# **Journal of Plant Production**

Journal homepage & Available online at: www.jpp.journals.ekb.eg

# Stability Analysis for some Agronomic and Quality Characters of New Bread Wheat Genotypes under Multi Environmental Trials in Egypt

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## ABSTRACT



Trials conducted across multiple environments are critical for characterizing the ideal cultivar for diverse locations. This study aimed to assess the stability of twelve new bread wheat genotypes using certain agronomic and qualitative characteristics in four different agro-climate conditions in Egypt (Sakha, Nubaria, Sids and Shandaweel) in 2022/23 and 2023/24 seasons. To achieve these goals, AMMI, GGE and Eberhart and Russel methods were used. Environments, genotypes, their interaction and interaction principal component axis IPCA1 and IPCA2 showed significant mean squares for all the studied characters. The studied genotypes G7, Misr 3 and Sakha 95 combined stability using AMMI, GGE and Eberhart and Russel methods and the high grain yield. In addition, the genotype G9 showed the same trend for wet and dry gluten contents and protein content. Also, the genotype G2 was the highest one for grain yield as mean across the studied environments but did not show stability using the used methods.

Keywords: Stability, AMMI, GGE, Agronomic traits, Quality traits.

## INTRODUCTION

Wheat (Triticum *spp.*) plays a peppy role in enhancing food security and nutrition in Egypt and globally, making it a crucial crop for human civilization. Wheat participates around twenty percent of the total alimentary calories and plant proteins globally (Shiferaw *et al.*, 2013). Common wheat is a versatile cereal, cultivated in diverse climatic zones, including hot, dry, cool, and humid environments (Zaïm *et al.*, 2017). The ability of wheat to thrive in various climates is largely genetically determined, but its actual performance is influenced by its interaction with the environment. Egypt spans from 22° N to 32° N latitude. The primary ecological characteristics of Egypt include wheat production regions concentrated in the Nile Valley and delta, which are characterized by clay loam soil, while most of the region is dominated by desert (Asseng *et al.*, 2018).

The goal of plant breeding program is to identify and cultivate a stable genotype adapted to a particular region (Yan, 2019). Genetic improvements for grain yield and quality are intended to suit the target environment, as they are crucial for breeding new varieties while ensuring food security (Braun *et al.*, 2010 and Fischer *et al.*, 2014). Several studies have compared the stability of old varieties with new and promising genotypes (Curin *et al.*, 2021 and Bosi *et al.*, 2022). These studies aimed to show the progress of breeding and the need for a changing environment for variety (Hanif *et al.*, 2022 and Pour-Aboughadareh *et al.*, 2022). The assessment of variety stability has traditionally focused on the impact of the environment on not only yield but also numerous quantitative traits (Öztürk and Korkut, 2020 and Curin *et al.*, 2021) and qualitative parameters (Živančev *et al.*, 2021).

The process of quality selection is laborious, costly, and time-intensive, leading to a slow and protracted quality selection process. The primary challenges in enhancing physiologically complex attributes are the substantial impact of the environment and the scarcity of stable donors with high trait value (Krishnappa *et al.*, 2019).

Univariate linear regression models (Eberhart and Russell, 1966) and multivariate models of additive main effects and multiplicative interactions (AMMI) (Zobel et al., 1988) and genotype  $\times$  genotype-environment (GGE) interaction (Yan et al., 2001) were used to study and interpret the  $G \times E$  interaction. The (AMMI) model is a vastly used statistical method and helps to understand the interactions among environments and different genotypes (Gauch, 1992). Gauch (2013) outlined the AMMI procedure in four stages: (i) analysis of variance, (ii) model diagnosis, (iii) identification of the mega-environment, and, (iv) agricultural recommendations. Genotypic main effect and, GE interaction (GGE biplot) analysis, utilized by plant breeders, has undergone significant enhancements for the analysis of multienvironment test (MET) data (Yan et al., 2007). Recent literature reviews indicate efforts to disentangle the effects of GHG on the agronomic and quality traits of wheat and many other crops using advanced multivariate statistical methods (Yan, 2016 and Yan and Frégeau-Reid, 2018).

This investigation aimed to assess the stability of twelve new bread wheat genotypes using different stability measures for certain agronomic and qualitative characteristics,

### MATERIALS AND METHODS Plant materials and experimental procedures

Twelve genotypes of bread wheat as shown in Table 1 were investigated in the study. Exotic materials obtained from CIMMYT (including several yield trials, such as the 30<sup>th</sup> ESWYT and 46<sup>th</sup> HTWYT) were surveyed during the

growing seasons from 2022 to 2024 to identify elite bread wheat genotypes. The decided elite genotypes, along with three newly released cultivars Misr 3, Sids 14, and Sakha 95 (used as checks), were included in the study.

 Table 1. Code, origin of the studied bread wheat genotypes

Code	Origin
G1	CIMMYT
G2	CIMMYT
G3	CIMMYT
G4	CIMMYT
G5	CIMMYT
G6	CIMMYT
G7	CIMMYT
G8	CIMMYT
G9	Egypt
G10	Egypt
G11	Egypt
G12	Egypt

The studied genotypes were assessed in four different Research Stations of Agricultural Research Center ARC, Egypt, Sakha, Nubaria, Sids and Shandaweel (Table 2) in the two growing seasons 2022/2023 and 2023/2024. The studied locations represent four different agro-climate conditions and represent most latitudes of Egypt (22°N - 32°N). Table 2 displays various soil kinds ranging from sandy soil to clay soil and calcareous sandy loam, as well as the altitude, which varies from 270 m in the South of Egypt to 6.5 m above sea level in North Egypt, and the temperature differences across the sites. The evaluated genotypes were assessed in each environment using a randomized complete block design (RCBD) with three replicates, in plots consisting of 6 rows, each 4 m long and 20 cm apart, with an area of 4.8 m<sup>2</sup>. The wheat was cultivated in each environment following the agricultural practices outlined by the Agricultural Research Center (ARC) and the Ministry of Agriculture and Land Reclamation of Egypt.

	Table 2.	The studied	locations and	their agro	o-climatic	conditions
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Environmont	Location	Growing	Latituda Langituda		Soil	Elevation	Tempera	Temperature ( <sup>0</sup> C)		
Environment	Location	season	Lautuue	Longitude	type	m	Min.	Max.	Ave.	
E1	Sakha	2022-2023	31° 5′ N	30° 56' E	Clay	6.5	17.84	23.42	20.6	
E2	Sakha	2023-2024	30° 38' N	30° 4' E	Calcareous sandy loam	11	17.45	23.19	20.7	
E3	Nubaria	2022-2023			-		13.45	23.68	18.56	
E4	Nubaria	2023-2024					13.09	22.98	17.36	
E5	Sids	2022-2023	28° 54' N	30° 56' E	Clay	31	10.65	25.14	17.36	
E6	Sids	2023-2024			-		10.72	25.11	17.34	
E7	Shandaweel	2022-2023	26° 33′ N	31° 42 ′ E	Clay	61	11.40	25.75	18.53	
E8	Shandaweel	2023-2024			-		11.52	26.00	18.76	

#### Studied traits

The studied traits were grouped into agronomic and quality traits. The agronomic characters were no. of kernels spike-1, no. of spikes m<sup>-2</sup>, 1000-kernel weight and grain yield plant<sup>-1</sup>. In addition, the quality characters were germination % (ISTA, 1999), wet and dry gluten % : (AACC, 10-38, Anonymous, 1983) and grain protein content (AOAC., 1990). **Statistical analyses** 

Homogeneity of variance was tested to determine whether individual experiments (RCBD) were included in identifying (GE) interaction using combined analysis. The traits under study were subjected to statistical analyses based on across different environmental repeated experiments interaction between genotypes and combinations. The environments (GEI) was analyzed by using additive main effects and multiplicative interaction (AMMI) (Gauch and Zobel, 1988; Gauch, 1988), which involved univariate ANOVA and multivariate principal component analysis (PCA) to partition the GE component, as outlined by Gauch (2013). Furthermore, AMMI Stability Value (ASV) proposed by (Purchase et al., 2000), was calculated to determine which genotypes exhibit stability across different environments. The obtained data were analyzed by GenStat Statistical Software 19th Edition. Graphical analyses for GGE biplot (genotype G + GEI) illustrated by (Yan et al. 2000 and 2001), were accomplished using GenStat 19th to establish genotype rankings based on both mean performance and stability, as well as to identify ideal genotypes across various environments. Parameters of stability givin by Eberhart and Russell (1966) were graphed utilizing META-R (Alvarado et al., 2020).

### **RESULTS AND DISCUSSION**

#### Results

#### **AMMI** analysis

Results in Table 3 showed AMMI analysis of variance for the studied characters. Environments, genotypes,

their interaction and interaction principal component axis IPCA1 and IPCA2 showed significant mean squares (P < 0.01) for all the studied characters. Environmental sum of squares contributed to the greatest variation percentage for all characters, except for wet and dry gluten to which genotypes contributed the greatest percentage. The combined analysis of variance showed that environments contributed 13.99% for dry gluten content to 87.15 % for no. of spikes m<sup>-2</sup>, while genotypes contributed 1.29 % for no. of spikes m<sup>-2</sup> to 59.49 % for dry gluten to the total sum of squares. In addition, GEI contributed to 7.07 % for no. of spikes m<sup>-2</sup> to 23.58% protein content to the total sum of squares of the studied characters.

IPCA1 showed the greatest percentage of the environmental genotypic interactions for all studied traits and share with 29.69 % for no. of kernels spike<sup>-1</sup> to 81.32 % for no. of spikes m<sup>-2</sup> of total GEI variation of the studied traits. In addition, the second interaction principal component axis (IPCA2) accounted for 8.34 % for no. of spikes m<sup>-2</sup> to 31.5 % for protein content of the sums of squares for studied traits of the total GEI variation.

The preferred environment (Al-Naggar *et al.* 2018) and genotype located on the central circle (Figure 1). Thus, Figure 1 illustrates the comparison plot for genotypes, with a model genotype positioned near or at the center of the central circle. Consequently, the most optimal genotypes with high stability and high mean for the agronomic characters G5 for no. of spikes m<sup>2</sup>, G2, G11 and G4 for no. of kernels spike<sup>-1</sup>, G7, G3, G10, G1, G4 and G5 for 1000-kernel weight and G9, G5, G7, G10, G1 and G12 for grain yield m<sup>-2</sup>. The perfect genotypes which gave high mean and high stability for the quality characters were G4, G11 and G2 for germination, G4, G2, G11 and G7 for protein content, G6 for wet gluten, G5 and G11 for dry gluten. Thus, G5 and G10 (Misr 3) were the most stable genotypes for most agronomic characters, while G4 and G11(Sids 14) were the most stable genotypes for quality characters.

#### J. of Plant Production, Mansoura Univ., Vol. 15 (12), December, 2024

Table 3. AMMI analysis of variance for the studied characters of the studied wheat genotypes across 8 environments

Source	DE	No. of spikes m <sup>-2</sup>		No. of kernels spike <sup>-1</sup>		1000-kernel weight		Grain yield g m <sup>-2</sup>	
Source	Dr -	MS*	SS%	MS*	SS%	MS*	SS%	MS*	SS%
Genotypes (G)	11	10859**	1.29	142.2**	3.01	247.3**	19.70	34715**	4.46
Environments(E)	7	1153891**	87.15	5136.8**	69.27	1016**	51.50	794396**	64.91
Block	16	4005*	0.69	100.1**	3.08	8.4	0.97	21068**	3.93
Interactions (GE)	77	8510**	7.07	69.4**	10.29	27.4**	15.26	18072**	16.24
IPCA 1	17	31346**	81.32	93.3**	29.69	57.8**	46.65	31714**	38.75
IPCA 2	15	3642*	8.34	94.6**	26.56	38.2**	27.20	26524**	28.59
Residuals	45	1505	10.34	51.9	43.75	12.2	26.10	10100**	32.66
Error	176	2002.00	3.80	42.30	14.34	9.90	12.57	5092.00	10.46

Table 3. Cont.									
Courses	DE	DE Germination %		Protein content %		Wet gluten content %		Dry gluten content %	
Source	Dr -	MS*	SS%	MS*	SS%	MS*	SS%	MS*	SS%
Genotypes (G)	11	447.5**	14.24	0.33**	3.29	367.97**	58.62	84.28**	59.49
Environments(E)	7	1905.1**	38.59	8.08**	51.73	146.1**	14.82	31.14**	13.99
Block	16	64.7	3.00	0.12	1.72	4.26	0.98	1.79**	1.84
Interactions (GE)	77	99.9**	22.26	0.34**	23.58	16.44**	18.33	3.25**	16.04
IPCA 1	17	208**	45.96	0.86**	56.52	53.02**	71.17	10.82**	73.56
IPCA 2	15	159.1**	31.02	0.54**	31.50	14.91**	17.69	2.8**	16.80
Residuals	45	39.4	23.02	0.07	11.99	3.13	11.14	0.54	9.64
Error	176	43.00	21.91	0.12	19.67	2.84	7.24	0.77	8.64

\* and \*\* significant at 0.05 and 0.01 respectively.



Figure 1. AMMI biplot presenting the studied agronomic and quality characters for 12 bread wheat genotypes. E1 = Sakha in 2022/23, E2 = Sakha in 2023/24, E3 = nubaria in 2022/23. E4 = Salha in 2023/24, E5 = Sids in 2022/23, E6 = Sids in 2023/24, E7 = shandaweel in 2022/23 and E8 = Shandaweel in 2023/24. G1 - G9 = Line 1 - 9, G10 = Misr 3, G11 = Sids 14 and G12 = Sakha 95. X = genotype scores, + = environment scores and — (blue) = vectors

The analysis of AMMI stability values (ASV) revealed that certain bread wheat genotypes exhibit high adaptation, while most genotypes demonstrate specific adaptability (Table 4). The ASV values showed variations in the studied agronomic and quality characters among the twelve studied bread wheat (Table 4). In line with Purchase *et al.* (2000), for the stable genotype, its AMMI stability values (ASV) are near to zero. A higher ASV value, whether negative or positive, indicates a more specific adaptation of a genotype to environments. A lower ASV value suggested greater stability of a genotype across different environments (Purchase 1997). Consequently, the most stable genotypes for

the agronomic characters were G5 for no. of spikes m<sup>2</sup>, G2, G11 and G3 for no. of kernels spike<sup>-1</sup>, G7 and G3for 1000kernel weight and G9 and G5 for grain yield m<sup>-2</sup>. The optimal genotypes with high stability and high mean for the quality characters were G2 and G5 for germination, G4 for protein content, G6 and G8 for wet gluten and G5, G11 and G3 for dry gluten.

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For mean performance of no of spikes., G1 showed the lowest mean (389), while G8 exhibited the highest one (455.9). for no of kernels/spike, the lowest value was (44.07) for G1 and the maximal value was (56.93) for G3. The lowest and highest values for grain yield were 659.9g and 778.49g

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for G5 and G2, respectively.G7 gave the lowest germination percent (91.46%). For protein content, all genotypes showed close values, and the highest one was 12.64 for G8. G9

exhibited the highest values for both wet and dry gluten contents (34.25 and 14.93, respectively).

fable 4. Means and AMMI stabili	y value	(ASV) of	f 12 genoty	pes for t	he studied	characters.
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Canatama	No. of Spikes m <sup>-2</sup>		No. of kern	els spike <sup>-1</sup>	1000-kernel weight		Grain Yield g m <sup>-2</sup>	
Genotype —	Mean	ASV	Mean	ASV	Mean	ASV	Mean	ASV
G1	389.00	119.12	49.07	1.32	56.46	1.25	705.80	5.82
G2	424.00	54.22	55.90	0.26	53.01	5.18	778.40	15.13
G3	393.80	23.85	56.93	2.91	53.48	0.65	733.50	13.91
G4	448.40	83.93	52.09	0.90	49.51	2.04	733.80	9.06
G5	403.30	11.48	55.20	2.00	51.72	2.21	659.90	3.51
G6	433.60	56.00	56.05	1.90	52.36	3.20	695.10	15.11
G7	432.90	20.56	55.13	2.96	46.07	0.47	766.00	6.72
G8	455.90	93.29	51.05	1.15	52.41	2.66	748.20	10.38
G9	398.30	45.87	52.12	3.11	50.71	2.49	710.40	2.39
G10 (Misr 3)	428.20	15.59	51.81	2.42	48.08	1.19	771.00	7.87
G11 (Sids 14)	415.20	19.35	53.26	0.75	48.10	1.29	696.90	9.93
G12 (Šakha 95)	414.90	19.34	51.67	2.37	45.80	1.52	775.30	6.69

Table 4. Cont.

Construes	Germination %		Protei	Protein content %		ntent %	Dry gluten content %		
Genotype –	Mean	ASV	Mean	ASV	Mean	ASV	Mean	ASV	
Gl	78.50	4.08	12.47	1.08	27.16	4.73	11.94	5.02	
G2	82.12	1.03	12.45	0.18	25.73	2.46	10.62	1.95	
G3	81.17	2.07	12.16	1.59	26.02	1.52	10.25	0.58	
G4	85.00	0.96	12.45	0.16	31.33	9.88	13.57	4.44	
G5	86.38	1.36	12.34	0.27	23.81	6.55	9.48	0.23	
G6	86.96	3.64	12.35	1.01	24.29	0.78	8.95	2.14	
G7	78.12	2.30	12.42	0.38	23.46	6.05	9.55	4.37	
G8	87.83	5.48	12.64	1.10	25.73	0.96	11.13	3.01	
G9	88.25	3.45	12.51	1.01	34.25	1.47	14.93	5.11	
G10(Misr 3)	91.46	1.83	12.42	0.49	34.16	7.16	12.75	3.17	
G11(Sids 14)	89.71	1.64	12.52	0.21	26.14	3.04	10.00	0.47	
G12 (Sakha 95)	87.25	3.50	12.45	1.11	23.64	4.27	9.47	5.98	

#### GGE biplot analysis

The GGE biplot results (Figure 2) illustrates the mode of mean performance and stability, as stable genotypes exhibited a short rating on the line with an arrow, surpassing the other line (overall mean).



Figure 2. GGE biplot presenting the studied agronomic and quality characters for 12 bread wheat genotypes. E1 = Sakha in 2022/23, E2 = Sakha in 2023/24, E3 = nubaria in 2022/23. E4 = Salha in 2023/24, E5 = Sids in 2022/23, E6 = Sids in 2023/24, E7 = shandaweel in 2022/23 and E8 = Shandaweel in 2023/24. G1 - G9 = Line 1 - 9, G10 = Misr 3, G11 = Sids 14 and G12 = Sakha 95. X = genotype scores, + = environment scores and — (blue) = vectors

The high estimates and stability of the studied genotypes for agronomic characters were detected by G8 for no. of spikes m<sup>-2</sup>, G2 and G5 for no. of kernels spike<sup>-1</sup>, G1 and G3 for 1000-kernel weight and G7, G10, and G12 for grain yield m<sup>-2</sup>. The highest genotypes with high stability for the quality characters were G10 for germination, G8, G2 and G12 for protein content, G9 and G10 for wet gluten, G9 and G4 for dry gluten.

#### Eberhart and Russell's stability analysis

The regression coefficient (bi) and deviation from the regression  $S^2$ di estimates for the traits under investigation were graphed for the genotypes under examination in Figure 3. The analysis identified adaptable genotypes, G7 for no. of spikes m<sup>-2</sup>, G1 and G5 for 1000-kernel weight, G5 and G7 for germination, G2 for protein content, G3 and G8 for wet gluten and G7, G8 and G9 for dry gluten. Moreover, genotypes G1 for 1000-kernel weight and G4 for germination were the most stable.



Figure 3. Yield stability for the studied agronomic and quality characters among 12 bread wheat genotypes plotted from Eberhart and Russell joint regression coefficients. bi = regression coefficient and S2di = deviation from regression. G1 - G9 = Line 1 - 9, G10 = Misr 3, G11 = Sids 14 and G12 = Sakha 95. X = genotype scores. Genotypes with black are not significant, with red are adaptible with blue are stable and with green are adaptible and stable.

#### Discussion

Environmental factors represent a big challenge for wheat breeders to develop a new cultivar, consequently multi environments trails are necessary to attain this goal (Yan, 2014). Consequently, breeders use AMMI, GGE and Eberhart and Russel methods. AMMI separate GE from PCA1 to PCA<sub>n</sub> and shows it in ANOVA table, but GGE estimates the PCA from G + GE the source of variation for the investigated trait for visually demonstrating (Yan *et al.*, 2007 and Yan, 2019). These analyses are purposed on evaluation of the studied genotypes (Gauch, 2013 and Yan, 2015) using G and GE components (Gauch, 2013).

The significant  $G \times E$  impacts as shown in Table 3 denote that the genotypes did not gave the same performance over the studied environments (Zaïm et al., 2017 and Thungo et al., 2020). In addition, studying the variation between different genotypes and environments allowed for an examination of the nature and extent of  $G \times E$ , which cannot be fully captured by a standard joint analysis of variance. (Purchase et al., 2000, Gauch, 2013 and Horn et al., 2018). Commonly, the main results of AMMI multivariate ANOVA followed a similar trend to previous studies. The main effects of the environment on wheat data, which elucidate the impact of environmental factors on wheat, accounted for a significant portion of the total variation, reaching 81% (Kaya et al., 2006), 84% (Mohammadi et al. 2018) and 85% (Mohammadi et al. 2021). In addition, Darwish et al. (2022) found that the three components had the same trend, especially, genotypes variation percent and were 1.0% and 2.2%, but GE interaction contributed 9.5 %, respectively. In this respect, Ahmed et al. (2020) reported that (PC1, PC2 and PC3) were highly significant for 1000 kernels weight and AMMI1 was only significant in case of grain yield. The AMMI stability value distinguished genotypes G3, G7, G9, G12, and G14. Additionally, G3 exhibited the most promising stability and adaptation in terms of grain yield performance in different environments.

The agronomic and quality characters are a form of multi-locations, multi-years, and several genotypes' trials (Yan, 2015 and 2016). The variety's high stability was particularly valuable when linked solely to high average productivity (Yan, 2021). The high estimates of agronomic and quality traits, along with the ability to maintain increased values across diverse environments, suggest that the cultivar is well-suited for continued growth in various agro-climatic regions. Consequently, the genotypes G7, G10 and G12 combined between the stability using AMMI, GGE and Eberhart and Russel methods and the high grain yield. In addition, the genotype G9 showed the same trend for protein content and wet and dry gluten contents whereas, the genotype G2 was the highest one for grain yield as mean across the studied environments, but did not show stability using the used methods. These findings are in line with those obtained by Mohammadi et al. (2018) and Abraha et al. (2019). In addition, Powell et al. (2013) and Sharma and Duveiller (2003) indicated the potential for selecting wheat genotypes with a blend of high yield and superior kernel quality traits.

Khazratkulova *et al.* (2015), Saleem *et al.* (2015), and Krishnappa *et al.* (2019) have highlighted that the environmental component contributes significantly to the total variance, with the environmental effect being more pronounced than the genotypic effect and GEI.

Consistent with the findings of Darwish *et al.* (2022), Sakha 95 (which exhibited stability and high yield performance in another multi-environment trial), Misr 3, and Sids 14 are currently widely cultivated cultivars and account for the majority of bread wheat production in Egypt.

#### CONCLUSION

The AMMI, GGE biplot and Eberhart and Russel findings indicated that certain genotypes exhibit broad and limited adaptability to different environments. Seasons, genotype and season  $\times$  genotype interaction contributed to variation in the studied agronomic and quality traits. Genotypes G7 and G9 in addition to the two cultivar checks Misr 3 (G10), Sids 14 (G11) and Sakha 95 (G12) were identified as the entries with high agronomic and quality estimates.

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# تحليل الثبات لتراكيب وراثية جديدة من قمح الخبز لصفات الجودة والمحصول تحت ظروف بيئية مختلفة في مصر محمد عدالكريم حسن درويش1، احمد على زين العابدين1، محمد مصطفى محمد يسن1، الحسين غلاب جلال احمد1، بسمة السيد السماحي2

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تحد التجلرب التي تجري في بيئك متحدة حلسمة التعرف علي الصنف المثلي للمواقع المختلفة. وتهدف هذه الدراسة لتقييم الثبك الوراثي لإنتي عشر تركيب وراثي من قمح الخبز بابستخدام الصفات المحصولية وصفات الجودة تحت أربعة ظروف مناخية مختلفة في جمهورية مصر العربية خلال موسمي 2023/2023 و 2024/2023. ولتحقق هذه الأهداف تم استخدام تحليل AMMI GGE , Eberhart and Russell , وكن هنك اختلافت معنوية في جميع الصفات المدروسة ترجع إلى تأثير كل من البيئك والتراكي الوراثي لإنتى عشر تركيب وراثي من قمح الخبز بابستخدام التراكيب الوراثية GGE , Eberhart and Russell , وكن هنك اختلافت معنوية في جميع الصفات المدروسة ترجع إلى تأثير كل من البيئك والتراكيب الوراثية والتفاعل بينهما و IPCAI , IPCA2 , و2021 و GGE , Eberhart and Russell , التراكيب الوراثية GI, Misr3, Sakha95 بينا البكت الوراثي والمحصول العلي باستخدام تحليل GGE المعاد ما Russell , GGE الفراغية والتفاعل بينهما و GGE ، و2021 و Gu الشراكيب الوراثية G1, Misr3, Sakha95 بينا وراثي والمحصول العلي باستخدام تحليل GGE المتوسط البيئات والتراكيب الوراثية والتفاعل بينهما و GGE ، و2021 و GL