

**ESTIMATION OF COMBINING ABILITY, GENE ACTION
AND HETEROSIS IN DURUM WHEAT USING
NESTED MATING DESIGN**

**تقدير مقدرة الانتلاف والفعل الجيني وقوة الهجين
في الحنطة الخشنة باستخدام تصميم التزاوج المتشعب**

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ABSTRACT

An experiment was conducted by using the nested mating design involved 15 hybrids and 20 parents (5 male and 15 female) in durum wheat during 2011-2012 at the station of Directorate of Agricultural Researches/Erbil under dry farming conditions using a randomized complete block design with three replications. Some growth characters, grain yield and its components were studied. Genetic statistical analysis were done to estimate general combining ability (GCA) of the parents, genetic variance components (additive and dominance), environmental variance, average degree of dominance, heritability in broad and narrow sense, expected genetic advance, heterosis and correlation coefficients among the characters. The results showed highly significant differences among genotypes for all studied characters. Three parents had a positive general combining ability effect in most characters including grain yield. The additive was greater than dominance genetic variance in most characters. Heritability in narrow sense was high for plant height, spike no./plant, 1000-grain weight and grain yield/plant. The values of average degree of dominance was greater than one for flag leaf area, number of grains/spike and biological yield/plant, while less than unit for spike no./plant. Expected genetic advance was high for plant height, spike no./plant and grain yield/plant and it were moderate for plant height, grain no./spike, 1000-grain weight, biological yield/plant and harvest index, while it was low for flag leaf area. Maximum number of hybrids showed significant positive heterosis for grain no./spike, 1000-grain weight and grain yield/plant . The cross [14 × 3] had the highest positive heterosis for most studied characters including grain yield followed by [8 × 1] and [16 × 4]. Grain yield/plant revealed a significant positive genetic correlation with spike no./plant, grain no./spike, 1000-grain weight and harvest index.

Key words: Durum wheat, nested mating, combining ability, gene action, heterosis, genetic correlation.

الخلاصة

نفذت هذه التجربة باستخدام تصميم التزاوج المتشعب الذي تضمن 15 هجيناً فردياً و 20 تراكيباً وراثياً (5 آباء ذكور و 15 أم) في الحنطة الخشنة خلال الموسم 2011-2012 في محطة البحوث الزراعية/أربيل تحت الظروف الدبمية باستخدام تصميم القطاعات العشوائية الكاملة بثلاثة مكررات. درست بعض صفات النمو والحاصل ومكوناته. أجري التحليل الإحصائي الوراثي لتقدير القدرة على الانتلاف ومكونات التباين الوراثي (الإضافي والسيادي) والتباين البيئي ومعدل درجة السيادة وقوة التوريث بالمعنيين الضيق والواسع والتحسين الوراثي المتوقع وقوة الهجين، بالإضافة الى إيجاد معامل الارتباط الوراثي بين الصفات المدروسة. أظهرت النتائج وجود اختلافات معنوية بين التراكيب الوراثية في جميع الصفات. كان لثلاثة آباء قدرة عامة موجبة ومعنوية على الانتلاف في معظم الصفات بضمنها حاصل الحبوب. كان التباين الوراثي الإضافي أكبر من قيم التباين الوراثي السيادي في معظم الصفات. كانت قوة التوريث بالمعنى الضيق عالية لارتفاع النبات وعدد السنابل/نبات ووزن 1000 حبة وحاصل الحبوب/نبات. بلغت قيم معدل درجة السيادة أكبر من واحد لمساحة ورقة العلم وعدد الحبوب/سنبله والحاصل البيولوجي وأقل من واحد لعدد السنابل/نبات. كان التحسين الوراثي المتوقع عالياً لارتفاع النبات وعدد الحبوب/سنبله ووزن 1000 حبة وحاصل الحبوب. أظهر الهجين (14 × 3) قوة هجين معنوية موجبة في أكثر عدد من الصفات يليه الهجينان (8 × 1) و (16 × 4). أظهر حاصل الحبوب/نبات ارتباطاً وراثياً معنوياً وموجباً مع عدد السنابل/نبات عدد الحبوب/سنبله ووزن 1000 حبة ودليل الحصاد.

INTRODUCTION

Yield is the most complex character in wheat crop plants. So the information on genetic control of yield and its components is more helpful for future breeding program. The combining ability and gene action can be studied through the diallel crossing technique developed by earlier scientists [1]. This breeding methodology is still considered as an important tool to work out the genetic basis for the control of traits. However, plant breeders sometimes wish to increase the number of parents in the hybridization program, with making few crosses by using another mating method nested mating. In this method every male crossed with few females differed from another male. Such programs need testing the combining ability of genotypes that are used as parents according to the general combining ability and then selecting the best hybrid combination. Nested mating method which described by [2] is considered one of the ways for estimating the general combining ability to select the best parents. General combining ability, gene action, heritability and heterosis had been studied for the different characters in wheat by many researchers using F₁ generation. Knowledge about combining ability is important in selecting suitable parents for hybridization, understanding of inheritance of quantitative traits and also in identifying the promising crosses for further use in breeding programs. Many researchers have studied the combining ability and genetic structure of bread wheat hybrid populations by using nested mating design and diallel analysis methods related to yield and yield components. Combining ability has been defined and categorized originally by [3] who described that high general combining ability (GCA) effects were due to additive type of gene action, whereas high specific combining ability (SCA) indicated non-additive gene effects. [4] reported that (GCA) effects were significant for number of grains per spike and grain yield. [5] and [6] describe additive type of gene action with partial dominance controlling this trait. [7] and [8] showed that over dominance type of gene action controls this parameter. Over-dominance type of gene has been reported for plant height ([9, 10] and flag leaf area [8, 11]. Over-dominance type of gene action has been reported by [12] for plant height, flag leaf area and grain yield per plant, but transgressive segregates can be found for plant height, flag leaf area, and grain yield per plant in later segregating generations. On the other hand Heterosis and combining ability are the two most important aspects of any hybrid crop. Many reports have been published establishing the fact that heterosis does occur with proper combinations of parents [13]. In fact, heterosis shows combining ability of parents so their usefulness in hybridization programs. Because of self-pollinating nature of wheat plant, limited investigation on hybrid grain has so far been devoted to wheat. Exploitation of heterotic effect for grain yield increase was largely attributed to cross-pollinated crops [14]. [15] revealed that heterosis relative to mid-parent was found to be significantly positive for grain weight /spike, no of grains /spike, grain yield/plant, biological yield and harvest index in the three crosses under study. [16] reported negative magnitude of heterosis for plant height and positive for spike length, number of grains/spike and harvest index. The knowledge of combining ability provides a useful clue for selection of desirable parents for development of superior hybrids. Thus, the information regarding heterosis, combining ability and nature of gene action are the basic requirements for a thorough understanding of genetic architecture of yield and its components.

The objective of this research were to estimate some genetic parameters in order to evaluate the ability of some durum wheat genotypes to predicate heterosis in F₁ hybrids for the choice of best parents and their crosses at early stages in the program under rainfall conditions.

MATERIALS AND METHODS

Fifteen durum wheat (*Triticum durum* Desf.) F₁ hybrids were created by crossing 5 pollinator parents with three standard females in the 2010-2011 growing season (Table, 1) followed the nested design (Design I mating scheme) [17]. Grains of genotypes were received from the International Center for Agricultural Research in the Dry Areas (ICARDA). The hybrids and parents were evaluated using randomized complete block design with three replications during the 2011-2012 growing season at the station of Directorate of Agricultural Researches/Erbil under dry

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farming conditions in the area of Ainkawa in Erbil/Kurdistan region of Iraq under the circumstances amounted to rain (172.6 mm) with good distribution depend on meteorological in the research site. The grains were manually drilled into one row of 2.5 m length, spaced 20 cm apart and 10 cm plant to plant distance. Data were collected for plant height (cm) [PH], flag leaf area (cm²) [FLA], spikes no. /plant [SN], grains no. /spike [GN], 1000-grain weight (g) [GW], grain yield/plant (g) [Gy], biological yield/plant (g) [By] and harvest index (%) [HI].

Table (1) Pedigree of genotypes (females and males) used in the study.

No.	Pedigree
Males	
1	ICD86-0471-ABL-0TR-8AP-0TR-20AP-0TR
2	ICD85-1340-ABL-6AP-0TR
3	ICD83-0050-4AP-14AP-TR-3AP-0TR
4	ICD 523-3Y-1Y-2M-0Y
5	ICD88-1233-ABL-8AP-0AP-6AP-0AP
Females	
6	Icajihhan36 ICD01-0251-T-14AP-AP-4AP-0AP
7	13307/Azn1/6/Zna-1/5/AW11/4/Ruff//Jo/Cr/3/F9.3 ICD00-0361-T-6AP-AP-4AP-AP
8	Marsyr-3//saadi 1989/Chan ICD02-1230-T-TR-12AP-0AP-4AP-0AP
9	Atlast1/961081//Icasyr-1 ICD02-0494-T-11AP-0TR-5AP-6AP-2AP-0AP
10	Atlast1/961081//Icasyr-1 ICD02-0494-T-11AP-0TR-5AP-6AP-4AP-0AP
11	Icasyr-1/3/Gen//Stj/Mrb3 ICD02-1016-C-6AP-0TR-1AP-0AP-1AP-0AP
12	Icasyr-1/3/Gen//Stj/Mrb3 ICD02-1016-C-6AP-0TR-1AP-0AP-5AP-0AP
13	Azeghar-2/4/Stj3/3/GdfI/T. dicds/SY20013//Ber ICD02-1272-W-3AP-0TR-3AP-0AP-5AP-0AP
14	Marsyr-3/3/ Gen//Stj/Mrb3 ICD02-1043-C-1AP-0TR-6AP-0AP-6AP-0AP
15	Icasyr-1/3/Ber/Sb15//T. urartu ICD02-1257-W-4AP-0AP-4AP-0AP-4AP-0AP
16	12938-5L-1AP-1AP-4AP-0AP
17	ICD78-0030-2AP-2AP-3AP-2AP-0AP
18	ICD79-0852-13AP-3AP-2AP-0AP
19	ICD79-1463-1AP-2AP-2AP-1AP-0SH
20	ICD91-0083-AB-1AP-0AP-5AP-0AP

Data analyzed according to nested mating design according to the following statistical model:

$y_{ijk} = \mu + mi + fj(i) + rk + eijk$ { $i = 1, 2, \dots, m; j = 1, 2, \dots, f; k = 1, 2, \dots, r$ } Where, y_{ijk} =experimental unit value; μ =grand mean; mi =general combining ability for i th parent; $fj(i)$ =effect of j female which crossed with i th male; rk = effect of k replicate; $eijk$ =effect of experimental unit for ij cross in k replicate. Analysis of variance table and calculate the sum of squared of the variation sources and degrees of freedom for these sources are shown in the Table (2):

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The effects of general combining ability (GCA) of parents were calculated according to the following two equations:

- Effect of GCA of male parents: $\hat{g}_i = \bar{y}_{i..} - \bar{y}_{...}$
- Effect of GCA of female parents: $\hat{g}_j = \bar{y}_{.j.} - \bar{y}_{...}$

The standard error of the effect of GCA for parents (males and females) was estimated according to the following equation: $SE = \sqrt{2\sigma^2 e / r}$

The components of genotypic variation (Dominance variance $\sigma^2 D$, Additive variance $\sigma^2 A$) and environmental variance $\sigma^2 E$ have been estimated based on the expected mean square (EMS) according to the following equations:

$$\sigma^2 m = \frac{Msm - Mse}{rf} = \sigma^2 G.C.A. = \frac{1}{2} \sigma^2 A$$

Table (2): ANOVA Table of nested mating design.

SOV	df	SS	MS	EMS (Fixed Model)
Re pl.	$r - 1$	$\frac{\sum y_{i..}^2}{mf} - \frac{Y_{...}^2}{mfr}$		
Males (m)	$m - 1$	$\frac{\sum Y_{i..}^2}{fr} - \frac{Y_{...}^2}{mfr}$	MSm	$\sigma^2 e + fr \sigma^2 m$
Females / Males	$m(f - 1)$	$\frac{\sum Y_{ij.}^2}{r} - \frac{\sum Y_{i..}^2}{fr}$	$MS F/M$	$\sigma^2 e + r \sigma^2 f/m$
Error	$(mf - 1)(r - 1)$	$\sum y_{ijk}^2 - \frac{\sum Y_{ij.}^2}{r} - \frac{\sum Y_{i..}^2}{mf} + \frac{Y_{...}^2}{mfr}$	MSe	$\sigma^2 e$
Total	$mfr - 1$	$\sum y_{ijk}^2 - \frac{Y_{...}^2}{mfr}$		

$$\therefore \sigma^2 A = 2\sigma^2 m$$

$$\sigma^2 F/M = \frac{MS f/m - MSe}{r} = (\sigma^2 GCA + \sigma^2 SCA) = \frac{1}{2} \sigma^2 A + \sigma^2 D$$

$$\therefore \sigma^2 D = \sigma^2 F/M - \sigma^2 m$$

In order to test the significant of each one of these variances, the following equations were used to find a variance of each variance:

$$V(\sigma^2 A) = \frac{2}{f^2 r^2} \left[\frac{2(MSm)^2}{k+2} + \frac{2(MSe)^2}{k+2} \right]$$

$$V(\sigma^2 D) = \frac{1}{r^2} \left[\frac{2(MS f/m)^2}{(k+2)} + \frac{2(MSe)^2}{k+2} \right] + \frac{1}{r^2 f^2} \left[\frac{2(MSm)^2}{k+2} + \frac{2(MSe)^2}{k+2} \right]$$

$$V(\sigma^2 E) = \frac{2(MSe)^2}{k+2}$$

Taking the square root of the variations above we then get the standard error (SE) for each variance for the test of significant of each one of these variances using statistical t-test.

Heritability in broad $h^2_{b.s.}$ and narrow sense $h^2_{n.s.}$ estimated by using the following equations:

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$$H^2_{b.s.} = \frac{\sigma^2 m + \sigma^2 f/m}{\frac{\sigma^2 e}{r} + \sigma^2 m + \sigma^2 f/m}$$

$$H^2_{n.s.} = \frac{2\sigma^2 m}{\frac{\sigma^2 e}{r} + \sigma^2 m + \sigma^2 f/m}$$

$$\text{Averaged degree of dominance } (\bar{a}) = \sqrt{2\sigma^2 D/\sigma^2 A}$$

$$\text{Expected genetic advance} = H^2_{n.s.} \sigma P i$$

$$\text{EGA\%} = \frac{GA}{\bar{X}} \cdot 100$$

Where, σP is the phenotypic standard deviation, and i is constant =1.76), at 10% selection intensity.

Each of heritability in broad sense, narrow sense, and genetic advance was categorized as low, moderate and high as suggested by [81, 19 and 20], respectively.

Heterosis over mid parents was computed according to the following equation:

$\text{Heterosis } (H) = \bar{F}_1 - [\bar{p}i + \bar{p}j/2]$. Then, heterosis significant was tested using the following statistical t-test for each hybrid: $t(H) = H/\sqrt{V(H)}$. The variance of heterosis were calculated from the following equation: $V(H) = (3/2)(Mse/r)$. Also genetic correlation between studied characters was calculated and tested with a t-test as follows: $Calc.t. = r/S_r$ where, $S_r = \sqrt{1-r^2/n-2}$ and $df = n-2$.

RESULTS AND DISCUSSION

Analysis of variance for characters indicated highly significant differences among genotypes (Males, females and hybrids) indicating that there was enough variation to be successful in selecting the desirable parents and cross combinations in this study (Table 3). The mean performance of males, females and hybrids for studied characters are presented in Table (4). The parent [12] was shorter than others in plant height (56.67 cm) and the parent [10] was the tallest one (70.33 cm).

Table (3): Mean squares of genotypes (males, females and hybrids) for studied characters.

Characters	Mean squares			F. value
	Replications df = 2	Genotypes df = 34	Error df = 68	
PH	156.753	79.706	10.645	7.89*
FLA	7.800	13.215	7.090	1.86*
SN	3.010	2.721	1.256	2.18*
GN	6.895	39.702	2.895	13.08*
GW	5.826	18.635	2.937	6.10*
BY	17.943	28.917	4.551	6.22*
GY	1.649	1.571	0.568	2.78*
HI	13.409	48.615	10.016	4.66*

* = Significant at 0.05 probability level.

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Table (4): Mean performance of parents and hybrids for the studied characters.

	PH	FLA	SN	GN	GW	BY	GY	HI
Males								
1	62.67	25.00	6.67	12.67	26.67	18.00	2.79	15.36
2	62.00	28.33	5.67	12.00	24.00	18.33	2.66	14.41
3	63.67	24.67	6.00	10.00	21.67	19.00	2.14	11.25
4	66.00	22.33	5.33	11.33	25.00	19.00	2.79	14.20
5	68.33	25.33	4.67	11.67	23.33	17.00	1.54	8.99
Mean	64.53	25.13	5.67	11.53	24.13	18.27	2.38	12.84
Females								
6	66.00	25.33	4.67	14.00	32.11	17.00	3.33	19.38
7	68.00	26.00	4.00	11.67	24.84	16.00	3.13	19.37
8	69.67	26.00	5.00	10.67	23.33	20.00	1.71	8.53
9	62.00	26.67	5.00	13.33	27.57	16.33	4.35	26.68
10	70.33	25.33	3.67	10.33	24.49	12.67	2.60	20.51
11	66.67	25.00	4.00	12.33	27.94	17.67	3.91	22.07
12	56.67	25.00	3.67	12.67	25.00	15.00	3.00	19.94
13	68.67	23.67	4.67	10.00	25.82	18.33	2.96	16.19
14	62.00	27.33	4.67	18.00	27.19	17.00	3.28	19.30
15	65.67	26.33	4.00	11.67	26.00	17.33	3.28	18.71
16	69.67	24.33	4.00	15.00	28.67	16.67	2.30	13.56
17	69.33	26.33	3.67	13.67	28.00	16.00	2.02	12.31
18	66.00	24.33	3.67	16.67	26.67	16.67	2.48	14.20
19	67.33	26.00	3.67	10.67	28.33	17.00	2.00	11.44
20	66.00	28.33	3.00	11.00	25.67	16.00	1.57	9.78
Mean	66.27	25.73	4.09	12.28	26.78	16.64	2.79	16.80
Hybrids								
6×1	64.67	24.00	3.33	11.67	30.33	14.67	1.98	13.37
7×1	60.00	24.33	3.67	12.67	29.67	15.67	2.46	15.67
8×1	70.67	32.00	3.00	17.67	29.00	18.33	2.12	11.57
9×2	71.00	23.67	4.00	16.00	25.00	15.33	1.85	11.95
10×2	68.33	27.00	3.67	12.67	29.33	15.33	2.30	14.95
11×2	71.33	24.67	3.67	16.33	29.00	19.33	3.00	15.50
12×3	86.33	24.67	3.00	13.67	26.67	16.00	1.94	12.10
13×3	76.00	28.33	5.00	18.00	29.16	17.67	2.58	14.56
14×3	73.33	26.00	6.33	27.33	28.33	32.00	3.59	11.13
15×4	67.33	25.67	4.33	21.33	32.00	23.00	3.90	17.05
16×4	66.00	23.33	5.33	18.00	31.00	19.33	4.16	21.48
17×4	69.33	23.33	5.67	14.67	28.00	18.67	3.17	16.65
18×5	60.33	27.00	5.33	11.67	26.00	18.33	2.80	15.22
19×5	66.67	26.00	4.67	13.67	26.67	17.67	2.79	15.90
20×5	68.67	27.33	4.67	17.67	24.67	19.67	2.73	13.94
Mean	69.33	25.821	4.38	16.20	28.32	18.73	2.76	14.74
G. M.	67.33	25.69	4.44	14.07	27.06	17.77	2.72	15.35
LSD _{0.05}	5.32	3.61	1.83	2.77	2.79	3.48	1.23	5.16

G. M. = Grand mean.

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The hybrid [13×3] was the tallest hybrids (76.00 cm) whereas hybrid [7×1] was the shortest in plant height (60.00 cm). The largest flag leaf area was found in parents [2 and 20] (28.33 cm²), whereas the lowest leaf area was that of parent [4] (22.33 cm²). The hybrid [8×1] gave the largest flag leaf area (32.00 cm²), while the lowest one was observed in hybrids [16×4 and 17×4] (23.33 cm²). The largest spikes no. /plant was found in parent [1] (6.67), whereas the lowest value of this trait was obtained in parent [20] (3.00). For hybrids, the hybrid [14×3] gave the largest number (6.33); the hybrids [8×1 and 12×1] gave the lowest number for this character (3.00). The maximum grains no. /spike showed in parent [14] (18.00) among parents and (27.33) from [14 × 3] among hybrids. 1000-grain weight is more stable character under rainfall conditions [21], the results for this character indicated that the parent [6] had highest value (32.11 g) among parents and (32.00) from [3 × 8] and [15 × 4] among hybrids. In biological yield/plant, parent [8] gave the highest value (20.00 g) among parents and [14 × 3] from hybrids showed maximum mean value (32.00 g) for this character. It is further revealed that the parent [9] produced the highest grain yield/plant (4.35 g) while maximum grain yield/plant was obtained in the hybrid [16 × 4] (4.16 g) followed by [15 × 4] (3.90 g) and [14 × 3] (3.59 g). Parent [9] exceeded over the other parents in harvest index (26.68%) and [16 × 4] from hybrids showed maximum mean value (21.48%) for this character. Similarly, significant differences among genotypes for grain yield and related characters in different sets of material of wheat were also reported [21, 22, 23]. The significant differences among the genotypes [Parents (males and females) and hybrids] for all the characters studied indicating that, material used had significant genetic diversity. These results are supported by the significant differences between male parents as well as between female/male (Table 5); in addition to the superior of overall mean of hybrids on the overall mean of males and females in most characters.

Table (5): Mean squares of nested mating design for studied characters.

SOV	df	Mean squares							
		PH	FLA	SN	GN	GW	BY	GY	HI
Re pl.	2	31.200	5.089	0.822	2.067	13.919	0.067	0.998	29.306
Males (m)	4	278.39*	12.422	5.42*	56.30*	28.07*	52.03*	3.24*	44.64*
Female/Males	10	60.11*	17.49*	2.16*	50.20*	4.61*	55.67*	0.816	11.513
Error	28	5.033	5.922	0.346	4.781	2.559	2.067	0.469	10.168
Total	44								

General combining ability (GCA) effects can be considered as the numerical values assigned to the parents in relation to their mean performance in cross-combinations. Table (6) showed the relative values of GCA effects of all the parents (males and females) for the studied characters. The GCA effects of 2, 7 and 18 for PH were negative and significant. Thus parents 2, 7 and 18 could be utilized to reduce plant height in bread wheat under rainfall conditions. Parent 2 also had positive and obvious GCA effects on GN and BY. In FLA, SN and HI only parents 8, 14 and 16, respectively had positive and remarkable significant GCA. It is quite evident from the results that parents 3, 15, 14 and 16 proved as better general combiners for GN, GW, BY and GY, respectively. The comparison of values revealed that those parents which mentioned above can be further used as the source material in the development of segregating generation. Other researchers also obtained parents which showed desirable GCA effects for different mentioned characters [15, 23, 24]

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Table (6) Estimates of general combining ability effects of males and females for studied characters.

	PH	FLA	SN	GN	GW	BY	GY	HI
Males								
1	2.89	-0.57	-0.66	0.93	0.72	-1.10	-0.33	-1.22
2	11.22*	0.65	0.34	5.60*	0.99	4.12*	-0.02	-2.75
3	0.22	-1.57	0.67	3.93*	3.27*	2.56*	1.03*	3.05
4	-2.11	1.09	0.45	0.27	-1.28	0.78	0.05	-0.33
5	-2.22	1.09	-1.10*	-0.07	2.61*	-1.55	-0.53	-1.81
Females								
6	-2.67	-1.69	-1.10*	-2.40	3.27*	-3.10*	-0.74	-1.98
7	-7.33*	-1.35	-0.77	-1.40	2.61*	-2.10*	-0.26	0.32
8	3.33*	6.31*	-1.44*	3.60*	1.94	0.56	-0.60	-3.78
9	3.67*	-2.02	-0.44	1.93	-2.06	-2.44*	-0.87	-3.40
10	1.00	1.31	-0.77	-1.40	2.27*	-2.44*	-0.42	-0.40
11	4.00*	-1.02	-0.77	2.27	1.94	1.56	0.28	0.15
12	19.00*	-1.02	-1.44*	-0.40	-0.39	-1.77	-0.78	-3.25
13	8.67*	2.65	0.56	3.93*	2.10	-0.10	-0.14	-0.79
14	6.00*	0.31	1.90*	13.27*	1.27	14.23*	0.87	-4.22
15	0.00	-0.02	-0.10	7.27*	4.94*	5.23*	1.18*	1.70
16	-1.33	-2.35	0.90	3.93*	3.94*	1.56	1.44*	6.13*
17	2.00	-2.35	1.23	0.60	0.94	0.90	0.45	1.30
18	-7.00*	1.31	0.90	-2.40	-1.06	0.56	0.08	-0.13
19	-0.67	0.31	0.23	-0.40	-0.39	-0.10	0.07	0.55
20	1.33	1.65	0.23	3.60*	-2.39	1.90	0.01	-1.41
<i>SE(gi - gj)</i>	1.83	1.99	0.48	1.79	1.31	1.17	0.56	2.60

Table (7) revealed that values of additive genetic variance and environment variance were significant for all characters, while values for dominance genetic variance were not significant for all the studied characters. The values of additive genetic variance were greater than dominance genetic variance for PH, SN, GN, GW and GY which depicts the importance of additive gene effect for controlling these characters, whereas the values of dominance genetic variance were greater than the additive genetic variance for FLA and BY, which indicates to the importance of dominant gene effect for controlling these characters. These results are in agreement with other researchers [21, 25].

The average degree of dominance (\bar{a}) was more than one for FLA, GN and BY, indicates that these characters are controlled by over dominance, while it was less than one for SN indicating that this character was controlled by partial dominance, whereas equal to zero for PH, GW, GY and HI indicating that no dominance controlled these characters. These results are in agreement with previous results [15, 26, 27]. The values of heritability in broad sense ($H^2_{b.s.}$) were high for PH, SN, GN, GW and BY ranged between (68.895%) for GW and (91.890%) for BY and moderate for FLA, GY and HI. These findings correspond with the results published by [12 and 28]. Heritability in narrow-sense ($H^2_{n.s.}$) varied between high for PH, SN, GW and GY and moderate for GN, BY and HI, while were low for FLA. These results agreed with those previously reported by [15 and 29]. The expected genetic advance (EGA) was between 0.785 for FLA and 12.710 for PH. The expected genetic advance as a percent of mean (EGA %) was high for SN and GY and it were moderate for

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PH, GN, GW, BY and HI, while it was low for FLA. These results are in agreement with those reported by [30].

Table (7) Estimates of genetic parameters for studied characters.

Parameter s	PH	FLA	SN	GN	GW	BY	GY	HI
$\sigma^2 A$	60.746* ±15.467	1.444 ±0.996	1.128* ±0.316	11.449* ±2.052	5.668* ±1.580	11.104* ±3.691	0.616* ±0.184	7.660* ±2.539
$\sigma^2 D^*$	0.000 ±0.000	3.133 ±2.435	0.039 ±.307	9.415 ±6.898	0.000 ±0.000	12.315 ±7.579	0.000 ±0.000	0.000 ±0.000
$\sigma^2 E$	5.033* ±1.300	5.922* ±1.529	0.346* ±.089	4.781* ±1.234	2.559* ±0.661	2.067 ±0.285	0.469* ±0.121	10.168* ±2.625
\bar{a}	0.000	2.083	0.263	1.282	0.000	1.489	0.000	0.000
$H^2_{b.s.}$	85.800	43.595	77.132	81.357	68.895	91.890	56.774	42.966
$H^2_{n.s.}$	85.800	13.754	74.545	44.644	68.895	43.569	56.774	42.966
EGA	12.710	0.785	1.614	3.979	3.48	3.871	0.869	3.195
EGA %	18.870	3.060	36.400	28.280	12.860	21.78	31.949	20.814

*=The $\sigma^2 D$ value was set to zero when estimated variance turned out to be a negative.

The number of hybrids showing significant heterosis levels over mid-parent with respective directions and ranges for all the eight characters are presented in Table (8). Results of hybrids showing significant desirable heterosis revealed that maximum number of hybrids showed heterosis for GN, GW, GY, SN, BY, HI, PH and FLA, respectively. Heterosis of F1 hybrids over mid parents for the studied characters are presented in Table (9) revealed that the significant heterosis in desirable direction were observed in hybrids [7 × 1] and [18 × 5] for PH and [8 × 1] and [13 × 3] for FLA. 5 hybrids in significant heterosis for SN were observed in desirable direction. Hybrid [14 × 3] had the highest positive heterosis for GN and [15 × 4] for GW. The significant heterosis in desirable direction was observed in most hybrids for GN and GW. Significant positive heterosis was observed in three hybrids in BY, the hybrids [14 × 3] showed the highest value for heterosis (14.00). Heterosis values of the hybrids for HI varied from (-8.60– 7.60). The hybrids which exhibited significant heterosis for GY are [16 × 4], [18 × 5], [19 × 5], [20 × 5], [14 × 3] and [15 × 4]. It indicated that high yielding varieties involved in the hybrids were predominantly responsible for enhancing the yield. Similar finding were reported by [31].

It's better to remind that the information on heterosis and combining ability considered together will be more meaningful. If the heterotic hybrids involve both the parents with high general combining ability effects, then it implies that the parental contribution to heterosis is mainly through additive gene action. As a rule, hybrid with the highest value of heterosis had a line with high GCA as one of its parents [32]. Therefore, Based on general combining ability effects best parents were identified using scoring techniques (Table 10). Among 20 parents, parents 3, 14 and 15 exhibited high GCA effects for maximum number of characters and produced heterosis in higher number of traits of the hybrids that participated in the composition. Thus, these parents can be used as genetic material to improve or derive new varieties of durum wheat under rainfall conditions.

Genetic correlation coefficients between studied characters are shown in Table (11). There were significant and positive correlation between GY and most of its components and between themselves, thus selection for any of these characters lead to improve other characters including GY. Similar results have been reported by [30]. The results of this study revealed that parents (3), (14) and (15) had the possibility to use in crossing programs because they have showed desirable GCA effects for most of the studied characters and obtaining some crosses like (14×3), (15×4), which had high desirable heterosis for most of the characters.

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Table (8): Number of hybrids showing significant heterosis levels with respective directions and ranges.

Characters	Relative heterosis		
	Positive	Negative	Range
PH	2	2	[16.33 – (-6.84)]
FLA	2	0	[-3.50 – 6.5]
SN	5	7	[-2.84 – 1.17]
GN	10	1	[-2.50 –13.30]
GW	9	0	[-0.79 – 6.50]
BY	3	2	[-2.83– 14.00]
GY	6	3	[-3.29 – 1.62]
HI	3	3	[-8.60 – 7.60]

Table (9) Heterosis relative to the mid-parent for studied characters.

	PH	FLA	SN	GN	GW	BY	GY	HI
6×1	0.33	-1.17	-2.34*	-1.67	0.94	-2.83*	-1.08*	-4.00*
7×1	-5.34*	-0.34	-1.67*	0.50	3.92*	-1.33	-0.50	-1.70
8×1	4.50*	6.50*	-2.84*	6.00*	4.00*	-0.67	-0.13	-0.38
9×2	9.00*	-3.50*	-1.34*	3.34*	-0.79	-2.00*	-1.66*	-8.60*
10×2	2.17	1.16	-1.00*	1.51	5.09*	-0.17	-0.33	-2.51
11×2	7.00*	-2.00	-1.17*	4.17*	3.03*	1.33	-3.29*	-2.74
12×3	16.33*	-0.17	-1.84*	2.34	3.34*	-1.00	-0.77	-3.50
13×3	9.83*	4.16*	-0.34	8.00*	5.42*	-1.00	0.03	-0.84
14×3	10.5*	0.00	1.00*	13.30*	3.90*	14.00*	0.88*	-4.15*
15×4	0.17	1.34	-0.34	9.83*	6.50*	4.84*	0.87*	0.60
16×4	-1.84	0.00	1.00*	4.84*	4.17*	1.50	1.62*	7.60*
17×4	1.67	-1.00	1.17*	2.17*	1.50	1.17	0.77	3.40
18×5	-6.84*	2.17	1.16*	-2.50*	1.00	1.50	1.03*	3.63
19×5	-1.16	0.34	0.50	2.50*	0.84	0.67	1.02*	5.69*
20×5	2.17	0.60	0.84*	6.34*	0.17	3.17*	1.18*	4.56*

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Table (10): Scoring of parents based on their GCA effects for studied characters.

Males										
1	0	0	0	0	0	0	0	0	0	5
2	1	0	0	1	0	1	0	0	3	2
3	0	0	0	1	1	1	1	0	4	1
4	0	0	0	0	0	0	0	0	0	5
5	0	0	-1	0	1	0	0	0	0	5
Females										
6	0	0	-1	0	1	-1	0	0	-1	6
7	-1	0		0	1	-1	0	0	-1	6
8	1	1	-1	1	0	0	0	0	2	3
9	1	0	0	0	0	-1	0	0	0	5
10	0	0	0	0	1	-1	0	0	0	5
11	1	0	0	0	0	0	0	0	0	5
12	1	0	-1	0	0	0	0	0	0	5
13	1	0	0	1	0	0	0	0	2	3
14	1	0	1	1	0	1	0	0	4	1
15	0	0	0	1	1	1	1	0	4	1
16	-1	0	0	1	1	0	1	1	3	2
17	0	0	0	0	0	0	0	0	0	5
18	-1	0	0	0	0	0	0	0	-1	6
19	0	0	0	0	0	0	0	0	0	5
20	0	0	0	1	0	0	0	0	1	4

Scoring: 1 = Significant GCA effects in desired direction.

0 = Non-significant GCA effect.

-1 = Significant GCA effects in undesired direction.

Table (11): Genetic correlation coefficients between studied characters.

	FLA	SN	GN	GW	BY	GY	HI
PH	-0.003	-0.031	0.265	0.114	0.161	-0.076	-0.193
FLA		-0.064	0.083	-0.031	0.048	-0.084	-0.110
SN			0.159	-0.060	0.549*	0.453*	0.175
GN				0.368*	0.602*	0.355*	0.059
GW					0.140	0.343*	0.270
BY						0.484*	-0.045
GY							0.838*

* = Significant at 0.05 probability level.

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