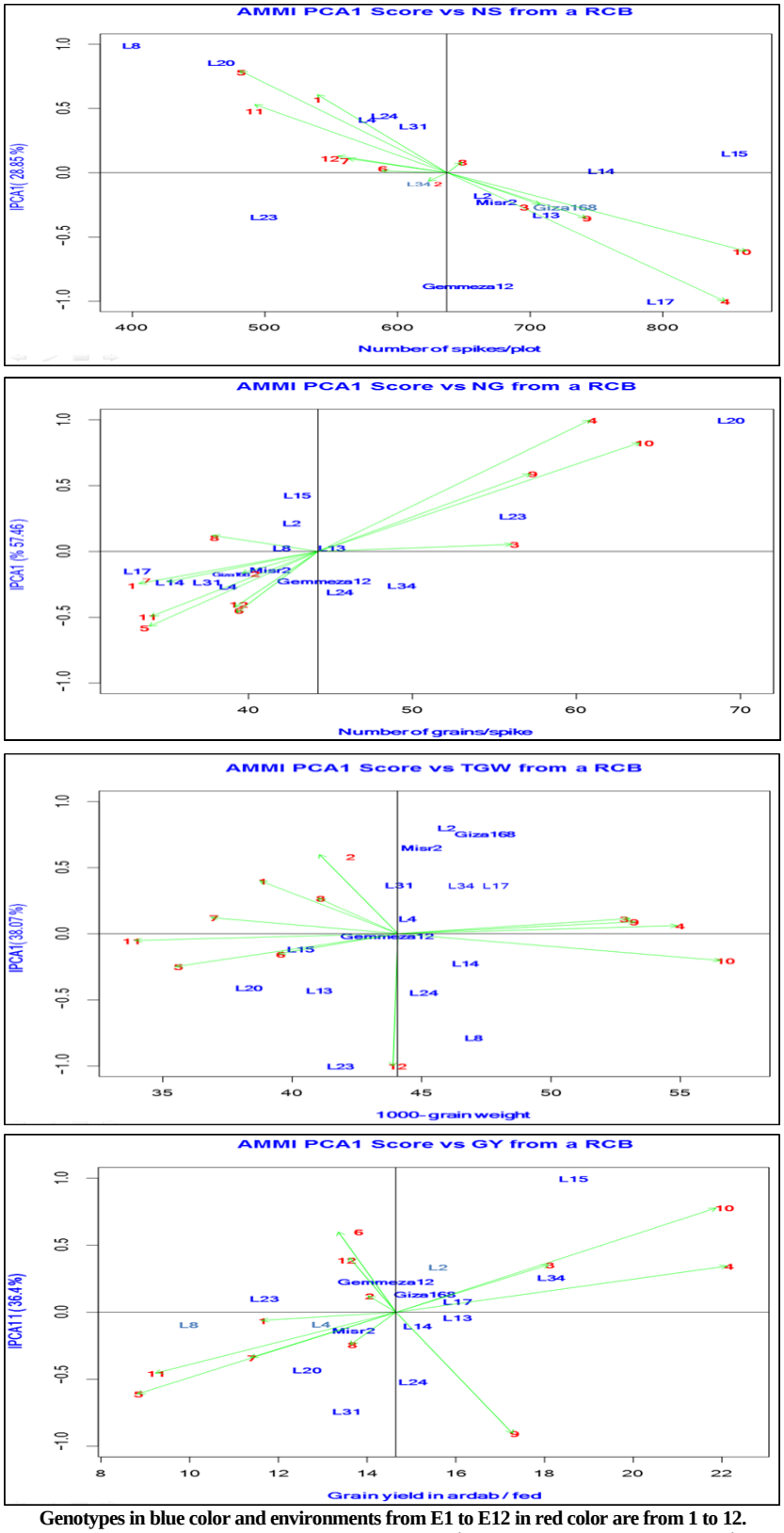
The biplot of AMMI analysis

The biplot of AMMI analysis provides information about the effects of genotypes, environments and their interaction. Crossa (1990) reported that the relationship between two environments or two genotypes in biplot is proportion to their similarity for GxE interaction. Fig. 2 indicated representation of 1st interaction principle component analysis IPCA1 on y-axis and means of the genotypes and environments of the studied traits on x-axis. The genotypes or environments that located in the right side of the midpoint of the perpendicular line characterized with high mean of the studied trait and vice versa for the left side. Genotypes located near to the origin of the biplot indicate its low contribution to GxE interaction referring that these genotypes were stable. Accordingly, genotypes L2, 13, 14, 15, 17, Misr 2 and Giza 168 for number of spikes plot^{-1}, five lines no. 13, 20, 23, 24 and 34 for number of grains spike^{-1}, eight lines 2, 4, 8, 14, 17, 24, 34 and Giza 168 for 1000 grains weight, eight genotypes L2, L13, L14, L15, L17, 24, 34 and Giza 168 for grain yield fed^{-1}. These genotypes were located in the right side of the midpoint of the perpendicular line characterized with high mean of the studied trait and vice versa for genotypes in the left side.

Misr 2 for number of spikes plot^{-1}, L13 for number of grains spike^{-1}, L34 for TGW and L13 and L14 for grain yield Fed^{-1} were the nearest genotypes from biplot origin so they were stable genotypes with mean higher than grand mean. These genotypes were stable according to both regression analysis of Eberhart and Russel (1966) and GSI of Farshadfar (2008), indicating the agreement of the results.

The environments E3, E4, E8, E9 and E10 for number of spikes plot^{-1}, E3, E4, E9 and E10 for each of number of grains spike^{-1}, 1000 grains weight and grain yield fed^{-1} were located in the right side of perpendicular line were the favorable conditions where gave mean higher than grand mean and vice versa for environments located in the left side.

The environments E4 and E5 for NS P^{-1} and NG S^{-1}, E10 and E11 for TGW and E5 and 9 for grain yield fed^{-1} were located in distant from the biplot origin implying had higher contribution to GxE interaction and resulted in unstable performance of genotype. While, the environments E8 for NS P^{-1}, E2 for NG S^{-1}, E6 for TGW and E2 for grain yield fed^{-1} were nearly located to the biplot origin with low contribution to GxE interaction and contributes to the stable genotypes performance. Amiri et al. (2013) in a study of GxE interaction in durum wheat revealed that those genotypes which are far from the biplot origin, have high GxE interaction and those genotypes that nearest to biplot origin have high stability.



Genotypes in blue color and environments from E1 to E12 in red color are from 1 to 12.

Figure 2. AMMI Biplot of IPCA-1 against number of spikes P^{-1}, number of grains spike $^{-1}$, 1000 grain weight and grain yield fed^{-1} of 15 bread wheat genotypes across 12 environments.

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الطرق الأحادية والمتعددة المتغيرات لتقدير ثبات بعض التراكيب الوراثية من قمح الخبز

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الملخص

اجريت الدراسة لتقييم الثبات المظهري في ١٥ تركيب وراثي من قمح الخبز (١٢ سلالة و٣ أصناف) خلال موسمين زراعيين ٢٠٢١/٢٠٢٢ و ٢٠٢٢/٢٠٢٣ تحت مستويين للتسميد النيتروجيني وثلاث مواعيد زراعة فى المزرعة التجريبية بكلية الزراعة – جامعة المنيا – مصر ، أظهر التحليل المشترك للثبات المظهري وجود اختلافات عالية المعنوية بين الاصناف ، البيئات ، والتفاعل بينهما لجميع الصفات المدروسة مما يدل علي وجود تفاعل للتراكيب الوراثية مع البيئات المختلفة ، وبالنسبة لمحصول الحبوب للفدان اعتبرت السلالات ٢ و ١٣ و ١٤ و ٢٤ والصنف جيزة ١٦٨ ثابتة حيث زادت متوسطات محصولها عن المتوسط العام علاوة على أن معامل الانحدار والانحراف عن الانحدار لهذه التراكيب كانا غير معنويين عن الواحد والصفر على الترتيب ، وأظهر تحليل المكونات الأساسية الإضافية والتفاعل المضاعف وجود اختلافات عالية المعنوية بين البيئات والتراكيب الوراثية والتفاعل بينهم لكل الصفات المدروسة ، وعن طريق دليل انتخاب التركيب الوراثي أمكن تمييز السلالات ١٣ و ١٤ و ٣٤ والصنف جيزة ١٦٨ كتراكيب وراثية ثابتة ذات محصول حبوب عالى حول البيئات مما يدعم نتائج تحليل الانحدار والانحراف عن الانحدار وكذلك كانت البيئات ١٠ و ١١ هي أفضل البيئات في حين كانت البيئات ٥ و ١١ هي غير المفضلة