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Genetic Analysis of Some Agronomic Traits in Two Durum Wheat Crosses under Heat Stress

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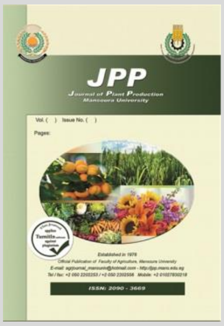

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ABSTRACT

Six populations derived from the Sohag 4 x Beni-Swif 5 and Sohag 4 x Beni-Swif 6 durum wheat hybrids were cultivated under two experimental conditions: regular sowing date and late sowing date (mimicking heat stress). This study was conducted at the Experimental Farm of the Faculty of Agriculture, Al-Azhar University, Assiut branch, Egypt, over three consecutive growing seasons from 2021–2022 to 2023–2024 Some characters i.e. plant height (PH), number of spikes per plant (NSP), number of kernels per spike (NKS), grain yield per plant (GY/P) and 100-grain weight (GW) were studied. Significant positive additive gene effects (d) were observed for DFF, PH and NKS under normal conditions for cross I, and for PH, NSP, GY/P and 100- kernels weight under heat stress for hybrid I. While positive and significant for DFF and PH, for cross II under heat stress, and negative significant for NKS and GY/P for cross II under normal condition. Moreover, positive insignificant for NSP and GY/P of the second cross under all conditions. Populations P1, F1, and BC1 (Cross 1) and P1, P2, F1, and BC2 (Cross 2) exhibited heat tolerance (HSI < 1) and high yield attributes. **** These resilient genotypes generally displayed high values for yield attributes. Notably, Sohag 4 maintained stability and outperformed other populations across both sowing dates. These findings offer significant insights for wheat breeders focused on enhancing yield potential, developing novel wheat genotypes, and improving Egyptian wheat germplasm.

Keywords: Wheat, Genetic advance, Heritability, Heat indices.

INTRODUCTION

As Egypt's most important cereal crop, wheat occupies the largest cultivated area and produces the highest yield. In 2023, global production of bread wheat reached approximately 777 million tons, with an additional 42.3 million tons of durum wheat contributing to the worldwide total. (USDA, 2023). Durum wheat occupies 8-10 % of the wheat – growing area and world production (FAO, 2018). Durum wheat is cultivated mainly in Upper and Middle Egypt for pasta production.

Abiotic stresses often limit durum wheat production by negatively affecting its development and grain filling.

Rising global temperatures are causing heat stress, which presents a significant challenge to agriculture in many regions worldwide (Wahid *et al* 2007). The potential number of grains was decreased by high temperatures during the flower initiation and spikelet development (a few weeks before anthesis), which affected the yield potential. By creating new-diverse genotypes with an include that may have both positive and negative effects on the traits of other components, the breeder is concentrating on increasing the potential for wheat yield (Chandra *et al*., 2004).

Furthermore, there are morphological features that affect wheat grain production that are more heritable than the crop itself, according to factors influencing the stated heritability estimates (Fatehi and Mohamed, 2010). Generation mean analysis serves as an effective approach for understanding the genetic basis of yield, its contributing components, and other key traits. In addition, it reveals important information regarding the specific types of gene action influencing the traits. This study investigates the genetic control of quantitative traits in two durum wheat crosses. Specifically, it aims to ascertain the relative importance of gene action, estimate heritability, and predict the expected genetic gain within these crosses. The research will utilize six populations derived from three parental durum genotypes for each hybrid, evaluating them under both optimal and heat stress environments.

MATERIALS AND METHODS

This experiment took place at the Experimental Farm of the Faculty of Agriculture, Al-Azhar University, Assiut branch, Egypt, spanning three consecutive growing seasons: 2021–2022, 2022–2023, and 2023–2024.Three cultivars of durum wheat were employed. Table 1 lists these broad wheat genotypes' names, pedigree origins, and characteristics. The parents were crossed to create F_1 hybrid grains in the 2021–2022 season, and they were given the following designation:

Table 1. The name, Pedigree and origin of parental genotypes used.

Hybrids	Parent		Pedigree	Origin
Hybrid 1	P1	Sohag - 4	Ajaia-16//Hora/Jro/3/Ga/4/Zar/S/Souk 7/6/Stot//Altar84/Aid. CDSSB007785-0T0PY-0M-OY129Y-0M-0Y-IB-0SH.	Egypt
	P2	Beni- Swif 5	DIPPER-2/BUSHEN-3. CDSS92B128-IM-0Y-0M-0Y-3B-0Y-0SD.	Egypt
Hybrid 2	P1	Sohag - 4	Ajaia-16//Hora/Jro/3/Ga/4/Zar/S/Souk 7/6/Stot//Altar84/Aid. CDSSB007785-0T0PY-0M-OY129Y-0M-0Y-IB-0SH.	Egypt
	P2	Beni- Swif 6	Boomer-21/Busca-3.- CDSS95-Y001158-8Y-0M-0Y-0B-1Y-0B-0SD.	Egypt

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The F_1 (the first generation) plants were backcrossed to their parents in the 2022–2023 season, and this breeding scheme produced backcross generations, specifically BC1 (F1 X P1) and BC2 (F1 X P2). To produce additional F_1 grains, crosses were also made. Some F_1 hybrids were selfed to create the F_2 generation at the same time.

The experiment utilized a randomized complete block design (RCBD) with three replicates to evaluate six populations (P1, P2, F1, F2, BC1, and BC2) from two distinct durum wheat hybrids. These populations were cultivated during the 2023-2024 season across two separate experiments, differentiated by sowing date: November 25th (normal) and December 25th (late sowing, simulating heat stress).

Each replication within the experiment comprised 44 rows, distributed as follows: 16 rows for the F_2 generation, 8 rows each for the BC1 and BC2 generations, and 4 rows each for the P1, P2, and F_1 populations. All rows were 5.0 meters in length, with individual plants spaced 20 cm apart and rows separated by 60 cm.

Data collection involved a specific number of individual plants from each population: 30 plants for P1, P2, and F_1; 60 plants for BC1 and BC2; and 120 plants for the F_2 population. The following agronomic traits were measured beside days to 50% flowering (DFF):

- Plant height (PH, cm)
- Number of spikes per plant (NSP)
- Number of kernels per spike (NKS)
- 100-grain weight (GW, g)
- Grain yield per plant (GYP, g)

In accordance with the guidelines established by the Ministry of Agriculture, all agricultural techniques were implemented as they are frequently used to cultivate wheat. Fertilizer containing nitrogen, phosphorus, and potassium were applied in the prescribed amounts. Over the course of two planting dates, 75 kg of nitrogen fertilizer per acre was sprayed in the form of urea (46% N). The first dose was applied before irrigation following planting, and the second dose was given at the tillering stage prior to the second irrigation. Before planting, 100 kg of calcium super phosphate (15.5% P_2O_5), a phosphorus fertilizer, was applied in a single dose. At the same time as the nitrogen fertilizer was applied, two equal doses of potassium fertilizer in the form of potassium sulphate (48% K_2O_5) were delivered at a rate of 120 kg/hectare. Table (2) list some of the physical and chemical characteristics of the experimental site prior to cultivation.

Table 2. The physical and chemical characteristics of the experimental site as determined prior to cultivation.

Chemical properties

Depth Cm	pH	ECE (dS/m)	Water-soluble ion concentrations (mq/L) in the soil paste were determined.							Available nutrient in soil (ppm)		
			$CO_{3}+HCO_{3}$	Cl^-	SO_4^-	Ca^{++}	Mg^{++}	Na^+	K^+	N	P	K
0-30	7.80	1.05	2.50	1.25	6.10	2.70	1.35	5.70	0.10	75	9.60	375
30-60	7.90	1.25	2.86	3.16	6.60	3,20	2.20	7.34	0.27	55	8.55	350

Physical properties

Depth (cm)	Percentage %			Texture Class	O.M %	$CaCO_3$ %
	Sand	Silt	Clay			
0-30	25	39.60	35.00	Clay loam	1.24	3.55
30-60	25.60	40.00	33.40	Clay loam	0.70	2.25

Statistical and genetic analyses:

Genetic analysis was performed using generation means analysis, which included the application of scaling tests (A, B, and C). These tests, developed by Mather and Jinks (1982), were specifically utilized to ascertain the presence of non-allelic interactions. The methodology involved the following steps:

$$A = 2\bar{B}_1 - \bar{P}_1 - \bar{F}_1$$
$$B = 2\bar{B}_2 - \bar{P}_2 - \bar{F}_1$$
$$C = 4\bar{F}_2 - 2\bar{F}_1 - \bar{P}_1 - \bar{P}_2$$

The genetic model parameters, encompassing (m), (a), (h), and the epistatic interactions of (aa), (ad), and (dd), were estimated using the established methodologies of Jinks and Jones (1958) and Hayman (1958). These parameters are calculated as follows:

m: Represents the mean of the genetic model.

a: Defined as the additive effect, calculated as B1−B2.

h: Represents the dominance effect, determined by the formula $F1-4F2-\frac{1}{2}p1-\frac{1}{2}p2+2BC1+2BC2$

aa: Represents the additive x additive gene interaction, calculated as 2 (BC1+BC2−٢F2).

ad: Represents the additive x dominance interaction, derived from $BC1-\frac{1}{2}p1-BC2+\frac{1}{2}p2$.

dd: Represents the dominance x dominance interaction, calculated as P1+P2+2F1+4 (F2−BC1−BC2).

The statistical significance of the genetic components was assessed using a t-test, calculated as:

$$t = \frac{\textbf{effect}}{\sqrt{\textbf{variance of the effect}}}$$

Heterosis:

Heterosis, or hybrid vigor, was calculated as the percentage difference between the mean performance of the F1 generation and either the mid-parent or the better parent value.

The formulas employed for these calculations were:

- **Mid-parent heterosis (M.P.)**:

$$\mathbf{M.P.}\ (\%) = \frac{(\textbf{first generation} - \textbf{Mid Parents})}{\textbf{Mid Parents}} \times \mathbf{100}$$

- **Better-parent heterosis (BP)**:

$$\boldsymbol{B}.\mathbf{P}.\ (\%) = \frac{(\textbf{first generation} - \textbf{Better Parents})}{\textbf{Better Parents}} \times \mathbf{100}$$

A t-test was applied to assess the statistical significance of the deviation of the F1 mean from its respective mid-parent and better-parent values.

*- MID PARENT

$$\mathbf{T} = \mathbf{T(Tabuler)} \times \frac{\sqrt{\mathbf{VP1 + VP2 + VF1}}}{\mathbf{3}}$$

*- Better parent

$$\mathbf{T} = \mathbf{T(Tabuler)} \times \frac{\sqrt{\boldsymbol{BP}\mathbf{ + VF1}}}{\mathbf{2}}$$

Inbreeding Depression (I.D.%) was quantified using the following equation:

$$(\text{I.D}\ \%) = \frac{F1 - F2}{F1} \times 100$$

Variances of I.D deviation = $VF_1 + VF_2$

T: I.D =$F_1 + F_2$ / (V.I.D) $^{0.5}$

Phenotypic and genotypic coefficients of variability were determined using the methods described by Burton (1952) The average degree of dominance (ā), $\bar{a} = (H/D)^{1/2}$ was estimated according to Mather and Jinks (1982).

Heritability:

Two distinct estimations of heritability were calculated:

- **Broad-sense heritability (h2b)** was determined using the formula provided by Mather and Jinks (1982):

$$h^2\text{b} = \frac{\text{VG}}{\text{VP}} \times 100$$

where

VG represents genetic variance and VP represents phenotypic variance.

- **Narrow-sense heritability (h^2n)** was estimated using the following formula, also from Mather and Jinks (1982):

$$h^2\text{n}\% = \frac{\frac{1}{2}D}{\text{VP}} \times 100$$

h^2n%=VP21D×100

where D represents the additive genetic variance and VP represents phenotypic variance.

Expected Genetic Gain from Selection:

The expected genetic gain from selection (G.S.) was calculated using the following formula:

G.S% = [(K * σ ph x $h^2{}_n$) / mean of F_2] x 100. (Allard, 1960):

Heat tolerance indices:

To differentiate genotypes based on their response to drought across all evaluated traits, heat tolerance indices were calculated for each genotype. These indices were derived from the studied traits under both non-stress (Yp) and drought stress (Ys) conditions, utilizing the specific formulas outlined in Table 4.

Table 3. Details the heat tolerance indices employed to assess the response of two durum wheat varieties to heat stress.

No.	Heat tolerance indices	Equation	Reference
1	Stress tolerance index (STI)	(Yp × Ys)/ (Ȳ p)^2	Fernandez, 1992 -- 11
2	Tolerance index (TOL)	Yp– Ys	Rosielle and Hamblin, 1981---12
3	Mean productivity index (MP)	(Yp+Ys)/2	
4	Heat tolerance index (HSI)	(1-YS/ YP)/ SI	Fisher and Maurer 1978---13
5	Harmonic mean (HM)	[2(Yp×Ys)/(Yp+Ys)	Chakherchaman *et al.*, 2009---14
6	Relative performance (P)	(YS/YP)/R	Abo-Elwafa and Bakheit 1999----15

Grain yield for each genotype under non-stress (Yp) and stress (Ys) conditions was recorded.

The Environmental Stress Intensity (SI) was calculated as:

$$SI = 1 - \frac{(\text{Mean of YS for all genotypes in stress}}{\text{mean of YP for all genotypes in non} - \text{stress environments})}$$

Additionally, a ratio (R) was determined by dividing the grain yield under stress by the grain yield under non-stress:

$$R = \frac{\text{YS}}{\text{YP}}$$

RESULTS AND DISCUSSION

Mean values and standard errors were determined for six traits across the six generations of two distinct wheat crosses. These data, collected under both normal and heat stress conditions, are summarized in Tables 4 and 5. A notable finding was the significant variation observed among the means of the six populations within each cross, suggesting substantial genetic diversity for all traits investigated. In both hybrids, the F_1 generation exhibited higher mean values than all parents, BC_1 and BC_2 for (PH), (NSP), (NKS), (GYP), and 100-kernel weight under both conditions—except for days to 50% flowering (DFF) in one hybrid, where no such trend was observed.

Table 4. Mean performance and standard error of parents, F_1, F_2, and back crosses generations in two durum wheat crosses for all studied traits under two sowing dates.

Cross I	Sohag 4 X Beni-swif 5					
Traits	DH		PH		N.S/P	
Sowing dates	N	H	N	H	N	H
P1	90.17±0.287	83.97±0.55	104.60±0.74	96.72±0.65	9.67±0.23	8.72±0.20
P2	85.40±0.390	79.84±0.51	109.40±0.70	102.13±0.67	8.37±0.26	7.94±0.14
F1	90.63±0.367	86.25±0.65	110.09±0.80	107.19±0.70	11.13±0.38	9.06±0.23
F2	91.38±0.410	89.60±0.54	97.36±0.60	97.38±0.60	9.24±0.23	7.99±0.15
BC1	89.18±0.450	82.43±0.65	107.17±0.72	103.66±0.68	10.53±0.28	8.92±0.19
BC2	87.03±0.530	83.60±0.61	98.81±0.66	101.21±0.60	10.18±0.29	8.08±0.18
LSD 5%	0.80	1.05	1.17	1.17	0.45	0.28
LSD 1%	1.05	1.38	1.54	1.54	0.59	0.37
Traits	NK/S		GY/P		100-KW	
Sowing dates	N	H	N	H	N	H
P1	57.13±0.74	40.03±0.53	25.95±0.36	19.46±0.30	5.96±0.07	4.86±0.08
P2	55.58±0.79	37.69±0.49	30.11±0.38	18.15±0.35	5.93±0.04	4.39±0.06
F1	58.11±0.99	43.94±0.69	36.69±0.84	24.05±0.56	6.21±0.05	4.92±0.10
F2	41.14±0.77	40.50±0.65	29.93±0.59	20.89±0.41	5.44±0.07	4.49±0.06
BC1	49.49±0.95	41.56±0.65	31.84±0.66	22.51±0.45	5.91±0.09	4.72±0.08
BC2	53.17±0.93	42.15±0.79	32.57±0.67	20.24±0.62	5.83±0.07	4.47±0.08
LSD 5%	1.51	1.26	1.61	0.80	0.14	0.12
LSD 1%	1.98	1.66	1.52	1.05	0.18	0.16

DH, days to 50% flowering; PH, plant height; N.S/P, number of spikes per plant; NKS, number of kerenels per spike; GY/P, grain yield per plant; 100-KW, weight of 100 grains, N, normal sowing date; H, late sowing date; LSD 5%, least significant difference at 5%; LSD 1%, least significant difference at 1%

Table 5. The mean performance and standard error for the parental, F1, F2, and backcross generations of two durum wheat crosses were determined for all investigated traits across two distinct sowing dates.

Cross II	**Sohag 4 X Beni-swif 6**					
Traits	**DH**		**PH**		**N.S/P**	
Sowing dates	**N**	**H**	**N**	**H**	**N**	**H**
P1	90.17±0.28	83.97±0.55	104.60±0.74	96.72±0.65	9.67±0.23	8.72±0.20
P2	91.03±0.33	85.91±0.37	108.56±0.78	102.44±0.74	8.96±0.27	7.88±0.24
F1	86.72±0.33	88.63±0.76	106.81±0.78	105.97±0.25	10.29±0.34	9.22±0.53
F2	91.30±0.29	89.12±0.57	98.97±0.69	99.26±0.61	9.41±0.21	8.56±0.19
BC1	91.31±0.37	90.39±0.66	105.56±0.78	103.75±0.72	10.18±0.25	8.40±0.21
BC2	90.84±0.33	86.34±0.77	99.80±0.86	101.08±0.76	9.98±0.28	8.60±0.25
LSD 5%	0.565	1.11	1.358	1.19	0.40	0.37
LSD 1%	0.741	1.146	1.781	1.56	0.534	0.49
Traits	NK/S		GY/P		100-KW	
Sowing dates	N	H	N	H	N	H
P1	57.13±0.74	40.03±0.53	25.95±0.36	19.46±0.30	5.96±0.07	4.86±0.08
P2	45.03±0.80	39.56±0.38	29.57±0.37	23.65±0.31	6.00±0.048	4.52±0.04
F1	58.63±1.10	44.13±0.532	35.47±0.97	28.22±0.592	6.09±0.09	4.97±0.07
F2	41.80±0.82	36.62±0.70	31.66±0.65	23.52±0.53	5.59±0.07	4.63±0.06
BC1	48.58±1.06	43.33±0.76	34.08±0.81	24.91±0.71	5.84±0.07	4.61±0.06
BC2	52.10±0.91	43.28±0.75	33.51±0.83	27.11±0.59	5.67±0.08	4.54±0.07
LSD 5%	1.612	1.36	1.280	1.04	0.129	0.11
LSD 1%	2.113	1.79	1.679	1.37	0.169	0.14

The backcross generations (BC_1 and BC_2) showed higher mean values than both parents for DFF and PH in both crosses. Under heat stress, the backcross generations exceeded both parents in all traits for the first cross, and in DFF, NSP, NKS, and GYP for the second hybrid. Under normal conditions, the BC_1 and BC_2 generations also recorded higher mean values than all parents for NKS and GYP in both hybrids.

In contrast, the second generation showed lower mean values than the F_1 for NSP, NKS, GYP, and 100-kernel weight in both hybrids, except for DFF and PH, which remained higher across both conditions. High genetic variance was observed for all traits, with the exception of PH and 100-kernel weight in both hybrids. Additionally, the F-values for these traits were lower than those observed in all parents. (Awad 1996), Amin (2013), Zaazaa (2017), El-Masry, Al-Nahhas (2018), Ahmed (2021) and Haridy *et al* (2021) reported the same conclusion. Also, Zaazaa (2017) revealed that the F_1 population recorded the highest average values compared with other populations for all traits in the three crosses, except grain weight / spike in the third hybrids. Abd El-Rady and Koubisy (2023) found that the DFF, PH, yield and yield components significantly decreased under water deficit stress.

Scaling test: -

Significant scaling test parameters (A, B, C) indicated deviations from the additive-dominance model, suggesting epistatic interactions that play an important role in the inheritance of the studied traits in the evaluated durum wheat materials (Mather and Jinks, 1982). Table 6 shows the estimated scaling test parameters (A, B, and C) for traits evaluated in two durum wheat hybrids under both normal and heat stress conditions. The consistent significance of at least one scaling test across both hybrids and environmental conditions for all traits suggests that a simple additive–dominance model is insufficient to fully explain the observed gene action. This supports the application of a more comprehensive six-parameter model to accurately describe the genetic behavior of these traits.

However, in certain instances, the non-significance of parameters A, B, or C indicates that even the interactive model may not completely capture the underlying gene action, highlighting the intricate nature of genetic control. These findings align with previous research, such as those reported by Shafey et al. (1993), Tammam (2005), El-Aref et al. (2011), Zaazaa et al. (2012), and Amin (2013) for traits like (NSP), (NKS), and (GYP). Similarly, observations regarding (DFF), (PH), and (GW) are consistent with reports by Moussa (2010) and Lal *et al.* (2013). Conversely, Abdel-Rady (2018) observed that the scaling test revealed an absence of non-allelic interactions for the majority of traits. However, exceptions were noted for of (NSP) in hybrid 2 and for (NKS) and (GYP) in hybrid 1 under normal conditions.

Gene effects:

Nature of gene effect, was determined using six Table (7). The estimates of F_2 means s were positive and highly significant (**) for the six characters in two hybrids under two conditions. Additive gene effects (d) were positive and significant (*) for DH, PH and NKS under normal conditions for cross I, PH, NSP, GYP and 100- kernels weight under heat stress for hybrid I. While positive and significant for DH, PH, for cross II under heat stress, and negative significant for NKS and GY/P for cross II under normal condition. Moreover, positive in significant for NSP and GY/P of the second cross under all conditions. Our findings align with previous studies conducted by Khattab *et al*. (2010), Abd El-Rahman (2013), Elmassrya and El-Nahas (2018), and Ahmed (2021). However, Zaazaa *et al.* (2012) reported a different pattern, noting non-significant additive gene effects for most characters, except for NGS and GYP in one hybrid, and only NGS in another. Similarly, Haridy *et al*. (2021) documented significant additive gene effects for the majority of traits, specifically excluding DH and 100-grain weight.

Dominance gene effects (h) demonstrated high significance (**) for PH, NKS, and GY/P in both crosses under both normal and heat stress conditions. Furthermore, significant to highly significant positive dominance effects were evident for NSP and 100-kernel weight in hybrid 2 under both environmental conditions. Conversely, dominance effects for DH were notably negative and highly significant in hybrid 1 under both conditions, and under natural condition in hybrid 2.

In general, the additive gene effects (d) were smaller in magnitude than the dominance effects (h). This suggests that non-additive gene action is the primary driver in the inheritance of most traits. These findings are consistent with earlier work by Khattab *et al.* (2010) and Wafaa El-Awdy (2011), who reported similar patterns for (PH), (NSP), (NKS), 100-kernel weight, and (GYP). Dominance effects generally exceeded additive effects for the majority of traits, with NKS in cross 2 being an exception, a result supported by Khaled (2013). Similarly, Ahmed (2021) observed highly significant dominance effects across all traits investigated, excluding NKS in cross 2. Abd-Allah and Mostafa (2011) also noted significant dominance gene effects for all traits, with the exception of NKS in both hybrids.

Table 6. Scaling test parameters A, B, and C were determined for all investigated traits in two durum wheat hybrids across various sowing dates.

Traits	Crosses	S. D	A	B	C
DH	C1	N	-2.43**±1.01	-1.96±1.20	8.71**±1.86
		H	5.36**±1.24	1.10±1.50	22.10**±2.63
	C2	N	5.73**±0.86	3.93**±0.80	10.57**±1.41
		H	8.18**±1.63	-1.85±1.80	9.37**±2.83
PH	C1	N	-0.36±1.72	-11.43**±1.80	-44.76**±3.80
		H	3.42*±1.66	-6.89**±1.60	-23.70**±2.95
	C2	N	-0.28±1.88	-15.77**±2.10	-30.89**±3.36
		H	-1.59±1.76	-6.24**±1.90	-20.46**±3.06
NS/P	C1	N	0.28±0.72	0.88±0.70	-3.33**±1.26
		H	0.86±0.49	-0.84±0.50	-2.82**±0.80
	C2	N	0.59±0.64	0.91±0.70	-1.16±1.13
		H	-1.13*±0.53	0.10±0.60	-0.79±0.97
NK/S	C1	N	-16.27**±2.26	-7.35**±2.30	-654.37**±3.83
		H	-0.84±1.57	2.68±1.80	-3.59±3.03
	C2	N	-18.61**±2.50	0.55±2.30	-52.21**±4.11
		H	2.50±1.70	2.87±1.60	-21.36**±3.06
G Y/ P	C1	N	1.04±1.60	-1.66±1.60	-9.72**±2.96
		H	1.51±1.10	-1.72±1.20	-2.14±2.04
	C2	N	6.74**±1.92	1.97±2.00	-1.78±3.33
		H	1.68±1.59	2.35±1.40	-5.96*±2.49
100kw	C1	N	-1.36±0.20	-0.48±0.21	-2.57**±0.32
		H	-0.34±0.208	-0.38±0.20	-1.14**±0.34
	C2	N	-0.37±0.192	-0.75±0.20	0.16±0.33
		H	-0.61**±0.16	-0.41*±0.20	-0.81**±0.28

DH, days to 50% flowering; PH, plant height; N.S/P, number of spikes per plant; NKS, number of kernels per spike; GY/P, grain yield per plant; 100-KW, weight of 100 grains, N, normal sowing date; H, late sowing date; C1, cross 1; C2, cross 2 and (A, B and C) = Scaling test parameters.

Table 7. The types of gene action were investigated for all traits in two durum wheat crosses across different sowing dates. This analysis utilized generation means ± standard error.

Traits	Crosses	S. D	M	D	h	dd	hh	dh
DH	C1	N	91.38**±0.35	2.15**±0.69	-10.25**±2.19	-13.10**±2.15	17.49**±3.34	-0.23±0.73
		H	89.60±0.33	-1.17±0.88	-22.02**±2.89	-26.36**±2.79	30.62**±4.41	-3.23**±0.96
	C2	N	91.30**±0.21	0.47±0.49	-4.79**±1.57	-0.91±1.52	-8.75**±2.44	0.90±0.54
		H	89.12**±0.35	4.05**±1.01	0.65±3.16	-3.04±305	-3.28±4.95	5.02**±1.07
PH	C1	N	98.81**±0.60	3.13*±0.98	36.07**±3.25	32.97**±3.10	-21.19**±4.99	5.23**±1.10
		H	97.38**±0.62	2.45±0.90	27.99**±3.13	20.22**±3.01	-16.75**±4.67	5.15**±1.02
	C2	N	98.97**±0.69	5.76**±1.16	15.07**±3.73	14.83**±3.61	1.22±5.73	7.47**±1.27
		H	99.26**±0.60	2.67*±1.04	15.81**±3.33	12.62**±3.20	-4.79±5.18	2.33*±1.15
NS/P	C1	N	9.24**±0.23	0.35±0.40	6.59**±1.30	4.48**±1.23	-5.63*±2.06	-0.30±0.44
		H	7.99**±0.24	0.84*±0.26	2.77**±0.83	2.04*±0.78	-1.25±1.32	0.45±1.08
	C2	N	9.41**±0.20	0.19±0.37	3.45**±1.18	2.67*±1.11	-4.17*±1.87	-0.16±0.41
		H	8.56**±0.25	0.19±0.32	0.68±1.05	-0.24±1.01	1.27±1.63	-0.62±0.36
NKS	C1	N	41.14**±1.01	-3.68**±1.32	42.51**±4.22	40.75**±4.07	-17.14**±6.54	-4.46**±1.43
		H	40.50**±1.02	0.59±1.02	10.50**±3.38	5.42±3.29	-7.26±5.08	-1.76±1.08
	C2	N	41.80**±0.82	3.53*±1.39	41.70**±4.48	34.16**±4.31	-16.10*±6.92	-9.58**±1.49
		H	36.62**±1.04	0.05±1.06	31.07**±3.57	26.74**±3.51	-32.11**±5.29	-0.18±0.16
G Y/ P	C1	N	29.93**±0.59	0.73±0.93	17.75**±3.15	9.09**±3.02	-8.47±4.78	1.35±0.97
		H	20.89**±0.61	2.27**±0.69	7.17**±2.23	1.93±2.14	-1.72±3.43	1.61*±0.72
	C2	N	31.66**±0.065	0.57±1.15	16.26**±3.63	8.55*±3.49	-17.26**±5.69	2.38*±1.18
		H	23.52**±0.57	2.20*±0.92	16.42**±2.89	9.99**±2.87	-14.01**±4.46	-0.34±0.96
100kw	C1	N	5.44**±0.071	0.08±0.11	1.99**±0.38	1.73**±0.37	-0.90±0.57	0.06±0.12
		H	4.49**±0.075	0.29**±0.11	0.71*±0.35	0.42±0.57	-0.30±0.57	0.02±0.13
	C2	N	5.59**±0.065	0.17±0.11	0.76*±0.36	0.66±0.36	-0.46±0.55	0.19±0.12
		H	4.63**±0.073	0.07±0.09	0.08±0.31	-.021±0.29	-1.23*±0.48	-0.10±0.10

M= mean effects, D= additive gene effects, h= dominance effect, dd= additive x additive gene interaction, hh= dominance x dominance gene interaction and dh= additive x dominance gene interaction

The additive × additive (dd) type of gene effects was consistently positive and highly significant for PH, NKS, and GY/P in both hybrids. They were also notably significant for NSP in cross I under both normal and heat stress conditions. In contrast, dd effects for DFF were negative and highly significant in cross I, while being non-significant for both DFF and 100-kernel weight in cross II under both environmental conditions. These results suggest that early generation selection may be effective for improving these traits, particularly in self-pollinated crops such as wheat, where additive × additive interactions play a crucial role in trait expression. This contrasts with hybrid crops, where dominance × dominance interactions are more critical due to the reliance on heterosis. Such findings support the potential of incorporating dd effects into wheat breeding programs aimed at improving key agronomic traits. These findings align with those reported by Amin (2013), who emphasized the significance of additive × additive effects in wheat breeding. Conversely, Akhtar and Chowdhry (2006) observed negative dominance × dominance (dd) effects for (PH) and (GYP). In contrast, Zaazaa *et al.* (2012) found that additive × additive gene effects were significantly positive for most traits, whereas dominance × dominance interactions were significantly negative across three different hybrids.

The (ad) parameters additive × dominance was highly significantly and positive for (PH) in both hybrids under both normal and heat stress conditions. In contrast, ad effects were significantly negative for (NKS) in both crosses under normal conditions, and significantly positive for (GY/P) in hybrid I under heat stress. However, these effects were not significant for (NSP) and GW across both crosses and conditions. These findings align with those reported by Abd El-Rahman and Hammad (2009), who observed similar patterns for NKS and GW.

Data in Table (7) showed that, the estimates (dd) dominance × dominance gene effects were significant to highly significant positive effects were observed in cross I for (DH), while negative significant effects were found for PH under both conditions and for NSP in both crosses under normal conditions. These results underscore the important role of dominance-based epistasis in the inheritance of certain traits. Additionally, significant (*) to highly significant (**) negative dd interactions were recorded for PH, GW, and DH in hybrid I. Conversely, dd effects was insignificant for DH and NKS in hybrid I and for GY/P in both hybrids. El-Aref et al. (2011) and Amin (2013) reported the same conclusion.

The type of epistasis was classified as complementary when the dominance (h) and dominance × dominance (dd) gene effects had the same sign, and as duplicate epistasis when the signs were opposite. Accordingly, selection in early generations is expected to be effective when additive effects outweigh non-additive effects. Conversely, when non-additive effects dominate, improvement of the traits requires intensive selection in later generations. These findings are consistent with those reported by Amin (2013), and Abd El-Rady (2018), who emphasized the importance of understanding gene action to determine the appropriate selection strategy in breeding programs.

Heterosis %, inbreeding depression (%) and phenotypic (PCV) and genotypic (GCV) coefficient of variation:

Heterosis, defined as the percentage deviation of the first generation mean from both the (MP) and (BP) values, was assessed across various traits. As detailed in Table 8, highly significant positive heterosis, relative to both MP and BP, was consistently observed for number of (NSP) and (GY/P) in both crosses under normal and heat stress conditions. Similarly, significant positive heterosis over the MP was noted for (PH), (NKS), and GW in both crosses and environments. However, exceptions included (DFF) and NKS under heat stress, where heterosis was either non-significant or negative. Specifically, DFF displayed negative heterosis, and PH showed non-significant positive heterosis in cross 2 under natural condition. These findings align with the results reported by Abd Alla and Hassan (2012), Zaazaa (2017), and Elmassry and El-Nahas (2018). Kumar *et al.* (2018) and Ahmed (2021) also observed significant positive mid-parent and better-parent heterosis in several hybrids for GY/P. Wafaa El-Awdy (2011) reported highly significant heterotic effects in the second cross for GY/P, NSP, NKS, and 100-kernel weight (8.69%, 9.78%, 6.71%, and 9.78%, respectively). In contrast, negative heterotic effects were recorded in the third cross for NSP (-17.45%) and NKS (-3.08%), leading to a reduction in GY/P (-10.37%).

Table 8. Heterosis, inbreeding depression %, phenotypic (PCV) and genotypic (GCV) coefficient of variation and average degree of dominance in two durum wheat hybrids for all characters under two sowing dates.

Traits	Crosses	S. D	Heterosis MP	Heterosis B*P*	ID	PCV%	GCV%	$(H/D)^{1/2}$
DH	C1	N	3.24**	0.51	-0. 83	4.93	4.45	1.40
		H	5.30**	2.72**	-3.89	6.60	5.57	1.09
	C2	N	-4.28	-3.82**	-2.58	3.55	2.95	1.31
		H	4.34**	5.55**	-0.55	7.01	6.02	1.61
PH	C1	N	2.89**	5.25**	11.57**	6.22	4.55	1.20
		H	7.81**	10.82**	9.15	6.76	5.58	1.09
	C2	N	1.05	2.12	7.34	7.67	6.38	1.15
		H	6.42**	2.76	6.33	6.70	5.36	1.22
NS/P	C1	N	23.38**	15.09**	16.96**	27.61	20.97	1.19
		H	8.82**	3.94**	11.82**	20.11	14.72	1.20
	C2	N	4.15**	6.45**	8.51**	24.2	16.44	1.18
		H	11.11**	5.73**	7.15**	24.70	19.69	1.13
NKS	C1	N	3.11*	1.71	29.62**	20.17	17.29	1.10
		H	13.07**	9.76**	7.82**	17.50	15.33	1.06
	C2	N	1.29**	2.61	28.70**	21.55	17.14	1.12
		H	10.88**	10.23**	17.01**	20.90	19.57	1.05
G Y/ P	C1	N	30.90**	41.39**	12.44**	14.87	13.68	0.62
		H	27.87**	23.57**	8.77**	15.22	11.24	1.73
	C2	N	15.50**	36.68**	8.16**	12.90	9.71	1.02
		H	29.92**	41.61**	6.93**	13.43	10.71	1.21
100kw	C1	N	4.41**	4.16**	18.42**	21.69	18.93	0.95
		H	6.38**	1.29	13.12**	21.56	18.52	1.23
	C2	N	1.03	2.08	10.76**	22.61	17.55	1.34
		H	6.01**	2.31	16.68**	24.86	22.55	1.53

MP, mid parent; BP, better parent; ID, inbreeding depression; PCV%, Coefficient of phenotypic variance; GCV%, coefficient of genotypic variance; $H/D)^{1/2}$ **average degree of dominance** respectively.; * & ** Significant and high Significant at 0.05 & 0.01 level of probabilities.

Inbreeding depression (ID) values were positive and highly significant (**) for (NSP), (NKS), (GY/P), and GW in both hybrids under the two sowing dates. In contrast, ID was insignificant and negative for (DFF) in both hybrids. These results are expected, as the expression of heterosis in the first generation is typically followed by a marked reduction in the second generation due to increased homozygosity. These findings align with previous research. For instance, Zaazaa *et al.* (2012), reported similar observations for (NSP), (NKS), and (GY/P). Similarly, Moussa (2010) found comparable results for days to heading.

Also noted significant inbreeding depression for yield and its related traits across multiple genotypes by Kumar *et al.* (2018). Furthermore, Wafaa El-Awdy (2011) documented significant and positive inbreeding depression (ID) values for NSP in the first and third crosses, and for NKS and GY/P across all crosses. Conversely, a significant negative ID was observed in the second hybrid, specifically for GW in the second and third crosses.

As presented in Table 8, the phenotypic coefficient of variation (PCV) consistently ranged from moderate to high and was invariably greater than the genotypic coefficient of variation (GCV) for all characters examined across both hybrids and sowing dates. The close proximity between PCV and GCV values indicates that a substantial proportion of the observed variation is genetically controlled, primarily through additive genetic variance. However, the consistently higher PCV values also suggest that environmental factors had a notable influence on trait expression. Similar results were reported by Zaazaa et al. (2012), Fouad et al. (2020), and Ahmed (2021), who highlighted similar trends in wheat and related crops.

As shown in Table 8, the average degree of dominance $(H/D)^{½}$ indicated that over-dominance for all studied traits in both hybrids across the two sowing dates. Exceptions to this pattern were grain yield per plant (GY/P) and GW in hybrid 1 under natural conditions. These observations are consistent with reports from Khattab *et al.* (2010), Amin (2013), and El-Gammaal and Yahya.(٢٠١٨)

Conversely, Abd-Allah and Mostafa (2011) noted complete dominance for number of spikes per plant (NSP) and GW in the first cross, while over-dominance (H/D > 1) was detected for grain yield and related traits in the second cross. Ahmed (2021), on the other hand, found partial dominance for all traits in cross 1, and for GW in the second cross. Furthermore, the results indicated over-dominance towards the better parent (BP) for all traits in cross 2, and for (PH) in cross 1, with the exception of (NKS) in cross 2.

Magda Abd El Rahman (2013) reported that $(H/D)^{½}$ was less than unity for (DFF), PH, and GY/P in the second hybrid, and for kernel weight in the third hybrid. Additionally, $(H/D)^{½}$ was less than unity for NKS in the last two crosses and for NSP in all crosses, which suggests the presence of partial dominance.

Heritability in broad (Hb) and narrow (Hn) senses and genetic advance:

Heritability estimates offer crucial insights into the feasibility of selecting plant characteristics within a breeding program, indicating the ease or difficulty of achieving progress through selection. Broad-sense and narrow-sense heritability estimates, along with genetic advance (G.S.%), are presented in Table 9.

Table 9. Estimates of heritability in broad sense (H^2b) and narrow sense (h^2n) and expected genetic advance (G.S%) in two durum wheat hybrids for all characters under two sowing dates.

Traits	Crosses	S. D	VP	VG	VE	H^2b	H^2n	GS%
DH	C1	N	20.27	16.75	3.70	81.76	57.08	5.79
		H	34.95	24.92	10.03	71.31	65.18	8.86
	C2	N	9.98	6.89	3.09	69.03	50.62	3.70
		H	39.05	28.76	10.28	73.66	41.12	5.94
PH	C1	N	36.67	19.60	17.07	53.44	42.19	5.41
		H	43.36	29.57	13.79	68.20	62.09	8.65
	C2	N	57.66	39.92	17.74	69.23	59.84	9.46
		H	44.26	28.31	15.95	63.96	51.45	7.10
NS/P	C1	N	6.50	3.75	2.75	57.68	47.32	26.91
		H	2.58	1.38	1.20	53.61	38.31	15.87
	C2	N	5.19	2.40	2.80	46.16	38.64	19.26
		H	4.47	2.84	1.63	63.57	56.03	28.51
NKS	C1	N	71.74	50.03	21.71	69.74	52.77	22.51
		H	50.23	40.08	10.16	79.78	75.28	27.14
	C2	N	81.18	51.35	29.82	63.26	56.17	24.94
		H	58.60	51.38	7.22	87.68	83.07	35.77
G Y/ P	C1	N	42.13	32.10	10.30	76.19	74.40	33.24
		H	20.29	14.96	5.33	73.76	58.61	26.03
	C2	N	51.24	30.85	20.39	60.22	42.91	19.99
		H	34.17	28.12	6.05	82.29	49.10	25.14
100kw	C1	N	0.65	0.55	0.10	84.63	68.71	21.05
		H	0.47	0.25	0.22	54.59	27.32	8.56
	C2	N	0.52	0.29	0.23	56.65	55.58	14.77
		H	0.39	0.25	0.14	63.61	51.40	14.22

Vp, Phenotypic variance; Vg, Genotypic variance; VE, environmental variance; Hb, Broad sense heritability; Hn, narrow sense heritability; GS%, expected genetic advance.

In the second generation, broad-sense heritability values ranged from moderate to high for all studied traits across both hybrids. Specifically, values varied from 46.16% for (NSP) in cross 1 under normal sowing conditions to 87.68% for (NKS) in cross 2 under heat stress. Narrow-sense heritability values were moderate for (DFF), (PH), and NKS in cross 1 under normal conditions. While low for GW in cross 1 under heat stress, narrow-sense heritability was high for DFF, PH, and NKS in cross 1 under heat stress, and for (GYP) and GW in hybrid 1 under normal conditions. Generally, narrow-sense heritability estimates were moderate to high for all traits under both conditions, except for NKS in hybrid 2 under heat stress.

This suggests that these traits are substantially influenced by both additive and non-additive genetic effects, indicating a considerable amount of table variation. Conversely, traits with low narrow-sense heritability estimates imply that selection for improvement will be challenging due to significant environmental influence. These findings align with reports from Amin (2013), El-Massry and El-Nahas (2018), and El-Gammaal and Yahya (2018).

Additionally, El-Said Rania (2018) noted high broad-sense heritability for all traits studied, suggesting primary genetic control, while low narrow-sense heritability for NSP and GY/P indicated a lesser contribution from additive genetic effects. Zaazaa (2017) also found low to moderate narrow-sense heritability for all traits across three crosses, with values ranging from 0.01 for NSP in the second hybrid to 0.56 for NKS in the first hybrid. More recently, Haridy *et al.* (2022) reported high narrow-sense heritability for GY/P (53.37%), GW (49.56%), spike number per plant (48.56%), and plant height (45.55%), with the smaller value being 30.25% for the NSP in the second mutational generation.

Agreeing to Johnson et al. (1955), genetic advance as a percentage of the mean is classified as less (<10%), moderate (10-20%), or greater (>20%). The expected genetic advance as a percentage of the F_2 average (Table 9) was moderate to high for both hybrids under both environmental conditions, with the exception of DFF, PH, and 100-grain weight in hybrid 1 under heat stress. This indicates a strong potential for developing high-yielding genotypes through early generation selection. Conversely, traits with lower expected genetic advance values suggest a substantial influence of environmental factors and dominance gene action on their inheritance. Similer conclusion by Khattab et al. (2010), El-Aref et al. (2011), Amin (2013), and Ahmed (2021), who reported the highest genetic advances for PH, 1000-grain weight, and GY/P. In a related study, Manal Eid (2009) observed low heritability and less genetic advance for PH and NKS, noting that heritability was generally lower under drought stress conditions.

Heat tolerance indices:

Six heat tolerance indices, based on (GY/P) potential and response, were computed to evaluate the heat tolerance of two durum wheat hybrids under normal sowing (YP) and heat stress (YS) conditions (Table 10). The Stress Tolerance Index (STI) for GY/P revealed that in cross 1, the P1 population exhibited the highest heat tolerance (74.99%), followed by BC1 (70.73%), F2 (69.79%), F1 (65.52%), BC2 (62.14%), and P2 (60.27%). In cross 2, BC2 demonstrated the highest STI value (80.92%), with P2 (79.98%), F1 (79.56%), P1 (76.79%), F2 (74.29%), and BC1 (73.12%) following. These findings suggest that segregating populations could effectively generate lines with tolerance to heat stress and high GY/P. These results are in agreement with those obtained by Amin (2013), and Abd El-Rady and Koubisy (2023).

Table 10. Comparison of heat indices for two crosses durum wheat based on GY/P under normal date (YP) and late sowing date (heat stress) (YS) conditions.

populations	Heat tolerance indices							
Cross 1	**YP**	**YS**	**STI**	**TOL.**	**Performance relative (P)**	**HSI**	**MP**	**HM**
Sohag4 (P_1)	25.95	19.46	74.99	6.49	1.119	0.757	22.70	22.24
Beni- swif 5(P_2)	30.11	18.15	60.27	11.96	0.9000	1.202	24.13	22.64
F_1	36.69	24.04	65.52	12.65	0.978	1.043	30.36	29.04
F_2	29.83	20.89	69.79	9.04	1.042	0.914	25.41	24.60
BC_1	31.81	22.5	70.73	9.31	1.056	0.886	26.75	26.35
BC_2	32.57	20.24	62.14	12.33	0.927	1.146	25.67	24.96
Mean	31.17	20.88	62.24	10.29	1.00	0.991	26.02	24.97
Cross 2								
Sohag4 (P_1)	25.95	19.92	76.79	6.02	0.991	0.757	22.93	22.54
Beni- swif 6(P_2)	29.57	23.65	79.98	5.91	1.032	0.888	26.61	26.28
F_1	35.47	28.22	79.56	7.24	1.027	0.900	31.63	31.43
F_2	31.65	23.51	74.29	8.13	0.959	1.140	27.28	26.98
BC_1	34.07	24.91	73.12	9.15	0.943	1.192	29.49	28.78
BC_2	33.50	27.11	80.92	6.38	1.044	0.846	30.30	29.69
Mean	32.04	24.55	76.57	7.49	0.999	1.002	28.04	27.79

According to the heat stress tolerance data in Table 10, cross 1 indicated that genotypes with superior relative performance (P), specifically BC1 (1.044), P2 (1.032), and F1 (1.027), displayed comparatively smaller differences in yield under stress and non-stress conditions. This was reflected by their lower Tolerance Index (TOL) values of 6.38, 5.91, and 7.24, respectively. In cross 2, P1 exhibited the highest relative performance (P) (1.119), followed by BC1 (1.056) and F2 (1.042), which yielded less varied TOL estimates (6.49, 9.31, and 9.04, respectively).

The remaining wheat populations (P1, F_1, and BC1 in cross 1, and P1, P2, F_1, and BC2 in hybrid 2) appeared to tolerate heat stress, recording Heat Susceptibility Index (HIS) values less than unity. These genotypes generally possessed high yield attributes. These results align with the findings of Mahdy *et al.* (2022), Hamam *et al.* (2022), Abd El-Rady (2022), and El-Saady *et al.* (2024).

The F_1, BC1, and BC2 populations in both crosses exhibited superior performance, as evidenced by their highest Mean Productivity (MP) and Harmonic Mean (HM) index values. This suggests high productivity under both potential yield (YP) and stress yield (YS) environments. Based on these results, these populations were categorized as heat tolerant under both sowing date conditions, a conclusion supported by the work of Kamrani *et al.* (2017).

CONCLUSION

Heat stress, induced by late sowing, negatively impacted all studied traits. However, specific wheat populations exhibited tolerance to this condition. In cross 1, P1 (Sohag 4), BC1, and BC2 demonstrated heat stress tolerance, as indicated by their heat tolerance indices (HIS) of less than unity. Similarly, in cross 2, P1 (Sohag 4), P2 (Beni-Swif 6), F_1, and BC2 showed tolerance. These resilient genotypes generally displayed high values for yield attributes. Notably, Sohag 4 maintained stability and outperformed other populations across both sowing dates. These findings offer significant insights for wheat breeders focused on enhancing yield potential, developing novel wheat genotypes, and improving Egyptian wheat germplasm.

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التحليل الوراثي لبعض الصفات الزراعية في هجينين من قمح المكرونة تحت الإجهاد الحرارة

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الملخص

زُرعت ستة تراكيب وراثية، مشتقة من هجن قمح المكرونة (سوهاج ٤ × بني سويف ٥) و(سوهاج ٤ × بني سويف ٦)، تحت ظروف بيئية مختلفة: الظروف العادية (الزراعة في الموعد المعتاد)، وظروف الإجهاد الحراري (الزراعة المتأخرة). أُجريت هذه الدراسة في مزرعة كلية الزراعة-جامعة الأزهر-أسيوط، خلال ثلاثة مواسم زراعية متتالية من ٢٠٢١-٢٠٢٢ إلى ٢٠٢٣-٢٠٢٤.النتائج الهجين الأول: لوحظت تأثيرات جينية مضافة إيجابية ومعنوية لصفات ارتفاع النبات، عدد الحبوب لكل سنبلة وعدد الأيام حتى الإزهار تحت الظروف العادية، ولصفات ارتفاع النبات، عدد السنابل لكل نبات، محصول الحبوب لكل نبات و وزن ١٠٠ حبة تحت ظروف الإجهاد الحراري.الهجين الثاني: لوحظت تأثيرات جينية مضافة إيجابية ومعنوية لصفات ارتفاع النبات، عدد الأيام حتى الإزهار تحت ظروف الإجهاد الحراري، بينما كانت سلبية ومعنوية لصفات عدد الحبوب لكل سنبلة و محصول الحبوب لكل نبات تحت الظروف العادية. كما كانت التأثيرات إيجابية وغير معنوية لصفات عدد السنابل لكل نبات و محصول الحبوب لكل نبات في هذا الهجين تحت كلتا الظروف.التحمل الحراري: أظهرت التراكيب الوراثية سوهاج ٤ ، الجيل الأول والهجين الرجعي الأول من الهجين الأول، وكذلك سوهاج ٤، بني سويف ٦ ، الجيل الأول والهجين الرجعي الثاني من الهجين الثاني، قدرة على تحمل الحرارة) مؤشر تحمل الحرارة (HSI < 1 وامتلكت صفات إنتاجية عالية.بشكل عام، أظهرت هذه الأنماط الوراثية المرنة قيمًا عالية لصفات المحصول. ومن الجدير بالذكر أن سلالة "سوهاج ٤" حافظت على استقرارها وتفوقت على السلالات الأخرى في كلا تاريخي الزراعة.تقدم هذه النتائج رؤى هامة لمربّي القمح الذين يسعون إلى•: تعزيز إمكانات المحصول.تطوير أنماط وراثية جديدة.تحسين السلالات الوراثية.