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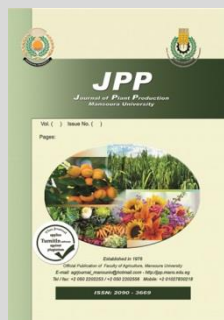
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Performance and Stability of some Bread Wheat Genotypes across Terminal Water and Heat Stresses Combinations Using Biplot Techniques

Feltaous, Y. M.* and Y. S. I. Koubisy



Wheat Research department-Field Crop Research Institute- Agricultural Research Center



ABSTRACT

The current study was conducted at Shandaweel Agric. Res. Stat., Agric. Res. Center, Egypt. Eighteen bread wheat genotypes were grown under four treatments during 2018/19 and 2019/20 seasons. The treatments were (1) normal conditions (sowing on 25th November and 5 irrigations). (2) Terminal water stress conditions (sowing on 25th November and 3 irrigations). (3) Terminal heat stress conditions (sowing on 25th December and 4 irrigations). (4) Combined stresses (sowing on 25th December and 3 irrigations). The combined analysis of variance showed significant differences between the genotypes, treatment, seasons for all the studied traits. The mean performance of the genotypes showed that L11 was the highest grain yield and grain filling rate under normal, water stress, heat stress, combined stresses as well as overall treatments. Genotype by genotype-environment biplot (GGE biplot) illustrated that the best performing genotype under normal conditions was Baj 1 while Shandaweel 1 was the best performing genotype under stress combinations. Genotype x trait biplot (GT biplot) showed a positive correlation between all the traits except, days to heading and days to maturity. Genotype by yield*trait biplot (GY*T biplot) was constructed to estimate superiority and stability for the genotypes. GY*T biplot showed a positive correlation between all yield*trait combinations. Based on superiority index (SI), the best performing genotypes was L11 (SI = 1.830) and the worst was L7 (SI = 1.935). L11 genotype can be utilized in breeding program as a source for abiotic stresses tolerance or can be evaluated in preliminary yield trials at the national level.

Keywords: wheat genotypes, GE interaction, GT biplot, yield, superiority, stability

INTRODUCTION

Wheat as a staple food crop takes a big consideration for its importance in sustainable food security. It cultivated over a wide area all over the world; its cultivated area was 214 million hectares produced 734.05 million metric tons (FAO 2018), while its cultivated area and total production in Egypt were 3.17 million feddan and 8.5 million metric tons, respectively in 2020 (Economic Affairs 2020). A similar situation in Egypt but it is more drastic where Egypt is an overpopulated country and is not wheat self-sufficient country. The gap between production and consumption is filled by imports where Egypt considers as largest wheat importer.

Drought and heat stresses are the most limitation factors threatening wheat production, especially when it occurs at reproductive stages known as terminal or end-season drought and heat stresses. They have a direct impact on photosynthesis and respiration therefore disrupts the metabolic pathways causing irreversible injuries which in turn result in drastic reduction in yield (Gol *et al.*, 2017). Water deficit and elevated temperature elicit stress responses which are different for tolerant and sensitive genotypes. It is advisable to measure other related traits to ensure that the traits of interest are not confound by another trait (Lopes *et al.*, 2012). Heat stress is a serious constraint for wheat production results from a rise in temperature beyond the optimal temperature for physiological processes during the growth stages. Heat stress may occur at any growth stage *i.e.* early-season heat stress and end-season or terminal heat stress. Terminal drought and heat stresses are more aggressive than vegetative drought and heat stresses because they occur at critical growth stages of plant lifetime *i.e.* reproductive and grain development stages. Both of them affect

on grain size, grain number/spike, and 1000-grain weight, and grain filling rate. Consequently result in a substantial reduction in wheat grain yield up to 42% under drought conditions as reported by Mehraban *et al.* (2019) and 48% reduction under terminal heat stress as reported by Abro *et al.* (2019).

Drought and heat stresses impact on source-sink relationship by altering partitioning, accumulation, and distribution assimilates. It was reported that drought and heat stress are linked; drought detrimental effects were more aggressive when it was combined with high temperature than when it was not (Urban *et al.*, 2018). Accordingly, combined drought and heat stresses have to be considered together. Due to their drastic effects of terminal heat and drought stresses either independently or combined. Therefore, wheat breeders are looking forward to develop new stable cultivar with physiological, morphological, molecular traits unique to heat and drought tolerance without yield penalty.

The most obstacle faces genotypes evaluation is interfering the genotype main effect (G) and genotype by environments interaction (G x E). Multi environments trials (MET) is helpful in estimating G x E interaction and accordingly selecting the most stable genotype/s with lowest G x E interaction. The ANOVA technique is not of much useful in varietal selection because it does not consider the positivity and negativity of factors. Biplot techniques represent a powerful, effective, informative, and meaningful graph for breeder in making decisions and recommendations (Yan *et al.*, 2007).

The objectives of this study were: 1) Determining how the studied wheat genotypes will respond under heat, drought, and combined stresses relative to normal conditions. 2) Examining G x E interaction between the studied wheat

* Corresponding author.
E-mail address: Feltaous80@yahoo.com
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genotypes under combination of drought and heat stresses using several biplot techniques. 3) Point out the most stable and high yielding wheat genotype/s based on yield or yield*trait combinations overall stress environments.

MATERIALS AND METHODS

Plant material

The current study was undertaken at Shandaweel Agric. Res. Sat., Agric. Res. Center during 2018/2019 and

2019/2020 winter growing seasons. The study included 18 bread wheat genotypes (Table 1); Shandaweel 1 “high yielding and local check”, Sokoll “drought and heat tolerant variety”, Baj 1 (heat tolerant variety), Borlaug 100 “high yielding variety” plus 14 advanced lines were selected from CIMMYT materials viz 7th stress adaptive traits yield nurseries “7th SATYN 2017/2018”.

Table 1. The genotypes under investigation, source, pedigree, and their origin

Code	Source	Pedigree	Origin
L1	line# 2 7 th SATYN	CHEN/AE.SQ//2*WEAVER/3/BAV92/4/JARU/5/OLI2/SALMEJA/6/CROC1/AE.SQUARR OSA(205)//BORL95/3/PRL/SARA//TSI/VEE#5/4/FRET2 PTSA08M00026T-050Y-050ZTM-050Y-8ZTM-010Y-0B-OSH	CIMMYT
L2	line# 3 7 th SATYN	SOKOLL/3/PASTOR//HXL7573/2*BAU/4/ASTREB PTSA08M00047S-050ZTM-050Y-36ZTM-010Y-0B	CIMMYT
L3	line# 4 7 th SATYN	SOKOLL/3/PASTOR//HXL7573/2*BAU/5/CROC_1/AE.SQUARROSA(205)//BORL95/3/P RL/SARA//TSI/VEE#5/4/FRET2 PTSA08M00052S-050ZTM-050Y-31ZTM-010Y-0B-OSH	CIMMYT
L4	line# 5 7 th SATYN	SOKOLL/3/PASTOR//HXL7573/2*BAU/4/SOKOLL/WBLL1 PTSA08M00053S-050ZTM-050Y-50ZTM-010Y-0B-OSH	CIMMYT
L5	line# 6 7 th SATYN	CROC_1/AE.SQUARROSA(256)/4/PASTOR//HXL7573/2*BAU/3/WBLL1/5/BABAX/LR 42//BABAX/3/ER2000 PTSS12SHB00050T-0TOPB-099Y-099B-3Y-020Y-0B-OSH	CIMMYT
L6	line# 9 7 th SATYN	IWA8612949/3/2*ATTILA*2/PBW65//MURGA PTSS13Y00137T-099B-099Y-59B-020Y-0B-OSH	CIMMYT
L7	line# 10 7 th SATYN	IRAN-880/3/2*ATTILA*2/PBW65//MURGA PTSS13Y00139T-099B-099Y-5B-020Y-0B	CIMMYT
L8	line# 12 7 th SATYN	IRAN-880/3/2*ATTILA*2/PBW65//MURGA PTSS13Y00139T-099B-099Y-19B-020Y-0B-OSH	CIMMYT
L9	line# 14 7 th SATYN	SOKOLL/WBLL1/4/PASTOR//HXL7573/2*BAU/3/WBLL1 PTSS11Y00144S-0SHB-099SHB-099Y-099B-099Y-19Y-020Y-0B-OSH	CIMMYT
L10	line# 17 7 th SATYN	CHEN/AE.SQ//2*OPATA/3/FINSI/5/W15.92/4/PASTOR//HXL7573/2*BAU/3/WBLL1 PTSS11Y00152S-0SHB-099B-099Y-099B-099Y-5Y-020Y-0B-OSH	CIMMYT
L11	line# 22 7 th SATYN	Waxing*2/vivisti CGSS01B00056T-099Y-099M-099M-099Y-099M-14Y-0B-OSH	CIMMYT
L12	line# 23 7 th SATYN	KACHU #1 CMSS97M03912T-040Y-020Y-030M-020Y-040M-4Y-2M-0Y-0SH	CIMMYT
L13	line# 24 7 th SATYN	SOKOLL/WBLL1 PTSS02Y00021S-099B-099Y-030ZTM-040SY-040M-31Y-0M-0SY-0B-0Y-0SH	CIMMYT
L14	line# 25 7 th SATYN	BAV92/SERI CMSS96Y04084S-0Y-1B-93TLA-0B-0Y-106B-0Y-0Y-0Y-0Y-0SH	CIMMYT
Sh1	Shandaweel 1	Site / Mo / 4/ Nac / Th. Ac //3* Pvn /3/ Mirlo / Buc CMSS93 B00S 67S -72Y - 010M - 010Y - 010M - 3Y - 0M - 0THY - 0SH	Egypt
Sok	Sokoll	Pastor/3/altar84/Ae.SQ(TR.TA)//OPTAM85 CMSS97M00316S-0P20M-0P20Y-43M-010Y-0SH	CIMMYT
Baj	Baj 1	Waxing/4/sni/Trap#1/3/Kauz+2/Trap/Kauz CGSS01Y00134S-099Y-099M-099M-13Y-0B-0SH	India
Bor	Borlaug 100	ROLF07/4/BOW/NKT/CBRD/5/FRET2/TUKURO/FRET2 CMSS06Y00605T-099TOPM-099Y-099ZTM-099Y-099M-11WGY-0B-0MEX-0SH	CIMMYT

Experimental set-up:

The studied wheat genotypes were grown for two seasons under the following conditions:

- **Normal conditions (T1):** recommended sowing date (25th November) and irrigation (five irrigations plus planting irrigation).
- **Water stress (T2):** recommended sowing date (25th November) and water deficit after heading (three irrigations plus planting irrigation).
- **Heat stress (T3):** late sowing date (25th December) and normal irrigation (four irrigations plus planting irrigation).
- **Combined stresses (T4):** late sowing date (25th December) and water defect after heading (two irrigations plus planting irrigation).

The study comprised of the above treatments during the two seasons counting eight environments; each treatment

joined with season number produced an environment as follow i.e. T1S1, T2S1, T3S1, T4S1, T1S1, T2S2, T3S2, and T4S2. The experiments were laid in randomized complete block design “RCBD” with three replications for each experiment.

The plot and harvested area was 4.2 m² and consisted of 6 rows with 3.5 m long spaced by 20 cm. The herein measured traits were: days to heading (DH), days to maturity (DM), grain filling rate (GFR) in g/day, plant height (PLH) in cm, number of spikes/m² (S/M²), thousand kernels weight (TKW) in g, number of kernels/spike (K/S), and grain yield/plot in kg.

Meteorological conditions

Sohag Governorate classified as a hot desert (BWh) because it has a wide difference of temperatures between days and nights according to Koppen-Geiger climate classification system (Kottek *et al.*, 2006). Figer 1 showed the maximum and minimum temperature during grain filling

development and reproductive stages *i.e.* from March to mid of May for 2018/2019 and 2019/2020 seasons.

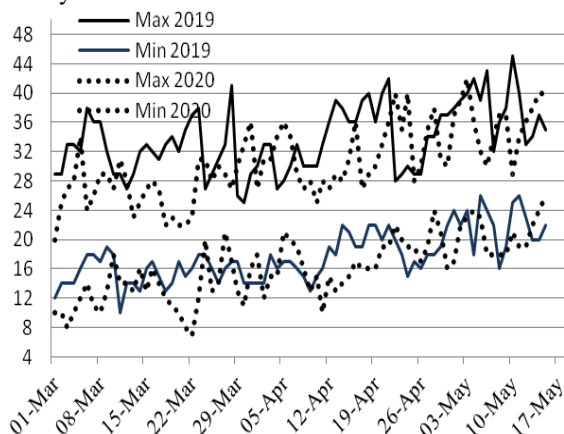


Figure 1. Maximum and minimum temperature degrees during grain filling stage 2018/19 and 2019/20 seasons

Statistical analysis

Different statistical softwares were used in calculations and statistical analysis. Single as well as combined analysis of variance (ANOVA) were performed according to Gomez and Gomez (1984) using SAS V9.3 (2011).

Genotype by genotype-environment biplot (GGE biplot) technique was performed according to Yan and Tinker (2006). Genotype by trait biplot (GT biplot) was constructed as suggested by Yan *et al.* (2000). Genotype x yield*trait biplot (GYT biplot) was performed according to the procedure of Yan and Fregeau (2018). Superiority index (SI) for all genotype x yield*trait combinations was calculated based on the standardized genotype x yield*trait combination according to Yan and Fregeau (2018). All biplot techniques and data visualization were performed using GenStat 19th Ed. statistical software.

RESULTS AND DISCUSSION

Analysis of variance

The analysis of variance for each experiment was performed independently. Before combining the data, Bartlett's test was used to determine the homogeneity of variances between experiments to determine the validity of the combined ANOVA. The results of the combined analysis of variance showed significant or highly significant differences between genotypes, treatments, and seasons. All interactions were significant or highly significant, except treatment x season interaction for days to heading, plant height, thousand kernels weight, and number of kernels/spike. Mean squares and coefficient of variation (%) for the studied traits are presented in table 2.

Table 2. Combined analysis of variance for the studied wheat genotypes under normal conditions and stress combinations.

S.O.V	D.F	Mean squares							
		DH	DM	GFR	PLH	S/M2	TKW	K/S	GY
Seasons (S)	1	1309.1**	1144.0**	1617.1**	4800.0**	2740.7*	8.4	274.7**	1.73**
Y/Rep	4	16.7	5.4	62.4	3.7	591.2	2.6	8.9	0.01
Treat. (T)	3	10904.5**	25374.3**	3362.5**	14550.7**	184700.6**	3234.9**	3112.1**	36.42**
T x S	3	48.2**	7.9	118.9*	27.2	4155.3**	3.1	7.2	0.53**
Genotype (G)	17	203.4**	80.5**	2299.2**	1016.8**	19536.1**	91.6**	95.2**	2.57**
G x S	17	78.4**	50.1**	380.8**	206.9**	3127.8**	13.3**	26.7**	0.40**
G x T	51	43.1**	39.5**	210.2**	63.1**	1300.9**	18.7**	17.1**	0.29**
G x T x S	51	31.2**	28.3**	166.2**	52.9**	1550.3**	12.1**	9.7**	0.17**
Error	284	11.1	9.5	52.1	12.6	533.3	4.7	4.3	0.04
C.V.	---	3.6	2.4	12.5	3.2	8.1	5.2	5.2	9.4

Where: *, and ** significant, and highly significant at 0.05 and 0.01 probability level, respectively.

Performance of genotypes under the test environments

Days to heading (days)

The response of the studied genotypes for days to heading (Table 3) showed high variability between the studied genotypes. It ranged from 89.50 days (Bor) to 106.3 days (L14), 94.65 days (L7) to 105.85 days (L12), 79.65 days (L7 and Bor) to 90.65 days (L10), and 73.35 days (Bor) to 89.30 days (L10) under T1, T2, T3, and T4, respectively. Average means for days to heading under T1, T2, T3 and T4 were 100.32 days, 100.93 days, 84.06, and 82.44 days, respectively. The overall means ranged from 84.88 days for Bor to 96.65 days for L10 with grand mean of 91.94 days. The results showed that the decrease in days to heading was occurred in case of T3 and T4 treatments but was not in case of T2 treatment. This can be attributed to the time of occurrence of stress where in case of T2 the time of stress was after heading itself, consequently there are no significant effects (Vara Prasad and Djanaguiraman, 2014).

Days to maturity (days)

The results in Table 3 showed a wide range of days to maturity between the studied wheat genotypes under the normal and stress combinations. The mean values under

normal conditions (T1) ranged from 141.35 days for Bor to 152.65 days for L13 and L14. While in case of stress combinations, the mean values ranged from 129.50 days (L13) to 140.80 days (Baj), 118.5 days (L13) to 126.50 days (L10), and 108.35 days (Bor) to 119.15 days (L3) under T2, T3, and T4, respectively. Concerning the averages, the average mean values under T1, T2, T3, and T4 were 148.92 days, 136.96 days, 122.67 days, and 114.29 days, respectively. The average overall mean values were ranged from 125.59 days (Bor) to 133.15 days (L3) with grand mean of 130.71 days.

A notable decrease in days to maturity was observed under stress conditions either independently or under stresses combinations. The results indicated that all stress combinations negatively affected on days to maturity compared to normal conditions. Similar results were obtained by Feltaous *et al.* (2020), where they declared a high reduction in number of days to maturity as a result of terminal heat stress conditions. Mehraban *et al.* (2019) stated a considerable reduction in number of days to maturity under water stress conditions.

Table 3. Mean values of days to heading and days to maturity under normal and stress combinations across the two seasons and overall.

Genotype	Days to heading (day)				Overall	Days to maturity (day)				Overall	
	T1	T2	T3	T4		T1	T2	T3	T4		
L1	94.00	98.30	85.00	84.65	90.49	146.85	138.35	124.15	116.70	131.51	
L2	99.00	99.35	83.80	85.85	92.00	148.50	134.30	122.50	113.00	129.58	
L3	104.30	100.15	86.00	89.15	94.90	151.00	136.15	126.30	119.15	133.15	
L4	98.15	100.50	85.00	78.65	90.58	144.80	135.65	123.15	114.65	129.56	
L5	103.80	102.30	85.80	83.30	93.80	150.00	138.65	123.85	115.50	132.00	
L6	99.80	102.00	84.65	79.50	91.49	150.00	135.35	125.85	111.65	130.71	
L7	93.50	94.65	79.65	77.65	86.36	151.00	137.50	120.65	113.85	130.75	
L8	101.80	100.35	83.15	82.50	91.95	147.15	138.20	122.00	116.15	130.88	
L9	101.85	102.85	83.00	85.30	93.25	149.50	138.85	124.15	116.85	132.34	
L10	103.15	103.50	90.65	89.30	96.65	151.20	139.00	126.50	115.65	133.09	
L11	103.85	104.50	87.50	78.15	93.50	148.65	140.50	122.85	110.20	130.55	
L12	103.85	105.85	86.00	82.80	94.63	149.00	139.85	121.50	114.00	131.09	
L13	105.85	101.35	82.65	82.50	93.09	152.65	129.50	118.50	114.15	128.70	
L14	106.30	102.20	82.00	85.15	93.91	152.65	139.30	123.15	117.00	133.03	
Sh1	101.30	96.15	80.35	83.80	90.40	152.35	130.15	122.00	114.50	129.75	
Sok	99.35	102.85	87.65	82.50	93.09	145.70	140.20	122.50	110.50	129.73	
Baj	96.35	102.85	80.65	79.85	89.93	148.20	140.80	118.85	115.35	130.80	
Bor	89.50	97.00	79.65	73.35	84.88	141.35	133.00	119.65	108.35	125.59	
Mean	100.32	100.93	84.06	82.44	91.94	148.92	136.96	122.67	114.29	130.71	
L.S.D _{0.05}	S	1.34	1.06	1.31	1.34	0.63	1.20	1.09	1.14	1.21	0.58
	T					0.89					0.82
	G	4.01	3.17	3.92	4.01	1.89	3.61	3.27	3.42	3.63	1.75
	T x S					1.06					0.98
	G x T					3.17					2.93
	G x S	6.67	4.48	5.55	5.67	2.24	5.10	4.63	4.83	5.13	2.07
G x T x S					4.48					4.14	

Grain filling rate (g/day)

The results of mean values for grain filling rate (g/day) are presented in Table 4. It showed that the best genotypes under T1 conditions, high grain filling rate with no significant differences from mean, were 76.30 (L11), 71.75

(L14), 71.60 (L3), and 70.50 (L3 and Baj). In the same context, the best genotypes under T2 conditions were L11 (81.20), L13 (74.80), and L12 (70.90). The situation slightly differed under T3 where L11 (72.05) and L13 (67.35) still the best genotypes in addition to Sok (65.45) and L10 (62.45).

Table 4. Mean values of grain filling rate (g/day) and plant height (cm) under normal, stress combinations across the two seasons and overall.

Genotype	Grain filling rate (g/day)				Overall	Plant height (cm)				Overall	
	T1	T2	T3	T4		T1	T2	T3	T4		
L1	63.90	60.40	52.05	60.50	59.21	117.30	106.50	96.15	92.85	103.20	
L2	68.25	66.05	52.90	62.35	62.39	120.85	109.20	100.85	92.35	105.81	
L3	71.60	67.40	54.75	56.10	62.46	117.50	107.85	97.00	89.00	102.84	
L4	67.55	69.95	60.40	42.25	60.04	124.80	108.35	98.50	97.50	107.29	
L5	44.15	59.65	49.35	36.90	47.51	139.20	124.15	114.85	115.00	123.30	
L6	47.75	57.60	40.15	39.95	46.36	135.15	124.50	112.65	98.50	117.70	
L7	33.00	38.60	36.90	32.45	35.24	132.50	127.50	107.50	100.00	116.88	
L8	43.65	41.10	41.05	37.25	40.76	140.15	120.65	110.50	105.80	119.28	
L9	63.75	59.50	39.30	55.10	54.41	117.50	119.20	107.65	94.65	109.75	
L10	65.90	64.90	62.45	66.65	64.98	117.85	109.00	99.35	92.35	104.64	
L11	76.30	81.20	72.05	69.95	74.88	117.35	109.35	101.85	97.65	106.55	
L12	65.75	70.90	56.40	48.00	60.26	126.15	114.00	105.00	97.85	110.75	
L13	70.50	74.80	67.35	62.65	68.83	130.70	113.85	106.35	102.00	113.23	
L14	71.75	60.55	49.80	52.30	58.60	124.35	113.00	105.50	103.00	111.46	
Sh1	68.75	67.50	51.00	63.20	62.61	110.50	106.85	94.65	86.85	99.71	
Sok	66.70	56.00	65.45	65.95	63.53	115.35	111.50	100.00	93.15	105.00	
Baj	70.50	63.05	52.05	41.05	56.66	118.35	112.15	101.50	94.35	106.59	
Bor	64.30	67.20	56.65	50.85	59.75	113.50	109.65	99.85	91.65	103.66	
Mean	62.45	62.58	53.34	52.41	57.69	123.28	113.74	103.32	96.92	109.31	
L.S.D _{0.05}	S	2.36	2.66	2.63	3.23	1.37	1.25	1.48	1.37	1.28	0.67
	T					1.93					0.95
	G	7.09	7.98	7.89	9.70	4.10	3.75	4.43	4.13	3.83	2.01
	T x S					2.29					1.12
	G x T					6.86					3.46
	G x S	10.02	11.28	11.15	13.72	4.85	5.31	6.26	5.83	5.42	2.39
G x T x S					9.70					4.77	

Regarding T4 the genotypes, with highest grain filling rate and no significant differences from mean, were L11 (69.95), L10 (66.65), Sok (65.95), Sh1 (63.20), L13 (62.65), and

L2 (62.35). The results of the overall mean values showed that the best genotypes were L11 (74.88), L13 (68.83), L10 (64.98), Sok (63.53), Sh1 (62.61), L3 (62.46), and L2 (62.39). A worthy

notable point was observed; L11 has superior grain filling rate under all treatments (T1, T2, T3, and T4) as well as overall means. Regarding the treatments, significant differences were found between recommended sowing date treatments (T1 and T2) and late sowing date treatments (T3 and T4). These results are in agreement with those obtained by Feltaous *et al.* (2020); where they found considerable differences between recommended and late sowing dates. These can be attributed to the variability between genotypes' ability for compensation as a results of stress as reported by Wu *et al.* (2018). These results declared the importance of screening the genotypes under a wide range of environments to identify the most adapted genetic makeup.

Plant height (cm)

The results of plant height (Table 4) showed high variability among the genotypes and between the treatments. The mean values under normal conditions ranged from 113.50 cm for Bor to 140.15 cm for L8 with an average of 123.28 cm. Under stress combinations a notable decrease in plant height was observed where, the mean values under T2 conditions ranged from 106.50 cm for L1 to 127.50 cm for L7 with an average of 113.74 cm. In the same manner, the mean vales under T3 and T4 conditions ranged from 94.65 cm (Sh1) to 114.85 cm (L5) with an average of 103.32 cm

and 86.85 cm (Sh1) to 115.00 cm (L5) with an average of 96.92 cm, respectively. Concerning the overall means, the values ranged from 99.71 cm for Sh1 to 123.00 cm for L5 with a grand mean of 109.31 cm. The results indicated that all stress combinations decreased plant height compared to normal conditions. These results are in harmony with those obtained by Poudel *et al.* (2020) and Feltaous *et al.* (2020).

Number of spikes/m²

The results of mean values for number of spikes/m² are presented in table 5. It showed that the highest mean values for number of spikes/m² under T1, T2, T3, T4, and across all treatments were 373.30 for L10, 363.80 spikes/m² for L11, 304.00 spikes/m² for L10, 300.80 spikes/m² for Sh1, and 332.25 spikes/m² for Sh1, respectively. While, the lowest mean values were 241.55 spikes/m² for L5, 265.00 spikes/m² for L8, 209.50 spikes/m² for L8, 203.50 spikes/m² for L5, and 241.70 spikes/m² for L8, respectively. The average mean values were 328.80 spikes/m², 313.77 spikes/m², 257.82 spikes/m², 244.36 spikes/m², and 286.19 spikes/m², respectively.

These results indicated a considerable reduction in number of spikes/m² under combination of heat and drought stresses which, are in agreement with those reported by many wheat researchers *e.g.* Rebetzke *et al.* (2008), Dreccer *et al.* (2009), Dreccer *et al.* (2012) and Mehraban *et al.* (2019).

Table 5. Mean values of number of spikes/m² and thousand kernels weight (g) under normal, stress combinations across the two seasons and overall.

Genotype	Number of spikes/m ²				Overall	Thousand kernels weight (g)				Overall	
	T1	T2	T3	T4		T1	T2	T3	T4		
L1	360.20	343.35	284.65	272.85	315.26	52.15	37.65	37.35	36.35	40.80	
L2	345.50	335.30	258.00	257.35	299.04	50.35	45.10	42.00	36.15	43.40	
L3	342.35	326.65	278.35	235.00	295.59	46.30	40.10	41.35	34.80	40.64	
L4	335.70	340.00	267.35	253.00	299.01	47.65	41.85	37.75	35.95	40.80	
L5	241.55	289.00	235.00	203.50	242.26	44.05	40.95	38.55	33.35	39.23	
L6	323.35	278.30	219.35	229.35	262.59	48.45	41.25	38.75	36.55	41.25	
L7	287.65	281.40	244.50	204.65	254.55	52.50	44.75	42.15	34.55	43.49	
L8	284.00	265.00	209.50	208.30	241.70	47.45	45.15	42.05	35.05	42.43	
L9	366.00	308.15	248.00	269.70	297.96	50.40	40.85	38.25	35.90	41.35	
L10	373.30	341.85	304.00	291.00	327.54	50.70	44.10	40.75	35.75	42.83	
L11	348.35	363.80	301.35	266.65	320.04	50.50	45.30	41.40	39.50	44.18	
L12	315.00	310.00	260.85	234.80	280.16	49.30	46.20	42.45	36.50	43.61	
L13	338.35	298.35	226.65	231.15	273.63	52.25	43.75	42.10	40.15	44.56	
L14	300.80	273.35	232.35	214.85	255.34	43.20	39.25	37.25	33.15	38.21	
Sh1	385.00	347.50	295.70	300.80	332.25	52.15	37.35	37.35	36.35	40.80	
Sok	281.65	292.00	239.65	231.15	261.11	50.35	45.10	42.00	36.15	43.40	
Baj	328.35	333.00	281.70	245.00	297.01	46.30	40.10	41.35	34.80	40.64	
Bor	361.30	320.80	253.85	249.35	296.33	47.65	41.85	37.75	35.95	40.80	
Mean	328.80	313.77	257.82	244.36	286.19	48.98	42.24	40.03	35.94	41.80	
L, S, D ^{0.05}	S	9.71	8.98	7.51	8.27	4.36	0.94	0.85	0.77	0.77	0.41
	T					6.17					0.58
	G	29.12	26.94	22.52	24.80	13.08	2.83	2.54	2.30	2.30	1.23
	T x S					7.31					0.69
	G x T					21.95					2.06
	G x S	41.18	38.09	31.84	35.07	15.52	4.00	3.59	3.25	3.25	1.46
G x T x S					31.04					2.79	

Thousand kernels weight (g)

The results of mean values for thousand kernels weight are presented in Table 5. It showed that the highest mean values for thousand kernels under T1, T2, T3, T4, and across all treatments were 52.50 g for L7, 46.20 g for L12, 42.45 g for L12, 40.15 g for L13, and 44.56 g for L13, respectively. While, the lowest mean values were 43.20 g for L14, 37.35 g for Sh1, 37.25 g for L14, 33.15 g for L14, and 38.21 g for L14, The average mean values were under T1, T2, T3, T4 and across 48.98 g, 42.24 g, 40.03 g, 35.95 g, and 41.80 g, respectively.

The results indicated that average mean of thousand kernels weight was drastically reduced from 48.98 under T1 conditions to 35.94 under T4 conditions. These results are in consistent with those obtained by Poudel *et al.* (2020). In regards to combined terminal and heat stresses, Kaur *et al.* (2011) stated that combined terminal heat and drought stresses resulted in stronger reduction in pericarp thickness and endosperm size than either alone which in turn lead to reduction in thousand kernels weight. For all these aspects, thousand kernels weight was used extensively as a major selection criterion under terminal heat and water stresses.

Number of kernels/spike (k/s)

The results of mean values for number of kernels/spike are presented in Table 6. It indicated that the highest mean values for number of kernels/spike under T1, T2, T3, T4, and across all treatments were 50.65 kernels/spike for L9, 44.10 kernels/spike for L4, 41.90 kernels/spike for L11, 38.35 kernels/spike for L11, and 43.38 kernels/spike for L11, respectively. While, the lowest mean

values under T1, T2, T3, T4, and across all treatments were 41.20 kernels/spike for L8, 37.95 kernels/spike for L1, 35.35 kernels/spike for L8, 30.50 kernels/spike for L7, and 36.60 kernels/spike for L8, respectively. The average mean values under T1, T2, T3, T4, and overall treatments were 46.76 kernels/spike, 40.99 kernels/spike, 38.43 kernels/spike, 33.90 kernels/spike, and 40.02, respectively. These results are in a line with those obtained by Poudel *et al.* (2020).

Table 6. Mean values of number of kernels/spike and grain yield under normal, stress combinations across the two seasons and overall.

Genotype	Number of kernels/spike				Overall	Grain yield/plot (kg)				Overall
	T1	T2	T3	T4		T1	T2	T3	T4	
L1	42.10	37.95	38.80	31.15	37.50	3.357	2.342	1.992	1.862	2.388
L2	47.45	39.60	36.85	34.75	39.66	3.371	2.305	2.028	1.717	2.355
L3	49.00	43.30	39.70	34.85	41.71	3.390	2.377	2.230	1.742	2.435
L4	50.15	44.10	38.70	34.25	41.80	3.155	2.442	2.143	1.513	2.313
L5	42.85	38.50	38.65	35.15	38.79	2.034	2.113	1.867	1.184	1.799
L6	43.15	39.85	39.85	35.00	39.46	2.396	1.917	1.650	1.284	1.812
L7	43.00	38.30	36.20	30.50	37.00	1.886	1.631	1.501	1.167	1.546
L8	41.20	38.65	35.35	31.20	36.60	1.979	1.563	1.584	1.249	1.593
L9	50.65	39.00	38.35	34.20	40.55	3.000	2.135	1.567	1.720	2.105
L10	50.30	42.85	39.85	35.00	42.00	3.142	2.242	2.227	1.805	2.354
L11	49.60	43.65	41.90	38.35	43.38	3.565	2.879	2.417	2.217	2.769
L12	44.20	39.80	37.50	32.50	38.50	2.967	2.546	1.989	1.462	2.241
L13	49.00	43.00	38.20	36.65	41.71	3.193	2.179	2.388	1.925	2.421
L14	44.65	42.50	36.10	33.15	39.10	3.352	2.225	2.038	1.663	2.319
Sh1	53.10	42.85	40.85	33.85	42.66	3.486	2.288	2.108	1.999	2.470
Sok	45.50	40.65	37.30	32.65	39.03	3.081	2.080	2.208	1.817	2.296
Baj	48.35	43.00	41.50	33.20	41.51	3.650	2.350	1.967	1.467	2.358
Bor	47.50	40.30	36.05	33.85	39.43	3.325	2.417	2.279	1.821	2.461
Mean	46.76	40.99	38.43	33.90	40.02	3.018	2.224	2.010	1.645	2.224
L.S.D _{0.05}	S	0.85	0.79	0.77	0.77	0.39	0.095	0.082	0.073	0.039
	T					0.55				0.56
	G	2.55	2.38	2.31	2.24	1.17	0.285	0.246	0.220	0.195
	T x S					0.66				0.063
	G x T					1.97				0.190
	G x S	3.61	3.36	3.26	3.16	1.39	0.403	0.348	0.311	0.277
G x T x S					2.79				0.269	

Grain yield/plot (kg)

The results of mean values for grain yield/plot are presented in Table 6. It showed that the highest mean performance under T1, with no significant differences from mean, were for Baj (3.650 kg), L11 (3.565 kg), Sh1 (3.486 kg), L3 (3.390 kg), L2 (3.371 kg), and L1 (3.357 kg). While under T2 conditions, the best performing genotypes were L11 with 2.879 kg and L12 with 2.546 kg. Similarly, the best performing genotypes under T3 conditions were L11 (2.417 kg), L13 (2.388 kg), and Bor (2.279 kg). The results showed that the best genotypes under T4 were L11, Sh1, L13, and L1 with mean values of 2.217 kg, 1.999 kg, 1.925 kg, and 1.862 kg, respectively. The results indicated that the superior genotypes under a particular condition can be recommended for their respective conditions. The most stable and superior genotypes can be recommended through a wide range of environments. The results of average means overall treatments indicated that the best genotypes are L11 (2.769 kg), Sh1 (2.470 kg), Bor (2.461 kg), L3 (2.435 kg), L13 (2.421 kg), L1 (2.388 kg), L2 (2.355 kg), Baj (2.358 kg) and L10 (2.354 kg). Though, these genotypes can be characterized as high yielding and well adapted genotypes across a wide range of environments.

It is apparent that L11 were the best superior and stable genotype either under dependant treatments or under the combinations of treatments. Furthermore, this genotype can be utilized as a source for terminal heat and drought stresses or recommended for affected heat and drought stresses region. These results indicated that a detrimental effects on grain yield

when heat and drought combined together than either alone these results in harmony with those obtained by Abro *et al.*, (2019), Mehraban *et al.*, (2019) and Feltaous *et al.*, (2020). Consequently, selecting the most high yielding and stable genotype/s is an effective breeding strategy for heat and drought tolerance. A worthy notable point that L11 has the highest mean value for grain filling rate under all the treatments combination as well as average overall. These findings revealed that grain filling rate is a major determining factor for grain yield as reported previously by Pireivatlou *et al.*, (2011) and Wu *et al.*, (2018).

Genotype by genotype environment biplot (GGE biplot)

GGE is a powerful and informative graphical technique for illustration and identification of superior and stable genotype/s in a specific environment. It was suggested by Yan and Tinker (2006). It can be used to estimate genotype main effect (G) as well as genotype by environment interaction effect (GE) in multi-environment trials. GGE biplot is based on singular value decomposition (SVD) by decomposition the three-way table into many two-way tables. GGE biplot is constructed based on the first and second component (PC1 and PC 2) of principal component analysis (PCA). In our study, PC2 and PC 2 explained 86.06% of the total variation. GGE can be used for (1) determining the relationship between the test environments. (2) Evaluation of environments; the power of discriminating among studied genotypes. (3) Determine which genotype perform the best in each environment (Which – Won – Where). (4) Ranking genotypes in the test environments using average test coordination (ATC).

Scatter plot

GGE biplot was constructed based on grain yield trait for 18 genotypes under eight environments *i.e.* T1S1, T2S1, T3S1, T4S1, T1S2, T2S2, T3S2, and T4S2. Each environment represented by vector and its length refer to its discriminating ability between the genotypes *i.e.* Long vector means high discriminating power and vice versa. Cosine of the angle between the vectors determine the correlation coefficient between the tested environments; if angle is $<90^\circ$ or $>90^\circ$ or $=90^\circ$ these means positive or negative or no correlation between the environments, respectively. Scatter plot of GGE biplot (Fig. 2) with origin point represent a virtual genotype that has average performance for grain yield in each environment. Scatter plot illustrated that there is a positive correlation between the test environments.

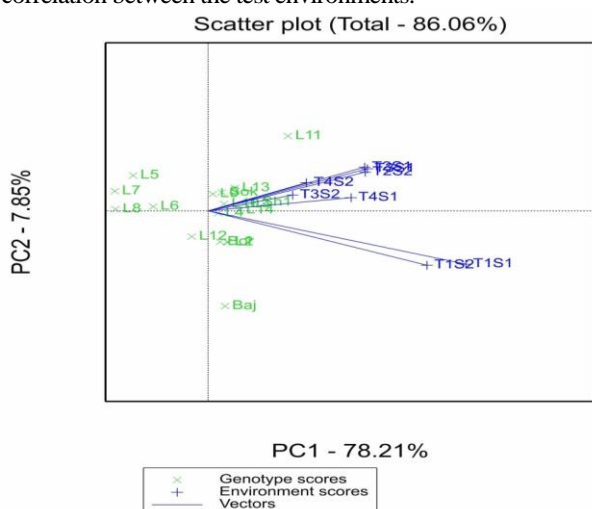


Figure 2. GGE scatter biplot viewing the interrelation between the test environments and the studied genotypes.

Which-Won-Where polygon

A convex hull (Figure 3) has been drawn by connecting the furthest genotypes to form a polygon encompasses all the genotypes. The convex hull was divided into sectors by drawing lines from the origin perpendicular to each side of the hull. Also mega environments were determined by drawing ellipses around the environments fall into in the same sector.

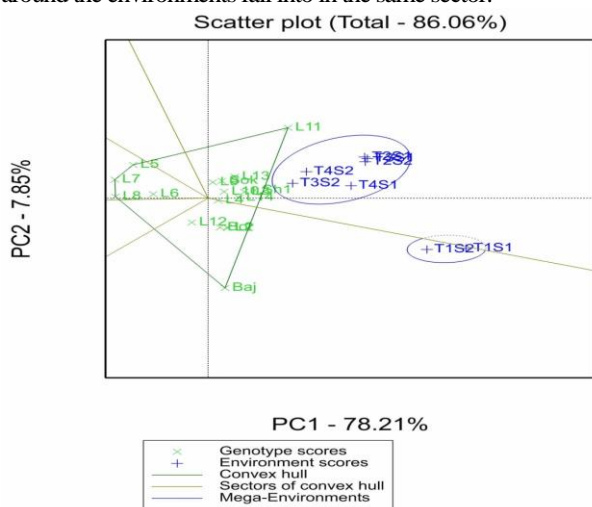


Figure 3. Which-won-where polygon of GGE biplot viewing omega environments and genotypes profile for the test environments.

“Which - Won - Where” polygon showed that there are two mega environments; first mega environment (ME1) contains T1S1 and T1S2 “normal conditions” while the second mega environment (ME2) contains T2S1, T3S1, T4S1, T2S2, T3S2, and T4S2 “stress combinations”. The best performing genotypes under ME1 are Baj, Bor, L2, and L12 while the best genotypes under ME2 are L11, Sh1, L3, L14, L13, Sok, L10, L1, L9, and L4. The rest of genotypes *i.e.* L5, L6, L7, and L8 locate in a separate sector which were not belonging to any sector because their performance was lower than average performance of any the test environments.

Ranking biplot

Identification of high yield and stable genotypes were done by using the average environment coordinate (AEC), which is defined by the average PC1 and PC2 scores for all environments (Yan and Tinker, 2006). The average environment ordinate is represented as a double-headed arrow and points towards lower stability in both directions. The genotypes on the left side of the ordinate line had yield lower than mean yield but the genotypes on the right side of the ordinate had yield higher than mean yield across environments. In concerns, GGE ranking biplot (Fig 4) illustrated that L12, L6, L5, L7, and L8 had yield less than the grand mean. While, the rest of genotypes (L11, Sh1, L3, L14, L13, L10, Sok, L2, Bor, Baj, L9, L1) were located on the right side which they exceeded the grand yield mean. Regarding stability, L11 and Baj have the greatest GE interaction (unstable), whereas the most stable with yield greater than mean yield were Sh1, L3, L14, L13, L10, and Sok.

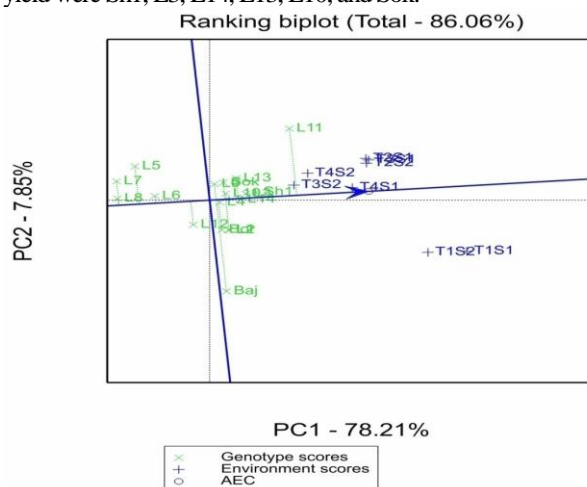


Figure 4. The AEC view of GGE biplot to rank the genotypes based on grain yield data across all environments

Evaluation based on multiple traits GT biplot

Genotypes selection, in multi environments trial, based on multiple traits is a quite significant issue in plant breeding. GGE biplot evaluates the genotypes based on only one trait; usually grain yield. Genotype by trait biplot (GT biplot) is another powerful technique for visualization genotypes based on multiple traits simultaneously (Yan *et al.*, 2000). It was constructed from data of mean performance overall the test environments for each trait (Table 7). GT biplot was generated using standardized data (will be discussed soon); standardization was done to remove the units followed by performing PCA and plotting PC1 against PC2. GT biplot (Fig. 5) showed the association among the traits (angle between vectors) as well the level of genotype relative to trait (distance from the origin). It showed presence of sufficient variability (long vector for traits)

for most of the traits and strong fitness for GT biplot *i.e.* 71.59% of the total variation was explained GT biplot. Except DM and PLH, all traits tend to correlate positively with grain yield, this

due to that these traits are yield components. Similar results were stated by Kendal (2019), Feltaous (2019) and Merrick *et al.* (2020).

Table 7. Mean performance of the studied traits for genotypes over all environments.

Genotype	DH	DM	GFR	PLH	S/M ²	TKW	K/S	GY
L1	90.50	131.51	59.20	103.20	315.26	40.80	37.50	2.388
L2	92.00	129.58	62.40	105.80	299.04	43.40	39.66	2.355
L3	94.90	133.15	62.50	102.80	295.59	40.64	41.71	2.435
L4	90.60	129.56	60.00	107.30	299.01	40.80	41.80	2.313
L5	93.80	132.00	47.50	123.30	242.26	39.23	38.79	1.799
L6	91.50	130.71	46.40	117.70	262.59	41.25	39.46	1.812
L7	86.40	130.75	35.20	116.90	254.55	43.49	37.00	1.546
L8	92.00	130.88	40.80	119.30	241.70	42.43	36.60	1.593
L9	93.20	132.34	54.40	109.80	297.96	41.35	40.55	2.105
L10	96.70	133.09	65.00	104.60	327.54	42.83	42.00	2.354
L11	93.50	130.55	74.90	106.60	320.04	44.18	43.38	2.769
L12	94.60	131.09	60.30	110.80	280.16	43.61	38.50	2.241
L13	93.10	128.70	68.80	113.20	273.63	44.56	41.71	2.421
L14	93.90	133.03	58.60	111.50	255.34	38.21	39.10	2.319
Sh1	90.40	129.75	62.60	99.70	332.25	37.53	41.51	2.47
Sok	93.10	129.73	63.50	105.00	261.11	41.44	39.43	2.296
Baj	89.90	130.80	56.70	106.60	297.01	40.96	42.66	2.358
Bor	84.90	125.59	59.80	103.70	296.33	41.26	39.03	2.461
Mean	91.94	130.71	57.70	109.30	286.19	41.55	40.02	2.224
Std. Dev.	2.90	1.83	9.79	6.51	28.53	1.96	1.99	0.327

It is clear that GGE biplot deals with genotypes and traits while GT biplot deals with genotypes and environments. A noteworthy point that despite GT biplot is helpful in visualizing and revealing the correlation between traits and trait profiles of the genotypes. But it is not in making decision about recommending or discarding the genotypes. Therefore, genotype by yield*trait (G Y*T) was proposed by Yan and Fregeau (2018) to overcome this issue.

Scatter plot (Total - 71.59%)

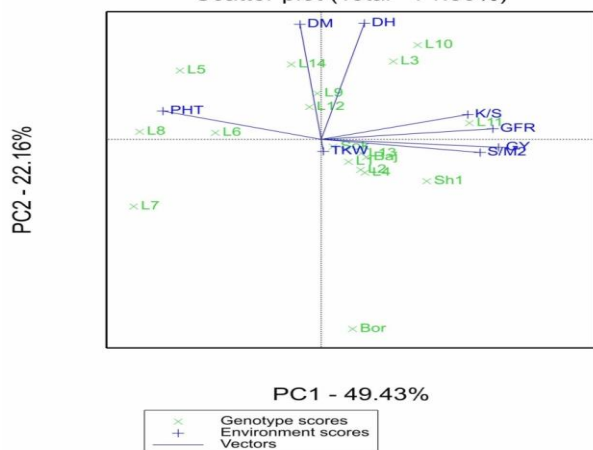


Fig. 5. Genotype by trait biplot for the studied genotypes over all the test environments.

G Y*T biplot

During breeding process, plant breeders try to develop high yield genotypes; they might disrupt another trait/s. Therefore other traits should be taken in consideration. G Y*T biplot is a new, comprehensive, and effective technique mainly relay on selecting superior genotypes based on combining yield with other traits (yield*trait combinations) rather than yield solely or traits individually.

The GYT approach can be executed following few simple steps; yield*trait combinations (GYT data), followed by data standardization, mean of the standardized across yield*trait combinations (superiority index), the last step is

visualizing the rank of genotypes based on their superiority in yield*trait combination across all the test environments.

Yield*trait combinations can be obtained by multiplying yield value with the trait value from data present in Table 7 to generate Table 8 (GYT data). Note that when the trait negatively correlated with yield its combination will obtain by dividing yield value by trait value for each genotype. Some traits *e.g.* lodging and disease scores are usually measured with 0 as the best and a larger value is less desirable. In this case it is advisable to reverse the values such that 0 means worst and a larger value means more desirable before calculating the yield*trait combinations.

GYT data (Table 8) were standardized so that the mean for each yield*trait combination was 0 and the variance was the unit. Data standardization was performed as:

$$P_{ij} = \frac{T_{ij} - T_j}{S_j}$$

Where: P_{ij} is the standardized value of genotype *i* for trait or yield-trait combination, *j* in the standardized table, T_{ij} is the original value of genotype *i* for trait or yield-trait combination *j* in the GYT table, T_j is the mean across genotypes for trait or yield*trait combination *j*, and S_j is the standard deviation for trait or yield*trait combination *j*. The standardized data along with superiority index are given in Table 9.

Superiority index (SI)

It was estimated according equation given by Yan and Fregeau (2018); it was shown in table 9. Consequently, genotypes have been ranked based on superiority index mean over trait/s (Table 10). Hereby, breeder’s can judge which superior genotypes can be selected and which one can be discarded according to his objectives and based on its rank in yield trait combination. This approach enables the breeder to identify and select the superior as well as the stable genotype/s.

GY*T biplot construction

Scatter GY*T biplot graph (Fig. 6) showed that there is a positive correlation between all yield*trait combination “acute angle” and they were well represented in the test

environments and among genotypes “long vectors”. The positive correlation can be attributed to that all the studied traits are yield components. The which-won-where polygon (Fig. 7) showed that all yield*trait combinations locate in one

sector, can be attributed to the same reason above. It showed that genotypes were distributed in the graph based on their performance and trait profile.

Table 8. Genotype by yield*trait combinations for the studied genotypes.

Genotype	GY/DH	GY/DM	GY*GFR	GY/PLH	GY*(S/M ²)	GY*TKW	GY*(K/S)
L1	0.026	0.018	141.370	246.442	752.841	97.430	89.550
L2	0.026	0.018	146.952	249.159	704.239	102.207	93.399
L3	0.026	0.018	152.188	250.318	719.762	98.958	101.564
L4	0.026	0.018	138.780	248.185	691.610	94.370	96.683
L5	0.019	0.014	85.453	221.817	435.826	70.575	69.783
L6	0.020	0.014	84.077	213.272	475.813	74.745	71.502
L7	0.018	0.012	54.419	180.727	393.534	67.236	57.202
L8	0.017	0.012	64.994	190.045	385.028	67.591	58.304
L9	0.023	0.016	114.512	231.129	627.206	87.042	85.358
L10	0.024	0.018	153.010	246.228	771.029	100.822	98.868
L11	0.030	0.021	207.398	295.175	886.191	122.334	120.119
L12	0.024	0.017	135.132	248.303	627.839	97.730	86.279
L13	0.026	0.019	166.565	274.057	662.458	107.880	100.980
L14	0.025	0.017	135.893	258.569	592.133	88.609	90.673
Sh1	0.027	0.019	154.622	246.259	820.658	92.699	102.530
Sok	0.025	0.018	145.796	241.080	599.509	95.146	90.531
Baj	0.026	0.018	133.699	251.363	700.350	96.584	100.592
Bor	0.029	0.020	147.168	255.206	729.268	101.541	96.053
Mean	0.024	0.017	131.224	241.519	643.072	92.417	89.443
Std. Dev.	0.004	0.003	37.817	27.059	142.847	14.536	16.205

Table 9. The standardized data for the studied genotypes and mean superiority index over all yield*trait combination.

Genotype	GY/DH	GY/DM	GY*GFR	GY/PLH	GY*(S/M ²)	GY*TKW	GY*(K/S)	Mean SI
L1	0.616	0.442	0.268	0.182	0.768	0.345	0.007	0.376
L2	0.395	0.448	0.416	0.282	0.428	0.674	0.244	0.412
L3	0.412	0.492	0.554	0.325	0.537	0.450	0.748	0.503
L4	0.375	0.323	0.200	0.246	0.340	0.134	0.447	0.295
L5	-1.410	-1.325	-1.210	-0.728	-1.451	-1.503	-1.213	-1.263
L6	-1.235	-1.234	-1.247	-1.044	-1.171	-1.216	-1.107	-1.179
L7	-1.772	-2.029	-2.031	-2.247	-1.747	-1.732	-1.990	-1.935
L8	-1.934	-1.894	-1.751	-1.902	-1.806	-1.708	-1.922	-1.845
L9	-0.452	-0.437	-0.442	-0.384	-0.111	-0.370	-0.252	-0.350
L10	0.042	0.258	0.576	0.174	0.896	0.578	0.582	0.444
L11	1.524	1.633	2.014	1.983	1.702	2.058	1.893	1.830
L12	-0.142	0.027	0.103	0.251	-0.107	0.366	-0.195	0.043
L13	0.509	0.697	0.935	1.203	0.136	1.064	0.712	0.751
L14	0.141	0.159	0.123	0.630	-0.357	-0.262	0.076	0.073
Sh1	0.880	0.785	0.619	0.175	1.243	0.019	0.808	0.647
Sok	0.131	0.262	0.385	-0.016	-0.305	0.188	0.067	0.102
Baj	0.572	0.391	0.065	0.364	0.401	0.287	0.688	0.395
Bor	1.347	1.003	0.422	0.506	0.603	0.628	0.408	0.702
Mean	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
Std. Dev.	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000

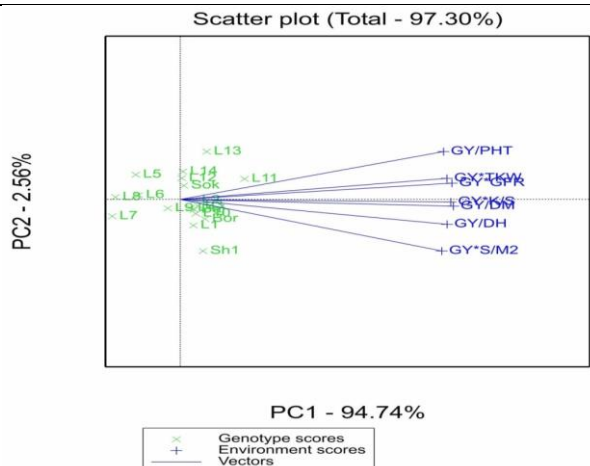


Figure 6. The interrelation between the genotypes and yield*trait combinations across all environments

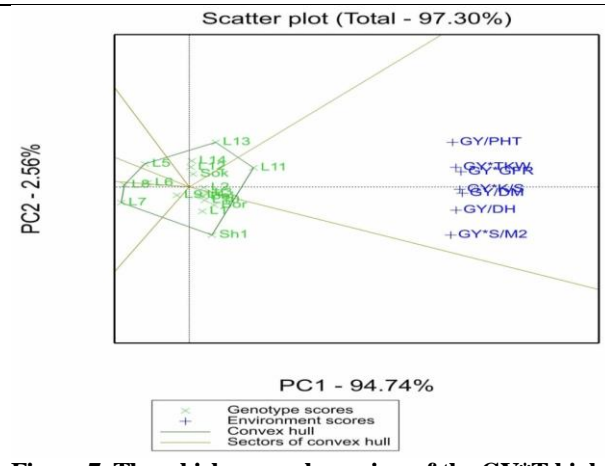


Figure 7. The which-won-where view of the GY*T biplot to highlight genotypes with outstanding profiles based on over all environments data

Ranks of the genotypes based on superiority:

Based on mean superiority index for each genotype, the genotypes were ranked based overall yield*trait combinations (Table 10), where highest value is the best genotype/s and the lowest value is the worst genotype/s. mean superiority index, over all yield*trait combination, indicated that the best ranked genotypes were L11, L13, Bor, Sh1, L3, L10, L2, Baj, L1, L4 and with mean superiority index of 1.830, 0.751, 0.702, 0.647, 0.503, 0.444, 0.412, 0.395, 0.376, and 0.295. While, the poorest genotypes based on its performance were L 9, L5, L8, L5, and L7 with mean superiority index of -1.179, -1.263, -1.845, and -1.935 with negative effects with all trait combinations. It is appear that L11 is the best performance genotype with the highest superiority index (1.83) has good combinations with all traits. The same situation for L13 has good combinations with all traits except GY*(S/M²) with 0.136. Similarly the rank for the other genotypes can be interpreted in the same manner. Merrick *et al.* (2020) obtained similar results.

Moreover the superiority can be detected based in a specific yield trait; in this case superiority index will be calculated based on yield combinations of interest rather than based on all yield*trait combinations. These results can be more informative and comprehensive, meaningful for breeders in making decisions when it plotted as a biplot graph.

GY*T biplot (Fig. 8) showed that the genotypes located below the average tester coordinate “ATC” tend to have high values of GY*S/M², GY*DH, GY*DM, and GY*K/S. while, the genotypes located above the ATC ordinate tend to have high values of GY*GFR, GY*TKW, and GY*PLH. GY*T biplot might rank genotypes based on one single year or based on overall years Mohammadi (2019). It showed the rank for the

studied genotypes based on their performance and stability across all test environment, considering all yield trait combinations, were L11, L13, Bor, Sh1, L3, L10, L2, Baj, L1, L4, Sok, L14, L12, L9, L6, L5, L8, and L7. Recently, this technique was effectively used by few numbers of researchers like Mohammadi (2019) and Kendal (2019) and Merrick *et al.* (2020). Looking back and reviewing the rank of genotypes by GGE biplot (GGE ranking biplot); it is different than GGE ranks. Only L11 rank is the same in both two rank lists. Similar results were obtained by Yan and Fregeau (2018).

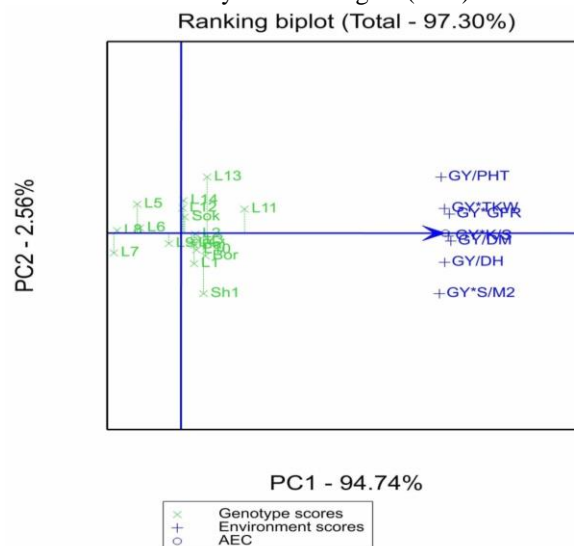


Figure 8. Ranking GY*T biplot highlighting the mean vs. stability for the studied genotypes

Table 10. Ranks of the studied genotypes based on superiority index overall the test environments.

Ranke	Genotypee	GY/DH	GY/DM	GY*GFR	GY/PLH	GY*(S/M ²)	GY*TKW	GY*(K/S)	SI
1	L11	1.524	1.633	2.014	1.983	1.702	2.058	1.893	1.830
2	L13	0.509	0.697	0.935	1.203	0.136	1.064	0.712	0.751
3	Bor	1.347	1.003	0.422	0.506	0.603	0.628	0.408	0.702
4	Sh1	0.880	0.785	0.619	0.175	1.243	0.019	0.808	0.647
5	L3	0.412	0.492	0.554	0.325	0.537	0.450	0.748	0.503
6	L10	0.042	0.258	0.576	0.174	0.896	0.578	0.582	0.444
7	L2	0.395	0.448	0.416	0.282	0.428	0.674	0.244	0.412
8	Baj	0.572	0.391	0.065	0.364	0.401	0.287	0.688	0.395
9	L1	0.616	0.442	0.268	0.182	0.768	0.345	0.007	0.376
10	L4	0.375	0.323	0.200	0.246	0.340	0.134	0.447	0.295
11	Sok	0.131	0.262	0.385	-0.016	-0.305	0.188	0.067	0.102
12	L14	0.141	0.159	0.123	0.630	-0.357	-0.262	0.076	0.073
13	L12	-0.142	0.027	0.103	0.251	-0.107	0.366	-0.195	0.043
14	L9	-0.452	-0.437	-0.442	-0.384	-0.111	-0.370	-0.252	-0.350
15	L6	-1.235	-1.234	-1.247	-1.044	-1.171	-1.216	-1.107	-1.179
16	L5	-1.410	-1.325	-1.210	-0.728	-1.451	-1.503	-1.213	-1.263
17	L8	-1.934	-1.894	-1.751	-1.902	-1.806	-1.708	-1.922	-1.845
18	L7	-1.772	-2.029	-2.031	-2.247	-1.747	-1.732	-1.990	-1.935

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سلوك وثبات بعض التراكيب الوراثية من قمح الخبز تحت توليفات من الاجهاد المائي والحرارى باستخدام التحليلات الثنائية المحاور (Biplot techniques)

يوسف محسن فلتاؤوس* و ياسر سيد ابراهيم قبيصي

قسم بحوث القمح – معهد بحوث المحاصيل الحقلية – مركز البحوث الزراعيه

أجريت هذه الدراسة بمحطه البحوث الزراعيه بشندويل – مركز البحوث الزراعيه – مصر. اشتملت الدراسه على 18 تركيب وراثي تم زراعتها وتقييمها تحت اربع معاملات للاجهاد المائي والحرارى خلال موسمين زراعيين 2018/2019 و 2019/2020 كما يلي: (1) بيئات الظروف المثلى : الظروف الموصى لميعاد الزرع مع خمس ريات. (2) بيئات الاجهاد المائي: ميعاد الزراعة الموصى به مع ثلاث ريات. (3) بيئات الاجهاد الحرارى: الزراعة بعد شهر من الميعاد الامثل مع اربع ريات. (4) بيئات الاجهاد المائي الحرارى: الزراعة بعد شهر من الميعاد الامثل مع ثلاث ريات. أظهر تحليل التباين وجود اختلافات بين التراكيب الوراثيه وبين البيئات والتفاعل بين التراكيب الوراثيه مع البيئات. أظهرت نتائج متوسط أداء التراكيب الوراثيه أن السلالة رقم 11 كانت الأفضل تحت كل البيئات وأيضاً الأفضل على مستوى متوسط كل المعاملات. أظهر تحليل GGE biplot وجود ارتباط موجب بين البيئات الثمانيه وقد قسمت البيئات الى مجموعتين. أظهرت نتائج GGE biplot أن Baj 1 هو الأعلى محصولاً وثباتاً تحت ظروف الإجهاد الحرارى. أظهر تحليل GT biplot وجود ارتباط ايجابي بين معظم الصفات المدروسة عدا صفتي عدد أيام النضج وطول النبات، حيث أظهرت هاتين الصفتين ارتباط سلبى مع محصول الحبوب. أظهر GY*T biplot وجود ارتباط ايجابي بين جميع Yield*trait combinations. أظهر دليل التوق (SI) أن السلالة رقم 11 هي الأكثر توقفاً وأن السلالة رقم 7 هي الأقل توقفاً مع الأخذ في الاعتبار توليفات المحصول مع الصفات الاخرى. يمكن الإستفادة من السلالة رقم 11 بتقييمها في تجارب محصوليه أوليه على مستوى الجمهوريه أو إستخدامها كمصدر لتحمل الحراره والجفاف فى برامج التربيه.