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GENETIC ANALYSIS FOR EARLINESS AND GRAIN YIELD OF BREAD WHEAT (*Triticum aestivum* L.) UNDER HEAT STRESS

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ABSTRACT: This investigation aimed to study mean performance, genotypic variances, types of gene action and heritability for earliness, yield and components in four bread wheat crosses using six populations *i.e.* (P_1, P_2, F_1, F_2, BC_1 and BC_2) under different thermal conditions. Wheat crosses populations were sown on 19th November and 3rd January at the Experimental Farm, Faculty of Agriculture, Zagazig University, Egypt in a randomized complete block design in 2017/2018 season. Scaling test provide evidence of non-allelic interaction in controlling all studied characters in the four crosses on both sowing dates except No. of spiklets/spike in the 3rd and 4th crosses and grain yield/plant in the 2nd and 3rd crosses on normal sowing date, indicated the presence of epistasis and the digenic model proved to be satisfactory in explaining the inheritance of the previous characters in the corresponding crosses. Narrow-sense heritability estimates recorded high values (>50%) for days to heading in the 1st and 2nd crosses on normal sowing date and the 3rd cross on both sowing dates; days to maturity in the 1st and 4th on normal sowing date and the 3rd cross on both sowing dates, No. of tillers/plant in the 3rd cross on both sowing dates and the 2nd and 4th crosses on normal sowing date; No. of spiklets/spike in all crosses on both sowing dates except the 1st and 2nd crosses on normal sowing date; No. of grains/spike in the 2nd cross on both sowing dates, the 4th cross on normal sowing and the 1st cross on late sowing date; weight of grains/spike in the 2nd cross on both sowing dates and the 3rd on normal sowing date, 1st and 4th crosses on late sowing date and grain yield/plant in the 1st cross on both sowing dates and the 3rd and 4th crosses on late sowing date.

Key words: Genetic component, heat stress, heritability, six populations, *Tritium aestivum* L., wheat.

INTRODUCTION

Wheat (*Tritium aestivum* L.) is the first strategic crop grow during the winter season and the most important and staple food crop for about third of the world population due to its multiple uses, the cultivated area of wheat in Egypt is about 1.34 million hectares with a production of approximately 8.80 million tons **FAO (2017)**. Therefore, one of the requirements for obtaining high yield is the choice of the suitable sowing date due to the variations in weather conditions among seasons. Climate change is one of the important factors responsible for low yield in wheat. The low productivity of wheat is due to shorter favorable growing period, high temperature with low humidity during growing season with more change in temperature **Akter and Rafiqul (2017).** Global climate models predict an increase in mean ambient temperatures between 3.7˚ to 4.8˚C by the end of this century **IPCC (2014)**. The optimum temperature for wheat anthesis and grain filling ranges from 12 to 22˚C **Joshi *et al.* (2007)**. Wheat genotypes are very sensitive to high temperature **(Slafer and Satorre, 1999l; Alexander *et al.*, 2006)**. Heat stress during the reproductive stage is more harmful than during the vegetative stage due to the direct effect on grain number and dry weight accumulation **Wollenweber *et al.* (2003)**. Additionally, when temperature is elevated between anthesis to grain maturity, grain yield is reduced because of the reduced time to capture resources. 1°C

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increase in global temperature could decrease the global wheat yield by 4.1– 6.4% **Liu *et al*. (2016).** Generation mean analyses provide information on the relative importance of mean effects of the genes (additive effects), dominance deviations, and effects due to non-allelic genetic interactions in determining genotypic values of the individuals and, consequently, mean genotypic values of families and generations effects for a polygenic trait **Singh and Singh (1992**). Genetic information obtained from multi generation are reliable compared with those based on one generation therefore, six populations (P_1, P_2, F_1, F_2, BC_1 and BC_2) are considered the one which may give detailed genetic information for the employed genotypes.

Heritability estimate is a valuable breeding parameter for determining the magnitude of genetic gain from selection. It indicates higher importance of genetic effects in controlling the inheritance of economic characters. Wheat grain yield is a complex character, highly influenced by the environment, but most of yield contributing characters are not only less complex and simply inherited, but are also less influenced by environment deviations. Therefore, the present study was carried out to identify magnitude and types of gene action, heritability for earliness, yield and its components in four bread wheat crosses in six populations (P_1, P_2, F_1, F_2, BC_1 and BC_2) growing under different thermal conditions.

MATERIALS AND METHODS

This study was conducted at Ghazala Experimental Farm, Faculty of Agriculture, Zagazig University, Egypt. during the successive growing seasons of 2015/2016, 2016/2017 and 2017/2018 to study types of gene action controlling yield and its attributes in six bread wheat populations (P_1, P_2, F_1, F_2, $BC_1$and BC_2) for four crosses *i.e.* line-4 × line-27, line-15 × Shandaweel-1, Misr-1 × line-15 and Shandaweel-1 × line-27. The origin and pedigree of these bread wheat genotypes are presented in Table 1. In 2015/2016 season, the parents were crossed to produce F_1 hybrid grains. In 2016/2017 season, the F_1 hybrid plants were backcrossed to their parents to produce BC_1 ($F_1 \times P_1$) and BC_2 ($F_1 \times P_2$) generations. In addition F_1 plants were selfed to produce F_2 grains. In 2017/2018 season the parents of each cross as well as their, F_1, F_2, $BC_1$and BC_2) populations were sown on two sowing dates *i.e.*, optimum (19^{th} November) and late (3^{rd} January) in a randomized complete block design with three replications. Each replicate consisted of 30 plants in one row for each of the parents and F_1; 60 plants in two rows each of back cross and 120 plants in four rows for the F_2 population. Rows were 3 m long and 10 cm was the distance between plants. All recommended cultural practices for wheat production and inputs like irrigation, manuring and weed control, were kept uniform for all entries from sowing till harvesting to minimize environmental variation to the maximum extent. The meteorological data for monthly average during 2017/2018 growing season are presented in Table 2. Data were recorded on 15 individual plants for non-segregate populations (P_1, P_2 and F_1) and 30 plants for BC_1 and BC_2 and 60 plants for F_2 population for each replicate for the following: days to heading, days to maturity, number of tillers/plant, number of spiklets/spike, number of grains/spike, weight of grains/spike (g) and grain weight/plant (g).

Statistical Analysis

Types of gene action and heritability

The A, B, C and D scaling tests as outlined by **Mather (1949)** and **Hayman and Mather (1955)** were applied to test the presence of non-allelic interactions as follows:

$A = \overline{2\,BC_1} - \bar{P}_1 - \bar{F}_1$ $\quad VA = 4V(BC_1) + V(P_1) + V(F_1)$

$B = \overline{2\,BC_2} - \bar{P}_2 - \bar{F}_1$ $\quad VB = 4V(BC_2) + V(P_2) + V(F_1)$

$C = 4\bar{F}_2 - 2\bar{F}_1 - \bar{P}1 - \bar{P}_2$ $\quad VC = 16V(F_2) + 4V(F_1) + V(P_1) + V(P_2)$

$D = \overline{2F_2} - \overline{BC}_1 - \overline{BC}_2$ $\quad VD = 4V(F2) + V(BC_1) + V(BC_2)$

In the presence of non-allelic interaction, the analysis was proceeded to compute the interaction types involved using the six-parameters genetic model according to **Jinks and jones (1958)** as follows:

m = Mean of $\bar{F}_2$

d = Additive effect = $\overline{Bc}_1 - \overline{Bc}_2$

h = Dominance effect = $\bar{F}_1 - 4\bar{F}_2 - (1/2)\bar{P}_1 - (1/2)\bar{P}_2 + 2\overline{Bc}_1 + 2\overline{Bc}_2$.

Table 1. Pedigree and origin of the parents used in the four bread wheat crosses under study

No.	Genotype	Pedigree
1	**Misr 1**	Oasis/SKAUZ//4×BCN/3/2×PASTOR.CMss00Y01881T-050M-030Y-030M-030WGY-33M-0Y-0S
2	**Line 15**	WBLLI×2/BRAMBLING
3	**Line 4**	BABAX/LR42//BABAX×2/3/BRAMBLING/
5	**Shandaweel 1**	SITE//MO/4/NAC/TH.AC//3×PVN/3MIRLO/BUC.CMSS93B00567S-72Y-010M-010Y-010M-0HTY-0SH.
6	**Line 27**	ICB91-0539-7APP-0AP-3AP-0AP

Table 2. Meteorological data for monthly average during 2017/2018 wheat growing season

2017/2018	Temp. (°C)			Humidity (%)		
	High	Low	Avg.	High	Low	Avg.
November	24	16	20	80	31	55
December	22	14	18	82	35	58
January	19	12	15	78	33	56
February	24	14	19	81	21	51
March	28	16	22	77	15	46
April	29	18	24	73	19	46
May	34	22	28	73	18	46

i= Additive x Additive type of gene interaction = $2\,\overline{Bc}_1 + 2\overline{Bc}_2 - 4\,\overline{F}_2$

j= Additive x Dominance type of gene interaction= $\overline{Bc}_1 - {}^1/_2\,\overline{P}_1 - \overline{Bc}_2 + {}^1/_2\,\overline{P}_2$.

I= Dominance x Dominance type of gene interaction = $\overline{P}_1 + \overline{P}_2 + 2\overline{F}_1 + 4\overline{F}_2 - 4\overline{Bc}_1 - 4\overline{Bc}_2$

Whereas, in the absence of epitasis, the simple genetic model (m, d and h) was applied using the formula by **Jinks and Jones (1958)** as follows:

Mean (m) = $\frac{1}{2}\,\overline{P}_1 + \frac{1}{2}\,\overline{P}_2 + 4\overline{F}_2 - 2\overline{Bc}_1 - 2\overline{Bc}_2$

Additive (d) = $\frac{1}{2}\,\overline{P}_1 - {}^1/_2\,\overline{P}_2$

Dominance (h)=$6\overline{Bc}_1+6\overline{Bc}_2-8\overline{F}_2-\overline{F}_1-3/2\,\overline{P}_1-3/2\,\overline{P}_2$.

Components of the genetic variance were estimated as follows:

$VE = 1/3\,(VP_1 + VP_2 + VF_1)$

$VD = 2(VF_2 - VBC_1 + VBC_2)$

$VH = 4(VF_2 - 1/2\,VD - VE)$

The following genetical parameters were estimated:

(a) Degree of dominance= $\sqrt{\frac{H}{D}}$

(b) Heritability:

Heritability in narrow sense "T_n" was estimated according to Hallauer (1989).

$T_n = (0.5VD) / (0.5VD + 0.25VH + VE)$

RESULTS AND DISCUSSION

Analysis of Variance

The results of analysis of variance revealed that mean squares due to genotypes of the six populations (P_1, P_2, F_1, F_2, BC_1, and BC_2) of four wheat crosses for the earliness characters are given in Table 3. The results indicated that, parental wheat genotypes and their populations mean squares were significant for days to heading on normal sowing date in all wheat crosses and in the 3rd cross on late sowing date; for days to maturity the 2nd cross on both sowing dates and the 4th cross on normal sowing date and 3rd cross on late sowing date were significant (Table 3). While all wheat crosses showed significant differences among genotypes for number of tillers/plant at both sowing dates. Number of spiklets/spike had significant differences for all crosses on both sowing dates except the 4th cross on both sowing dates and the 3rd cross on late sowing date. Moreover, number of grains/spike exhibited significant differences among genotypes for all crosses on both sowing dates except the 2nd cross on late sowing date. For weight of grains/spike, it recorded significant differences among genotypes for all crosses except the 3rd cross on normal and the 4th cross on late sowing dates, respectively. Also, grain yield/plant showed significant differences for all wheat crosses on both sowing dates except the 2nd and 3rd crosses on normal sowing date. Analysis of variance results for yield are presented in (Table 4).These results indicating the existence of genetic variation and possibility of selection for heat tolerance. These results are in well agreement with those of **Rashid *et al*. (2012), Adel and Ali (2013), Said (2014), Mahpara *et al*. (2018) and Raza *et al*. (2019)** they reported high variability for different characters among wheat genotypes.

Mean Performance

Earliness characters

Means and standard errors of the six populations (P_1, P_2, F_1, F_2, BC_1, and BC_2) of four crosses are shown in Table 5. For days to heading the F_1 means were earlier than the mean of their parents for all wheat crosses on both sowing dates except the 2nd cross on late sowing date. Also, the 1st and the 2nd crosses on normal sowing date and the 1st, 3rd and 4th crosses on late sowing date were earlier than the mean of their parents for days to maturity. These results provide evidence for the presence of heterotic effects and over-dominance gene effects and the decreasing alleles were more frequent than increasing ones in the genetic constitution of wheat genotypes. These results are in line with those reported by **LjubiČIĆ *et al*. (2017)** and **Raza *et al*. (2019)** recorded the inheritance of days to heading and maturity revealed complex inheritance due to the involvement of non-allelic interactions.

The F_2 means were earlier than the F_1 means for days to heading and maturity in the 1st and 2nd crosses on normal sowing date, indicating accumulation of decreasing alleles. Whereas it was more than the F_1 mean in the 4th cross on normal sowing date and the 1st, 2nd and 4th crosses on late sowing date, indicating accumulation of increasing alleles for these characters. Results indicated the presences of appreciable amount of genetic variability.

The means of $Bc_1$and Bc_2 were earlier than the means of $P_1$and P_2 in all crosses on both sowing dates except the 3rd cross for $Bc_1$and Bc_2 and the 4th cross for Bc_2 on late sowing date for days to heading as well as the 3rd and 4th crosses for Bc_2 on normal and late sowing dates for days to maturity. Similar results were obtained by **Rashid *et al*. (2012).**

Yield and its attributes

The results in Table 6 reveal that, F_1 means were higher than those of the highest parent or mid-parent in all wheat crosses on normal sowing date and the 1st and 4th crosses on late sowing date for number of tillers/plant; in all crosses on late sowing date and the 1st and 2nd crosses on normal sowing date for number of spiklets/spike; for number of grains/spike, in all crosses on both sowing dates except the 3rd cross on normal sowing date; in all crosses on both sowing dates except the 1st cross on normal sowing date for weight of grains/spike; as well as in the 1st and 4th crosses on normal sowing date and all crosses on late sowing date for grain yield/plant (Table 6).

Table 3. Mean squares for earliness characters in the four bread wheat crosses on the two sowing dates

SOV	d.f	Normal sowing (19th November)				Late sowing (3rd January)			
		1	2	3	4	1	2	3	4
						Days to heading			
Replication	**2**	3.79	3.50	2.06	2.20	0.99	7.25	1.85	2.72
Genotypes	**5**	11.59**	7.83**	5.30**	8.19**	6.02	8.73	5.77**	7.52
Error	**10**	2.16	2.23	1.34	1.51	2.79	3.09	0.98	2.49
						Days to maturity			
Replication	**2**	1.27	5.72	1.37	3.29	0.60	4.84	0.88	1.39
Genotypes	**5**	3.34	11.79**	3.86	9.17**	12.09	15.46**	5.47*	7.59
Error	**10**	1.63	2.19	1.32	1.74	4.38	2.28	1.14	3.26

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

Crosses: 1(line-4 × line-27), 2(line-15 × Shandaweel-1), 3(Misr-1 × line-15) and 4(Shandaweel-1 × line-27)

Table 4. Mean squares for yield, its components in the four bread wheat crosses on the two sowing dates

SOV	d.f	Normal sowing (19th November)				Late sowing (3rd January)			
		1	2	3	4	1	2	3	4
						Number of tillers/plant			
Replication	2	1.21	0.84	1.24	0.35	1.48	0.59	0.19	0.56
Genotypes	5	6.44**	12.36**	8.37**	12.45**	5.65**	4.94**	5.12**	10.72**
Error	10	0.81	0.65	0.98	0.43	1.00	0.80	0.53	1.36
						Number of spiklets/spike			
Replication	2	1.81	2.87	2.30	0.62	1.48	0.91	0.24	0.56
Genotypes	5	6.73**	9.80*	5.50*	3.73	4.58*	3.22*	0.93	2.50
Error	10	0.81	2.00	1.14	1.23	1.00	0.59	0.42	1.36
						Number of grains/spike			
Replication	2	3.76	12.55	7.89	0.02	5.42	1.20	0.58	1.24
Genotypes	5	73.78**	101.85**	139.76**	69.17*	17.60*	10.57	31.33*	29.00**
Error	10	8.36	10.68	6.67	17.16	5.09	3.81	9.03	3.14
						Weight of grains/spike (g)			
Replication	2	0.08	0.09	0.10	0.01	0.001	0.07	0.05	0.01
Genotypes	5	0.45**	0.37*	0.49	0.42*	0.42**	0.18*	0.35**	0.04
Error	10	0.08	0.11	0.28	0.12	0.07	0.05	0.03	0.02
						Grain weight /plant (g)			
Replication	2	0.14	0.15	1.27	3.01	0.45	1.81	0.37	0.01
Genotypes	5	13.45**	2.51	1.71	13.81**	23.47**	19.38**	13.00**	8.61*
Error	10	1.19	2.31	1.31	1.31	1.21	1.03	1.25	1.76

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

Crosses: 1(line-4 × line-27), 2(line-15 × Shandaweel-1), 3(Misr-1 × line-15) and 4(Shandaweel-1 × line-27)

Table 5. Mean ± SE for the six populations for earliness characters in the four bread wheat crosses on the two sowing dates

Crosses	Normal sowing (19th November)				Late sowing (3rd January)			
	1	2	3	4	1	2	3	4
Genotypes				**Days to heading**				
P_1	98.00±0.58	96.00±0.58	96.61±0.60	97.32±0.34	87.47±0.52	86.50±0.29	83.46±0.29	83.63±0.67
P_2	97.33±0.33	96.33±0.33	96.52±0.29	96.33±0.33	87.10±0.56	85.15±0.45	82.83±0.44	82.50±0.29
F_1	96.83±0.44	93.67±0.33	95.35±0.18	95.83±0.44	86.43±0.54	86.07±0.23	81.60±0.29	82.27±0.44
F_2	94.67±1.45	93.33±1.76	98.00±1.15	98.00±1.15	87.33±1.20	89.33±1.76	81.67±1.20	83.33±1.45
Bc_1	92.67±0.88	95.33±0.88	95.00±0.58	93.29±0.84	85.00±1.53	86.00±1.53	85.00±0.58	83.33±1.20
Bc_2	96.00±1.16	92.33±0.67	94.33±0.88	95.33±0.88	84.00±0.58	84.33±1.33	84.33±0.33	86.67±0.88
LSD 0.05	2.67	2.72	2.10	2.23	3.04	3.20	1.80	2.87
LSD 0.01	3.79	3.86	2.98	3.17	4.31	4.53	2.55	4.07
				Days to maturity				
P_1	149.33±0.33	148.67±0.33	147.68±0.32	148.65±0.33	142.13±0.58	141.50±0.29	138.13±0.44	137.29±0.33
P_2	149.67±0.33	150.33±0.33	149.52±0.29	148.67±0.33	141.77±0.15	139.48±0.29	137.50±0.29	136.50±0.29
F_1	148.77±0.16	147.67±0.33	147.80±0.36	150.50±0.29	139.77±0.50	139.73±0.15	135.93±0.17	135.93±0.17
F_2	148.67±1.45	147.00±1.53	147.33±1.20	151.33±1.76	142.00±1.53	145.00±1.53	135.67±1.20	137.33±1.45
Bc_1	149.00±0.56	147.67±1.20	149.33±0.33	146.63±0.37	138.67±1.76	140.33±1.20	139.00±0.58	136.33±1.33
Bc_2	146.67±0.67	144.33±1.20	146.67±0.88	147.67±0.67	137.33±1.20	138.67±1.20	138.33±0.33	140.33±1.33
LSD 0.05	2.32	2.69	2.09	2.40	3.81	2.75	1.94	3.28
LSD 0.01	3.29	3.82	2.96	3.40	5.40	3.89	2.76	4.66

*, **=significant at 0.05 and 0.01 levels of probability, respectively.
Crosses: 1(line-4 × line-27), 2(line-15 × Shandaweel-1), 3(Misr-1 × line-15) and 4(Shandaweel-1 × line-27)

Table 6. Mean ± SE for the six populations for yield, its components in the four bread wheat crosses on the two sowing dates

Crosses	Normal sowing (19th November)				Late sowing (3rd January)			
	1	2	3	4	1	2	3	4
Genotypes				**Number of tillers/plant**				
P1	8.33±0.55	5.47±0.34	7.63±0.32	4.40±0.15	6.17±0.25	4.59±0.11	4.96±0.13	5.43±0.30
P2	5.87±0.43	5.90±0.45	5.17±0.13	8.43±0.49	4.19±0.61	3.85±0.45	4.67±0.40	4.70±0.40
F1	6.90±0.50	10.60±0.06	7.03±0.19	7.73±0.18	4.86±0.29	5.44±0.29	4.77±0.17	5.96±1.01
F2	6.02±0.65	6.02±0.79	6.75±1.23	6.27±0.55	2.87±0.83	2.34±0.64	4.25±0.57	5.43±0.39
Bc1	8.80±0.71	6.67±0.58	8.00±0.61	7.80±0.17	3.83±0.92	4.42±0.09	3.41±0.53	9.50±0.76
Bc2	9.27±0.30	8.83±0.20	10.23±0.12	10.43±0.47	3.01±0.33	3.85±0.75	4.60±0.29	8.25±0.66
LSD 0.05	1.64	1.46	1.80	1.20	1.82	1.40	1.17	2.12
LSD 0.01	2.32	2.07	2.55	1.70	2.58	1.98	1.67	3.00
				Number of spiklets/spike				
P1	15.00±0.29	16.72±0.49	18.83±0.30	15.80±0.61	14.02±0.32	15.33±0.34	15.21±0.21	14.47±0.29
P2	16.00±0.29	17.34±0.49	17.91±0.27	15.98±0.04	13.11±0.06	14.32±0.38	16.26±0.32	14.83±0.39
F1	19.31±0.89	19.51±0.33	18.69±0.24	16.80±0.28	14.06±0.12	16.35±0.33	15.68±0.17	15.18±0.59
F2	15.96±0.16	16.23±1.17	15.76±1.21	14.53±0.99	12.54±1.08	15.22±1.12	14.30±0.60	14.77±0.89
Bc1	16.29±0.65	19.83±1.04	16.08±0.94	14.05±0.48	11.16±0.29	16.44±0.82	15.58±0.38	15.22±0.75
Bc2	17.26±0.74	20.50±1.11	16.49±0.30	16.63±0.78	12.46±0.33	12.43±0.62	15.70±0.51	13.06±0.23
LSD 0.05	1.64	2.57	1.94	2.02	1.53	2.10	1.10	1.74
LSD 0.01	2.32	3.65	2.75	2.87	2.18	2.98	1.56	2.46

*, **=significant on 0.05 and 0.01 levels of probability, respectively.
Crosses: 1(line-4 × line-27), 2(line-15 × Shandaweel-1), 3(Misr-1 × line-15) and 4(Shandaweel-1 × line-27)

Table 6.Cont.

Crosses	Normal sowing (19th November)				Late sowing (3rd January)			
	1	2	3	4	1	2	3	4
Genotypes	**Number of grains/spike**							
P_1	54.82±0.51	51.29±1.16	64.18±0.98	52.58±0.87	44.47±0.15	47.23±0.79	48.52±0.63	45.97±0.55
P_2	49.48±0.48	62.94±1.28	56.71±0.22	56.45±1.05	45.36±0.55	46.95±0.54	46.00±1.15	45.67±0.33
F_1	53.09±0.29	63.58±1.06	49.34±0.53	60.95±1.34	49.14±0.35	50.00±0.58	48.33±0.88	47.90±0.10
F_2	57.82±2.40	49.98±3.58	46.29±2.44	59.12±3.60	43.37±2.81	44.93±1.77	44.69±2.44	42.28±1.46
Bc_1	63.42±2.59	55.38±2.04	46.44±1.71	51.99±3.19	49.12±0.99	48.02±1.46	40.67±1.74	39.25±1.07
Bc_2	51.84±1.45	59.59±0.96	49.38±2.65	48.22±1.36	45.52±1.71	45.20±0.48	42.03±2.50	43.04±1.39
LSD 0.05	5.26	5.95	5.81	7.54	4.10	3.55	5.47	3.22
LSD 0.01	7.46	8.43	8.24	10.69	5.82	5.04	7.75	4.57
	Weight of grains/spike (g)							
P_1	3.09±0.09	3.25±0.14	3.38±0.23	2.64±0.17	1.44±0.05	1.89±0.01	1.93±0.04	1.64±0.07
P_2	3.30±0.16	3.11±0.05	3.28±0.22	3.24±0.13	1.65±0.02	1.61±0.03	1.90±0.03	1.54±0.06
F_1	3.42±0.12	3.70±0.13	3.20±0.09	3.29±0.14	2.35±0.03	2.08±0.07	2.12±0.03	1.66±0.08
F_2	2.87±0.23	3.01±0.37	2.50±0.55	2.90±0.26	1.72±0.26	1.66±0.29	1.81±0.18	1.64±0.09
BC_1	2.77±0.14	2.82±0.16	2.46±0.14	2.30±0.15	1.40±0.08	1.74±0.07	1.73±0.14	1.80±0.10
BC_2	2.36±0.19	3.63±0.09	3.08±0.24	2.83±0.23	1.32±0.19	1.37±0.13	1.79±0.13	1.45±0.11
LSD 0.05	0.50	0.60	0.96	0.63	0.47	0.42	0.27	0.29
LSD 0.01	0.72	0.85	1.36	0.90	0.67	0.59	0.32	0.41
	Grain weight /plant (g)							
P_1	23.53±0.48	23.88±0.81	26.25±0.25	23.17±0.52	8.40±0.52	14.00±0.58	17.20±0.61	13.81±0.59
P_2	19.49±0.17	23.48±0.24	25.37±0.19	25.52±0.63	8.55±0.26	16.10±0.10	17.18±0.24	15.68±0.34
F_1	25.13±0.37	23.00±0.67	24.99±0.28	27.21±0.81	9.21±0.03	15.85±0.45	17.63±0.61	15.42±0.74
F_2	22.68±1.04	23.49±1.14	24.30±1.01	23.63±0.86	8.60±0.99	9.05±0.83	12.63±0.89	14.51±1.04
Bc_1	25.31±0.61	22.61±0.43	24.18±1.01	21.01±0.60	14.92±0.88	14.16±0.94	17.56±0.69	15.43±0.21
Bc_2	23.49±0.42	25.26±0.67	24.92±0.45	25.01±0.88	6.91±0.27	13.51±0.44	14.42±0.38	11.20±0.88
LSD 0.05	1.98	2.76	2.08	2.08	2.00	1.84	2.03	2.41
LSD 0.01	2.81	3.92	2.96	2.95	2.84	2.61	2.88	3.42

*, **=significant at 0.05 and 0.01 levels of probability, respectively.
Crosses: 1(line-4 × line-27), 2(line-15 × Shandaweel-1), 3(Misr-1 × line-15) and 4(Shandaweel-1 × line-27)

These results provide evidence for the presence of over-dominance gene effects and increasing alleles were more frequent than decreasing ones in the genetic makeup of parental materials. These results are in accordance with those reported **by Erkul *et al*. (2010), Zaazaa *et al*. (2012), LjubiČIĆ *et al*. (2017), Maqsood *et al*. (2018) and Raza *et al*. (2019)** they recorded that The F_1 population was higher than the respective parents in most crosses in studied traits.

The F_2 means were lower than the F_1 means in all crosses on both sowing dates for yield and its attributes, indicating the presence of inbreeding depression and transgressive segregations.

The means of $Bc_1$and Bc_2 were higher than the means of P_1 and P_2 for number of tillers/plant in all crosses on normal sowing date and lower than all crosses on late sowing date; the means of $Bc_1$and Bc_2 were higher than the means of $P_1$and P_2 in all crosses except the 3rd and BC_1 in the 4th cross on normal sowing date and BC_1 in the 2nd, 3rd and 4th crosses on late sowing date, as well as for number of spiklets/spike. Moreover, for number of grains/spike, the means of BC_1 were higher than the means of P_1 in the 1st and 2nd crosses on both sowing dates, While, BC_2 was higher than the means of P_2 in all crosses on normal sowing date except the 1st cross and the 1st and 2nd crosses on late sowing date; for weight of grains/spike, the means of $BC_1$and BC_2 were less than the means of $P_1$and P_2 in all crosses on normal sowing date except BC_2 in the 2nd cross while the means were less in all crosses except BC_1 in the 4th cross on late sowing date and grain yield/plant the mean of BC_1 were less than P_1 in all crosses except the 1st cross on normal sowing date, While, it was higher in all crosses on late sowing date. The mean of BC_2 were less than P_2 in all crosses on both sowing dates except the 1st and 2nd crosses on normal sowing date. These results are in harmony with those obtained by **Amin (2013).**

Types of Gene Action and Heritability

Earliness characters

The one of least from scaling test measures (A, B, C and D) had significant variations in all crosses on both sowing dates for days to heading and maturity, it provide evidence for the failures of a simple genetic model to explain the genetic mechanism controlling, indicate the presence of non-allelic interaction (epistasis) and the digenic model was adequate to explain the inheritance of both characters in corresponding crosses. In this connection, the complex genetic model was found to be controll the inheritance of these characters Tables 7. These results are in accordance with those reported by **Mahpara *et al*. (2018), Maqsood *et al*. (2018) Raikwar (2019)** they reported that genetic analysis showed that all traits under study were under the control of complex inheritance due to presence of epistasis

The mean (m) was highly significant for days to heading and maturity in all crosses under normal and late sowing dates, reflecting the contribution due to the overall mean plus the low effects and interaction of the fixed loci.

The additive (d) was the main type controlling the inheritance of days to heading in the 1st and 2nd crosses on normal sowing date and the 4th cross on late sowing date. For days to maturity it was significant in the 1st, 2nd and 3rd crosses on normal sowing date and the 4th cross on late sowing date. Therefore, phenotypic selection was more effective for improving earliness characters in those crosses.

The interaction types of gene action additive × additive (i) and dominance × dominance (l) in the 3rd cross on both sowing dates and the 4th cross on normal sowing date of days to heading, and the 4th cross on normal sowing and all crosses except the 4th cross on late sowing date, and additive × dominance (j) only in the 1st and 2nd crosses on normal sowing date and the 4th cross on late sowing date for days to heading and days to maturity, and the 3rd cross on normal sowing date of days to maturity were involved in the inheritance of earliness characters, These cross combinations could be considered the most promising materials for recurrent selection programs for earliness.

The dominance (h) and its digenic interaction type dominance × dominance (l) were significant and involved in the inheritance in the 3rd and 4th crosses on normal sowing date and the 3rd cross on late sowing date for days to heading and the 4th cross on normal sowing and all crosses except the 4th cross on late sowing date for days to maturity. The considerable amount of non-fixable gene action type displayed by these characters in the corresponding crosses may suggest the improving of these characters could be achieved through hybrid bulk breeding method. The negative value of (h) detected in most wheat crosses for earliness traits, indicated that the alleles responsible for less value of the trait were dominant over the alleles controlling high value.

In addition, it is worth noting to the dominance (h) and its digenic interaction dominance × dominance (l) were significant and have different signs indicating that interaction is predominantly of duplicate type. Various investigators stated similar results by **Raikwar (2019) and Raza *et al*. (2019).**

Additive genetic variance (D) was controlling days to heading in the 2nd cross on normal sowing date and the 3rd cross on late sowing date, as well as for days to maturity in the 3rd cross on both sowing dates and the 1st and 4th

Table 7. Scaling test and gene action for earliness characters using six populations in the four bread wheat crosses on the two sowing dates

Sowing date	Normal sowing (19th November)				Late sowing (3rd January)			
Crosses	**1**	**2**	**3**	**4**	**1**	**2**	**3**	**4**
Character				**Days to heading**				
Scaling test								
A	-9.50**	1.00	-1.96	-6.57**	-3.90	-0.57	4.94**	0.77
B	-2.17	-5.33**	-3.21	-1.50	-5.53**	-2.55	4.23**	8.57**
C	-10.33	-6.33	8.16	6.68	1.90	13.55	-2.83	2.67
D	0.67	-1.00	6.67**	7.37**	5.67	8.33*	-6.00*	-3.33
Adequacy genetic model								
m	94.67**	93.33**	98.00**	98.00**	87.33**	89.33**	81.67**	83.33**
d	-3.33*	3.00**	0.67	-2.04	1.00	1.67	0.67	-3.33*
h	-2.17	-0.50	-14.55**	-15.74**	-12.18*	-16.43*	10.45*	5.87
i	-1.33	2.00	-13.33**	-14.75**	-11.33	-16.67*	12.00*	6.67
j	-7.33*	6.33**	1.24	-5.07*	1.63	1.98	0.71	-7.79**
l	13.00	2.33	18.50**	22.81**	20.77*	19.78	-21.17**	-16.01
Components of genetic variance								
D	6.33	15.00	4.67	3.53	0.67	6.33	7.33	6.00
H	10.11	5.11	4.79	7.26	12.54	23.29	1.22	10.44
E	0.64	0.56	0.47	0.42	0.87	0.34	0.36	0.72
√H/D	1.26	0.58	1.01	1.43	4.34	1.92	0.41	1.32
T(n)%	50.00	80.36	58.33	44.11	7.69	33.93	84.62	47.37
				Days to maturity				
Scaling test								
A	-0.10	-1.00	3.19**	-5.90**	-4.57	-0.57	3.94**	-0.56
B	-5.10**	-3.33**	-3.99*	-3.83**	-6.87**	-1.88	3.23**	8.23**
C	-1.87	-6.33	-3.46	7.01	4.57	19.55**	-4.83	3.67
D	1.67	2.00	-1.33	8.37*	8.00*	11.00**	-6.00*	-2.00
Adequacy genetic model								
m	148.67**	147.00**	147.33**	151.33**	142.0**0	145.00**	135.67**	137.33**
d	2.33**	3.33*	2.67**	-1.04	1.33	1.67	0.67	-4.00*
h	-4.07	-5.83	1.87	-14.91*	-18.18*	-22.76**	10.12*	3.04
i	-3.33	-4.00	2.67	-16.75*	-16.00*	-22.00**	12.00*	4.00
j	5.00**	8.33*	7.18**	-2.07	2.30	1.32	0.71	-8.79*
l	8.53	14.33	-1.87	26.48**	27.43**	24.45**	-19.17**	-11.67
Components of genetic variance								
D	10.33	5.33	6.00	16.92	0.33	5.33	7.33	2.00
H	3.69	16.00	4.07	2.30	24.89	16.58	1.44	20.44
E	0.24	0.33	0.31	0.30	0.61	0.19	0.31	0.22
√H/D	0.60	1.73	0.82	0.37	8.64	1.76	0.44	3.20
T(n)%	81.58	38.10	69.23	90.62	2.38	38.10	84.62	15.79

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

Crosses: 1(line-4 × line-27), 2(line-15 × Shandaweel-1), 3(Misr-1 × line-15) and 4(Shandaweel-1 × line-27)

crosses on normal sowing date, resulting in $(H/D)^{1/2}$ ratio was less than unity, suggesting the effectiveness of phenotypic selection for improving the foregone characters in these crosses. Similar results were found by **Awaad (2002)**.

The dominance genetic variance (H) was the prevailed type controlling the inheritance of days to heading in all crosses on both sowing dates except the 2nd cross on normal sowing date and the 3rd cross on late sowing date; days to maturity in the 2nd cross on normal sowing date and all crosses except the 3rd cross on late sowing date, resulting in $(H/D)^{1/2}$ more than unity. Indicating the importance of over-dominance in the genetic mechanism controlling the abovementioned characters in these crosses, therefore the effectiveness of using hybrid breeding method when commercial seed production of wheat is feasible.

Narrow sense heritability estimates recorded high to moderate values (>44%) for days to heading in all crosses except the 1st and 2nd crosses on late sowing date, and days to maturity in all crosses except the 2nd cross on both sowing dates and the 1st and 4th crosses on late sowing date. These results allowing for considerable progress from selection. Various investigators stated similar results by **(El-Marakby *et al.* 2007; Magda and El-Rahman, 2013; Raza *et al*., 2019)**

Yield and its attributes

Results presented in Table 8 show that scaling test (A, B, C and D) revealed the presence of non-allelic gene interaction for number of tillers/plant, number of spiklets/spike, weight of grains/spike in all crosses on both sowing dates, number of spiklets/spike except in the 3rd and 4th crosses on normal sowing date and grain yield/plant except the 2nd and 3rd crosses on normal sowing date. These results indicated the presence of epistasis and the complex genetic model was found to adequate for explaining the inheritance of the aforementioned characters in the corresponding crosses .In this connection, the model was found to be adequate to explain the genetics of yield components. Similar results were recorded by **Usman and Kashif (2013), LjubiČIĆ *et al.* (2017), Mahpara *et al*. (2018) and Raikwar (2019)**.

The insignificancy of non-allelic interaction tests were observed in number of spiklets/spike in the 3rd and 4th crosses on normal sowing date and grain yield/plant in the 2nd and 3rd crosses on normal sowing date. The previous results indicated that, the simple additive-dominance genetic model proved to be satisfactory in explaining the inheritance of these characters. Similar results were recorded by **Magda and El-Rahman (2013) and Bilgin *et al*. (2016)**

The mean parameter (m) values were highly significant for yield and its attributes in all crosses on both sowing dates, indicated that these traits were quantitatively inherited.

The additive gene action (d) was significant for number of tillers/plant in the 2nd, 3rd and 4th crosses on normal sowing date and the 3rd and 4th crosses on late sowing date; number of spiklets/spike in the 4th cross on normal sowing date and all crosses on late sowing date except the 3rd cross; number of grains/spike in the 1st and 2nd crosses on normal sowing date and the 4th cross on late sowing date; weight of grains/spike in all crosses except the 1st cross on normal sowing date and the 2nd and 4th crosses on late sowing date and grain yield/plant in all crosses except the 3rd cross on normal sowing date and all crosses except the 2nd cross on late sowing date. Furthermore, the additive gene action (d) and its digenic type, additive × additive were significant for number of tillers/ plant in the 2nd and 4th crosses on normal sowing date, the 3rd cross on late sowing date of grain yield/plant. These results indicated that, the superior genotypes could efficiently identified from its phenotypic expression, therefore phenotypic selection was more effective for improving these characters in those crosses. Similar results were recorded by **Mahpara *et al.* (2018) and Raza *et al*. (2019)**

The dominance gene action (h) and its digenic type dominance × dominance (l) values were significant and have opposite signs and involved in the inheritance of number of tillers/plant in the 1st, 3rd and 4th crosses on normal sowing date; number of spiklets/spike in the 2nd cross on normal sowing date; weight of grains/spike in the 1st cross on normal sowing

Table 8. Scaling test and gene action for yield, its components using six populations in the four bread wheat crosses on the two sowing dates

Sowing date	Normal sowing (19th November)				Late sowing (3rd January)			
Crosses	**1**	**2**	**3**	**4**	**1**	**2**	**3**	**4**
Character	**Number of tillers/plant**							
Scaling test								
A	2.37	-2.73*	1.33	3.47**	-3.36	-1.19**	-2.91**	-0.66
B	5.77**	1.17	8.27**	4.70**	-3.04**	-1.59	-0.25	-4.01**
C	-3.93	-8.50**	0.13	-3.23	-8.61*	-9.96*8	-2.19	0.17
D	-6.03**	-3.47*	-4.73	-5.70**	-1.11	-3.59*	0.49	2.42
Adequacy genetic model								
m	6.02**	6.02**	6.75**	6.27**	2.87**	2.34**	4.25**	5.29**
d	-0.47	-2.17**	-2.23**	-2.63**	0.83	0.57	-1.19*	2.04*
h	11.87**	11.85**	10.10*	12.72**	1.89	8.41**	-1.02	-4.48
i	12.07**	6.93*	9.47	11.40**	2.21	7.19*	-0.97	-4.84
j	-3.40*	-3.90**	-6.93**	-1.23	-0.32	0.39	-2.66*	3.35
l	-20.20**	-5.37	-19.07**	-19.57**	4.19	-4.41	4.13	9.52
Components of genetic variance								
D	0.76	2.64	7.84	1.05	1.25	0.76	1.21	3.05
H	0.59	0.88	1.71	0.30	3.64	2.23	0.45	4.55
E	0.74	0.35	0.15	0.30	0.52	0.30	0.25	0.40
√H/D	0.88	0.58	0.47	0.54	1.71	1.71	0.61	1.22
T(n) (%)	29.95	69.86	87.08	58.51	30.35	30.60	62.65	49.80
	Number of spiklets/spike							
Scaling test								
A	1.63	3.44	-2.42	-2.24	-5.77**	1.21	0.79	0.79
B	2.56	4.16	-0.69	2.75	-2.65**	-5.80**	-0.50	-3.90**
C	14.34**	-8.15	6.50	6.35	-5.08	-1.45	-5.63*	-0.58
D	5.08*	-7.87**	4.80	2.92	1.67	1.57	-2.96*	1.26
Adequacy genetic model								
m	19.31**	16.23**	18.69**	16.80**	12.54**	15.22**	14.30**	14.77**
d	-0.97	-0.67	-0.41	-2.58**	-1.10*	4.01**	0.13	2.16**
h	-9.69*	18.22**	-12.23*	-7.19	-2.84	-1.62	5.87*	-2.00
i	-10.15*	15.74**			-3.34	-3.14	5.92*	-2.53
j	-0.93	-0.72			-3.12**	7.01**	1.29	4.68**
l	5.96	-23.34**			11.76*	7.73	-6.22	5.64
Components of genetic variance								
D	1.83	1.22	5.90	3.35	6.35	4.33	1.26	2.89
H	5.06	11.57	4.90	3.21	0.71	4.89	1.06	1.39
E	0.19	0.60	0.23	0.45	0.12	0.37	0.18	0.58
√H/D	1.66	3.08	0.91	0.98	0.33	1.06	0.92	0.69
T(n)%	38.53	14.91	67.02	57.16	91.47	57.65	58.54	60.83

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

Crosses: 1(line-4 × line-27), 2(line-15 × Shandaweel-1), 3(Misr-1 × line-15) and 4(Shandaweel-1 × line-27)

Table 8. Cont.

Sowing date	Normal sowing (19th November)				Late sowing (3rd January)			
Crosses	1	2	3	4	1	2	3	4
Character	**Number of grains/spike**							
Scaling test								
A	18.94**	-1.31**	-20.65**	-9.55	4.63*	-1.20	-15.52**	-15.37**
B	1.11	0.46*	-7.30	-20.96**	-3.47	-6.56**	-10.28**	-7.49**
C	20.78*	-1.72	-34.40**	5.56	-14.63	-14.47*	-12.42	-18.33**
D	0.37	-0.43	-3.23	18.03*	-7.90	-3.36	6.69	2.27
Adequacy genetic model								
m	57.82**	3.01**	46.29**	59.12**	43.37**	44.93**	44.69**	42.28**
d	11.58**	-0.82**	-2.94	3.77	3.61	2.82	-1.36	-3.79*
h	0.20	1.39	-4.65	-29.64	20.01	9.62	-12.31	-2.46
i	-0.74	0.86	6.45	-36.07*	15.79	6.71	-13.38	-4.54
j	17.83**	-1.77**	-13.35**	11.41	8.10*	5.36	-5.25	-7.88*
l	-19.30	0.00	21.50	66.57**	-16.95	1.05	39.18**	27.40**
Components of genetic variance								
D	8.21	0.73	13.02	41.78	35.74	11.81	15.30	3.60
H	50.68	0.05	26.05	57.33	21.71	9.11	30.72	16.80
E	0.57	0.04	4.80	3.66	0.45	1.25	2.50	0.42
√H/D	2.48	0.27	1.41	1.17	0.78	0.88	1.42	2.16
T(n)%	23.66	87.66	36.53	53.72	75.25	62.58	42.89	28.00
	Weight of grains/spike (g)							
Scaling test								
A	-0.42	-1.31*	-1.66**	-1.34**	-1.00**	-0.48**	-0.58*	-0.02
B	-1.46**	0.46*	-0.32	-0.88	-1.35**	-0.96**	-0.45	-0.33**
C	1.52	-1.72	-3.06	-0.88	-0.90	-1.02	-0.82	-0.31
D	1.70**	-0.43	-0.54	0.67	0.73	0.21	0.10	0.02
Adequacy genetic model								
m	3.42**	3.01**	2.50**	2.90**	1.72**	1.66**	1.81**	1.64**
d	0.42	-0.82**	-0.62*	-0.53*	0.07	0.38*	-0.05	0.22**
h	-3.73**	1.39	0.95	-0.98	-0.65	-0.10	-0.01	0.12
i	-3.41**	0.86	1.08	-1.34	-1.45	-0.43	-0.21	-0.04
j	1.04*	-1.77**	-1.35*	-0.46	0.36	0.48	-0.14	0.31**
l	5.29**	0.00	0.90	3.56*	3.80**	1.87	1.24	0.39
Components of genetic variance								
D	0.15	0.73	1.62	0.19	0.29	0.43	0.08	0.04
H	0.16	0.05	0.02	0.19	0.23	0.11	0.21	0.01
E	0.05	0.04	0.11	0.06	0.01	0.01	0.01	0.01
√H/D	1.02	0.27	0.10	1.00	0.89	0.50	1.66	0.41
T(n)%	47.47	87.66	87.64	45.80	70.04	86.75	40.49	77.24

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

Crosses: 1(line-4 × line-27), 2(line-15 × Shandaweel-1), 3(Misr-1 × line-15) and 4(Shandaweel-1 × line-27)

Table 8. Cont.

Sowing date	Normal sowing (19th November)				Late sowing (3rd January)			
Crosses	1	2	3	4	1	2	3	4
Character	grain weight/plant (g)							
Scaling test								
A	4.41**	-1.66	-2.18	-8.36**	12.85**	-1.53	0.28	1.63
B	4.82**	4.04	0.16	-2.72	-3.32**	-4.93**	-5.97**	-8.71**
C	12.17**	0.62	-0.25	-8.59*	2.69	-25.60**	-19.10**	-2.29
D	1.47	-0.88	0.89	1.25	-3.42	-9.57**	-6.71**	2.40
Adequacy genetic model								
m	25.13**	23.49**	24.99**	23.63**	9.21**	9.05**	12.63**	14.51**
d	1.82*	-2.65*	-0.73	-4.00**	8.01**	0.65	3.13**	4.23**
h	-1.77	1.07	-3.28	0.37	6.96	19.93**	13.86**	-4.12
i	-2.94			-2.50	6.84	19.13**	13.42**	-4.79
j	-0.41			-5.65*	16.17**	3.40	6.25**	10.34**
l	-6.28			13.58*	-16.37**	-12.67*	-7.74	11.88*
Components of genetic variance								
D	4.85	3.47	2.45	1.06	3.40	0.95	2.86	4.09
H	1.69	3.94	5.87	1.51	3.70	4.25	0.49	0.84
E	0.40	1.17	0.37	1.32	0.34	0.55	0.80	1.02
√H/D	0.59	1.07	1.55	1.20	1.04	2.12	0.41	0.45
T(n)%	74.72	44.59	40.05	23.80	57.36	22.71	60.78	62.44

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

Crosses: 1(line-4 × line-27), 2(line-15 × Shandaweel-1), 3(Misr-1 × line-15) and 4(Shandaweel-1 × line-27)

date and grain yield/plant in the 3rd cross on late sowing dates. These results indicated that interaction is predominantly of duplicate type, the non-fixable gene action type displayed by these characters in these crosses may suggest that improving these characters could be achieved through hybrid breeding method. In this respect, **Mahpara *et al*. (2018)** found that the dominance (h) and type of gene action dominance × dominance (l) were involved in the inheritance of these characters.

Additive genetic variance (D) was the predominant type controlling number of tillers/ plant in all crosses on normal sowing date and the 3rd cross on late sowing date; number of spiklets/ spike in the 3rd and 4th crosses on both sowing dates and the 1st cross on late sowing date; number of grains/spike in the 2nd cross on both sowing dates and the 1st cross on late sowing date; weight of grains/spike in the 2nd cross on both sowing dates and the 3rd cross on normal sowing date, the 1st and 4th crosses on late sowing date and grain yield/plant in the 1st cross on normal sowing date and the 3rd and 4th crosses on late sowing date, resulting in $(H/D)^{1/2}$ ratio was less than unity, suggesting the effectiveness of phenotypic selection for improving the foregone characters in this crosses. These results are in accordance with those reported by **Adel and Ali (2013)**

The dominance genetic variance (H) was the prevailed type controlling the inheritance of number of tillers/plant in the 1st, 2nd and 4th crosses on late sowing date; number of spiklets/spike in the 2nd cross on both sowing dates and the 1st cross on normal sowing date;

number of grains/spike in the 3rd and 4th crosses on both sowing dates and the 1st cross on normal sowing date; weight of grains/spike in the 1st and 4th crosses on normal sowing date and the 3rd cross on late sowing date and grain yield/plant in the 2nd , 3rd and 4th crosses on normal sowing date and the 1st and 2nd crosses on late sowing date, resulting in $(H/D)^{1/2}$ more than unity. Indicating the importance of over-dominance in the genetic mechanism controlling the abovementioned characters in this crosses, therefore the effectiveness of using hybrid breeding method when commercial seed production of wheat is feasible. **Raikwar (2019)** which reported that magnitude of dominance effect (h) has a greater value than additive effect (d) in all the traits, digenic interaction indicated complex nature of inheritance means non-additive gene action.

Narrow sense heritability estimates recorded high values (>50%) for number of tillers/plant in the 3rd cross on both sowing dates and the 2nd and 4th on normal sowing date; number of spiklets/spike in all crosses on both sowing dates except the 1st and 2nd crosses on normal sowing date; number of grains/spike in the 2nd cross on both sowing dates and the 4th cross on normal sowing date and the 1st cross on late sowing date; weight of grains/spike in the 2nd cross on both sowing dates and the 3rd on normal sowing date , the 1st and 4th crosses on late sowing date and grain yield/plant in the 1st cross on both sowing dates and the 3rd and 4th crosses on late sowing date. These results allowing for considerable progress from selection. These results are in well agreement with those obtained by **Magda and El-Rahman (2013), Badran and Moustafa (2015), Maqsood *et al*. (2018) and Raza *et al*. (2019)** where they reported that most of the examined traits revealed moderate to high heritability grain weight/spike

Whereas, low to moderate heritability in narrow sense "T_n" estimates were reported for number of tillers/plant in the 1st cross on both sowing dates and the 4th cross on late sowing date; number of spiklets/spike in the 1st and 2nd crosses on normal sowing date; number of grains/spike in the 3rd cross on both sowing dates, the 1st cross on normal sowing and the 4th cross on late sowing date; weight of grains/spike in the 1st and 4th crosses on normal sowing date and 3rd on late sowing date and grain yield/plant in the 2nd cross on both sowing dates and the 3rd and 4th crosses on normal sowing date, Indicating that non-additive genetic effects controlling the inheritance of these traits. Similar results were obtained by **Erkul *et al*. (2010) and Rabbani *et al*. (2011).**

Conclusion

This study purpose to genetic analysis for earliness and grain yield of bread wheat under heat stress in four bread wheat crosses in six populations. Where, the results showed that the analysis of variance revealed significant differences between parental wheat genotypes and their crosses in non-segregating and segregating generations for most studied characters on both normal and late sowing dates providing evidence for the presence of adequate amount of genetic and the 3rd cross more tolerant of heat stress than the other crosses.

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التحليل الوراثى لصفات التبكير والمحصول فى قمح الخبز تحت ظروف الإجهاد الحرارى

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أجريت هذه الدراسة فى المزرعة البحثية- كلية الزراعة بغزالة- الزقازيق – محافظة الشرقية - مصر خلال الموسم الشتوى لأعوام ٢٠١٥/٢٠١٦ – ٢٠١٦/٢٠١٧ و ٢٠١٧/٢٠١٨ بهدف تحديد الموديل الوراثى الملائم وطرز الفعل الجينى المتحكم فى وراثة صفات التبكير والمحصول ومكوناتة لأربع هجن من قمح الخبز، تحت ميعادى زراعة ١٩ نوفمبر و ٣ يناير باستخدام نموذج تحليل العشائر الستة، وقد أظهرت نتائج اختبار المقياس (A, B, C and D) أن الموديل الوراثى المعقد هو الملائم لتفسير وراثة صفات التبكير، عدد الأشطاء/النبات، عدد حبوب السنبلة ووزن حبوب السنبلة فى جميع الهجن تحت ميعادى الزراعة، بينما صفات عدد السنيبلات/السنبلة فى كلا الهجينين الثالث والرابع وصفة محصول النبات الفردى فى الهجينين الثانى والثالث كان الموديل الوراثى البسيط ملائم لتفسير وراثة تلك الصفات تحت ميعاد الزراعة الأمثل، كانت قيم كفاءة التوريث في المعنى الضيق مرتفعة لصفة عدد الأيام حتى الطرد فى الهجينين الاول والثانى تحت ميعاد الزراعة الامثل والهجين الثالث تحت ميعادى الزراعة، وفى الهجينين الأول والرابع تحت ميعاد الزراعة الأمثل والهجين الثالث تحت ميعادى الزراعة لصفة عدد الأيام حتى النضج، بينما كانت مرتفعة فى الهجين الثالث تحت ميعادى الزراعة و الهجينين الثانى والرابع تحت ميعاد الزراعة الأمثل لصفة عدد الأشطاء/النبات، وفى جميع الهجن تحت ميعادى الزراعة ماعدا الهجينين الأول والثانى تحت ميعاد الزراعة الأمثل لصفة عدد السنيبلات/السنبلة، بالنسبة لصفة عدد الحبوب/السنبلة كانت مرتفعة فى الهجين الثانى تحت ميعادى الزراعة والهجين الرابع تحت ميعاد الزراعة الأمثل والهجين الأول تحت ميعاد الزراعة المتأخر، وفى الهجينين الثانى والثالث تحت ميعادى الزراعة والهجين الثالث تحت ميعاد الزراعة الأمثل و الهجينين الأول والرابع تحت ميعاد الزراعة المتأخر لصفة وزن حبوب/السنبلة و الهجين الأول تحت ميعادى الزراعة و الهجينين الثالث والرابع تحت ميعاد الزراعة المتأخر لصفة محصول النبات الفردى.

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