Genetic Analysis of Some Agronomic Traits in Two Bread Wheat Crosses under Heat Stress Conditions.

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ABSTRACT

The present study was carried out at Shandaweel Agric., Res., Station, ARC, Egypt, in 2014/2015, 2015/2016 and 2016/2017 seasons. The present investigation aimed to determine genetic parameters and type of gene action controlling some agronomic traits of the two bread wheat crosses, Shandawel 1 × Gemmeiza 11 and Misr 1 × Giza 168 under normal 20th Nov. and heat stress 20th Dec. conditions, using six populations model (P_1, P_2, F_1, F_2, B_{C1} and B_{C2}). Scaling test indicated the presence of non-allelic interactions for all studied traits except number of spikes/plant in cross 2 under normal conditions, number of grains/spike in cross1 under favorable conditions and in cross 2 under heat stress and grain yield/plant in cross 1 under normal conditions. The relative importance of additive and dominance effects varied for traits and crosses under normal and heat stress conditions. Dominance effects were generally greater than additive, except for days to heading in cross 2 under heat stress, plant height under normal conditions in cross 2 and biological yield in cross 1 under heat stress and in cross 2 under normal conditions, indicating that dominant genes playing major role in inheritance of these beside the additive one. Dominance × dominance gene interaction was higher in magnitude than additive × additive and additive × dominance in most traits, indicating that these traits greatly affected by dominance and non-allelic interactions. Therefore, it is advisable to delay selection to later generations with increased homozygosity. Positive highly significant heterosis over better parent values were observed for all studied traits, except for plant height in cross 2 under both sowing dates, number of grains/spike in cross 1 under heat stress and in cross 2 under both environments. Broad sense and narrow sense heritability and genetic advance ranged from moderate to high in most cases. Based on these results, these two crosses could be selected to produce high yielding lines under heat stress conditions.

Keywords: *Triticum aestivum*, six populations model, gene action, heritability, heterosis.

INTRODUCTION

Wheat is one of the most important food grain crops in the world and staple food for the people of Egypt. However, wheat production is insufficient to meet the domestic consumption of the growing population in Egypt, which resulted in increasing wheat imports. Heat stress is one of the major limitations facing wheat productivity in arid, semiarid, tropical and subtropical regions all over the world (Fischer, 1986). Many studies had confirmed the damaging effect of heat on wheat. El-Gizawy (2009), Tahir *et al*. (2009), Seleiman *et al*. (2011), Hamam (2014) and EL-Maghraby *et al*. (2016) reported that late sowing reduced days to heading, plant height, number of spikes/m^2, number of grains/spike, 1000-grain weight, biological yield and final grain yield. Genetic variability in heat tolerance has been found to exist among wheat cultivars and lines. Therefore, wheat breeders and geneticists must continue to increase the productivity to fill the gap by developing high yielding cultivars over a wide range of stress and non-stress environments with desirable genetic makeup. A detailed understanding of the genetics factors controlling agronomic characteristics is a primary step for breeding studies. Generation mean analysis is a simple estimate but it is one of the most important techniques for estimating main gene effects (additive and dominance) along with their interactions (additive × additive, additive × dominance and dominance × dominance) provided the pattern inheritance of yield and other associated traits. Additive dominance model was adequate for explain the type of gene action of grain yield and its components (Bayoumi *et al*., 2008). Amin (2013) found that additive dominance model was invalid to explain the inheritance of most studied traits under normal and heat stress. Hamam (2014) observed that heritability estimates in

narrow sense in F_2 were relatively moderate to high under favorable and heat stress for yield and itscomponents. The objectives of this study were to determine 1) The nature of gene action controlling yield and its components in two bread wheat crosses under normal and heat stress conditions, 2) Estimate heterosis, inbreeding depression, potence ratio, heritability in broad and narrow sense and expected genetic advance from selection.

MATERIALS AND METHODS

Three field experiments were carried out at Shandaweel Agric. Res. Station, ARC., Egypt, during the three successive growing seasons of 2014/2015, 2015/2016 and 2016/2017. Four bread wheat cultivars representing a wide range of diversity for several agronomic traits were used as parents to obtain the following crosses; Cross 1= Shandaweel 1 / Gemmeiza 11 and Cross 2= Misr 1 / Giza 168 (Table 1).

In the first growing season of 2014/2015, two crosses were performed using the four wheat cultivars to produce F_1 hybrid seeds. In the second growing season of 2015/2016, the F_1 of each cross was crossed to its respective parents to produced B_{C1} (F_1 × P_1) and B_{C2} (F_1 × P_2). At the same time , the other F_1 plants were selfed to produce F_2 grains. In the third growing season of 2016/2017, the six populations, i.e., P_1, P_2, F_1, F_2, B_{C1} and B_{C2} of the two wheat crosses were sown in two separate field experiments in a randomized complete block design with three replications under two sowing dates. The first sowing date was 20th Nov. a recommended sowing and the second sowing date was 20th Dec. as late sowing "heat stress" (Table 2). Each replicate consisted of 14 rows, one row for each of P_1, P_2 and F_1, 5 rows for F_2, 2 rows for each of $B_{C1}$and B_{C2} as well as two border rows. Each row was 2.0 m long and 30 cm apart with 10 cm plant spacing. All other

cultural practices were applied as recommended for wheat cultivation. Data were recorded on 10 guarded plants for each P_1, P_2 and F_1; 75 plants of F_2 and 20 plants of B_{C1} and B_{C2} in each replicate for: 1- days to 50% heading, 2- plant height (cm), 3- number of spikes/plant, 4- number of grains/spike, 5- 100-grain weight (g) 6- biological yield/plant (g) and 7- grain yield/plant (g).

Table 1. Pedigree and selection history of cultivars used in the two bread wheat crosses.

Cross	Parent		Pedigree and selection history
Cross 1	P1	Shandaweel 1	SITE//MO/4/NAC/TH.AC//3*PVN/3/MIRLO/BUC CM SS93B00S675S-72Y-010M-010Y-010M–3Y–0M–0THY–0SH
	P2	Gemmeiza 11	BOW"S"/KVZ"S"//7C/SERI-82/3/GIZA 168/SAKHA 61 GM7892-2GM-1GM-2GM-1GM-0GM
Cross 2	P1	Misr 1	OASIS/KAUZ//4*BCN/3/2*PASTOR CMSS00Y01881T-050M-030Y-030M-030WGY-33M-0Y- 0S
	P2	Giza 168	MIROL/BUC//SERI-82 CM-93046-8M-0Y-0M-2Y-2B;

Table 2. Mean maximum and minimum air temperatures (ºC) during 2014/2015, 2015/2016 and 2016/2017 growing seasons.

Month		November	December	January	February	March	April	May
2014/2015	Max.	27	23	20	23	28	31	37
	Min.	13	10	7	10	14	16	22
2015/2016	Max.	27	21	19	25	28	36	38
	Min.	15	9	7	10	15	19	23
2016/2017	Max.	28	21	20	21	26	33	38
	Min.	15	8	7	7	12	18	22

Statistical and genetic analysis:

Analysis of variance and mean comparison of the characters was performed using M-STAT statistical program. The scaling test was applied to detect the presence or absence of non-allelic interactions and their types as outlined by Mather (1949).

$A = 2\overline{B_{C1}} - \overline{P_1} - \overline{F_1}$

$B = 2\overline{B_{C2}} - \overline{P_2} - \overline{F_1}$

$C = 4\overline{F_2} - 2\overline{F_1} - \overline{P_1} - \overline{P_2}$

$D = 2\overline{F_2} - \overline{B_{C1}} - \overline{B_{C2}}$

$V(A) = 4V(\overline{B_1}) + V(\overline{P_1}) + V(\overline{F_1})$

$V(B) = 4V(\overline{B_{C2}}) + V(\overline{P_2}) + V(\overline{F_1})$

$V(C) = 16V(\overline{F_2}) + 4V(\overline{F_1}) + V(\overline{P_1}) + V(\overline{P_2})$

$V(D) = 4V\overline{F_2} + V\overline{B_{C1}} + V\overline{B_{C2}}$

The standard error (S.E) of A, B, C and D was obtained by taking the square root of their respective variances. T-test was calculated by dividing the calculated values of A, B, C and D on their respective standard error. The significance of any one of these scales is taken to indicate the presence of epistasis. In the presence of epistasis various gene effects were estimated using six parameters genetic model of Jinks and Jones (1958) and Hayman (1958).

m = mean effect= $\overline{F_2}$

d = additive effect = $\overline{B_{C1}} - \overline{B_{C2}}$

h = dominance effect = $\overline{F_1} - 4\overline{F_2} - 0.5\overline{P_1} - 0.5\overline{P_2} + 2\overline{B_{C1}} + 2\overline{B_{C2}}$

i= Additive x Additive gene interaction = $2\overline{B_{C1}} + 2\overline{B_{C2}} - 4\overline{F_2}$

j = Additive x Dominance gene interaction = $\overline{B_{C1}} - 0.5\overline{P_1} - \overline{B_{C2}} + 0.5\overline{P_2}$

l = Dominance x Dominance gene action = $\overline{P_1} + \overline{P_2} + 2\overline{F_1} + 4\overline{F_2} - 4\overline{BC_1} - 4\overline{BC_2}$

The variance values in this concern were obtained as follows:

$V_m = V(\overline{F_2})$

$V_d = V(\overline{B_{C1}}) + V(\overline{B_{C2}})$

$V_h = V(\overline{F_1}) + 16V(\overline{F_2}) + 0.25V(\overline{P_1}) + 0.25V(\overline{P_2}) + 4V(\overline{B_{C1}}) + 4V(\overline{B_{C2}})$

$V_i = 4V(\overline{B_{C1}}) + 4V(\overline{B_{C2}}) + \overline{16F_2}$

$V_j = V(\overline{B_{C1}}) + 0.25V(\overline{P_1}) + V(B_{C2}) + 0.25V(\overline{P_2})$

$V_1 = V(\overline{P_1}) + V(\overline{P_2}) + 4V(\overline{F_1}) + 16V(\overline{F_2}) + 16V(\overline{B_{C1}}) + 16V(\overline{B_{C2}})$

The significant of the genetic components were tested using the t test, where $\pm t$ = effect/(variance effect)$^{1/2}$

The genetic components of variance were calculated by the formulas of F_2 variance were obtained according to Mather and Jinks (1982) as:

E (environmental variance) = 1/3 ($V_{P1} + V_{P2} + V_{F1}$)

D (additive variance) = 4 V_{F2} – 2 ($V_{BC1} + V_{BC2}$)

H (dominance variance) = 4 ($V_{F2} - 1/2V_D - V_E$)

Broad-sense (H^2_b) and narrow-sense (h^2_b) heritability were estimated by Warner (1952) formulas:

$$H^2b = [V_{F2} - (V_{p1} + V_{p2} + F_1)/3]/V_{F2}$$

$$h^2_b = [2V_{F2} - (V_{BC1} + V_{BC2})]/V_{F2}$$

Genetic advance was computed according to Johnson *et al.* (1955) with selection intensity of K = 5% (2.06) for all characters as follows:

G.S = K × ($\sigma^2 F_2$)$^{1/2}$ × h^2_n. and (G.S %) = (G.S / $\overline{F_2}$) × 100

Heterosis was expressed as the deviation of F_1 generation from the mid-parent or better parent average values as follows:

Heterosis over mid-parent % (M.P) = $(\overline{F_1} - \overline{MP})/\overline{MP}$ × 100

Heterosis over the better-parent % (BP) = $(F_1 - \overline{BP})`/BP × 100$

Inbreeding depression was estimate as the average percentage decrease of the F_2 from the F_1 as follows:

$$(I.D \%) = (\overline{F_1} - F_2 / \overline{F_1}) × 100$$

Potence ratio (P), was estimated by using the following equation given.

$$P = (F_1 - MP) /1/2 (P_2 - P_1)$$

where: F_1: First generation mean, P_1: the mean of the lower parent, P_2: the mean of the higher parent, and MP: the mid-parent values = 1/2($P_1 + P_2$).

Stress tolerance index (STI) for grain yield was computed as formula using by Farshadfar, *et al.* (2001), as follow: STI = Yp x Ys /(Yp)^2 × 100

where , Yp grain yield under normal conditions, Ys grain yield under stress conditions**.**

RESULTS AND DISCUSSION

Mean performance:

Mean of the six populations P_1, P_2, F_1, F_2, B_{C1} and B_{C2} for the studied traits in the two bread wheat crosses under normal and heat stress treatments are presented in Table 3. Significant differences were found among the six generations for all the studied traits under the two environmental conditions, indicating the existence of genetic variation for these traits in the studied materials. The F_1 mean values surpassed the mid values of the two parental means for all studied traits in the two crosses under both recommended and late sowing, indicating the prevalence of heterotic effects and dominance effects controlling these traits. The F_1 means exceeded the better parent for studied traits in the two crosses under both environments except, days to heading in cross 1 under normal conditions and in cross 2 under both conditions, plant height in cross 2 under normal conditions, number of grains/spike in cross 2 and 100-grain weight in cross 1 under recommended sowing date, indicating over dominance. The F_2 population mean performance values were between the two parents and less than F_1 for days to heading in the two crosses under both environments, plant height in cross 2 under both conditions, number of spikes/plant in cross 1 under normal conditions, number of grains/spike in cross 1 under heat stress and in cross 2 under both conditions, 100-grain weight in cross 1 under both conditions and in cross 2 under normal conditions and grain yield/plant in cross 1 under heat stress, indicating the importance of non-additive components of genetic variance for these traits. Meanwhile, the remaining traits mean values of the F_2 generation were higher than the highest parents, indicating that superior parental lines can be selected depending on transgressive segregation for these traits. However, average value of B_{C1} and B_{C2} progenies of the two crosses varied under normal and late sown conditions and each tended toward the mean of its recurrent parent. Similar results were reported by Amin (2013), Hamam (2014), Said (2014) and Kumar *et al.* (2017).

Stress tolerance index (STI) for grain yield/plant (Table 3) showed that the F_1 hybrid had the highest value of heat tolerance (0.74) followed by P_1, F_2, B_{C2}, P_2 and B_{C1} which had 0.73, 0.70, 0.69, 0.68 and 0.64, respectively in cross 1. While in cross 2 the F_2 population had the highest value of STI (0.82) followed by P_2 (0.80), B_{C2} (0.79), F_1 (0.77), B_{C1} (0.77) and P_1 (0.64). These results suggest that segregating populations could be effective to produce lines tolerant to heat stress and give high grain yield. These results are in line with those found by Amin (2013).

Gene effects:

Results of scaling test of the studied traits in the two wheat crosses under the two environments are shown in Table 4. The calculated values of A, B, C and D scaling test revealed that significant of any of these tests in the two crosses under both environments, except for number of spikes/plant in cross 2 under normal conditions, number of grains/spike in cross1 under favorable sown and in cross 2 under heat stress and grain yield/plant in cross 1 under favorable sown. These findings indicated that the presences of non allelic gene interactions and additive-dominance model is inadequate for explaining the inheritance of these traits. Meanwhile, the scaling test estimates for expected traits, indicates the absence of non-allelic interactions and the adequacy of the additive-dominance model to explain the type of gen action for these traits. These results are in general agree with those reported by Tammam (2005), Moussa (2010), El-Aref *et al.* (2011), Zaazaa *et al.* (2012), Amin (2013), Abd El-Rahman (2013), Hamam (2014), El-Hawary (2016) and kumar *et al.* (2017).

Results of the six parameters analysis are listed in Table 5. The mean effect (m) which reflects the contribution due the overall mean plus the locus effects and interactions of the fixed loci was highly significant for all studied traits of the two crosses under normal and heat stress conditions, indicating that these traits are quantitatively inherited. Similar results were found by Moussa (2010), Amin (2013), Hamam (2014), Bilgin *et al.* (2016) and El-Hawary (2016).

Additive gen effects (d) were positive and significant or highly significant for days to heading in cross 1 and 2 under heat stress, plant height in cross1 under normal and in cross 2 under both treatments, number of spikes/plant in cross 1 under normal conditions, number of grains/spike in cross 1 under heat stress and biological yield/plant in cross 1 under heat stress and cross 2 under favorable sown, indicating the significant contribution of additive gene effect in the inheritance of these traits and the potential for obtaining further improvement of these traits by selection using pedigree method. Meanwhile, the negative and highly significant values found for 100-grain weight under both environments in cross 1 were due to the choice as to which parent was designated P_1 or P_2. These results are in agreement with those obtained by El-Aref *et al.* (2011), Amin (2013), Hamam (2014) and El-Hawary (2016). Kumar *et al.* (2017) reported that the additive gene effects were significantly negative for 1000-grain weight.

The dominance gene effects (Table 5) were positive and significant or highly significant for days to heading in cross 1 under both treatments, plant height in cross 1 under favorable sown, number of grains/spike in cross 1 under heat stress, 100-grain weight in the two crosses and environments and grain yield/plant in cross 1 under normal sown. Meanwhile, negative and highly significant effects were recorded for number of grains/spike in cross 2 under normal sown. These results show the great importance of the dominance gene effects in the inheritance of these traits. With regard to the negative sign for dominance effects indicated that the alleles responsible for less value for these traits were over dominant over the alleles controlling high value. Amin (2013) reported that a negative sign for dominance for 100-grain weight under heat stress. On

the other hand, significant additive and dominance gene effects were important in the inheritance of days to heading in cross 1 under heat stress, plant height in cross 1 under normal sowing, number of grains/spike in cross 1 under heat stress and 100-grain weight in cross 1 under both environments and the dominance gene effects were higher than additive effects, revealed that both additive and dominance gen effects were important

in inheritance of these traits. Also, selecting desirable characters may be practiced in the early generations but it would be effective in the late ones when dominant effect diminished. These results are in accordance with those obtained by El-Aref *et al*. (2011), Zaazaa *et al*. (2012), Abd El Rahman (2013), Amin (2013), Bilgin (2014), Hamam (2014), El-Hawary (2016) and Kumar *et al*. (2017).

Table 3. Mean performance ± stander error of P_1, P_2, F_1, F_2, B_{C1} and B_{C2} populations of two bread wheat crosses for the studied traits under normal (N) and heat stress (H) conditions.

Trait	Cross	Sowing date	Generations						L.S.D 0.05
			P_1	P_2	F_1	F_2	B_{C1}	B_{C2}	
Days to 50% heading	C_1	N	97.33±0.25	94.67±0.28	97.00±0.36	95.32±0.22	96.50±0.33	97.50±0.45	1.87
		H	92.93±0.16	90.73±0.21	93.87±0.20	91.09±0.13	92.00±0.22	91.23±0.27	1.91
	C_2	N	95.07±0.30	93.13±0.25	94.93±0.21	93.71±0.16	93.53±0.31	92.30±0.21	1.79
		H	90.47±0.22	88.53±0.27	90.07±0.28	88.51±0.15	89.07±0.25	88.03±0.28	1.70
Plant height, cm.	C_1	N	105.33±0.69	110.73±0.94	118.67±1.29	111.69±1.05	116.20±1.74	110.07±1.70	5.27
		H	100.13±0.76	106.87±0.88	110.73±0.81	107.65±1.25	109.27±1.96	104.77±1.64	4.88
	C_2	N	112.00±0.61	103.20±0.92	110.13±0.91	107.37±0.41	108.77±0.76	103.10±0.69	5.35
		H	104.20±0.89	97.27±0.81	104.53±0.70	101.51±0.46	100.43±0.79	98.03±0.75	4.82
Number of spikes /plant	C_1	N	13.67±0.32	11.73±0.31	14.00±0.52	12.48±0.21	13.10±0.39	12.03±0.32	1.04
		H	11.13±0.30	10.67±0.30	12.00±0.35	11.37±0.16	10.73±26	10.53±0.34	0.95
	C_2	N	11.67±0.34	12.87±0.27	14.20±0.33	13.36±0.19	12.97±0.31	13.00±0.31	1.36
		H	9.93±0.28	11.07±0.34	13.07±0.40	12.79±0.23	11.50±0.41	11.70±0.38	1.38
Number of grains / spike	C_1	N	47.93±0.83	45.62±0.92	50.32±0.90	48.31±0.51	50.14±0.73	47.77±0.99	2.68
		H	45.58±0.94	38.83±0.93	46.50±0.82	41.44±0.44	45.65±0.70	42.71±0.82	3.19
	C_2	N	48.94±0.88	44.44±0.86	47.69±0.90	45.43±0.44	43.60±0.73	43.04±0.86	3.33
		H	41.40±0.89	42.00±1.12	42.73±1.00	40.89±0.48	40.09±0.81	40.30±0.93	1.65
100-grain weight, g.	C_1	N	4.37±0.05	5.00±0.07	4.97±0.06	4.88±0.03	4.79±0.04	5.07±0.07	0.41
		H	4.22±0.07	4.43±0.07	4.60±0.06	4.33±0.03	4.15±0.05	4.61±0.06	0.30
	C_2	N	4.81±0.07	4.48±0.07	4.84±0.07	4.77±0.04	4.96±0.06	4.84±0.08	0.28
		H	4.34±0.07	4.32±0.06	4.55±0.06	4.49±0.04	4.69±0.06	4.56±0.06	0.23
Biological yield /plant, g.	C_1	N	81.33±2.47	84.93±2.17	96.93±3.79	87.52±1.94	84.87±3.38	81.60±2.81	7.68
		H	65.27±2.27	70.93±2.63	86.73±1.95	80.17±1.49	78.67±2.41	71.33±2.51	8.07
	C_2	N	79.80±2.10	76.67±2.20	90.27±2.99	88.16±1.43	87.30±2.53	80.13±2.24	8.93
		H	65.87±3.43	71.07±3.15	83.93±3.03	81.93±1.53	76.57±2.93	74.40±2.55	8.43
Grain yield/ plant, g.	C_1	N	28.75±0.88	26.48±0.72	34.29±1.15	29.51±0.72	31.73±1.24	29.54±1.17	3.52
		H	21.03±0.40	18.06±0.47	25.46±0.80	20.67±0.41	20.37±0.58	20.51±0.72	2.47
	C_2	N	27.03±0.61	25.37±0.54	32.57±0.88	28.76±0.54	28.14±0.99	26.91±0.82	3.49
		H	17.37±0.69	20.19±0.91	25.16±0.93	23.62±0.54	21.58±0.89	21.38±0.88	2.98
STI%	C_1		0.73	0.68	0.74	0.70	0.64	0.69	
STI%	C_2		0.64	0.80	0.77	0.82	0.77	0.79	

STI= Stress tolerance index for grain yield/plant, Cross 1= (Shandaweel 1 x Gemmeiza 11), Cross 2 = (Misr 1 x Giza 168)

Additive × additive gene effects (i) were positive and significant or highly significant (Table 5) for days to heading in cross 1 under two environments, number of grains/spike in cross 1 under heat stress and 100-grain weight in cross 2 under both environments, suggested that these traits have increasing genes and selection for its improvement could be effective. These results are in accordance with the findings of Moussa (2010), El-Aref *et al*. (2011), koumber and El-Gammaal (2012), Hamam (2014) and Kumar *et al*. (2017). However, negative and significant or highly significant values of additive × additive gene effects were reported for plant height in cross 2 under both treatments, number of spikes/plant in cross 1 and 2 under heat stress, number of grains/spike in cross 2 under normal sown, biological yield/plant in cross 1 under heat stress and in cross 2 under both environments and grain yield/plant in cross 2 under heat stress. These results showed dispersion of alleles in parents. Therefore, selection is of no use in early segregating generations because there is no additive genetic effect to be fixed in these traits. Similar results were obtained by Amin (2013) and Hamam (2014).

Negative additive × additive gene effects were recorded for plant height, number of tillers/plant, biomass/ plant and grain yield/plant (Akhtar and Chowdhry, 2006).

Significant or highly significant and positive additive × dominance gen effects (j) were found for days to heading in cross 2 under normal conditions, plant height in cross 1 under both environments and in cross 2 under normal conditions and biological yield/plant in cross 1 under heat stress. As additive × dominance epistasis tends to segregate in next generations, it would be better to delay selection to later generations with increased homozygosity, where additive and additive×additive variances are prevailing. These results are in harmony with those reported by Amin (2013), Hamam (2014) and kumar *et al*. (2017). Negative and significant or highly significant values were reported for days to heading in cross 1 under normal conditions and 100-grain weight in cross 1 under heat stress, indicating that the dominance genes are in the low performance parent and it is expected to obtain less days to heading and 100-grain weigh in infinity generations.

Table 4. Scaling test parameters A, B, C and D of two bread wheat crosses for all studied traits under normal (N) and heat stress (H) conditions.

Cross	Sowing date	Scaling test			
		A	B	C	D
		Days to heading			
C₁	N	-1.33±0.79	3.33**±1.00	-4.72**±1.20	-3.36**±0.71
	H	-2.80**±0.50	-2.13**±0.61	-7.03**±0.71	-1.05*±0.43
C₂	N	-2.93**±0.72	-3.47**±0.53	-3.24**±0.85	1.58**±0.49
	H	-2.40**±0.61	-2.53**±0.68	-5.11**±0.89	-.09±0.48
		Plant height			
C₁	N	8.40*±3.77	-9.27*±3.75	-6.63±5.07	-2.88±3.21
	H	7.67±4.07	-8.07*±3.49	2.15±5.38	1.27±3.57
C₂	N	-4.60*±1.87	-7.13**±1.88	-5.97±2.70	2.88±1.31
	H	-7.87**±1.94	-5.73**±1.84	-4.51±2.60	4.55**±1.42
		Number of spikes/plant			
C₁	N	0.47±0.99	-3.61**±0.88	-3.48±2.12	-0.17±1.03
	H	-1.20±0.70	-2.07*±0.83	-0.31±1.05	1.48**±0.54
C₂	N	-1.13±0.75	0.13±0.77	0.51±1.09	0.75±0.57
	H	-1.13±0.97	0.40±0.90	4.01**±1.31	2.37**±0.73
		Number of grains/spike			
C₁	N	2.04±1.91	-0.39±2.37	-0.97±3.00	-1.31±1.60
	H	-0.78±1.88	0.09±2.06	-11.64*±2.74	-5.48**±1.39
C₂	N	-9.43**±1.93	-6.04**±2.13	-7.03*±2.79	4.22**±1.43
	H	-3.94±2.10	-4.13±2.38	-5.30±3.12	1.38±1.56
		100-grain weight			
C₁	N	0.24*±0.12	0.17±0.16	0.21±0.20	-0.10±0.10
	H	-0.52**±0.14	0.18±0.15	-0.55**±0.20	-0.11±0.10
C₂	N	0.27±0.16	0.37*±0.18	0.10±0.23	-0.27*±0.13
	H	0.49**±014	0.24±0.15	0.18±0.21	-0.27*±0.11
		Biological yield/plant			
C₁	N	-12.13±8.13	-15.07*±7.21	-10.05±11.34	8.57±5.86
	H	-0.33±5.68	-9.33±5.85	11.03±7.93	10.35*±4.59
C₂	N	7.67±6.24	-9.80±5.77	15.64±8.82	8.89*±4.42
	H	-1.86±7.44	-1.00±6.85	22.94**±9.80	12.90**±4.95
		Grain yield/plant			
C₁	N	2.69±2.87	-3..95±2.76	-5.79±3.86	-2.26±2.23
	H	-2.79±1.47	-5.48**±1.69	-7.33**±2.36	0.47±1.23
C₂	N	-1.66±2.25	-5.78**±1.96	-2.50±2.90	2.47±1.68
	H	-2.18±2.13	0.24±2.11	6.60*±3.08	4.27**±1.66

* & ** Significant and high Significant at 0.05 & 0.01 level of probabilities, respectively.

Table 5. Types of gene action using generation means ± stander error for all studied traits of two bread wheat crosses under normal (N) and heat stress (H) conditions

Trait	Cross	Sowing date	Mean (m)	Additive (d)	Dominance (h)	Additive x Additive (i)	Additive x Dominance (j)	Dominance x Dominance (L)	Epistasis
Days to heading	C1	N	95.32**±0.22	-1.00±0.55	7.72**±1.48	6.72**±1.42	-2.33**±0.58	-8.72**±2.52	D
		H	91.09**±0.13	0.77*±0.34	4.13**±0.90	2.09*±0.86	-0.33±0.37	2.84±1.54	C
	C2	N	93.71**±0.16	1.23±0.38	-2.33±1.02	-3.16±0.98	0.27**±0.42	9.56*±1.73	D
		H	88.51**±0.15	1.03**±0.37	0.74±1.01	0.17±0.96	0.41±0.41	4.76**±1.74	C
Plant height, cm.	C1	N	111.69**±1.05	6.13*±2.43	16.39*±6.58	5.76±6.42	8.83**±2.50	-4.89±10.96	D
		H	107.65**±1.25	4.50±2.55	4.69±7.22	-2.55±7.15	7.87**±2.62	2.95±11.54	C
	C2	N	107.37**±0.41	5.67**±1.02	-3.23±2.84	-5.76±2.63	1.27**±1.16	17.49±4.89	D
		H	101.51**±0.46	2.40*±1.09	-5.29±2.99	-9.09**±2.84	-1.07±1.24	22.69**±5.06	D
Number of spikes /plant	C1	N	12.48**±0.45	1.07*±0.51	1.64±2.13	0.34±2.05	0.10±0.55	2.80±2.93	C
		H	11.37**±0.16	0.20±0.43	-1.86±2.13	-2.96**±1.08	-0.03±0.48	6.23**±2.02	D
	C2	N	13.36**±0.19	-0.03±0.43	0.43±1.21	-1.51±1.14	0.57±0.48	2.51±2.05	C
		H	12.79**±0.23	-.20±0.56	-2.18±1.52	-4.75**±1.45	0.37±0.60	5.48*±2.58	D
Number of grains / spike	C1	N	48.31**±0.51	2.37±1.23	6.16±3.39	2.61±3.20	1.22±1.38	-4.26±5.77	D
		H	41.44**±0.44	2.94**±1.08	15.25**±2.97	10.95**±2.78	-0.43±1.27	-10.27*±5.12	D
	C2	N	45.43**±0.44	0.55±1.13	-7.45**±3.05	-8.45*±2.85	-1.70±1.29	23.92**±5.31	D
		H	40.89**±0.48	-0.21±1.23	-1.73±3.35	-2.76±3.12	0.10±1.42	10.82±5.82	D
100-grain weight, g.	C1	N	4.88**±0.03	-0.28**±0.08	0.49*±0.22	0.20±0.21	0.03±0.09	-0.62±0.37	D
		H	4.33**±0.03	-0.46**±0.08	0.48*±0.22	0.21±0.21	-0.35**±0.09	0.1±0.38	C
	C2	N	4.77**±0.04	0.12±0.10	0.73*±0.27	0.53*±0.25	-0.05±0.11	-1.2*±0.46	D
		H	4.49**±0.04	0.14±0.08	0.77**±0.23	0.55*±0.22	0.13±0.09	-1.3**±0.39	D
Biological yield /plant, g.	C1	N	87.52**±1.94	3.27±4.39	-3.35±12.43	-17.15±11.73	5.07±4.69	44.35*±20.92	D
		H	80.17**±1.49	7.33±3.48	-2.06±9.54	-20.69**±9.17	10.17**±3.89	30.4±16.03	D
	C2	N	88.16**±1.43	7.17±3.37	-5.74±9.46	-17.77*±8.85	5.60±3.70	19.9±16.22	D
		H	81.93**±1.53	2.17±3.88	-10.34±10.61	-25.80**±9.89	4.77±4.53	28.7±18.37	D
Grain yield/ plant, g.	C1	N	29.51**±0.72	2.19±1.70	11.20*±4.64	4.53±4.46	1.05±1.80	-3.26±7.83	D
		H	20.67**±0.41	-0.14±0.92	4.99±2.61	-0.93±2.46	-1.63±0.97	9.20*±4.39	C
	C2	N	28.76**±0.54	1.23±1.28	1.42±3.49	-4.94±3.35	0.40±1.35	12.38*±5.90	C
		H	23.62**±0.54	0.20±1.25	-2.16±3.49	-8.54*±3.31	1.61±1.38	10.48±5.88	D

*p < 0.05, **p < 0.01.   C = Complementary   D = Duplicate

The dominance × dominance (l) gene interactions were significant or highly significant and positive in cross 1, for umber of spikes/plant and grain yield/plant under heat stress and biological yield/plant under normal conditions. As well as in cross 2 for days to heading under both conditions, plant height and number of spikes/plant under heat stress, number of grains/spike and grain yield/plant under favorable sown. These results confirm the important role of dominance × dominance gene action in the genetic system controlling these traits and selection should be effective in late generations. Significant or highly significant and negative dominance × dominance (l) gene interactions were obtained in cross 1 for days to heading under favorable sown and number of grains/spike under late sowing date. As well as in cross 2 for 100-grain weight under normal and heat stress conditions, indicating their reducing effect in the expression of these traits and there is no breeding importance in proceeding generations. These results are in agreement with those reported by Akhtar and Chowdhry (2006), El-Aref *et al.* (2011), Koumber and El-Gammaal (2012), Amin (2013), Hamam (2014) and Kumar *et al.* (2017).

The type of epistasis was determined as complementary when dominance (h) and dominance × dominance (l) gene effects have same sign and duplicate epistasis when the sign was different. The results in Table 5 showed that duplicate epistasis was prevailing for all studied traits in the two crosses and both environments, except for days to heading in cross 1 and 2 under heat stress, plant height in cross 1 under heat stress, number of spikes/plant in cross 1 and 2 under normal conditions, 100-grain weight in cross 1 under heat stress and grain yield in cross 1 under heat stress and in cross 2 under normal conditions, where complementary epistsis prevailed, indicating that

duplicate epistasis was of greater importance than complementary epistasis for most traits. Because non additive effects were higher than additive effects in most the studied traits, intensive selection through later generation was needed to improve these traits. Also, the possibility of obtaining desirable segregates through inter-mating in early segregations require breaking undesirable linkage or it is suggested to adopt recurrent selection for handling the above crosses for rapid improvement .These results are in harmony with those reported by Saint Pierre *et al.* (2010), Yadav and Singh (2011), Amin (2013), Hamam (2014) and El-Hawary (2016).

Heterosis, inbreeding depression and potence ratio:

Percentages of heterosis over mid-parent and better parent, inbreeding depression and potence ratio are presented in Table 6. Positive significant or highly significant heterosis over mid-parent and better parent values were observed for all studied traits in the two crosses and both conditions, except over mid-parent for days to heading in cross 2 under heat stress, number of grains/spike in cross 2 under normal conditions and over better parent for plant height in cross 2 under both sowing dates, number of grains/spike in cross 1 under heat conditions and in cross 2 under both conditions, 100-grain weight in cross 1 under normal conditions. These results are in accordance with those found by Abd El-Rahman (2013), Hamam (2014), Abd El-Hamid and El-Hawary (2015) and El-Hawary (2016). Highly significant and positive better parent heterosis values for grain yield/plant which was obtained in the two crosses, indicating that these could be considered as a promising crosses in wheat breeding program when planning for producing a hybrid wheat.

Table 6. Heterosis, inbreeding depression (I.D%), potence ratio (P.R%), components of variation, heritability percentage in broad (H^2b) and narrow (h^2n) senses and expected genetic advance (G.S) of two bread wheat crosses for all studied traits under normal (N) and heat stress (H) conditions.

| Trait | Cross | Sowing date | Heterosis (%) | | I.D % | P.R % | components of variation | | | $H/D^{1/2}$ | Heritabbility | | G.S% |
			M.P	B.P			H	D	E		H^2b	h^2n	
Days to heading	C_1	N	1.04*	2.46**	1.73**	0.75	18.52	7.56	2.68	1.57	75.82	34.08	2.45
		H	2.21**	3.45**	2.95**	1.85	8.08	1.60	1.09	2.25	72.05	20.47	0.92
	C_2	N	0.89**	1.93**	1.29**	0.86	3.95	5.11	1.97	0.88	64.30	46.39	2.39
		H	0.63	1.73**	1.73**	0.59	5.34	3.45	1.99	1.24	60.64	34.17	1.79
Plant height	C_1	N	9.84**	7.16**	5.88**	3.94	299.25	287.11	30.34	1.02	87.80	57.72	16.79
		H	6.99**	3.62**	2.78**	2.15	79.35	622.88	20.06	0.36	94.29	88.65	31.79
	C_2	N	2.35*	-1.67	2.51*	0.58	13.41	29.80	20.42	0.67	47.21	38.53	4.60
		H	3.77**	0.32	2.90**	1.1	17.36	46.47	19.47	0.61	58.61	49.38	6.87
Number of spikes/ plant	C_1	N	10.24**	2.44**	10.86**	1.34	3.67	8.38	4.65	0.66	52.36	42.95	22.15
		H	10.09**	7.78**	5.22**	4.71	7.96	2.00	3.06	2.00	49.42	16.52	7.36
	C_2	N	15.76**	10.36**	5.92**	3.22	2.21	8.46	2.98	0.51	61.64	54.52	23.41
		H	24.44**	18.07**	2.14**	4.53	10.73	12.18	3.56	0.94	71.14	49.39	27.94
Number of grains/ spike	C_1	N	7.58**	4.98 **	4.00**	3.06	32.42	55.12	23.56	0.77	60.22	46.53	15.27
		H	10.17**	2.01	10.87**	1.27	12.42	31.21	24.22	0.63	43.58	36.35	11.84
	C_2	N	2.14	-2.55*	4.74**	0.45	42.86	17.24	23.25	1.58	45.41	20.24	5.99
		H	2.46*	1.72	4.31**	3.38	33.13	26.79	30.37	1.11	41.65	25.74	9.36
100-grain weight	C_1	N	6.05**	-0.67**	1.78**	0.89	0.06	0.23	0.12	0.49	52.94	47.33	9.93
		H	6.24**	3.71**	5.94**	2.56	0.01	0.24	0.13	0.21	49.06	47.99	11.41
	C_2	N	4.29**	0.72**	1.53**	1.21	0.40	0.18	0.15	1.49	56.01	26.50	6.64
		H	5.17**	4.95**	1.48**	24.00	0.02	0.33	0.12	0.11	57.93	57.59	14.11
Biological yield/ plant	C_1	N	16.60**	14.13**	9.71*	7.67	231.73	1077.3	251.80	0.46	70.32	63.49	43.53
		H	27.36**	22.27**	7.56**	6.58	278.06	543.23	158.87	0.72	68.23	54.32	31.21
	C_2	N	15.38**	13.12**	2.33	7.68	163.51	475.43	18169	0.59	60.50	51.63	25.89
		H	22.59**	18.10**	2.38	5.95	275.37	299.60	308.91	0.96	41.44	28.40	16.40
Grain yield/ plant	C_1	N	24.17**	19.28**	13.95**	5.90	126.41	116.60	26.37	1.04	77.32	50.14	37.75
		H	30.28**	21.07**	18.82**	3.98	15.85	46.06	10.16	0.59	72.65	61.98	37.65
	C_2	N	24.29**	20.47**	11.69**	7.66	77.67	62.50	14.44	1.11	77.82	48.00	27.74
		H	33.94**	24.60**	6.12**	4.53	25.19	76.02	21.75	0.58	67.08	57.54	40.79

*p < 0.05, **p < 0.01. M.P= Heterosis over mid parents   B.P= Heterosis over better parent

Inbreeding depression measured as reduction in performance of F_2 generation relative to F_1 is presented in Table 6. Results showed significant or highly significant positive inbreeding depression values for all studied traits under normal and heat stress conditions, except for biological yield/plant in cross 2 under both conditions. These results are expected because the expression of heterosis in F_1 will be reduced in F_2 generation due to selfing and starting homozygosity. These results are in close agreements with those of Yadav and Singh (2011), Hamam (2014), Said (2014) and El-Hawary (2016).

Potence ratio (Table 6) refers to over dominance in the two crosses and environments for most studied traits, where its values exceeded the unity. Meanwhile, potence ratio values for days to heading in cross 1 under normal and in cross 2 under both conditions, plant height in cross 2 under normal conditions, number of grains/spike in cross 2 under normal conditions and 100-grain weight in cross 1 under normal sown were less than unity, indicating partial dominance for these traits. Similar findings were obtained by Yadav and Singh (2011), Amin (2013), Hamam (2014) and kumar *et al*. (2017).

Genetic components of variance:

The estimates of different variance components as well as the average degree of dominance are presented in Table 6. The results revealed that the dominance variance component was higher than additive one for days to heading in cross 1 under both conditions and in cross 2 under heat stress, plant height in cross 1 under normal conditions, number of spikes/plant in cross 1 under heat stress, number of grains/spike in cross 2 under both environments, 100-grain weight in cross 2 under normal sown and grain yield/plant in cross 1 and 2 under normal conditions, indicating that dominance gene effect played the major role in inheritance of these traits and selection may be effective in later segregation generations. On the other hand, additive gene effects were more important in the genetic system controlling the remaining traits, suggesting that practice selection in early segregating generations could be effective to isolate lines characterized by high grain yield under heat stress. Similar results obtained by El-Aref *et al*. (2011), Amin (2013), Hamam (2014) and El-Hawary (2016).

The average degree of dominance (Table 6) was less than unity in most traits, except cross 1 for days to heading in cross 1 under both conditions and in cross 2 under heat stress, plant height in cross 1 under normal conditions, number of spikes/plant in cross 1 under heat stress, number of grains/spike in cross 2 under both environments, 100-grain weight in cross 2 under normal sown and grain yield/plant in cross 1 and 2 under normal conditions. These results confirm the role of partial dominance gene effects in controlling in these traits and selection for these traits might be more effective in early generations. Meanwhile, the remaining traits which had degree of dominance more than unity, indicating that the over dominance gene effects in controlling in these traits and selection should be delayed to later generations for improving these traits. These results reported that the genetic system of these characters under the two conditions are controlled by additive and non-additive gene effects. These results are in accordance with those reported by Farshadfar *et al*. (2008), Khattab (2009), El-Aref *et al*. (2011), Amin (2013), Hamam (2014) and El-Hawary (2016).

Heritability in broad and narrow-senses and genetic advance:

Heritability estimates indicate that the progress from selection for plant characters is relatively easy or difficult to make in breeding program. Heritability estimates in broad and narrow-sense and genetic advance are presented in Table 6. The heritability values in broad sense were moderate to high for all studied traits in the two crosses under both environments, ranging from 41.44 % for biological yield/plant in cross 2 to 94.29% for plant height in cross 1 under heat stress, indicating that most of the phenotypic variability was due to genetic effects and possibility for improvement through selection for these traits. The difference between H^2b and h^2n exhibits the involvement of the dominance effect in the genetic constitution of these characters. Heritability values are categorized as low (0-30%), moderate (30-60%) and high (60% and above) as stated by Robinson *et al*. (1949). Narrow sense heritability values were moderate to high in most traits, except for days to heading in cross 1 under stress conditions, number of spikes /plant in cross 1 under heat stress, number of grains/spikes in cross 2 under both environments, 100-grain weight in cross 2 under normal conditions and biological yield/plant in cross 2 under heat stress, indicating that these traits were greatly affected by additive and non additive effects and there is appreciable amount of heritable variation. Meanwhile, the remaining traits which had low narrow sense heritability estimates, apparent that selection for these traits will be difficult and high environmental influence well be a problem. These results are in accordance with the findings of El-Sayed and El-Shaawawy (2006), El-Aref *et al*. (2011), Amin (2013) and El- Hawary (2016)

According to Johnson *et al*. (1955) genetic advance as percent of mean classified as low (<10%), moderate (10-20%) and high (>20%). Based on this argument, the expected genetic advance (G.S) as percent of F_2 mean (Table 6) was moderate to high of the two crosses under both environments, except for days to heading in cross 1 and 2 under both environments, plant height in cross 2 under both conditions, number of spikes/plant in cross 1 under heat stress, number of grains/spikes in cross 2 under both environments and 100-grain weight in cross 1 and 2 under normal conditions, indicating the possibility of practicing selection in early generations to enhance selecting high yielding genotypes. Meanwhile, the remaining traits, which showed the low values of expected genetic advance, suggesting the role of environmental factors and dominance gene action in inheritance system of these traits. These results are in agreement with those of El-Aref *et al*. (2011), Amin (2013), Hamam (2014) and El-Hawary (2016).

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التحليل الوراثي لبعض الصفات المحصولية في هجينين من قمح الخبز تحت ظروف الإجهاد الحراري

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أجريت هذه الدراسة بمحطة البحوث الزراعية بشندويل في ثلاثة مواسم زراعية هي 2014/2015، 2015/2016 و2016/2017 بهدف تقدير المقاييس الوراثية ونوع فعل الجين المتحكم في بعض الصفات المحصولية للهجينين من قمح الخبز (شندويل 1 × جميزة 11) و (مصر 1 × جيزة 168) تحت الظروف العادية (20 نوفمبر) وظروف الإجهاد الحراري (20 ديسمبر) باستخدام موديل الست عشائر (الأب الأول، الأب الثاني، الجيل الأول، الجيل الثاني، الهجين الرجعى الأول والهجين الرجعى الثاني). أشار تحليل اختبار المقياس إلى وجود تأثير التفاعلات الغير أليلية في معظم الصفات ماعدا صفة عدد السنابل/النبات في الهجين الثاني تحت الظروف العادية ، عدد الحبوب/السنبلة في الهجين الأول تحت الظروف العادية والهجين الثاني تحت الإجهاد الحراري ومحصول الحبوب/النبات في الهجين الأول تحت الظروف العادية. اختلفت الأهمية النسبية لتأثير كل من الفعل الوراثي الإضافي والسيادي تبعاً للصفات وظروف الإجهاد الحراري. كان التأثير السيادي بصفة عامة أكبر من التأثير الإضافي فيما عدا عدد أيام الطرد في الهجين الثاني تحت ظروف الإجهاد الحراري، طول النبات تحت الظروف العادية في الهجين الثاني والمحصول البيولوجي/النبات في الهجين الأول تحت ظروف الإجهاد الحراري وفي الهجين الثاني تحت الظروف العادية مؤكدا على الأهمية الأكبر للتأثير السيادي في وراثة هذه الصفات بجانب التأثير الإضافي. كان المكون السيادي × السيادي ذو تأثير أكبر من تأثير كل من الإضافي × الإضافي والإضافي × السيادي في معظم الصفات موضحا الدور الأكبر للتأثير السيادي والتفاعلات الغير أليلية للأجيال الانعزالية المتأخرة لزيادة الأصالة الوراثية. كانت تقديرات قوة الهجين بالمقارنة بالأب الأفضل عالية المعنوية وموجبة لكل الصفات فيما عدا طول النبات في الهجين الثاني تحت كلا ميعادي الزراعة وعدد الحبوب/السنبلة في الهجين الأول تحت الإجهاد الحراري وفي الهجين الثاني تحت كلا البيئتين. تراوحت قيم كل من درجة التوريث بالمعنى الواسع والضيق وكذلك التحسين الوراثي المتوقع من متوسطة إلى مرتفعة في معظم الحالات، وبناء على هذه النتائج يمكن الاستفادة من هذه الهجن للحصول على سلالات عالية المحصول تحت ظروف الإجهاد الحراري.