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Adaptability of Ten Bread Wheat Genotypes under Delta, Middle, and Upper Egypt Conditions

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ABSTRACT



Genotype by environment interaction (GXE) is a serious issue under multi environment trials. Therefore, many statistical models were implemented to deal with GXE *e.g.* Additive Main Effect and Multiplicative Effect (AMMI) model. Ten bread wheat genotypes were evaluated in three seasons at five locations *vz*. Sakha, Giza, Sids, Malawy, and Shandaweel Agric. Res. St., Egypt from 2020/21 through 2022/23 winter growing seasons. The results showed significant differences between seasons (S), locations (L), and their interactions for all traits, except in case of S, SXG, SXLXG in plant height, days to heading, No. of kernels/spike, respectively. The mean overall performance indicated that G5 had the highest mean performance in No. of spikes/m², 1000 kernels weight, and grain yield, while G7 has the highest performance in No. kernels/spike. The results indicated that the first two components of principal component of the interaction of matrix (IPCA 1 and IPCA 2) contributed with 45.69% and 20.71%, respectively with 66.40% of total G×E interaction variation. IPCA 2 was plotted against IPCA 2 for AMMI biplot; AMMI illustrated that G5 is the most adapted and stable genotype while G7 is the most sensitive genotype overall environments.

Keywords: GXE interaction, environments, wheat, AMMI model, stability

INTRODUCTION

Sustainable food security became an urgent need to cope the climate changes and world growing population which is expected to reach 9.8 billion by 2050 (UN,2022). Food security can be achieved by increasing the strategic food crops production e.g. wheat and rice while sustainability can be achieved by keeping the production increment in systematic manner. Wheat is the second staple food crop after rice for its importance and nutritional value as well as its cultivation all over the world. The total wheat cultivated area was 220.8 million hectare produced 791.4 million tonnes 2024 (USDA, 2023). In this regard, Egypt faces a critical and difficult situation where it is the world's largest wheat importer because it imports more than 50% of its consumption. The total cultivated area in Egypt was 1.45 million hectare (about 3.3 million feddan; Feddan = 0.42hectare) produced 9 million tonnes in 2023 (USDA-Egypt,2023). The gap between production and consumption costs the Egyptian government billions of Dollars which in turn puts overload responsibilities on the Egyptian government shoulders.

Developing new high yield, stable varieties and adapted to wide range of environments can increase the total production which is resulted in reducing the gap between production and consumption. Therefore, the stability took concerns of many investigators since the early investigations which were made by Haldane (1946). Evaluation of group of genotypes across number of environments might take one of the following classes; high yield with poor stability or low yield with high stability or high yield with strong stability genotypes. The later genotypes are the targeted genotypes which is the ultimate objective of any wheat breeding program. The genotype might be stable either over years or over locations which is known as temporal and spatial stability, respectively. However, the target for the wheat breeders is a high yield stable genotype over years and locations. The quantitative traits *e.g.* grain yield are controlled by many genes, highly influenced by environment and generally have low heritability. These traits are influenced by genotype main effect (G) and environment additive main effect (E) in addition to the interaction between genotype and environment (GXE). There are several ways to deal with GxE interaction *i.e.* ignoring, reducing or exploit it. Ignoring and avoiding can be used when the proportion of G x E is low and for identifying mega-environments, respectively (DeLacy *et al.*, 1996). The best way to deal with G x E interaction is to exploit it along with genotype effect (G).

Cross Mark

Many techniques were developed to deal with and characterize GXE interaction based on linear-bilinear or mixed models and were successfully widely used in wheat breeding programs. Genotype, genotype by environment interaction biplot (GGE biplot), Additive Main effects and Multiplicative Interaction (AMMI), and principal component analysis (PCA) used to determine the stability and compatibility of genotypes based on the quantitative analysis singular value decomposition (SVD). AMMI model uses ANOVA to test the genotypes main effects and environments main effect to analyze the residual interaction component, so it is best to handle them separately, while still considering all three in an integrated manner as mentioned by Gauch (2006). Also he stated that AMMI model, due to the separation of these effects from each other, is mostly superior to the GGE biplot. AMMI model combines additive components for main effects (genotype and environment) and multiplicative components for genotype-environment interaction (GEI). It combines a univariate technique (ANOVA) for the main effects and a multivariate technique (PCA; principal component analysis) for GEI; the use of multivariate techniques permits a better use of information than the regression methods in the MET analysis as suggested by Crossa (1990).

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Evaluation genotype under wide range of environments is a prerequisite for development a new superior stable cultivar. Therefore, this investigation aimed to 1) study performance and stability of some bread wheat genotypes using AMMI model, 2) select superior stable genotype/s either overall environments or under specific environment, consequently utilization of the stable genotype/s in breeding program, and enhance the stabilize wheat grain production.

MATERIAL AND METHODS

Experiment set-up and plant material

Ten bread wheat genotypes (Table 1) were studied through 2020/21 to 2022/2023 winter growing seasons and the experiment was laid out in RCBD design in each location and season. The plot area was 4.2 m² and consisted of 6 rows with 3.5 m long spaced by 20 cm.

Code	Source	Pedigree and selection history	Origin	Description
C1	Cize 171	Gemmiza 9/Sakha 93	Equat	High yield and
GI	Giza 1/1	GZ2003-101-1GZ-4GZ-1GZ-2GZ-0GZ	Egypt	adaptability cultivar
G	Mier 4	NS732/HER/3/PRL/ SARA// TSI/VEE 5/6/FRET 2/5/WHEAR/SOKOLL	Fount	High yield and
02	WII5I 4	CM SA09Y007125-050Y- 050ZTM-0NJ-099NJ-0B-0EG	Egypt	adaptability cultivar
G3	Sakha 05	PASTOR//SITE/MO/3/CHEN/AEGILOPS SQUARROSA (TAUS)//BCN/4/WBLL1	Fount	High yield and
05	Sakia 75	CMSA01Y00158S-040P0Y-040M-030ZTM-040SY-26M-0Y-0SY-0S	Lgypt	adaptability cultivar
G4	Sakha 06	MINO/6/Sakha 12/5/Kvz//Cno 67/Pj 62/2/Yd"s"/Blo"s"/4/K 134 (60)/Vee	Fount	Early mature
04	Sakila 70	S. 16869-010S-07S-1S-2S-0S	Lgypt	cultivar
G5	Line 1	SAKHA 94 // WBLL1 *2/BRAMBLING	Fount	High yield
05	Line 1	S.16945 -013S -016S-5S -0S	Lgypt	advanced line
G6	Line 2	SERI/RAYON*2//PFAU/WEAVER /3/ MISR 2	Fount	High yield
00	Line 2	S.2011-40-033S-013S-1S-0S	Egypt	advanced line
G7	line#14	MUU/KBIRD//2*KACHU/KIRITATI	CIMMYT	High yield
0/	18HTWYT	CMSS12Y01082T-099TOPM-099Y-099M-099NJ-099NJ-4Y-0WGY-0EG		advanced line
G8	line#21	BORL14*2//BECARD/QUAIU #1	CIMMYT	High yield
00	18HTWYT	CMSS12B00634T-099TOPY-099M-099NJ-099NJ-17Y-0WGY-0EG		advanced line
GQ	line#17	KENYA SUNBIRD/KACHU//KACHU/KIRITATI	CIMMYT	High yield
0)	27HRWYT	CMSS13Y00616S-099Y-099M-0SY-22M-0RGY-0EG		advanced line
G10	line#36	MANKU//MUTUS*2/TECUE #1	CIMMYT	High yield
010	27HRWYT	CMSS13B00893S-099M-099Y-2M-0RGY-0EG		advanced line
18 th H	FWYT (High	Temperature Wheat Yield Trial).27 th HRWYT (High Rainfall Wheat Yield Trial).		

Three high yielding and wide adapted cultivars and an early mature cultivar in addition to six high yielding advanced lines were included in the study. Hereafter, the term 'genotype' will be used to refer to both the cultivars and the advanced lines for the sake of simplicity. The description of the studied genotypes is presented in Table (1).

Testing locations

The studied genotypes were tested at five locations i.e., five Agricultural Research Stations, Agricultural Research Center, Egypt, *viz.* Sakha (SK) and Giza (GZ), representing Delta, Sids (SD) and Malawy (ML), representing Middle Egypt and Shandaweel (SH) representing Upper Egypt. Latitude, Longitude, and Altitude for each location are presented in Table (2) as well as air temperature for all studied locations through the three growing seasons in Figure (1).

Table 2. The description of the testing sites

Location	Agroecological zone	Latitude Longitud	le Altitude
Sakha (SK)	Delta	31° 09' N 30° 94' H	E 6 m
Giza (GZ)	Delta	30° 02' N 31° 21'E	E 19 m
Sids (SD)	Middle Egypt	30° 96' N 28° 91'E	E 35 m
Malawy(ML)	Middle Egypt	30° 83' N 27° 73'E	E 36 m
Shandaweel(SH)	Upper Egypt	26°63'N 31° 65'E	E 69 m



Figure 1. Monthly mean temperature for each location in each growing season.

The measured traits

A total of seven phenological and agronomic traits were measured; days to heading (DH), days to maturity (DM), plant height (PLH) in cm, number of spikes/ m^2 (S/M²), 1000 kernels weight (KW) in g, number of kernels/spike (K/S), and grain yield/plot (GY) in kg.

Statistical analysis

Different statistical software packages were used in calculations and statistical analysis. Single as well as combined analysis of variance (ANOVA) were performed according to Gomez and Gomez (1984). Bartlett test for homogeneity of errors variance according to Bartlett (1937) using SAS V9.3 (2015) was performed. Additive Main effects and Multiplicative Interaction (AMMI) models were performed to assess the relationships among genotypes, locations and genotypes by environment interaction based on the model described by Crossa (1990) using Genstat 21st Ed. statistical software package. The AMMI stability value (ASV) was calculated as described by Purchase *et al.* (2000).

RESULTS AND DISCUSSION

Analysis of variance

Analysis of variance for each location in each season were executed separately; based on the presence of variability and homogeneity of errors variance, the combined analysis were performed separately over locations and/over seasons as well as overall locations and seasons. The results of combined analysis of variance over all locations and seasons (Table 3) show the existence of variability among seasons (S), locations (L), genotypes (G), as well as seasons by location (S×L), seasons by genotypes (S×G), locations by genotypes (L×G), and season by locations by genotypes (S×L×G) interactions for all studied traits, except seasons for plant height, S×G interaction for days to heading, and L×G interaction for No. of kernels/spikes. These results are consistent with those obtained by Mulugeta et al., 2024 whom found that the combined analysis of variance indicated a significant difference between genotypes for all studied trait, while the interaction genotype by location and genotype by year was highly significant for most of the studied traits.

T	abl	le 3	3. (Com	bined	l anal	lvsi	s of	' vari	iance	for t	the	stud	lied	genot	vpes	s unde	r over	locati	ions	and	seaso	ns
							•								0								

SOV	DE	Mean squares											
5. U . V	D. r -	DH	DM	PLH	S/M ²	K/S	KW	GY					
Season (S)	2	1065**	1104.2**	72.5 ^{NS}	312767**	3869.7**	307.2**	38.334**					
Location (L)	4	884.2**	818.6*	1938.8**	26671**	374.1*	1542.8**	40.554**					
SxL	8	1141.1**	252.7**	447.7**	18340**	430.3**	364.8**	12.558**					
Error	30	24.3	19.8	39.9	1173	107.0	7.6	0.640					
Genotypes (G)	9	1712.9**	1046.5**	685.0**	36625**	772.9**	157.8**	7.836**					
GxS	18	20.6 ^{NS}	58.7**	169.8**	5426**	154.9**	84.3**	0.785**					
GxL	36	44.6**	28.9**	76.0**	5512**	366.0**	69.9**	0.761**					
GxSxL	72	39.1**	27.0**	72.7**	3214**	52.1 ^{NS}	21.8**	0.299**					
Error	270	21.4	15.2	30.2	1450	54.3	8.1	0.149					
C.V %		4.7	2.7	5.1	8.9	11.7	5.8	9.8					

Where: *, ** are significant at 0.01, and 0.05. NS is nonsignificant. C.V = coefficient of variation.

The genotypic mean performance: Phenological traits

Days to heading (DH)

The results for means of days to heading and days to maturity are in Table 4. The results indicate that mean days to heading ranged from 81.8 (G4) to 102.8 (G 2), 86.1 (G4) to 107.3 (G8), 86.8 (G 4) to 106.6 (G8), 83.3 (G4) to 104.8 (G5), 73.8 (G4) to 102.0 (G5), 80.3 (G4) to 98.9 (G8), 83.3 (G4) to 105.5 (G5), 83.5 (G4) to 104.0 (G3), 82.4 (G4) to 102.7 days (G5) in SK, GZ, SD, ML, and SH, S1, S2, S3, and overall location and seasons, respectively. With regards to the averages, it was 97.5, 101.1, 100.9, 98.5, 93.4, 95.2, 99.7, and 99.9 days in SK, GZ, SD, ML, SH, S1, S2 and S3, respectively, with grand mean of 98.3 days. Similar results were obtained by Zotova *et al.* (2024).

Days to maturity (DM)

The results for days to maturity, presented in Table (4), indicate that mean days to maturity ranged from 137.4 (G4) to 151.1.8 (G2), 138.7 (G4) to 150.4 (G2), 126.8 (G4) to 146.6 (G2), 134.7 (G4) to 152.4 (G2), 130.2 (G4) to 146.3 (G7), 132.6 (G4) to 146.6 (G5), 136.1 (G4) to 152.2 (G2), 132.0 (G4) to 150.9 (G2), 133.6 (G4) to 149.3 days (G5) in SK, GZ, SD, ML, and SH, S1, S2, S3, and overall location and seasons, respectively. With regards to the averages, it was 147.1, 147.0, 141.0, 147.1, 142.2, 142.8, 148.0, and 143.9 days in SK, GZ, SD, ML, SH, S1, S2, and S3, respectively, with grand mean of 144.9 days. Due to the diverse environments and the genetic makeup of the studied genotypes, the variability for days to heading and days to maturity overall environments was very high *i.e.* 19.6 and 15.7 days for DH and DM, respectively. These results are in

agreement with those obtained by Zotova *et al.* (2024). Based on the above mentioned results, it is obviously that the earliest genotype is G4 with significant differences with all studied genotypes where it is an early mature cultivar recently was released in Egypt.

The phenological traits *i.e.* DH and DM has been acknowledged as major aspects of plant response to the environment which can serve as important bio-indicator in the era of climate change (Rezaei *et al.*, 2018). The adapted early flowering cultivars successfully advance onset of anthesis and enforce longer grain filling period to reduce or avoids the risks of exposure to terminal heat stresses in late spring (Yang *et al.*, 2019), While days to maturity is the major genotypic cause of genotype environment interaction where it is influenced by genetic and non-genetic parameters (Garatuza-Payan *et al.*, 2018). Phenological traits genes also regulate the physiological development of wheat, therefore beside the grain yield; the phenological traits should be taken into consideration in selection strategies in wheat improvement as concluded by Mohan *et al.*, 2022.

Morph-agronomical traits

Plant height (PLH)

The results for plant height are presented in Table (5); it indicate that mean plant height ranged from 103.9 (G4) to 119.0 (G2), 101.8 (G4) to 113.9 (G2), 97.8 (G4) to 112.3 (G2), 102.8 (G4) to 116.4 (G5), 94.2 (G4) to 112.3 (G5), 101.0 (G4) to 117.1 (G5), 100.0 (G4) to 113.3 (G1), 99.3 (G4) to 119.7 (G2), 100.1 (G4) to 113.4 cm (G2) in SK, GZ, SD, ML, and SH, S1, S2, S3, and overall location and seasons, respectively. With regards to the averages, they were 113.4, 108.2, 101.2, 111.2,

107.3, 107.8 and 108.5 cm in SK, GZ, SD, ML, SH, S1, S2, and S3, respectively, with grand mean of 108.3 cm.

Plant height trait variability overall environments was very high (13.3 cm). Plant height has a significant positive correlation with grain yield where taller germplasm, to a certain limit, tended to provide consistently higher yield as concluded by Morgounov *et al.* (2024).

Table 4. Days to heading and days to maturity means for the studied genotypes across the studied environments

Trait Days to heading Days to maturity																			
			Lo	cations	over		Sea	asons o	ver			Loc	ations	over		Sea	isons o	ver	
Geno	otype			seasor	ıs		1	ocatior	IS	Overall		1	season	s		le	ocation	IS	Overall
	• -	SK	GZ	SD	ML	SH	S1	S2	S3		SK	GZ	SD	ML	SH	S1	S2	S3	-
1		96.7	103.4	102.2	101.9	96.0	96.9	101.6	101.6	100.0	150.3	150.0	141.0	151.4	144.2	146.2	150.4	145.6	147.4
2		102.8	104.1	105.1	102.1	96.0	98.7	103.9	103.5	102.0	151.1	150.4	146.6	152.4	145.9	144.8	152.2	150.9	149.3
3		102.6	103.1	100.5	98.7	96.6	97.3	99.7	104.0	100.3	146.4	149.4	141.8	146.6	142.3	142.0	147.9	146.0	145.3
4		81.8	86.1	86.8	83.3	73.8	80.3	83.3	83.5	82.4	137.4	138.7	126.8	134.7	130.2	132.6	136.1	132.0	133.6
5		100.0	101.8	105.1	104.8	102.0	99.7	105.5	103.0	102.7	148.7	147.3	145.9	149.7	148.8	146.6	151.5	146.1	148.1
6		99.8	100.2	103.2	101.8	98.6	96.1	103.4	102.7	100.7	150.6	147.6	144.8	149.1	144.2	144.0	150.7	147.0	147.2
7		100.1	104.2	103.6	100.8	93.2	98.8	101.0	101.3	100.4	147.6	147.3	143.0	151.0	146.3	144.3	147.3	149.5	147.0
8		101.3	107.3	106.6	99.6	92.3	98.9	102.4	102.9	101.4	148.6	147.2	144.1	149.6	141.6	144.6	152.0	142.0	146.2
9		97.8	105.3	100.0	100.2	95.0	95.4	101.4	102.2	99.7	148.1	146.8	139.7	145.2	139.4	142.0	147.9	141.7	143.8
10		92.3	95.6	95.6	92.1	90.3	90.0	95.0	94.6	93.2	142.7	145.0	136.6	141.2	139.3	140.8	143.5	138.5	141.0
Mear	1	97.5	101.1	100.9	98.5	93.4	95.2	99.7	99.9	98.3	147.1	147.0	141.0	147.1	142.2	142.8	148.0	143.9	144.9
	S	2.4	3.4	3.4	3.6	2.1				1.2	3.6	2.1	4.0	3.6	1.2				1.1
	L						2.6	3.4	2.0	1.5						2.3	2.7	2.8	1.4
ICD	G	4.5	4.6	4.5	3.7	4.5	3.2	3.2	3.8	2.0	2.9	3.5	4.5	3.7	3.3	2.8	3.0	2.6	1.6
	SXL									2.6									2.3
0.05	SXG	7.6	8.0	8.0	6.8	7.6				3.3	5.6	6.0	8.1	6.8	5.5				2.8
	LXG						7.2	7.4	8.1	4.3						6.2	6.8	6.0	3.7
	SXLXG	ſ								7.5									6.4
					~~	-													

Where: L.S.D _{0.05} is least significant differences between treatments.

While Mohan *et al.* (2022) had different conclusion about difficulty to generalize the impact of plant height where most of the genotypes globally have one or two genes out of reduced plant height mutant genes (Rht-B1b and or Rht-D1b); Rht-B1b and Rht-D1b are gibberellins insensitive, leading to decreased sensitivity of vegetative tissues to endogenous gibberellins, consequently lead to reduce plant height. Plant height trait together with the phenological traits can be defined as non-grain parametric traits (Mohan *et al.*, 2022). Grain yield and its components

No. of spikes/ m^2 (S/ M^2)

The results in Table (5) indicate that mean no. of spikes/m² ranged from 343.8 (G4) to 479.1 (G1), 329.4 (G4) to 459.6 (G8), 391.9 (G1) to 467.8 (G8), 382.3 (G4) to 482.8 (G6), 353.3 (G4) to 493.8 (G5), 338.7 (G4) to 433.5 (G8), 372.6 (G4)

to 438.1 (G3), 380.3 (G4) to 517.0 (G5), 363.9 (G4) to 451.9(G5) spikes/m² (G 2) in SK, GZ, SD, ML, and SH, S1, S2, S3, and overall location and seasons, respectively. With regard to the average, it was 427.7, 399.9, 427.5, 445.5, 437.5, 396.6, 406.1 and 480.0 spikes/m² in SK, GZ, SD, ML, SH, S1, S2, and S3, respectively, with grand mean of 427.6 spikes/m². Based on the above results, the highest number of spikes/m² overall environments is G5 followed by G8, G3, G1, G6, and G2 with no significant differences, while the lowest value was for G4 with significant differences with the rest of genotypes. The results indicated considerable differences in number of spikes/m² between locations and seasons and overall locations and seasons revealing its influence with environments; numerous investigators concluded the same results for instance Feltaous et al. (2020), Philipp et al. (2018), Mohiy et al. (2021) and Slafer et al. (2022).

Table 5. Plant height and No. of spikes/m² means for the studied genotypes across the studied environments

Trait Plant height									No. of spikes/m ²										
Constru			L	ocatio	ns		5	Season	s	Oronall	1	L	ocatio	ns		S	Season	S	Oronall
Genoty	pe	SK	GZ	SD	ML	SH	S1	S2	S3	Overall	SK	GZ	SD	ML	SH	S1	S2	S3	Overall
1		116.2	113.7	100.9	113.7	111.0	113.1	113.3	106.8	111.1	479.1	449.8	391.9	445.3	453.1	393.4	432.8	505.3	443.8
2		119.0	113.9	112.3	111.7	110.0	107.8	112.7	119.7	113.4	463.7	401.7	432.6	457.6	439.4	401.4	404.8	510.7	439.0
3		114.1	113.7	100.6	115.0	107.8	109.1	109.2	112.3	110.2	460.0	402.4	432.1	455.6	484.4	395.1	438.1	507.6	446.9
4		103.9	101.8	97.8	102.8	94.2	101.0	100.0	99.3	100.1	343.8	329.4	410.6	382.3	353.3	338.7	372.6	380.3	363.9
5		118.1	109.8	103.8	116.4	112.3	117.1	109.6	109.5	112.1	463.6	430.7	426.7	445.0	493.8	423.3	415.5	517.0	451.9
6		109.2	103.9	100.0	106.1	109.8	100.4	108.4	108.6	105.8	452.9	394.8	444.8	482.8	427.8	419.4	411.3	491.1	440.6
7		115.1	110.8	95.7	111.2	106.9	106.1	108.8	108.9	107.9	403.8	363.6	424.0	451.7	416.4	380.5	383.5	471.7	411.9
8		114.6	106.0	103.4	115.2	109.2	110.0	109.6	109.5	109.7	440.4	459.6	467.8	453.3	431.3	433.5	417.7	500.3	450.5
9		113.4	102.4	97.2	111.2	104.2	103.0	108.3	105.8	105.7	397.1	418.5	430.1	452.6	455.5	393.1	404.4	494.8	430.8
10		110.0	106.1	100.0	109.1	107.7	107.0	107.8	104.9	106.6	372.9	348.1	414.8	428.9	418.6	387.7	380.7	421.5	396.6
Mean		113.4	108.2	101.2	111.2	107.3	107.5	108.8	108.5	108.3	427.7	399.9	427.5	445.5	437.4	396.6	406.1	480.0	427.6
	S	5.1	1.9	3.8	5.2	3.0				1.5	22.5	20.0	21.4	19.9	24.1				8.1
	L						4.1	4.2	3.4	1.9						23.6	16.4	16.5	10.4
LOD	G	5.1	5.1	6.0	4.7	5.2	4.2	4.0	3.4	2.3	30.2	27.2	51.5	31.3	34.7	30.8	27.6	25.0	15.8
LSD	SXL									3.3									18.1
0.05	SXG	9.4	8.4	10.2	8.8	8.8				4.0	52.8	47.4	86.3	53.8	60.1				22.7
	LXG						9.6	9.3	7.9	5.2						68.6	60.3	55.0	35.0
	SXLXC	ť								9.0									60.6

Where: L.S.D $_{0.05}$ is least significant differences between treatments.

No. of spikes/m² is a very important yield's component trait. It is determined by the ability of tillering; tillering is a significant agronomic trait which determines plant architecture and affect on grain yield. It is a complex trait

quantitatively inherited controlled by different factors either genetic or environmental factors. It is controlled by major and many small-effect loci. It is worthy to mention that it is controlled by tillering formation as well as tillering bud inhibition genes. Tillering bud inhibition, four genes, were named tin1, tin2, tin3, and ftin genes; all of them were mapped on 1AS, 2A, 3A, and 1AS chromosomes, respectively (Shang *et al.*, 2021). Tillering formation genes were identified and characterized *e.g.* Monoculm 1 "TaMOC1- 7A"and Teosinte branched 1 "TaTB1" (Zhang *et al.*, 2015).

In addition to the above mentioned genes some hormones affect on tillering in wheat *e.g.* Gibberellins which is influenced by plant height genes Rht genes, therefore number of tillers and plant height are negatively associated; plants defective gibberellins biosynthesis have massive tillers and short culms (Wang *et al.*, 2023). For all those aspects, complexity of no. spikes/m² and its contribution in increasing yield is not questioned.

No. of kernels/spike (K/S)

The results in Table (6) indicate that mean of no. of kernels/spike ranged from 47.1 (G9) to 72.4 (G7), 56.0 (G4) to 73.5 (G1), 55.7 (G1) to 76.7 (G2), 52.0 (G3) to 67.9 (G1), 52.3 (G4) to 71.0 (G1), 54.6 (G4) to 72.6 (G2), 50.7 (G4) to 64.2 (G1), 60.2 (G4) to 74.7 (G7), 55.1 (G4) to 68.4 (G7) kernels/spike in SK, GZ, SD, ML, and SH, S1, S2, S3, and overall location and seasons, respectively. With regards to the average, it was 61.5, 66.6, 66.0, 61.7, 64.7, 65.2, 59.3, and 67.9 kernels in SK, GZ, SD, ML, SH, S1, S2, and S3, respectively, with grand mean of 64.9 kernels. These results in line with those obtained by Muhammad *et al.* (2020), Vicentin *et al.* (2024) and Zotova *et al.* (2024).

 Table 6. No. of Kernels/spike and 1000-Kernels weight means for the studied genotypes across the studied environments

 Trait
 No. of Kernels/spike

 1000-Kernels weight

Halt		INO. OI KEI HEIS/SPIKE											1000-1	Xel lle	is weig	çin			
Constr	m 0		L	ocatio	ns		S	Season	IS	Orionall		L	ocatio	ns		S	Season	IS	Oronall
Genoty	ре	SK	GZ	SD	ML	SH	S1	S2	S3	-Overall	SK	GZ	SD	ML	SH	S1	S2	S3	Overall
1		66.1	73.5	55.7	67.9	71.0	65.1	64.2	71.1	66.8	56.9	50.7	51.1	52.7	41.2	50.4	49.4	51.8	50.5
2		68.8	68.0	76.7	58.6	65.6	72.6	59.6	70.4	67.5	53.3	49.1	47.7	47.2	44.7	46.6	45.9	52.7	48.4
3		66.1	72.0	65.0	52.0	72.8	65.4	61.1	70.3	65.6	52.4	48.0	49.5	52.1	39.5	48.5	46.6	49.8	48.3
4		57.2	56.0	50.3	60.0	52.3	54.6	50.7	60.2	55.1	53.6	46.9	52.4	47.4	36.9	51.0	48.1	43.3	47.5
5		63.8	65.3	70.5	64.4	62.6	72.1	56.8	67.1	65.3	52.5	60.7	50.0	49.6	53.3	51.7	52.2	55.7	53.2
6		55.1	69.0	72.3	64.9	67.1	63.7	62.3	71.1	65.7	51.4	45.8	46.2	46.1	41.8	45.4	44.5	48.9	46.3
7		72.4	69.3	64.5	65.2	70.6	67.1	63.5	74.7	68.4	52.5	45.3	48.1	46.6	35.5	45.0	45.0	46.7	45.6
8		63.6	62.8	62.8	65.8	56.3	67.6	56.1	63.0	62.2	53.6	51.6	57.2	48.8	46.1	48.7	51.5	54.1	51.5
9		47.1	66.2	75.3	57.7	63.6	60.6	59.6	65.8	62.0	50.1	51.2	48.2	46.3	43.1	46.9	46.3	50.1	47.8
10		56.8	63.8	66.7	60.4	65.0	62.8	59.5	65.3	62.6	49.6	51.0	48.5	49.2	43.1	47.3	48.1	49.4	48.3
Mean		61.7	66.6	66.0	61.7	64.7	65.2	59.3	67.9	64.1	52.6	50.0	49.9	48.6	42.5	48.1	47.8	50.3	48.7
	S	4.0	4.0	6.0	10.4	6.2				2.4	2.1	2.1	1.7	1.5	0.8				0.7
	L						7.4	5.3	4.8	3.2						0.9	1.3	2.2	0.8
ISD	G	5.8	5.8	9.2	5.7	7.6	4.9	5.0	6.0	3.1	2.2	2.2	2.7	2.2	3.8	1.6	2.0	2.4	1.2
0.05	SXL									5.5									1.5
0.05	SXG	10.1	10.1	15.9	13.0	13.5				5.6	4.0	4.0	4.7	3.8	6.2				2.0
	LXG						12.3	11.6	13.5	7.2						3.4	4.4	5.5	2.6
	SXLXG									12.4									4.5

Where: L.S.D $_{0.05}$ is least significant differences between treatments.

Thousand kernels weight (KW)

The results in Table (6) indicate that mean no. of 1000-kernels weight ranged from 49.6 (G 10) to 56.9 (G 1), 45.3 (G 7) to 60.7 (G 5), 46.2 (G 6) to 57.2 (G 8), 46.1 (G6) to 52.7 (G 1), 35.5 (G7) to 53.3 (G 5), 45.0 (G7) to 51.7 (G 5), 45.0 (G7) to 52.2 (G 5), 43.3 (G 4) to 55.7 (G 5), 45.6 (G7) to 53.2 (G 5) g SK, GZ, SD, ML, and SH, S1, S2, S3, and overall location and seasons, respectively. With regards to the average, it was 52.6, 50.0, 49.9, 48.6, 42.5, 48.1, 47.8, and 50.3 g in SK, GZ, SD, ML, SH, S1, S2, and S3, respectively, with grand mean of 48.7 g; Mohiy *et al.* (2021), Muhammad *et al.* (2020), Zotova *et al.*(2024) found similar results.

Grain yield/plot (GY)

The results in Table (7) indicate that mean no. of grain yield (Kg/plot) ranged from 3.940 (G4) to 5.344 (G3), 2.561 (G4) to 4.093 (G5), 3.561 (G4) to 5.411 (G5), 3.194 (G4) to 4.140 (G2), 2.256 (G4) to 3.811 (G2), 3.090 (G4) to 4.595 (G2), 2.705 (G4) to 3.881 (G5), 3.422 (G4) to 4.966 (G2), 3.103 (G4) to 4.432 (G5) kg in SK, GZ, SD, ML, and SH, S1, S2, S3, and overall location and seasons, respectively. With regards to the average, it was 4.739, 3.469, 4.573, 3.801, 3.198, 3.997, 3.431, and 4.440 kg in SK, GZ, SD, ML, SH, S1, S2, and S3, respectively, with grand mean of 3.956 kg/plot.

Heavy investigations were done on the influence of grain yield by its components; for example Xie *et al.* (2018), Muhammad *et al.* (2020), Isham *et al.* (2021) and Vicentin *et al.* (2024).

No. of kernels/spike and 1000 kernels weight are two major yield components traits where they lead to high grain yield; Muhammad *et al.* (2020) concluded that the breeding progress in elite cultivars compared to landraces was achieved by enhancement in no. of kernels/spike and 1000-kernel weight. Even though, the bottleneck of improving no. of kernels/spike and 1000-kernel weight is the negative correlation between them. Therefore, a trade-off between no. of kernels/spike and 1000-kernel weight has been reported by Vicentin *et al.*, (2024); where he reported that no. of kernels/spike and yield were increased, the proportion of smaller kernels in the distal spike position also augmented thus lowering the average kernels weight.

It is worthy to mention that the spike characteristics *i.e.* no. of spikelets/spike, no. of kernels/spikelet, and no. of kernels/spike are associated with Q gene which present in all modern wheat cultivars. Q gene reduces the ratio between grain length to weight, leading to shorter and rounded kernels (Xie *et al.*, 2018). A remarkable example for the trade-off was that an improvement was achieved in grain weight under field conditions at farmer's plant density rate, where grain weight and grain yield was increased by 12.3% and 11.3%, respectively without affecting grain number (Calderini *et al.*, 2021). With regards to grain yield, it is a complex trait heavily influenced by environmental factors. The association between grain yield and its components e.g. no. of kernels/spike and

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1000 kernels weight is very important; many investigations have detected quantitative trait loci (QTL) influence on grain yield and colocate with some yield components which in turn suggest partially shared genetic control for yield and these traits (Sukumaran *et al.*, 2015). In the same context, Philipp *et al.* (2018) found that approximately a half of 38% yield improvement was achieved in elite cultivars, compared to

genetic resources, was attributed to no. kernels/spike and grain yield/spikelet, while the other half of yield improvement was attributed to no. spike/m2. In sense of the above, grain yield results (Table 7) showed that the highest grain yield is for G5 with the highest no. of spike/m² and the highest 1000-kernel weight as well; these results are in agreement with the above conclusions.

Table 7. Grain	yield (Kg/plot) means f	for the studied genoty	ypes across the studied	d environments
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Construm				Locations					Orion all	
Genotyp	e –	SK	GZ	SD	ML	SH	S1	S2	S 3	Over all
1		5.195	3.986	4.728	3.754	3.563	4.204	3.677	4.855	4.245
2		5.188	3.861	4.939	4.140	3.811	4.595	3.603	4.966	4.388
3		5.344	3.691	5.217	3.704	3.419	4.327	3.743	4.756	4.275
4		3.941	2.561	3.561	3.194	2.256	3.090	2.705	3.513	3.103
5		5.162	4.093	5.411	3.710	3.782	4.480	3.881	4.934	4.432
6		4.196	3.352	4.633	3.943	3.086	4.027	3.314	4.185	3.842
7		4.592	2.843	3.702	4.000	2.282	3.788	3.242	3.422	3.484
8		4.822	3.581	4.989	4.081	3.031	4.067	3.667	4.569	4.101
9		4.589	3.349	4.639	3.893	3.404	3.903	3.200	4.822	3.975
10		4.359	3.367	3.911	3.588	3.344	3.485	3.277	4.379	3.714
Mean		4.739	3.468	4.573	3.801	3.198	3.997	3.431	4.440	3.956
	S	1.058	0.142	0.165	0.245	0.225				0.189
	L						0.174	0.165	0.175	0.244
LCD	G	0.342	0.361	0.391	0.392	0.337	0.293	0.253	0.295	0.160
	SXL									0.422
0.05	SXG	1.24	0.603	0.656	0.673	0.582				0.321
	LXG						0.640	0.556	0.645	0.414
	SXLXG									0.717

Where: L.S.D 0.05 is least significant differences between treatments.

Additive main effects and multiplicative interaction analysis "AMMI"

AMMI is an effective and powerful technique in investigating the main effects (G and E) and multiplicative interaction (GXE) in multi environments trials, where it combines ANOVA analysis as well as PCA analysis. AMMI can be performed only in case of G×E interaction significance.

Analysis of variance for AMMI model is presented in Table (8). The results indicated that first principal component of the interaction matrix (IPCA1) and second principal component of the interaction matrix (IPCA 2) were highly significant and explained 45.86%, 20.39% of GXE interaction, respectively. IPCA1 was plotted against IPCA2 of grain yield trait to visualize GXE in AMMI biplot. AMMI enables us to 1) visualizing GXE interaction, 2) identifying the genotypes that are adapted to particular environments, 3) identifying the genotypes that are broadly adapted overall wide range of environments, and 4) measure stability of a genotype.

Table 8.	AMMI ha	sed ANOV	A for the	studied ger	notvnes
I able of			in tor the	Staarea Se	not pes

S.O.V	D.F	Sum of squares	Mean squares
Genotypes (G)	9	23.51	2.612**
Environments (E)	14	113.12	8.080^{**}
Interactions (GXE)	126	21.01	0.167
IPCA 1	22	9.81	0.547**
IPCA 1	20	4.39	0.218**
Residuals	84	7 27	0.082

AMMI stability values (ASV)

AAMI analysis its self does not provide quantitative measures for ranking genotypes therefore Purchase *et al.* (2000) proposed an equation to estimate AMMI stability value (ASV) to rank the genotypes. ASV affects on the distance from the coordinate point to the origin in a twodimensional scattergram of IPCA1 scores against IPCA2 scores; this method depends on reducing the noise from the GEI effects. Since IPCA1 score is double to IPCA score to GEI sum of square, therefore it has to be weighted by the proportional difference between IPCA1 and IPCA2 scores to compensate for the relative contribution of IPCA1 and IPCA2 total G×E sum of squares. The ASVs, IPCA 1 and IPCA 2 are presented in Table (9). The genotypes which have least ASV and IPCA1score are the most stable genotypes. The results in Table (9) reveled that G5 is the most stable genotype and on the contrary G7 is the most sensitive genotype across all environments. These results are in a line with Khare *et al.* (2024) and Taherian *et al.* 2024).

Table 9. Alvin II stability values (AS V) for the studied genotypes										
Rank	Genotype	Number	Mean	ASV	IPCAg1	IPCAg2				
1	G5	5	3.837	0.192	-0.08461	0.02288				
2	C	2	1 272	0 552	0.21440	0 26774				

10	G7	7	3.473	3.241	-1.43646	0.14013
9	G9	9	3.972	1.421	0.57859	0.56312
8	G6	6	4.420	1.316	0.50281	-0.66909
7	G10	10	3.717	0.940	0.25112	0.75004
6	G4	4	3.129	0.828	-0.36696	0.04464
5	G3	3	4.253	0.826	0.23917	-0.62582
4	G1	1	4.227	0.768	0.34046	0.02819
3	G8	8	4.123	0.749	-0.23862	-0.52182
2	G2	2	4.373	0.553	0.21449	0.26774

Where: AVS is AMMI stability values, IPCA 1 and IPCA 2 are the first and second principal component analysis

AMMI biplot

The origin of biplot represents the overall mean performance of grain yield for the studied genotypes across all environments. The position of a genotype or an environment relative to the origin gives some insight into GXE interaction. Where, the genotype which is located near to the origin that is broadly adapted. In contrast, the genotype which is located far from the origin is sensitive to environmental interaction means that is specifically adapted. Similarly, the environment located near to the origin with a short vector has a weak interactive forces and the environment located far from the origin with long vector has a strong interactive forces. In light of the above, the AMMI biplot (Figure 2) showed that G 5 is the most adapted genotypes overall environments while G7, G9, and G10 are the most sensitive genotypes overall environments. The results showed that G 8 is the best performing genotype in GZ2 while G3 is the best performing in SD2 in addition G2 is the best performing in SH2 & SK3 & GZ3. In regard to environments, the most interactive environments are ML2 and SD2 and the least interactive environments are GZ1 and SH1, this is clear by the long and short vector, respectively. These results are in harmony with those obtained by Verma and singh (2021), Timalsina et al. (2023), Chaudhary et al. (2023), Khare et al. (2024) and Taherian et al. (2024).





AMMI biplot gives the behavior of genotypes across the environments as well as effect of the environments on the genotypes; the genotypes cluster together behave similarly across the environments and the environments cluster together influence genotypes in a similar way. The results revealed (Figure 2) indicated that G2 and G4 behave similarly across environments. In case of environments influences on genotypes, the environments clustered into groups as follow; (ML1 & SK2), (SD1 & GZ2), (SK1 & SK3), (GZ1 & SH1), and (SH2 & SK3 & GZ3) each group influence on genotypes in a similar way. Moreover, the correlation between the environments can be extracted from AMMI where the angle between the environments vector determine the correlation between them. Where, cute, obtuse, zero, and right angles indicate a positive, a negative, a complete, and no correlation, respectively. The results (Figure 1) showed that a complete correlation was found only between SD1 and GZ2. A positive correlation was found between most of the environments *e.g.* (ML1 and SK2), (SD1 & GZ2), (SK1 & SK3), (GZ1 & SH1), (SH2 & SK3 & GZ3)etc. it was expected that the three growing season for the same location tend to cluster together "influence similarly on the studied genotypes" as one cluster or slightly deviate from the cluster but the figure (2) illustrated that they did not; this can be attributed to the drastic reflection in temperature from season to season which resulted from climate change. In light of the above, selecting superior broadly adapted genotype across the studied environments is G5 which is superior across all studied environments. These findings are in agreement with Verma and singh (2021), Khare et al. (2024) and Taherian et al.(2024).

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تأقلم عشرة تراكيب وراثيه من قمح الخبز تحت ظروف مصر العيا والوسطى والدلتا

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الملخص

إن التفاعل الوراثي البيئي هو مشكله جدية تواجهنا عند دراسة التجارب متعددة البيئت. لذلك يوجد الكثير من النماذج الإحصائية لدراسة التفاعل البيئي الوراثي ومن النماذج الهامه لدراسة التفاعل البيئي الوراثي نموذج MMIA(التأثيرات الرئيسية الإضافية والتفاعل المضاعف) . تمت هذه الدراسة في خمس مواقع هي محطات البحوث الزراعية بسخا، الجيزة، سدس، ملوى وشندويل لتقييم عشرة تراكيب وراثيه خلال المواسم الزراعية من 21/2020 الى 23/2022. بحثيه أظهرت النتائج وجود اختلافات معنوية بين المواسم الزراعية، المواقع، التراكيب الوراثية، والتفاعلات فيما بينهم في كل الصفات عدا صفة طول النبات (المواسم)، عد ايام التزهير (تفاعل المواسم مع المواقع، التراكيب التراكيب الوراثية). أظهرت النتائج أن المكون الأول و الثاني النبائي الوراثي 1 APP و APP يساهمان بنسبة 60.00 و « التراكيب الوراثية). أظهرت النتائج أن المكون الأول و الثاني التفاعل البيئي الوراثي 1 APP و APP البعن البيئي عنه مع المواقع مع الوراثي. قد تم استخدام المكونين في تكوين نموذج الالموالي التفاعل البيئي الوراثي 1 APP و APP المعان بنسبة 60.00 و الوراثي. قد تم استخدام المكونين في تكوين نموذج المقال التفاعل البيئي الوراثي 10 APP و APP المحان بنسبة 64.00 % بلجمالي 66.40 % من تباين التفاعل البيئي وراثقاعل أوراثي معند منه من المول و الثاني التفاعل البيئي الوراثي 10 APP و APP المحناعف): فات المحاور الثمانية و الوراثي قد تم استخدام المكونين في تكوين نموذج العرالة المنا المينية و التفاعل الميني و التفائية و التفائية و الذي أوراثي مع 5 هو الاكثر شبتا وتألما وأن التركيب الوراثي رقم 7 هو الاكثر حسابير وتتراع المينية و التفاعل المعناعف البيئة تحت الدراسة.