



**Heat stress effect on the inheritance of yield, its components
and associated traits in two bread wheat crosses**



Amany N. Sayed

Department of Agronomy, Faculty of Agriculture, Ain Shams University, Cairo 11241, Egypt

تأثير الإجهاد الحراري على وراثته المحصول ومكوناته والصفات المرتبطة في هجينين من قمح الخبز

ABSTRACT

The six-population model supports the development of strategies for selecting genotypes with enhanced heat tolerance and yield stability, which are crucial for wheat improvement programs targeting adverse climate conditions. This study was dedicated to exploring the genetic control and heterosis of earliness, physiological, and yield traits under optimum and late sowing dates. The used plant material was six populations (P_1 , P_2 , F_1 , F_2 , BC_1 , and BC_2) derived from two crosses of bread wheat; Cross I (Line 606 \times Sakha 95) and Cross II (Cham 8 \times Masr 3). The results displayed highly significant mean squares due to generations. Heterosis estimates were negative and significant for earliness traits and positively significant for the remaining traits, with a few exceptions. Moreover, at least one of the non-allelic interactions is significant or highly significant, proving the appropriateness of the six parameters model to estimate the different gene effect types governing most studied characters. However, the simple additive-dominance genetic model clarified the inheritance of the number of spikes/plant and days to maturity in cross I (Line 606 \times Sakha 95), and number of spikes/plant and number of grains/spike in cross II (Cham 8 \times Masr 3) at late sowing. Heritability estimates are labeled as very high to moderately high in the broad sense and, in the meantime, varied as low, medium, and high in the narrow sense. The expected genetic advance had varied values, which ranged from 4.55% days to maturity at the recommended sowing in the cross II (Cham 8 \times Masr 3) to 76.07% for the weight of 100-kernel at the late date in the cross I (Line 606 \times Sakha 95). Our findings provide valuable insights for wheat breeding programs targeting enhanced yield and heat tolerance.

Keywords: *Triticum aestivum* L., Sowing dates, Generations mean analysis, Genetic parameters

Corresponding author E-mail: Amany87323@agr.asu.edu.eg

Submit date: 28-09-2024

Revise date: 29-10-2024

Accept date: 04-11-2024

1. INTRODUCTION

Evidently, climate change poses challenges to agriculture, which can severely impact crop yield, productivity (Shahin *et al.*, 2023) and quality around the world, particularly in the context of heat stress. One of the climate change scenarios illustrated that by 2100, the average temperature will have increased from 1.8 to 4 °C. (IPCC, 2007). During the growing season of crops, a temperature increment by one degree Celsius can cause a 17% reduction in these crops' yield (Öztürket *et al.*, 2015). Consequently, climate change poses a threat to the security of food globally (Ul-Allah *et al.*, 2023). Accordingly, cultivars with high yields must be produced and developed in stressed conditions for sustainable crop production. Wheat is one of these economic crops around the world where unfavorable climate conditions during critical growth periods can lead to substantial yield losses. Among these challenges was heat stress, which significantly affected wheat growth and yield (Karla *et al.*, 2023). Crops that are exposed to changing climate conditions during the growing season have limitations in yield prospects (Assenget *et al.*, 2013; Paymardet *et al.*, 2018). Late sowing dates limit wheat production and productivity because the plants are subjected to ultimate heat stress conditions that arise within the reproductive phase and early grain filling (Lobell *et al.*, 2012; Zheng *et al.*, 2012), leading to the termination of physiologic and metabolic processes (Gupta *et al.*, 2013), such as earliness traits, chlorophyll content in plants, and cell membrane thermostability. These metrics can be used as indicators to identify and select wheat genotypes that are heat-tolerant or resistant (Hamam, 2014; Bala, 2017; Hussain *et al.*, 2018).

In recent years, wheat productivity in arid or semi-arid regions has been significantly impacted by high temperature stress (Karla *et al.*, 2023), and Egypt is one of them. The total acreage of wheat was 219.15 million hectares in the 2021/22 season over the world; with total production of 808.44 million tons, China is the major wheat producing country, which produced 137 million tons of the global production for wheat, followed by India, the Russian Federation, and the United States of America (FAO, 2024). Egypt grew 1.53 million hectares in winter 2022 and produced 9.80 million metric tons of grain yield, with an average yield of 6.41 metric tons/hectare, whereas almost 19 million tons of wheat were consumed (MALR, 2022). However, Egypt's wheat production still needs to be increased. Therefore, it is essential to continue to produce and develop high-yielding and heat-tolerant cultivars by wheat breeders to keep up with this demand.

Modern wheat varieties are insufficiently heat tolerant and are liable to severe abiotic stresses (Hussain *et al.*, 2016). To mitigate heat stress, either by improving practices to manage heat stress or developing heat-tolerant cultivars (Farooq *et al.*, 2011; Hossain and Teixeira da Silva, 2012). Biometrical approaches are important for the breeder as a tool for genetic analysis and inheritance determination to identify candidates for new genotypes (Poodineh and Rad, 2015) and help to study the nature of gene actions of the different traits. Generation mean analysis is a precise biometrical approach depending on the phenotypic performance of characteristics (Mather and Jinks, 1982).

The six population model is employed to analyze the genetic inheritance patterns of critical traits under different conditions. The model includes

the parental (P_1 , P_2), F_1 , F_2 , and backcross (BC_1 , BC_2) generations provides a comprehensive framework to investigate the gene actions responsible for trait variation, including additive, dominance, and epistatic effects. By incorporating these six generations, the model allows for precise dissection of both simple and complex genetic interactions, particularly non-allelic interactions that are critical for understanding how crop genotypes respond to environmental stressors like heat. This approach enables the identification of traits

2. MATERIALS AND METHODS

2.1. Plant materials and field experimental work

Four bread wheat (*Triticum aestivum* L.) genotypes, including two local cultivars (Sakha 95 and Masr 3) acquired from the Agricultural Research Center (ARC), Egypt; the promising line (Line 606) obtained from the Plant Genetic Resources Department, Desert Research Center, Egypt, and the introduced genotype (Cham 8) from Syria, were selected based on their diversity to achieve this study. Names, origin and pedigree of the parental wheat genotypes are shown in **Table 1**.

During the 2020/21 growing season, the four parents were sown and

Table 1. Names, origin and pedigree of the four wheat genotypes used as parents in the study.

No.	Name	Origin	Pedigree
1	Line 606	Egypt	RCB-61/{Atlas 66 / Nap Hall // (NE70117) Skores Pelka35} 2RCB-61Su606- 13Su-2Su-0Su
2	Sakha 95	Egypt	SKAUZ*2_SRMA-CMBW91MO2694P-OTOPY-7M-010Y -010M-010Y-5Crow's CM 40457
3	Cham 8	Syria	JOPATICO6M67458-F-73/BLUEAY/VEE`S`-T-81
4	Masr 3	Egypt	ATTILA*2/PBW65*2/KACHU

In 2022/23 growing season, two separate and adjacent field trials (two sowing dates: at 15th November as a standard date and 15th December as a late sowing date) included the six populations (P_1 , P_2 , F_1 , F_2 , BC_1 and BC_2) of the two crosses were executed at the Experimental Farm of Giza Agriculture Research Station, Agriculture

governed by quantitative inheritance. It supports the development of strategies for selecting genotypes with enhanced heat tolerance and yield stability, which are crucial for wheat improvement programs targeting adverse climate conditions. **Therefore**, this study aimed to combine insights from genetic analysis, generation mean analysis, and the effects of sowing dates and heat stress to develop strategies that wheat breeders can use in breeding programs to lead to improvements in wheat production under heat stress.

crosses to generate F_1 hybrid grains of two crosses designated as follows: Cross I (Line 606 × Sakha 95) and Cross II (Cham 8 × Masr 3). In the next growing season, 2021/22, the F_1 grains were planted, F_1 plants were protected to obtain F_2 grains, crossing between other F_1 plants was made with their parents to develop backcrosses (BC_1 and BC_2) grains, and parents were protected to maintain parental purity. In addition, crossing was made between the parental genotypes again to produce additional F_1 hybrid grains for each cross in the Experimental Farm of the Faculty of Agriculture, Ain Shams University at Shoubra El-Kheima, Qalyubia Governorate, Egypt.

Research Centre, Egypt. The preceding summer crop was maize (*Zea mays*, L.).

The two field experiments were conceived using a randomized complete block (RCBD) design along with three replications. Each replicate comprises one row for non-segregating populations (parents and F_1 cross); while the segregating populations (F_2 and

backcrosses) were planted in four rows for each backcross and six rows for the F₂ population for each cross. The row was 3 m long with 20 cm apart between rows, and the hills spaced at 15 cm within the rows, where a row allowed a total of 20 plants. Plants were thinned at one plant/hill. The soil characterizations of the study location are presented in **Table 2**. according to **Soil Survey Staff (2010)**. Average monthly metrological data of the site are shown in **Fig. 1**. which was obtained from the Central Laboratory for Agricultural Climate, Giza, Egypt. Sprinkler irrigation was used. Calcium

superphosphate was added at rate of 36 kg ha⁻¹ of (P₂O₅ 15.5%) during soil preparation; then, the fertigation technique was used, the potassium element was added at rate of 79.2 kg ha⁻¹ potassium sulfate (K₂O 48%), while nitrogen fertilizer was added at rate of 7 equal doses as ammonium nitrate (N 33.5%) so that fertilization ends at flowering with amount 187.5kg N ha⁻¹. The recommended agricultural practices were followed for wheat production in the region of the experiment. Plants were harvested on 1st May.

Table 2. Properties of the experimental soil site in depth 0-30 cm

Physical properties			Chemical properties		
Coarse sand	(%)	10.80	Soil reaction pH		7.73
Fine sand	(%)	30.30	Organic matter	(%)	0.72
Silt	(%)	41.20	Electrical conductivity	(dS/m)	0.60
Clay	(%)	17.80			Ca ⁺² 2.4
Texture	loam		Cations	(meq /l)	Mg ⁺² 1.69
					Na ⁺ 1.63
Field capacity	(%)	16.8			K ⁺ 0.3
					Cl ⁻ 1.35
Wilting point	(%)	7.67	Anions	(meq/l)	CO ₃ ⁻² -
					HCO ₃ ⁻ 1.65
Bulk density	(g/cm3)	1.24			SO ₄ ⁻² 3.03

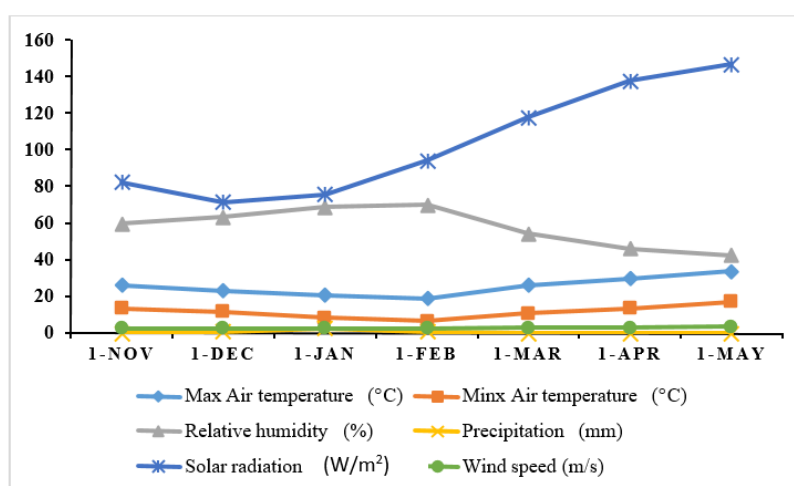


Fig. 1. Metrological data of the Giza location at the 2022/23 season

2.2. Traits measurement

Traits were measured on an individual guarded plant basis and the data were documented on 30 plants for non-segregating populations (P_1 , P_2 , and F_1). In contrast, segregating population measurements were recorded on 150 plants of BC_1 and BC_2 as well as 240 plants for each of the F_2 population from the three replications for each cross for earliness traits (days to heading and day to maturity), physiological traits, i.e., relative chlorophyll content (SPAD unit) was measured on flag leaf area of 10 guarded plants taken from each plot in the field by the chlorophyll meter by **Minolta (1989)**. Cell membrane stability (CMS) (%) was determined using the methodology outlined by **Blum and Ebercon (1981)** using the equation:

$$= \left[1 - \left(\frac{EC_1}{EC_2} \right) \right].$$

This involved incubating eight leaf discs in 10 ml of deionized water for 24 hours on a shaker, followed by measuring EC_1 values using EC meters. The discs were then autoclaved at 120°C for 20 minutes to measure the values of EC_2 , as well as yield traits: number of spikes/plant, number of grains/spike, 100-kernel weight (g) and grain yield/plant (g).

2.3. Statistical and genetic analyses

Analysis of variance and mean performance of generations for the characters were carried out following **Gomez and Gomez (1984)** using SAS Software (version 9.1).

Heterosis is calculated as the deviation of the F_1 mean from each of the mid-parents and better-parent percentages. It is expressed as a percentage based on the equations provided by **Bhatt (1971)**:

$$\text{Mid-parents heterosis (\%)} = \left(\overline{F_1} - \overline{M.P.} / \overline{M.P.} \right) \times 100.$$

$$\text{Better parent heterosis (Heterobeltiosis) (\%)} = \left(\overline{F_1} - \overline{B.P.} / \overline{B.P.} \right) \times 100.$$

where: $\overline{F_1}$ = the mean of the F_1 cross; $\overline{M.P.}$ = the mean of the mid parents; $\overline{B.P.}$ = the mean of the better parent.

The significance of differences between the F_1 means and their respective mid- and better-parent values were tested by the t-test was applied according to the following formulae:

$$\text{L.S.D. } \overline{M.P.} = (3\text{MSE}/2r)^{0.5} \times T \text{ tabulated};$$

$$\text{L.S.D. } \overline{B.P.} = (2\text{MSE}/r)^{0.5} \times T \text{ tabulated}$$

where: MSE = error mean squares; r = replications number

Generation means analysis was analyzed using a six-populations model and A, B, C and D scaling tests were estimated using **Mather and Jinks (1982)** method to compute the gene effects involved in the six parameters genetic model. In this method, the mean of each character is indicated as follows: $Y = m + \alpha[d] + \beta[h] + \alpha^2[i] + 2\alpha\beta[j] + \beta^2[l]$; where: Y = observed mean for generation; m = the mean effect, d = average additive effects, h = average dominance effects, i = average interaction between additive effects, j = average interaction between additive and dominance effects, and l = average interaction between dominance effects. The genetic attributes (m, [d], [h], [i], [j], and [l]) were tested using the t-test of significance.

Narrow sense heritability (h_{ns}) was calculated by **Mather and Jinks 1982** as the following = $\frac{(VF_2 - (VBC_1 + VBC_2)/2)}{VF_2}$

where: VE = the average environmental variances for the two parental genotypes and the F_1 populations, VBC_1 = variance of the backcross 1 population; VBC_2 = variance of the backcross 2 population.

Broad sense heritability (H_{bs}), expected genetic (G.S) and expected genetic advance relative to F_2 mean (GAM%) were calculated according to **Allard (1960)** as follows formulas: H_{bs}

$$= \frac{VF_2 - VE}{VF_2} = \frac{VG}{VF_2} \text{ where: } VE = \text{ the}$$

average environmental variances for the two parental genotypes and the F₁ populations, VF₂= the phenotypic variance of the F₂ population, and VG= the genotypic variance of the F₂ generation by subtracting the environmental variance (VE) from the F₂ variance (VF₂), *i.e.*, VF₂-VE. GAM (%) = G.S./F₂ × 100; G. S. (Δg)= K × δp × H_{bs}. where: K= selection differential with a value of 2.06 under 5% selection intensity. δp = genotypic standard deviation, and F₂= mean of the F₂ population.

3. RESULTS AND DISCUSSION

3.1. Analysis of variance and mean performance

Results in **Table 3.** displayed that generations mean squares were highly significant for the studied characteristics in the two crosses at normal and late sowing dates, referring to the contribution of the genetic variability among the six populations (P₁, P₂, F₁, F₂, BC₁ and BC₂) in the two crosses under normal and late sowing dates. **Raza *et al.* (2019)** mention that any breeding program's success requires genetic diversity in breeding material. Genetic variability can be clarified by the knowledge that all genotypes have highly different ancestors, for which the material has been carefully selected (**Kumar *et al.*, 2014**).

Table 3. Mean squares of analysis of variance under normal (N) and late (L) sowing dates for the studied traits in the six populations of two bread wheat crosses, in 2022/23 season

Trait	S.O.V. D.F.	Cross I (Line 606 × Sakha 95)			Cross II (Cham 8 × Masr 3)		
		Replications 2	Generations 5	Error 10	Replications 2	Generations 5	Error 10
Days to heading	N	0.09	15.67**	0.82	0.09	15.48**	0.83
	L	3.35	30.25**	1.92	2.52	43.75**	2.48
Days to maturity	N	0.57	23.82**	0.6	0.58	6.62**	0.6
	L	0.56	35.83**	3.23	2.00	26.71**	3.27
Cell membrane stability (%)	N	0.82	22.46**	0.45	0.88	15.92**	1.46
	L	1.26	34.98**	0.5	0.04	36.90**	5.70
Relative chlorophyll content (SPAD unit)	N	0.54	16.49**	0.2	0.55	16.65**	0.20
	L	0.03	12.74**	0.54	0.07	7.46**	0.44
Number of spikes/plant	N	0.09	2.15**	0.04	0.11	3.21**	0.04
	L	0.21	1.62**	0.14	0.26	1.40**	0.18
Number of grains/spike	N	1.96	26.12**	4.11	1.95	26.18**	4.02
	L	0.09	16.76**	0.36	0.61	20.23**	0.73
100-kernel weight (g)	N	0.04	0.34**	0.01	0.04	0.30**	0.01
	L	0.08	0.51**	0.08	0.02	0.33**	0.05
Grain yield/plant (g)	N	2.01	35.2**	0.46	2.01*	28.5**	0.45
	L	2.48	9.47**	0.58	3.73	22.17**	4.72

S.O.V.: source of variance; D.F.: degrees of freedom; *,** significant at 0.05 and 0.01 probability levels, respectively.

Also, data analysis showed that delaying sowing date decreased all studied characteristics in cross I and cross II. The mean performances of the six populations of the two wheat crosses under the two planting dates tended towards their earlier parent; the F₁ means were lower than the earlier parent. The F₂ means were more than the F₁ mean indicating the role of non-additive genetic variance components for

these traits. Furthermore, the means of F₁ followed by BC₂ gave the highest values in the cross I (Line 606 × Sakha 95) and cross II (Cham 8 × Masr 3) for traits under investigation, except grain yield/plant in cross I (**Figs. 2 and 3**). The identical outcomes were attained by **El Sabaghet *al.* (2019)**, **Ahmed (2021)**, and **Al-Naggaret *al.* (2021)**.

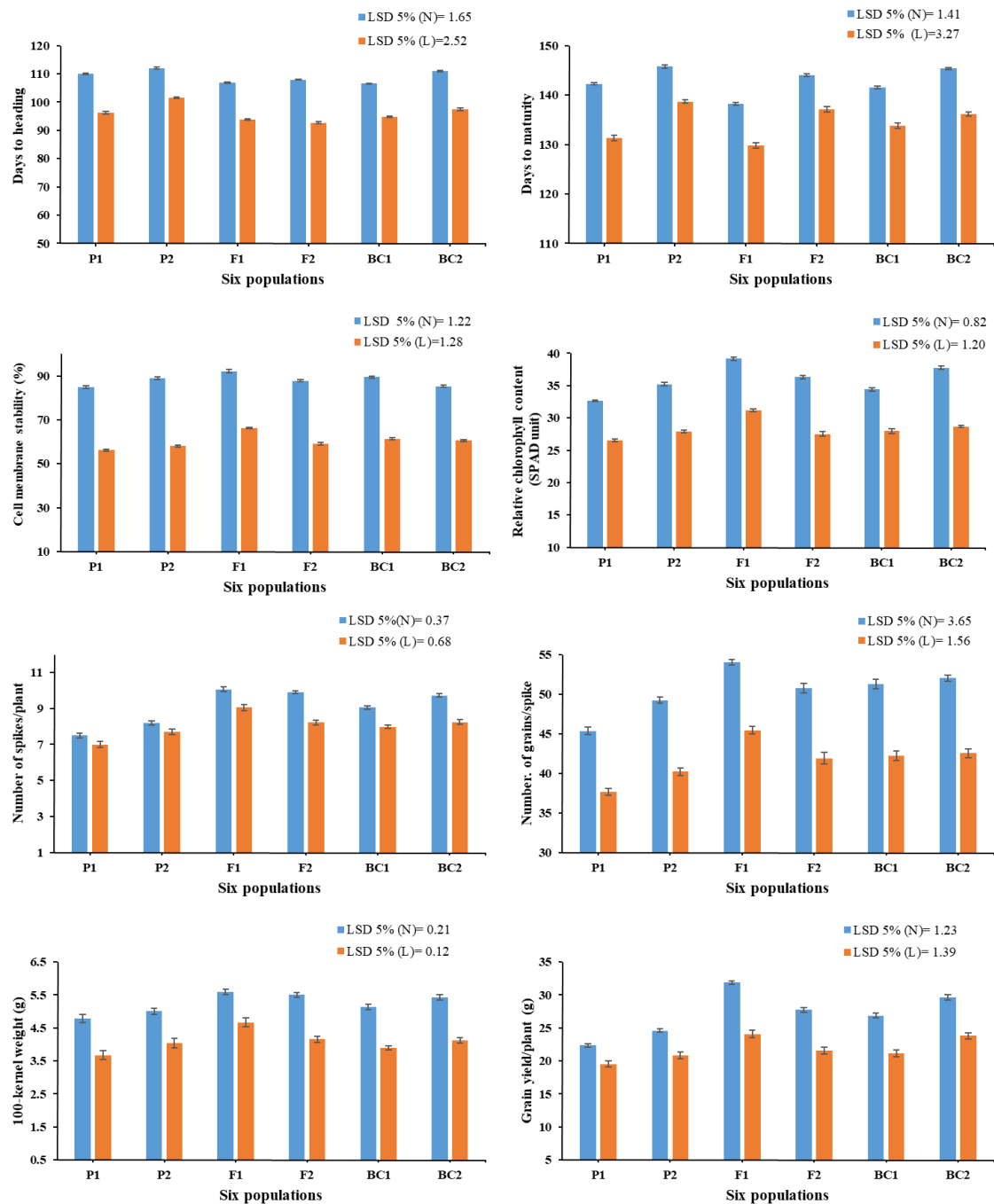


Fig. 2. Mean performance of six populations of the Cross I (Line 606 × Sakha 95) for the studied traits at normal (N) and late (L) sowing dates; 2022/23 season. (The bars at the top of the columns indicate the standard error)

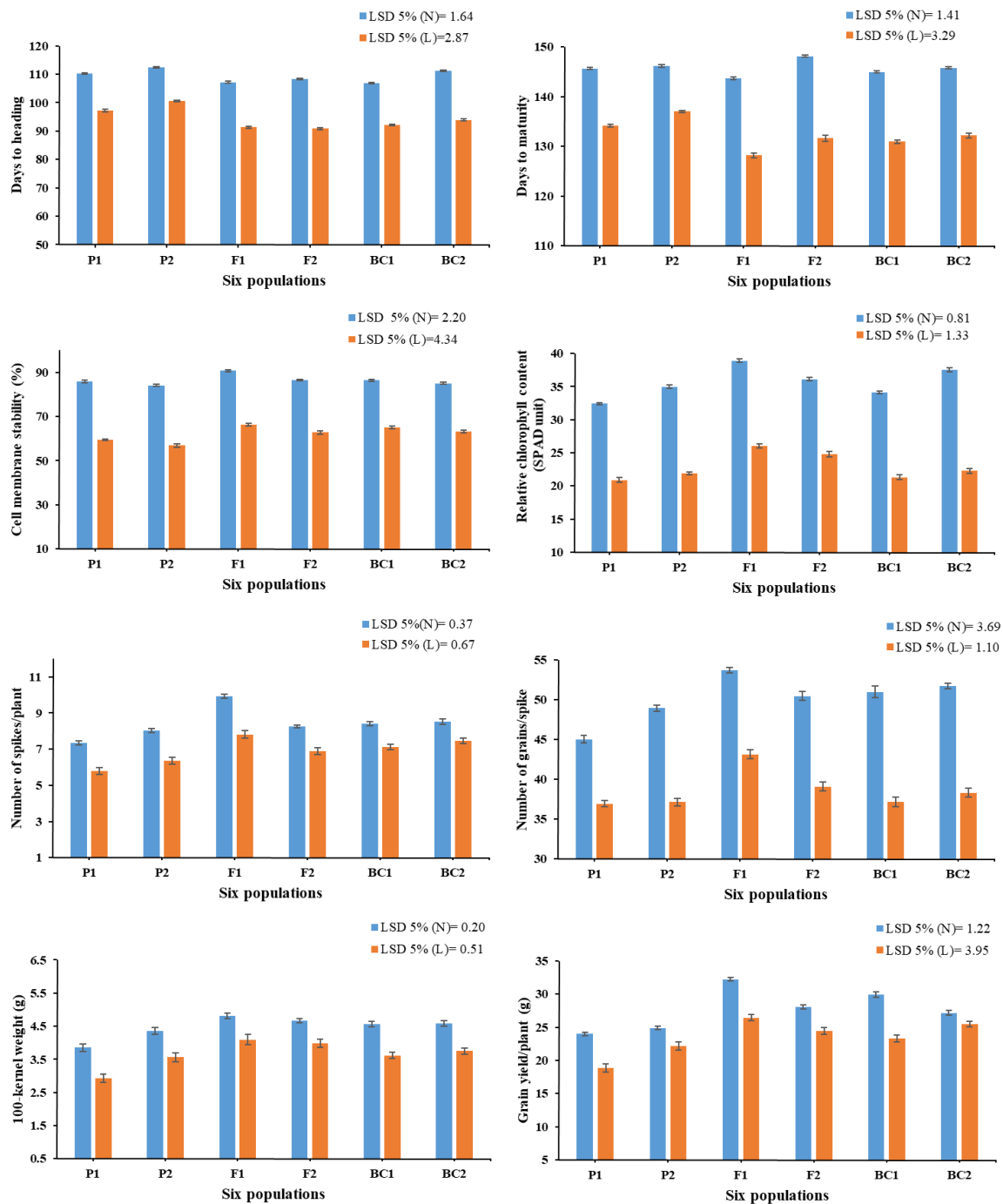


Fig. 3. Mean performance of six populations of the Cross II (Cham 8 × Masr 3) for the studied traits at normal (N) and late (L) sowing dates; 2022/23 season. (The bars at the top of the columns indicate the standard error)

3.2. Heterosis and heterobeltiosis

Heterosis percentage relative to mid-parents (MP) and heterobeltiosis (BP) were shown in **Table 4**. The values of heterosis (MP) and heterobeltiosis (BP) were negative and slightly significant for

earliness traits (days to heading and maturity), except heterobeltiosis at the late sowing date in cross I (Line 606 × Sakha 95) was negative but insignificant. The values ranged from -1.56 and -1.40% for days to maturity at standard date to -7.66

and 6.09% for days to heading at late date in cross II (Cham 8 × Masr 3) for heterosis and heterobeltiosis, respectively.

For physio-morphological traits (CMS and relative chlorophyll content), the values were slightly significant and positive under both dates in the two crosses, except heterosis and heterobeltiosis for CMS at the late date in cross I were non-significant. heterosis values ranged from 6.40% for CMS in cross II at the normal date to 21.64% for relative chlorophyll content at the late date in cross I; heterobeltiosis values ranged from 5.27% for CMS at the normal date in cross I to 18.98% for relative chlorophyll content at the late date in the same cross.

Regarding yield and its components, values were positive and significant or highly significant in yield and all components; heterosis ranged from

14.19% for 100-kernel weight in cross II to 35.89% for plant grain yield in cross I at normal date; likewise, heterobeltiosis ranged from 9.71% for number of grains/spike in cross II to 29.65% in cross I at normal date also.

In this connection, **Al-Naggar *et al.* (2021)** revealed that the F₁ mean values significantly outperformed the mid-parent values for wheat traits, which revealed the preponderance of heterotic and dominance effects in governing these traits. They also reported that the F₁ mean values slightly exceeded the higher parent values for such traits, evidenced that over-dominance controls the inheritance of such traits. More researcher's findings agreed with these results, such as **Abd El-Rady (2018)**, **Mohamed and EL-Gabry (2018)**, **Sayed and Koubisy (2019)**, and **Kamara *et al.* (2021)**.

Table 4. Estimates of heterosis relative to mid- parents (MP) and heterobeltiosis relative to better parent (BP) for the studied traits using the six populations data of the two wheat crosses at normal (N) and late (L) sowing dates; in 2022/23 growing season

Trait	Sowing dates	MP	BP	MP	BP
		Cross I (Line 606 × Sakha 95)		Cross II (Cham 8 × Masr 3)	
Days to heading	N	-3.77**	-2.86**	-3.71**	-2.79**
	L	-5.17**	-2.52	-7.66**	-6.09**
Days to maturity	N	-4.04**	-2.87**	-1.56**	-1.40**
	L	-3.85**	-1.16	-5.43**	-4.42**
Cell membrane stability (%)	N	7.42**	5.27**	6.40**	7.50**
	L	7.77	6.55	10.33**	12.23**
Relative chlorophyll content (SPAD unit)	N	15.47**	11.23**	15.48**	11.25**
	L	21.64**	18.98**	14.54**	11.69**
Number of spikes/plant	N	28.89**	23.28**	28.33**	22.85**
	L	28.37**	22.69**	23.4**	17.82**
Number of grains/spikes	N	14.31**	9.74*	14.25**	9.71*
	L	16.5**	16.19**	16.75**	13.05**
100-kernel weight (g)	N	17.26**	10.45**	14.19**	11.66**
	L	26.15**	14.98*	20.90**	15.46**
Grain yield/plant (g)	N	35.89**	29.65**	31.85**	29.40**
	L	19.33**	15.6**	29.03**	19.47*

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

3.3. Scaling test

The breeding approach for genetic enhancement of wheat relies on the

understanding of types of gene effects for different traits in plant materials under research. Six populations of wheat can be

analyzed using generation mean analysis to better understand the inheritance of important traits.

Joint scaling test (A, B, C and D) results were shown in **Table 5** displaying the significance of these tests for studied traits in the cross I and cross II under both planting dates that referred to the presence of non-allelic interaction, revealing the appropriateness of the six parameters model to estimate the different types of gene effect controlling these traits (**Hayman, 1958**), except number of spikes/plant at unfavorable sowing date in cross I as well as days to maturity, number of spikes/plant and number of grains/spike

in Cross II which showed that insignificant of scaling test proved to the lack of non-allelic interaction so, the simple additive-dominance genetic model (three parameters model) was confirmed to be acceptable in clarifying the inheritance of these traits (**Jinks and Jones, 1958**). These outcomes align with the findings of **Amin (2013)**, **Hamam (2014)**, **Raza et al. (2019)**, **Ahmed (2021)**, and **Al-Naggar et al. (2021)**. However, **Al-Azab et al. (2017)**; **Kandil et al. (2022)** confirmed that the simple additive-dominance genetic model (three-parameters model) provides clarity on the inheritance of some yield characteristics in bread wheat.

Table 5. Estimates of scaling tests for the studied traits using the six populations data of the two wheat crosses at normal (N) and late (L) sowing date; in 2022/23 growing season

Trait	Treatment	A	B	C	D
		Cross I (Line 606 × Sakha 95)			
Days to heading	N	-3.81**	3.03**	-3.95**	-1.59**
	L	-0.41	-0.49	-14.5**	-6.8**
Days to maturity	N	2.65**	6.8**	11.56**	1.06
	L	6.48**	3.88**	18.96**	4.3**
Cell membrane stability (%)	N	1.73	-10.6**	-7.4**	0.74
	L	0.37	-3.17**	-10.27**	-3.74**
Relative chlorophyll content (SPAD unit)	N	-3.04**	1.15	-0.86	0.51
	L	-4.3**	-3.3**	4.42**	6.01**
Number of spikes/plant	N	-0.45	-0.9**	-2.24**	-0.44
	L	0.62	0.76	-0.22	-0.8
Number of grains/spikes	N	3.22**	0.75	0.44	-1.77
	L	-5.75**	-3.66**	-4.01	2.7**
100-kernel weight (g)	N	0.45*	0.0037	0.82**	0.19
	L	0.22	-0.16	1.26*	0.6*
Grain yield/plant (g)	N	-0.55	2.73**	0.27	-0.96
	L	-1.37	2.66**	-2.28	-1.79
Cross II (Cham 8 × Masr 3)					
Days to heading	N	-3.79**	2.97**	-3.97**	-1.58**
	L	-4.26**	-4.09**	-16.84**	-4.24**
Days to maturity	N	0.66	1.77**	13.54**	5.56**
	L	-0.48	-0.79	-1.06	0.11
Cell membrane stability (%)	N	-3.88**	-4.73**	-5.59**	1.51
	L	4.38**	3.09	2.22	-2.63
Relative chlorophyll content (SPAD unit)	N	-3.02**	1.12	-0.89	0.51
	L	-1.74*	-1.7**	-6.72**	-1.64
Number of spikes/plant	N	0.55*	1.19**	3.77**	1.01**
	L	-0.08	-0.25	0.11	0.23
Number of grains/spikes	N	3.22*	0.76	0.45	-1.76
	L	1.39	-0.51	-1.08	-0.98
100-kernel weight (g)	N	-0.11	0.25	1.04**	0.45**
	L	-0.55*	-0.45	-0.40	0.30
Grain yield/plant (g)	N	3.64**	-2.8**	-1.08	-0.96
	L	1.33	2.40*	3.96	0.11

*, ** significant at 0.05 and 0.01 probability levels, respectively; N: Normal sowing date; L: late sowing date.

3.4. Types of gene actions

The gene actions for studied characteristics in the cross I (Line 606 × Sakha 95) and cross II (Cham 8 × Masr 3) under both treatments are shown in **Table 6**. Data revealed that the F_2 mean effect parameter (m) was highly significant for studied characteristics in the two wheat crosses under this investigation, which shows the contributions due to the grand mean.

Meanwhile, additive gene (d) effects were highly significant for earliness traits (days to heading and maturity), relative chlorophyll content and grain yield/plant under favorable and unfavorable dates number of spikes/plant at late date as well as cell membrane stability (CMS) at optimum sowing date in cross I; in cross II the values were significant or highly significant except relative chlorophyll content at normal date and number of grains/spike at late date were insignificant values.

Moreover, dominance gene (h) effects were significant or highly significant for days to maturity, relative chlorophyll content number of spikes/plant and grain yield/plant at both conditions as well as CMS and at late date and number of grains/spike at normal date in the two crosses, in addition to days to heading at late date and number of spikes/plant under both dates in the first cross only.

The findings suggested that selection for desirable characters could be successful in the early generations because both additive and dominant have significant contributions to the inheritance of the examined traits. But it is preferable to delay it to later segregating generations (**Al-Naggar *et al.* 2021**).

Regarding non-allelic interaction, additive × additive gene (i) effect for days to heading under both sowing dates, additive × dominance gene (j) effect for days to heading, relative chlorophyll

content and grain yield/plant at normal date, dominance × dominance gene (l) effect for days to maturity and cell membrane stability at normal date were highly significant in the two crosses.

Moreover, in the first cross, additive × additive gene (i) effects for days to maturity, CMS, relative chlorophyll content, number of grains/spike and 100-kernel weight at late date; additive × dominance gene (j) effects for days to maturity and grain yield at late date and CMS under both dates; dominance × dominance gene (l) effects for days to heading, relative chlorophyll content and Number of grains/spike were highly significant values. Whereas, in the second cross II, additive × additive (i) gene effects for days to maturity, number of spikes/plant were highly significant, in addition to 100-kernel weight being significant at the optimum sowing date; likewise, dominance × dominance gene (l) effects for CMS and 100-kernel weight at the late planting date were significant values.

According to the data above, for the two bread wheat crosses included in this study, the locus effects and the fixed loci's interaction were found to be marginally significant for the traits under consideration, indicating that these traits were quantitatively inherited. **Abdallah *et al.* (2019)** mention that the superior genotypes could be effectively discerned from their phenotypic expression; thus, phenotypic selection proved more efficacious for enhancing these traits in those crosses.

These results are in accordance with **Amin (2013)**, **Hamam (2014)**, **Mahpara *et al.* (2018)**, **Raikwar (2019)**, **Raza *et al.* (2019)**, and **Ahmed (2021)**. **Al-Naggar *et al.* (2021)** reported that genetic study revealed that these features in wheat were governed by intricate

inheritance patterns owing to the occurrence of epistasis. On the other hand, **Al-Azab et al. (2017)** and **Kandil et al. (2022)** reported that no epistasis was

identified for some yield traits in wheat, providing evidence that estimates of gene effects for such traits were free devoid linkage bias.

Table 6. Gene effects for the studied traits using the six populations data using the six populations data of the two wheat crosses at normal (N) and late (L) sowing dates; in 2022/23 growing season

Trait	Sowing date	m	d	h	i	J	l
Days to heading	N	107.94**	-4.46**	-1.01	3.17**	-3.42**	-2.39
	L	92.71**	-2.65**	8.49**	13.6**	0.04	-12.7**
Days to maturity	N	143.99**	-3.81**	-7.93**	-2.11	-2.08**	-7.33**
	L	137.14**	-2.37**	-13.79**	-8.6**	1.3	-1.77
Cell membrane stability (%)	N	87.71**	4.11**	3.75	-1.47	6.16**	10.34**
	L	59.09**	0.89	16.47**	7.47**	1.77*	-4.68
Relative chlorophyll content (SPAD unit)	N	36.08**	-3.38**	4.19**	-1.02	-2.1**	2.91
	L	24.8**	-0.98*	-7.39**	-12.02**	-0.5	19.62**
Number of spikes/plant	N	8.25**	-0.12	3.11**	0.89	0.23	0.47
	L	4.49**	-0.28*	6.30**	-	-	-
Number of grains/spikes	N	50.44**	-0.72	10.25**	3.53	1.24	-7.5
	L	39.07**	-1.14	0.71	-5.4**	-1.05	14.8**
100-kernel weight (g)	N	4.66**	-0.03	0.34	-0.37	0.22	-0.08
	L	3.98**	-0.13	-0.35	-1.20**	0.19	1.14
Grain yield/plant (g)	N	27.76**	-2.77**	10.34**	1.91	-1.64**	-4.09
	L	21.57**	-2.67**	7.48**	3.58	-2.01**	-4.87
Cross II (Cham 8 × Masr 3)							
Days to heading	N	108.25**	-4.43**	-0.97	3.16**	-3.38**	-2.34
	L	90.9**	-1.74**	0.91	8.48**	-0.08	-0.13
Days to maturity	N	148.15**	-0.79*	-13.39**	-11.12**	-0.55	8.69**
	L	131.62**	-1.28*	-7.57*	-	-	-
Cell membrane stability (%)	N	86.43**	1.30*	2.79	-3.02	0.43	11.64**
	L	62.75**	1.97*	13.32**	5.25	0.65	-12.72*
Relative chlorophyll content (SPAD unit)	N	36.34**	-3.36**	4.24**	-1.02	-2.07**	2.92
	L	27.51**	-0.71	7.24**	3.29	-0.02	0.15
Number of spikes/plant	N	9.9**	-0.67**	0.19	-2.03**	-0.32	0.29
	L	7.79**	-0.35**	0.47	-	-	-
Number of grains/spikes	N	50.75**	-0.72	10.26**	3.53	1.23	-7.50
	L	36.95**	-1.27**	11.31	-	-	-
100-kernel weight (g)	N	5.5**	-0.29*	-0.21	-0.90*	-0.18	0.77
	L	4.16**	-0.23*	0.20	-0.61	-0.05	1.61*
Grain yield/plant (g)	N	28.07**	2.76**	9.71**	1.92	3.22**	-2.76
	L	24.46**	-2.18**	5.73*	-0.22	-0.54	-3.51

*,** significant at 0.05 and 0.01 probability levels, respectively. m= mean, d= additive effect, h= dominance effect, i= additive × additive interaction, j= additive × dominance interaction, l= dominance × dominance interaction.

3.5. Heritability estimates and genetic advance

Broad (H_{bs}) and narrow (h_{ns}) sense heritability values and genetic advance after one generation of selection the best

5% of the F_2 population in percentage revealed in **Table 7**.

According to **Singh (2001)**, levels of heritability in broad sense (H_{bs}) are categorized as low (less than 40%), moderate (from 40 to 59%), moderately

high (from 60 to 79%), and high (more than 80%). In this study, broad sense (H_{bs}) heritability was classified as high for studied traits, except CMS, number of spikes/plant and 100-kernel weight at normal sowing date in the in the cross I and cross II, as well as 100-kernel weight in the second cross at late date, which was classified as moderately high, demonstrating that most of the phenotypic variability was attributed to the genetic effects and possibly for enhancement by selection for these traits. Consequently, Broad sense heritability ranged from 72.16 and 71.97% for 100-kernel weight at normal date to 93.97 and 95.96% for relative chlorophyll content at late date in the first and second cross, respectively. **Abd El-Rady (2018)** and **Sayed and Koubisy (2019)** reported that broad sense heritability was moderate to high for wheat traits under normal and late sowing dates. These findings are in good agreement with those of **Singh et al. (2013)**, **Hamam (2014)**, **Kumar et al. (2014)**, **Ahmed (2021)**, **Kamara et al. (2021)**, **Karla et al. (2023)**, and **Ul-Allah et al. (2023)**.

The estimates of heritability in the narrow sense (h_{ns}) have been classified by **Robinson (1966)** into three categories, viz., low (<10%), medium (10-30%) and high (> 30%). In this research, narrow sense heritability was categorized as low for 100-kernel weight at normal date in the two crosses and number of spikes/plan at normal date in cross II only; while its categorized as medium for CMS and grain yield/plant at normal date in the two crosses and number of grains/spike at late date in cross I; moreover, its categorized as high for others traits, evidencing that these traits which high to moderate heritability estimates were slightly affected by additive effect and there is respectful amount of heritable variation; furthermore, the others traits which had low heritability estimates in narrow sense were slightly affected by

non-additive gene effect, evident that selection for these traits will be arduous and the effects by environment well be issue. Accordingly, narrow sense heritability ranged from 3.86 and 3.72% for 100-kernel weight at normal date to 61.72% for 100-kernel weight and 68.31% for CMS at late date in the cross I and cross II, respectively. **Maqsood et al. (2018)**, **Raza et al. (2019)**, **Sayed and Koubisy (2019)**, and **Ul-Allah et al. (2021)** reported that the traits related to yield in wheat revealed moderate to high heritability in a narrow sense. On the other hand, **Abdallah et al. (2019)** displayed low to moderate heritability in the narrow sense for yield components. Other researchers agreed with the above results as **Singh et al. (2013)**, **Hamam (2014)**, **Ram et al. (2014)**, **Ahmed (2021)**, **Al-Naggaret al. (2021)**, and **Kamara et al. (2021)**.

High heritability coupled with high genetic advance is primarily due to the additive gene action. Moreover, high heritability with low genetic advance and moderate or low heritability with low genetic advance represent non-additional gene action (**Katiyar et al., 2020**). Expected genetic advance relative to F_2 mean (GAM) was labeled as low (less than 10%), moderate (from 10 to 20%), and high (more than 20%) according to **Johnson et al. (2010)**. GAM was labeled as low for days to heading and maturity at standard date in the two crosses, proposing the effect of environmental factors and dominance gene action in inheritance of such traits; meanwhile, it was labeled as moderate for days to heading and maturity at unfavorable sowing date and CMS at favorable sowing date in date in the cross I and cross II, as well as number of spikes/plant in cross II at normal date. On the other hand, other traits were labeled as high values of GAM, indicating the possibility of selecting in early generations to improve selecting genotypes with high

yielding. Thus, estimates ranged from 4.70 and 4.55% for days to maturity at the slandered date to 76.07% for 100-kernel weight and 60.65% for grain yield/plant at the late date in the first and second crosses,

respectively. These results are in harmony with Hamam (2014), Kumar *et al.* (2014), Abd El-Rady (2018), Sayed and Koubisy (2019), Ahmed (2021), Al-Naggar *et al.* (2021), and Karla *et al.* (2023).

Table 7. Heritability estimates in broad (H_{bs}) and narrow (h_{ns}) sense and genetic advance for the studied traits using the six populations data using the six populations data of the two wheat crosses at normal (N) and late (L) sowing dates; in 2022/23 growing season

Trait	Sowing date	Cross I (Line 606× Sakha 95)			Cross II (Cham 8 × Masr 3)		
		H_{bs}	h_{ns}	GAM	H_{bs}	h_{ns}	GAM
Days to heading	N	83.62	33.21	5.61	83.69	34.07	5.62
	L	91.95	56.31	13.73	90.28	48.79	11.44
Days to maturity	N	86.11	45.51	4.70	85.98	45.04	4.55
	L	92.26	58.87	12.53	95.46	66.26	13.35
Cell membrane stability (%)	N	75.18	19.29	12.74	73.27	22.16	10.19
	L	90.76	56.57	26.45	93.27	68.31	41.05
Relative chlorophyll content (SPAD unit)	N	90.74	35.96	20.52	90.79	36.79	20.54
	L	93.79	48.70	46.61	95.96	65.43	41.41
Number of spikes/plant	N	73.70	36.78	24.04	73.66	8.48	20.00
	L	86.87	59.29	74.29	82.53	55.13	44.17
Number of grains/spikes	N	93.97	36.23	34.41	94.92	60.69	37.69
	L	90.03	25.37	39.17	95.32	56.40	51.63
100-kernel weight (g)	N	72.16	3.86	33.83	71.97	3.72	28.56
	L	81.19	61.72	76.07	72.65	59.45	51.55
Grain yield/plant (g)	N	93.73	28.65	38.21	93.70	28.59	37.75
	L	89.11	55.51	72.08	85.19	53.82	60.65

H_{bs} : broad sense heritability; h_{ns} : narrow sense heritability; GAM: genetic advance after one generation of selection the best 5% of the F_2 population in percentage.

4. CONCLUSION

As a conclusion for this investigation, it would be mentioned that the heterosis values relative to mid-parents had highly significant with few exceptions, indicating the preponderance of dominance effect in governing the traits under study; in the same trend, the heterobeltiosis values, evidenced that over-dominance controls the inheritance of such traits. According to the aforementioned results, for the cross I (Line 606 × Sakha 95) and cross II (Cham 8 × Masr 3), included in this study, the locus effects and the fixed loci's interaction were found to be marginally significant for the traits under considerations, governing that these traits were quantitatively

inherited, so selection for desirable characters could be successful in the early generations but it is preferable to delay it to later generations. Furthermore, improvement of studied traits based on the moderate to high heritability and high genetic advance shown by the different traits, particularly relative chlorophyll content, number of grains/spike, grain yield/plant under favorable and unfavorable dates, governing the possibility of selecting in early generations to improve selecting genotypes with high economic yield.

REFERENCES

- Abd El-Rady, A. G. 2018.** Genetic analysis of some agronomic traits in two bread wheat crosses under heat stress conditions. *J. Plant Prod., Mansoura Univ.*, 9(1):21-28.
- Abdallah, E., Salem, A. H., Ali, M. M. A. and Kamal, K. Y. 2019.** Genetic analysis for earliness and grain yield of bread wheat (*Triticum aestivum*, L.) under heat stress. *Zagazig J. Agric. Res.*, 46(6A):1769-1784.
- Ahmed, B. H. 2021.** Estimates of genetic parameters using six populations in two bread wheat crosses. *Arch. Agri. Sci. J.*, 4(1):330-341.
- Al-Azab, K. F., Abdel-Lattif, H. M. and Al-Naggar A. M. M. 2017.** Allelic and non-allelic gene interactions controlling the inheritance of earliness and yield traits in three crosses of bread wheat. *Egypt. J. Plant Breed.*, 21(7):1309-1325.
- Allard, R. W. 1960.** Principles of Plant Breeding. John Wiley and Sons, Inc., New York, London, p. 274
- Al-Nagar, A. M. M., Al-Azabb, K. F., Younis, A. S. M, Hassan, I. O., Basyouny, M. A. E. and Ayaad, M. 2021.** Genetic parameters controlling the inheritance of glaucousness and yield traits in bread wheat. *Brazilian J. Biol.*, 82: e253864.
- Amin, A. 2013.** Genetic behavior of some agronomic traits in two durum wheat crosses under heat stress. *Alex. J. Agric. Res.*, 58(1):53-66.
- Asseng, S., Ewert, F., Rosenzweig, C., Jones, J. W., Hatfield, J. L., Ruane, A. C., Boote, K. J., Thorburn, P. J., Rötter, R. P. and Cammarano, D. 2013.** Uncertainty in simulating wheat yields under climate change. *Nat. Clim. Change*, 3:827-832.
- Bala, P. 2017.** Evaluation of heat tolerance of wheat genotypes through membrane thermostability test. *Mayfeb J. Agric. Sci.*, 2:1-6.
- Bhatt, G. M. 1971.** Heterotic performance and combining ability in a diallel cross among spring wheat (*Triticum aestivum*, L.). *Aust. J. Agric. Res.*, 22:356-369.
- Blum, A. and Ebercon, A. 1981.** Cell membrane stability as a measure of drought and heat tolerance in wheat, *Crop Sci.*, 21:43-47.
- El Sabagh, A., Hossain, A., Barutçular, C., Islam, M. S., Awan, S. I., Galal, A., Iqbal, A., Sytar, O., Yildirim, M., Meena, R. S., Fahad, S., Najeeb, U., Konuskan, O., Habib, R. A., Llanes, A., Hussain, S., Farooq, M., Hasanuzzaman, M., Abdelaal, K. H., Hafez, Y., Cig, F. and Saneoka, H. 2019.** Wheat (*Triticum aestivum*, L.) production under drought and heat stress – adverse effects, mechanisms and mitigation: A review. *Appl. Ecol. Environ. Res.*, 17(4):8307-8332.
- FAO. 2024.** Food and Agriculture Organization of the United Nations. Statistical Database, Available from: <http://www.fao.org/faostat/en/#data/QC>.
- Farooq, M., Bramley, H., Palta, J. A. and Siddique K. H. 2011.** Heat stress in wheat occurs during reproductive and grain-filling phases. *Crit. Rev. Plant Sci.*, 30:491–507.
- Gomez, K. A. and Gomez, A. A. 1984.** Statistical Procedures for Agriculture Research. John Wiley & Sons, New York.
- Gupta, N. K., Agarwal, S., Agarwal, V. P., Nathawa, N. S., Gupta, S. and Singh, G. 2013.** Effect of short-term heat stress on growth, physiology and antioxidative defence system in wheat seedlings. *Acta Physiol. Plant*, 35:1837-1842.
- Hamam, K. A. 2014.** Genetic analysis of agronomic traits in bread wheat using six parameters model under heat stress. *Egypt. J. Agron.*, 36(1):1-18.

- Hossain, A. and Teixeira da Silva, J. A. 2012.** Phenology, growth and yield of three wheat (*Triticum aestivum*, L.) varieties as affected by high temperature stress. *Not. Sci. Biol.*, 2, 4(3):97–109.
- Hossain, M. M., Hossain, A., Alam, M. A., EL Sabagh, A., Ibn Murad, K. F., Haque, M. M., Muriruzzaman, M., Islam, M. Z., Das, S., Barutcular, C. and Kizilgeci, F. 2018.** Evaluation of fifty spring wheat genotypes grown under heat stress condition in multiple environments of Bangladesh. *Fresen. Environ. Bull.*, 27:5993-6004.
- Hussain, S., Jamil, M., Napar, A. A., Rahman, R., Bano, A., Afzal, F., Kazi, A. G. and Mujeeb-Kazi, A. 2016.** Heat stress in wheat and interdisciplinary approaches for yield maximization, In plant-environment interaction: Responses and approaches to mitigate stress (Eds., Azooz MM, Ahmad P), John Wiley and Sons, Ltd., Chichester, UK.
- IPCC, 2007.** Climate Change The physical science basis summary for policymakers' contribution of Working Group I to the Fourth Assessment Report of the Intergovernmental Panel on Climate Change.
- Jinks, J. L. and Jones, R. M. 1958.** Estimation of the components of heterosis. *Genetics*, 43:223- 224.
- Johnson, H. W., Robinson, H. F. and Comstock, R. E. 2010.** Estimates of genetic and environmental variability in soybeans. *Agro. J.*, 47(7):314-318.
- Kamara, M. M., Ibrahim, K. M., Mansour, E., Kheir, A. M. S., Germoush, M. O., Abd El-Moneim, D., Motawei, M. I., Alhusays, A. Y., Farid, M. A. and Rehan, M. 2021.** Combining ability and gene action controlling grain yield and its related traits in bread wheat under heat stress and normal conditions. *Agronomy*, 11, 1450.
- Kandil, A. A., Abdel-Moneam, M. A., Hafez, S. H. and Gomaa, H. S. 2022.** Genetic analysis of two bread wheat crosses (*Triticum aestivum*, L.) using six populations techniques. *J. Plant Production, Mansoura Univ.*, 13(2):59-62.
- Karla, U., Choudhary, V. K., Singh, S. K., Vignesh, S. and Ellandula, A. 2023.** Genetic variability in wheat (*Triticum aestivum*, L.) under timely and late sown conditions for tolerance towards terminal heat stress. *Int. J. Bio-Resour. Stress Manag.*, 14(11):1460-1466.
- Katiyar, A., Sharma, A., Singh, S., Srivastava, A. and Vishwakarma, S. R. 2020.** A study on genetic variability and heritability in barley (*Hordeum vulgare*, L.). *Int.J.Curr.Microbiol.App.Sci.*, 9:243-247.
- Kumar, R., Prasad, B. K., Singh, M. K., Verma, A. and Tyagi, B. S. 2014.** Genetic analysis for phenological and physiological traits in wheat (*Triticum aestivum*, L.) under heat stress environment, *Indian J. Agric. Res.*, 48(1):62-66.
- Lobell, D. B., Sibley, A. and Ortiz-Monasterio, J. I. 2012.** Extreme heat effects on wheat senescence in India. *Nat. Clim. Change*, 2:186–189.
- Mahpara, S., Hussain, S. T., Iqbal, J., Noorka, I. R. and Salman, S. 2018.** Analysis of generation means for some metric plant traits in two wheat (*Triticum aestivum*, L.) hybrids. *Pure Appl. Biol.*, 7(1):93-102.
- MALAR. 2022.** Statistical Bulletin, Economic Affairs Sector, Ministry of Agriculture and Land Reclamation, Egypt.
- Maqsood, R. H., Khaliq, I., Kashif, M. and Ahmed, N. 2018.** Gene action

- array related to morpho-physiological traits using population genetics in *Triticum aestivum*, L. Pak. J. Agri. Sci., 55(3):513-519.
- Mather, K. and Jinks, J. L. 1982.** Biometrical Genetics (3rd ed.). Chapman and Hall Ltd., London, UK.
- Minolta. 1989.** Manual for chlorophyll meter SPAD-502. Minolta Camera Co., Osaka, Japan.
- Mohamed, A. Z. A. and EL-Gabry, Y. A. 2018.** Genetic analysis of some bread wheat crosses under normal and late sowing conditions, Egypt. J. Plant Breed., 22(4):827-848.
- Öztürk, M., Hakeem, K. R., Faridah-Hanum, I. and Efe, R. 2015.** Climate Change Impacts on High-Altitude Ecosystems. Springer Science Business Media New York, p. 736.
- Paymard, P., Bannayan, M. and Haghghi, R. S. 2018.** Analysis of the climate change effect on wheat production systems and investigate the potential of management strategies. Nat. Hazards, 911:237-1255.
- Poodineh, M., and Rad, M. 2015.** Genetic components for physiological parameters estimates in bread wheat (*Triticum aestivum*, L.). Annu. Res. Rev. Biol., 7:163-170.
- Raikwar, R. S. 2019.** Genetic architecture of yield and quality traits in wheat (*Triticum aestivum*, L.). Indian J. Genet., 79(1):100-103.
- Ram, M., Singh, R. M. and Agrawal, R. K. 2014.** Genetic analysis for terminal heat stress in bread wheat (*Triticum aestivum*, L. EM THELL). BioScan, 9(2):771-776.
- Raza, H., Khan, A. S. and Ahmed, N. 2019.** Genetic analysis for some phenological and morphological traits in wheat (*Triticum aestivum*, L.) under two different sowing windows. Appl. Ecol. Environ. Res., 17(2):2059-2071.
- Robinson, H. F. 1966.** Quantitative genetics in relation to breeding of the centennial of mendalism. Indian J. Genet., 26:171- 187.
- Sayed, Y. and Koubisy, I. 2019.** Generation mean analysis of two bread wheat crosses under normal and late sowing date conditions. Egypt. J. Agric. Res., 97(2):589-607.
- Shahin, M. G., Saady, H. S., El-Bially, M. E., Abd El-Momen, W. R., El-Gabry, Y.A., Abd El-Samad, G. A. and Sayed, A. N. (2023).** Physiological and agronomic responses and nutrient uptake of soybean genotypes cultivated under various sowing dates. J. Soil Sci. Plant Nutr., 23:5145–5158.
- Sing, B. D. 2001.** Plant Breeding: Principles and Methods. Kalyani Publishers, New Delhi, pp.896.
- Sing, M. K., Sharma, P. K., Tyagi, B. S. and Singh, G. 2013.** Genetic analysis for morphological traits and protein content in bread wheat (*Triticum aestivum*, L.) under normal and heat stress environments. Indian J. Genet., 73(3):320-324.
- Soil Survey Staff. 2010.** Keys to Soil Taxonomy. 11th ed. U.S. Department of Agriculture, Natural Resources Conservation Service, U.S. Government Printing Office, Washington, DC., USA.
- Ul-Allah, S., Azeem, A., Sher, A., Ijaz, M., Sattar, A., Saleem, M. A., Bibi, M., Abbas, N. and Hussain, M. 2021.** Assessment of genetic variability and direct-indirect contribution of post-anthesis traits to the grain yield in bread wheat (*Triticum aestivum*) at different sowing dates. Int. J. Agric. Biol., 26:193-200.
- Ul-Allah, S., Hussain, S., Mumyaz, R., Naeen, M., Abdul Sattar, Sher, A., Ijaz, M., Azeem, A., Hassan, Z., Ahmed, K., Ur Rehman, A., Hussain, I., Abbas, N., Ur Rehman, S.,**

Alharbi, S. A., Alfarraj, S. and Ansari, M. J. 2023. Phenotypic characterization of wheat germplasm for heritability and dissection of association among post anthesis traits under variable sowing dates. *J. King Saud Univ. Sci.*, 35:102578.

Zhen, B., Chenu, K., Fernanda, Dreccer, M. and Chapman, S. C. 2012. Breeding for the future: what are the potential impacts of future frost and heat events on sowing and flowering time requirements for Australian bread wheat (*Triticum aestivium*) varieties? *Glob. Change Biol.*, 18:2899-2914.