THE INHERITANCE OF SOME QUANTITATIVE CHARACTERS OF F_2 GENERATION FOR COMMON WHEAT IN SULAIMANI-IRAQ

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ABSTRACT

This study was aimed to testing 25 genotypes (5 parents + 10 diallel + 10 reciprocal crosses) using full Diallel mating design in winter season 2021-2022 for F_2 generation of common wheat, in two locations. The first was in Qlyasan Agricultural Research Station, College of Agricultural Engineering Sciences; University of Sulaimani located (Lat 35° 34′; N, Long 45° 21′; E, 765 MASL), the second was in Koya Agricultural Station-Ministry of Agricultural (Lat 36° 04′; N, Long 44° 37′; E, 582 MASL). The results of the study confirmed that the mean squares of genotypes was highly significant for all characters in both locations, the same for the mean squares for gca with the exception of grain weight plant^{-1} in Qlyasan location which was only significant. The mean square for sca was highly significant for most characters at Qlyasan location, while at Koya location it was significant only for grain weight plant^{-1}. The mean square for rca was significant for spike weight plant^{-1} at Qlyasan location and 1000-grain weight at Koya location and not significant for the other characters. The Diallel cross 1×4 at Qlyasan location and the reciprocal cross 2×1 at Koya location showed the best performance for grain weight plant^{-1} recording 58.083 and 40.941g plant^{-1} respectively. The magnitude of σ^2sca was more than σ^2gca for all characters in both locations indicating the importance of non-additive gene effects in controlling these characters. Heritability in broad sense for Diallel crosses due to grain weight plant^{-1} was found to be high in both locations, while for reciprocal crosses was low, and it was low for narrow sense for all crosses.

Keywords: Genetic Analysis, Gene Action, Heritability, Heterosis and Common Wheat.

توريث بعض الصفات الكمية للجيل الثاني للحنطة الناعمة في السليمانية-العراق

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المستخلص

تهدف هذه الدراسة إلى اختبار 25 تركيب وراثي (5 آباء + 10 هُجن تبادلية + 10 هُجن عكسية) باستخدام تصميم التهجينات التبادلية الكاملة في الموسم الشتوي 2021-2022 للجيل الثاني من الحنطة الناعمة، في موقعين مختلفين. الأول كان في محطة قلياسان للبحوث الزراعية بكلية علوم الهندسة الزراعية/ جامعة السليمانية′ (Lat 35 ° 34 ؛N ، ′ 21 ° Long 45؛E ، 765 MASL)، والثانية كانت في محطة كويه الزراعية – وزارة الزراعة′ (Lat 36 ° 04 ؛N ، 37 ° Long 44؛ E ، 582 MASL). أكدت نتائج الدراسة أن متوسطات المربعات للتراكيب الوراثية كانت عالية المعنوية لجميع الصفات في كلا الموقعين، ونفس الحال بالنسبة لمتوسط المربعات ال gca باستثناء وزن الحبوب نبات $^{-1}$ في موقع قلياسان والذي كان معنوياً فقط . كانت متوسط المربعات ل sca عالية المعنوية لمعظم الصفات في موقع قلياسان ، بينما كانت معنويًا فقط لوزن الحبوب للنبات $^{-1}$ في موقع كويه. كانت متوسط المربعات لـ rca معنويا بالنسبة لوزن السنبلة نبات $^{-1}$ في موقع قلياسان و وزن 1000 حبة في موقع كويه, بينما لم يكن معنوياً بالنسبة للصفات الأخرى .أظهر الهجين التبادلي 1×4 في موقع قلياسان والهجين العكسي 2 × 1 في موقع كويه أفضل أداء لوزن الحبوب نبات$^{-1}$ حيث سجلا 58.083 و 40.941 غم نبات $^{-1}$ على التوالي . و كانت مشاركة σ^2sca أعلى من σ^2gca لجميع الصفات في كلا الموقعين مما يشير إلى أهمية تأثير الفعل الجيني الغير مضاف في التحكم على توريث هذه الصفات . وجِدَت بأنَ درجة التوريث في معناها الواسع للهجن التبادلية لوزن الحبوب نبات$^{-1}$ عالية في كلا الموقعين ، بينما كانت واطئة للهجن العكسية ، أما بالنسبة لدرجة التوريث في معناها الضيق كانت منخفضة لجميع الهجن التبادلية والعكسية لكلا الموقعين.

الكلمات المفتاحية: التحليل الوراثي ، الفعل الجيني ، درجة التوريث ، قوة الهجين و الحنطة الناعمة.

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INTRODUCTION

Wheat is regarded as one of the major food crops in the world, accounting for about seventeen percent of all cultivated land (10, 12, 30) with 214 million hectares planted in 2018 and 34.254 tons of productivity per hectare. (*Triticum aestivum* L.) is an essential cereal crop globally, serving as a staple food source for most of the world's population, and it is an important part of these countries' diets, allowing them to attain food security (4, 6, 13, 21). FAO (17) arrived at the 6331 thousand dunums of wheat cultivated in Iraq for the winter of 2019, to a production capability of roughly 4343 thousand tons for the same year (14). A major factor in agricultural productivity keeping up with global population increase has been the creative thinking and hard work of agricultural experts. By 2050, the current 7.7 billion people on the planet are predicted to increase to 9.8 billion (36). We need to boost productivity and wheat production to fulfill our population's increasing demand (15 ,19, 20, 24). Finding acceptable parents with good combining ability for yield contributing qualities is the most crucial phase in any breeding program since it allows for the creation of genetic variability and the collection of data regarding the genetic architecture of component traits (8, 9, 11). The choice of suitable parents for evolving better hybrids and variations are a source of concern for the plant breeders (33). All breeding program's major objective is to produce high-yielding varieties with a good performance of genotypes in different environments (5, 21). Diallel Additionally, analysis offers a special chance to test some lines in all possible combinations (31). Diallel cross technique is a good tool for the identification of hybrid combinations that have the potential to produce maximum improvement and identify superior lines among the descendants of the early generations of segregation. The most used biometric technique for identifying parental lines based on their propensity to combine into hybrid combinations is the combination ability analysis of (18). With this method, the resulting total genetic variations is partitioned into the variance of general combining ability, as a measure of additive gene action and specific combining ability, as a measure of non-additive gene action (1, 2). The diallel cross designs are frequently used in plant breeding research to obtain information about genetic properties of parental linesb or estimates of general combining ability (gca), specific combining ability (sca), and heritability (16). Combining ability analysis helps in the identification of parents with high gca and parental combinations with high sca. Based on combining ability analysis of different characters, higher sca values refer to dominance gene effects and higher gca effects indicate a greater role of additive gene effects controlling the characters (35). The purpose of this study was to determine the general and particular combining abilities for yield and yield-contributing features in several wheat varieties genotypes to choose the best parents and crosses for breeding program and this study is to estimate the variability and ability to combine in the F2 generation arising from a set of dialect pairings for a few quantitative wheat crop characteristics.

MATERIALS AND METHODS

The present investigation was completed out in two distinct areas inside the Kurdistan Region of Iraq. Located at (Lat 35° 34′; N, Long 45° 21′; E, 765 MASL) was the first Qlyasan Agricultural Research Station, College of Agricultural Engineering Sciences, University of Sulaimani; the second was at Koya Agricultural Station, Ministry of Agricultural (Lat 36° 04′; N, Long 44° 37′; E, 582 MASL). Randomized Complete Block Design (RCBD) with three replicates was used to sow the seeds of twenty F2s with their parents on December 16, 2021, at the Qlyasan location, and on December 30, 2021, at the Koya location. One 2-meter-long row with 40 centimeters separating rows and 15 centimeters inside each treatment was used.

Table 1. The genotype names, pedigrees, and origins of the parents

No. of Parents	GenotypesName	Pedigree	Origin
1	Aras	(Sonora 64×Lerma Rojo 64) × Sentaelena	Mexico
2	Hasad	SNB//CMH79A55/3×CNO79/3/ATTILA	Iraq
3	Kauz	PVN/5×SUPER KAUZ	CIMMYT-Veery
4	Klal	KLEIN RECORD/38 MA//KLEIN PALANTELEN	CIMMYT
5	Ipa-95	Veery ″S”	Iraq

Statistical Analysis

For each character, a variety of statistical analyses were performed. Three repetitions of a randomized complete block design (RCBD) were used (7).

Combining Ability Analysis

The generic linear model for the analysis was used to estimate the (gca) and (sca), utilizing the formula of (34).

$$Y_{ijk} = \mu + g_i + g_j + s_{ij} + R_{ij} + r_k + \frac{1}{bc}\sum\sum \varepsilon_{ijk}$$

Where: Y_{ijk}: observed value of the experimental unit

μ: population means,

g_i: general combining ability (gca) effect for the i the parent

g_j: general combining ability (gca) for the j the parent

S_{ij}: special combining ability (sca) for the diallel crosses involving parent i and j

R_{ij}: special combining ability (rca) for the reciprocal crosses involving parent i and j

r_k: replication (block) impact

e_{ijk}: experimental error impact

Estimate of Heterosis

It was estimated as the percentage deviation of the F_1s hybrid from the mid-parental value. The percent increase (+) or F1 cross's decline (-) over the mid-parent was calculated to determined hetrotic values for every character (3).

Heterosis (H) % = $\frac{F_1' - M.P}{M.P} \times 100$

Where:

F'_1 = mean of hybrid,

M.P= Mid Parental value.

Where:

M.P = $\frac{P_1 + P_2}{2}$

P_1: Parent 1.

P_2 : Parent 2

Estimation of Heritability

In both broad and specific senses, heritability was estimated depending on the variance of general and specific combining abilities, and regarding the variation of experimental error according to (34). And as follows:

$$h^2_{b.s} = \frac{\sigma^2{}_G}{\sigma^2{}_P} = \frac{\sigma^2{}_A + \sigma^2{}_D}{\sigma^2{}_A + \sigma^2{}_D + \sigma^2 e} = \frac{2\sigma^2{}_{GCA} + \sigma^2{}_{SCA}}{2\sigma^2{}_{GCA} + \sigma^2{}_{SCA} + \sigma^2 e}$$

$$h^2_{n.s} = \frac{\sigma^2{}_A}{\sigma^2{}_P} = \frac{\sigma^2{}_A}{\sigma^2{}_A + \sigma^2{}_D + \sigma^2 e} = \frac{2\sigma^2{}_{GCA}}{2\sigma^2{}_{GCA} + \sigma^2{}_{SCA} + \sigma^2 e}$$

Where:

$h^2{}_{b.s}$: heritability in broad sense

$h^2{}_{n.s}$: heritability in narrow sense

$\sigma^2{}_{gca}$: the variance of general combining ability

$\sigma^2{}_{sca}$: the variance of specific combining ability

$\sigma^2{}_e$: the variance of experimental error i.e. environmental variance

$\sigma^2{}_A$: additive genetic variance,

$\sigma^2{}_D$: non-additive (dominance and epitasis) genetic variance,

$\sigma^2{}_G$: total genetic variance, and

$\sigma^2{}_P$: phenotypic variance (genetic and environmental variance).

Estimation of the mean degree of dominance (ā): The following estimate was made for the mean degree of dominance for all traits:

$$\bar{a} = \sqrt{\frac{2\sigma^2 D}{\sigma^2 A}} = \sqrt{\frac{2\sigma^2 sca}{2\sigma^2 gca}} = \sqrt{\frac{\sigma^2 sca}{\sigma^2 gca}}$$

If ā = 0 indicate no dominance

If ā < 1 indicate partial dominance

If ā =1 indicate complete dominance

If ā >1 indicate over dominance

Estimation of Reciprocal Effects: Reciprocal Effect (RE%) = $\frac{(F'_{1r} - F'_1)}{F'_1} \times 100$

$\bar{F}_1$: the average of diallel hybrid

$\bar{F}_1 r$: the average of reciprocal hybrid

Mean comparisons conducted by using Least Significant Difference (LSD) test at 5 % and 1 % significant levels according to the following equation:

$$L.S.D_{Location} = t_{\alpha}\left(df_{E(a)}\right) \times \sqrt{\frac{2MS_{E(a)}}{tr}}$$

Table 2. Variance Analysis for a Complete Diallel Cross According to 13, Parents + parallel crosses plus reciprocal crosses compose Method I, Model I. (34).

S.O.V	d.f	SS	MS	EMS
Block	***b-1= 2***	$\frac{\sum Y^2..k}{p^2} - \frac{Y^2...}{bp^2}$	***MSb***	
Genotype	***P^2-1= 24***	$\frac{\sum Yij^2.}{b} - \frac{Y^2...}{bp^2}$	***MSg***	
gca	***p-1= 4***	$\frac{1}{2p}\sum(Yi.+Y.j)^2 - \frac{2}{p^2}Y^2...$	***MSgca***	$\sigma^2 e + 2p(\frac{1}{p-1})\sum gi^2$
sca	$\frac{p(p-1)}{2} = 10$	$\frac{1}{2}\sum Yij(Yij+Yji)^2 \frac{1}{2p}\sum(Y.j+Yj.)^2 + \frac{1}{p^2} - Y^2...$	***MSsca***	$\sigma^2 e + \frac{2}{p(p-1)kj}\sum\sum_{1<j} Sij^2$
rca	$\frac{p(p-1)}{2} = 10$	$\frac{1}{2}\sum(Yij-Yji)^2$	***MSrca***	$\sigma^2 e + (\frac{2}{p(p-1)})\sum\sum_{1<j} rij^2$
Error	***(b-1)(p^2-1)=48***	***SST-SSb-SSg***	***MSe***	***σ^2 e***
Total	***bp^2 -1= 74***	$\sum Yijk^2 - \frac{Y^2...}{bp^2}$		

Data Collection

Data were obtained for both locations after five plants that were considered competitors (instead of border plants) were tagged.

1- Spikes number plant^{-1}
2- Spikes weight plant^{-1} (g)
3- Grains weight spike^{-1} (g)
4- 1000-grain weight (g)=
5- Grain weight plant^{-1} (g)

Table 3. Analysis of variance in mean squares in the typical genotype of wheat for grain yield and its components at Qlyasan location

S.O.V	d.f	M.S Spikes no. plant^{-1}	Spikes weight plant^{-1} (g)	Grains weight spike^{-1} (g)	1000-grain weight (g)	Grain weight plant^{-1} (g)
Blocks	**2**	**19.301**	**27.353**	**0.970**	**75.014**	**7.491**
Genotypes	**24**	**11.678****	**147.942****	**0.385****	**80.383****	**60.895****
Gca	**4**	**9.898****	**64.050****	**0.366****	**58.522****	**23.695***
Sca	**10**	**4.030****	**50.192****	**0.097N.S**	**29.470***	**25.236****
Rcs	**10**	**1.353N.S**	**42.542***	**0.065N.S**	**11.427N.S**	**14.002N.S**
Exp. Error	**48**	**2.182**	**50.593**	**0.162**	**32.893**	**23.347**
MSe¯		**0.727**	**16.864**	**0.054**	**10.964**	**7.782**

The character mean squares that were examined for Qlyasan location present in table (3). For every character, the genotype mean squares were extremely significant, while for gca it was highly significant for all characters except grain weight/plant which was only considerable. Except 1000-grain weight, which was significant, and grain weight/spike, which was not significant, the mean squares for sca were extremely significant for every character. All characters' mean squares for rca were not important, except for spike weight/plant, which was the only one that had significance. For every attribute, there were highly significant differences between the genotypes. indicating relatively high magnitude of genetic variability in these genotypes (11). The mean performance of hybrids was greater than parents for all characters, The results obtained were fairly consistent with the data that were published by (32). Significant differences among genotypes for the studied characters reported by (22).

Table 4. The average values of the characteristics that were studied for the parents, F_2 reciprocal crosses, and F_2 diallel at Qlyasan

Crosses and parents	Spikes no. plant^{-1}	Spikes weight plant^{-1} (g)	Grains weight spike^{-1}(g)	1000-grain weight (g)	Grain weight plant^{-1} (g)
1 x 2	5.067	62.273	2.359	42.413	43.087
1 x 3	7.933	68.823	1.955	39.907	47.022
1 x 4	9.400	79.050	2.587	34.347	58.083
1 x 5	9.000	72.770	1.954	36.880	43.343
2 x 3	6.667	67.590	2.194	41.280	41.844
2 x 4	4.143	70.203	1.964	30.273	41.011
2 x 5	5.400	47.247	1.949	34.093	39.491
3 x 4	3.100	68.260	1.631	26.193	47.854
3 x 5	5.550	56.063	2.026	35.877	40.872
4 x 5	5.067	56.180	2.093	38.493	42.244
2 x 1	5.377	57.320	2.511	44.067	44.482
3 x 1	5.000	75.320	1.517	34.067	51.320
4 x 1	8.433	68.987	1.760	36.013	39.347
5 x 1	7.533	63.793	1.849	33.893	42.403
3 x 2	5.333	65.133	1.431	42.267	44.295
4 x 2	6.267	64.350	2.135	36.880	42.176
5 x 2	4.333	66.597	1.631	25.227	43.476
4 x 3	2.903	65.400	1.082	33.360	48.686
5 x 3	4.967	51.503	1.827	33.593	43.677
5 x 4	7.800	65.840	1.993	38.053	41.140
1	7.420	66.247	2.043	42.173	48.609
2	4.467	64.593	1.809	38.329	51.145
3	5.333	65.613	1.611	33.150	51.780
4	7.800	68.283	1.234	32.520	45.347
5	10.533	67.177	1.646	25.447	45.207
LSD$_{(p\leq 0.05)}$	2.098	48.670	0.156	31.642	22.459

The mean performance of genotypes for studied characters presents in table (4). The maximum quantity of spikes/plant recorded by number of spikes/plant reached 10.533 spikes while the maximum weight of spikes/plant, grain weight/spike, and grain weight/plant were 79.050, 2.587, and 58.083 g respect recorded by the cross 1x4, while the highest weight of 1000 grains was 44.067 showed by the cross 2x1. Minimum spikes number/plant, grain weight/spike and weight/spike were 2.903 spikes and 1.082 g obtained from the cross 4×3. The lowest weight of spikes /plant was 47.247 g obtained from the cross 2x5. The cross 5x2 gave minimum weight of 1000 grains reached 25.227 g, while the lowest grains weight/spike was 39.347 g showed by the cross 4x1.

Table 5. F_2 diallel and reciprocal crosses' proportion Regarding grain yield heterosis and its constituent parts at Qlyasan location

Crosses	Spikes no. plant^{-1}	Spikes weight plant^{-1} (g)	Grains weight spike^{-1} (g)	1000-grain weight (g)	Grain weight plant^{-1} (g)
1 x 2	-14.750	-4.810	1.901	5.372	-13.614
1 x 3	24.412	4.388	7.026	5.961	-6.320
1 x 4	23.522	8.184	10.428	-8.033	-9.737
1 x 5	0.260	18.495	5.974	9.080	-7.601
2 x 3	36.054	3.820	4.510	15.503	-18.690
2 x 4	-32.446	5.667	2.800	-14.541	-14.997
2 x 5	-28.000	-28.289	-7.898	6.917	-18.027
3 x 4	-52.792	1.960	14.661	-20.227	-1.460
3 x 5	-30.042	-15.561	24.414	22.453	-15.717
4 x 5	-44.727	-17.053	45.358	32.812	-6.699
S.E Diallel Crosses	9.882	4.449	4.672	5.159	1.818
2 x 1	-9.534	-12.382	8.452	9.480	-10.816
3 x 1	-21.589	14.242	-16.934	-9.546	2.242
4 x 1	10.819	2.560	7.417	-3.570	-16.242
5 x 1	-16.079	-4.375	0.262	0.246	23.823
3 x 2	8.844	0.046	-31.825	18.264	-13.927
4 x 2	2.174	-3.143	11.751	4.109	-12.581
5 x 2	-42.222	1.080	-22.955	-20.889	-9.757
4 x 3	-55.787	-2.313	-23.942	1.599	0.253
5 x 3	-37.395	-22.429	12.233	14.660	-9.933
5 x 4	-14.909	-2.790	38.435	31.294	-9.137
S.E Reciprocal Crosses	7.028	3.022	6.881	4.677	3.754

The estimate of heterosis values as the F_2s deviation from mid-parental values for diallel and respect crosses of examined the characters at Qlyasan location is illustrated in table (5). Maximum positive heterosis for a number of spikes/plant was 36.054% recorded by the cross 2x3, However, the cross 1x5 revealed the highest positive heterosis for spikes weight/plant at 18.495%. Maximum positive heterosis for the characters grains weight /spike and 1000 grains weight were 45.358 and 32.812% respect obtain from the cross 4x5. The highest degree of positive heterosis for grains weight /plant was 23.823% exhibited by the cross 5x1. Both positive and negative heterosis values were present for every character. The cross Klal×Kauz at the first location recorded the maximum positive heterosis value for grain yield/plant at 7.425%, while the cross Hasad×Iba-95 at the second location recorded the highest positive heterosis for some components for weight of grains/spike at 71.402%. Every character had displayed a significant degree of heterosis over middle parents (14,15).

Table 6. Reciprocal effect values of reciprocal crosses about grain crop and its constituents for Qlyasan location

Reciprocal crosses	Spikes no. plant^{-1}	Spikes weight plant^{-1} (g)	Grains weight spike^{-1} (g)	1000-grain weight (g)	Grain weight plant^{-1} (g)
2 x 1	6.118	-7.954	6.429	3.898	3.238
3 x1	-36.975	9.440	-22.387	-14.634	9.140
4 x 1	-10.284	-5.199	-2.727	4.852	-7.207
5 x 1	-16.296	-19.300	-5.390	-8.098	34.008
3 x 2	-20.000	-3.635	-34.767	2.390	5.858
4 x 2	51.247	-8.338	8.707	21.823	2.842
5 x 2	-19.753	40.955	-16.347	-26.007	10.090
4 x 3	-6.344	-4.190	-33.667	27.361	1.739
5 x 3	-10.511	-8.134	-9.791	-6.364	6.862
5 x 4	53.947	17.195	-4.763	-1.143	-2.613
S.E	9.576	5.468	6.131	5.019	4.087

Data in table (6) illustrate the reciprocal effect values of studied characters in Qlyasan location. The 5x4 reciprocal cross produced the greatest favorable impact of spikes number/plant reached 53.947%, while the cross 5x2 showed the highest positive effect for spike weight/plant, and grain weight/plant with 40.955 and 10.090% respectively, and in addition gave highest possible negative effect for 1000-grains weight reached -26.007%. The highest positive effect of grains weight /spike was 8.707% recorded by the cross 4x2. The cross 4x2 exhibited the highest positive effect for 1000-grains weight reached 27.361%. Maximum negative effect of reciprocals for the characters spike number/plant, spike weight/plant, grains weight/spike, and grains weight/plant were -36.975, -19.300, -34.767, and -7.207% recorded by the crosses 3x1, 5x1, 3x2 and 4x1 respectively.

Table 7. Evaluation of the parents' overall combining ability with grain yield and its constituents at Qlyasan location

ĝii	Spikes no. plant^{-1}	Spikes weight plant^{-1} (g)	Grains weight spike^{-1} (g)	1000-grain weight (g)	Grain weight plant^{-1} (g)
1	1.065	3.098	0.108	3.042	1.513
2	-1.041	-1.995	0.263	1.764	-0.902
3	-0.981	-0.053	-0.183	-0.267	1.795
4	0.078	1.871	-0.178	-1.686	-1.562
5	0.879	-2.922	-0.010	-2.851	-0.844
C.D. (0.05) Critical Differences	0.381	1.837	0.104	1.481	1.248

The parental estimates of the gca impact for studied characters in Qlyasan location present in Table (7). Parent 1 was the most effective general combiner for the characteristics weight and number of spikes per plant, and 1000-grains weight recording 1.065, 3.098, and 3.042 respectively. The parents 2 and 3 were the best general combiner for the characters grains weight/spike and grains weight/plant, recording 0.263 and 1.795 respectively. Regarding the gca impacts of parents, all parents demonstrated a positive sca effect for one or more yield components under examination in both the F1 and F2 generations, but none of the parents was shown to be a good general combiner for all 11 features. (33).

Table 8. Estimation especially when skills are combined for the diallel crosses for grain yield and its components for Qlyasan location

ŝij	Spikes no. plant^{-1}	Spikes weight plant^{-1} (g)	Grains weight spike^{-1} (g)	1000-grain weight (g)	Grain weight plant^{-1} (g)
1 x 2	-0.996	-6.292	0.192	2.883	-1.944
1 x 3	0.016	6.385	-0.360	-2.988	2.560
1 x 4	1.580	0.924	-0.017	-1.727	-4.193
1 x 5	0.130	6.261	-0.068	-0.355	4.926
2 x 3	1.829	3.424	-0.139	4.725	-2.941
2 x 4	-0.025	2.416	0.093	-2.053	-1.060
2 x 5	-1.164	-3.146	-0.335	-4.804	-1.888
3 x 4	-2.289	0.027	-0.154	-3.821	2.919
3 x 5	-0.832	-8.227	0.248	2.302	-3.795
4 x 5	-0.717	-2.924	0.360	7.259	-1.020
C.D. (0.05) Critical Differences	0.763	3.673	0.208	2.962	2.495

The estimated of sca effect of diallel crosses in Qlyasan location illustrated in table (8). The crosses 2x3, 1x3, and 1x5 were the best specific combiners for the characters spike quantity plant^{-1}, spike weight plant^{-1} and grains weight plant^{-1} recording 1.829, 6.382, and 4.926 respectively, while the diallel cross 4x5 was discovered to be the greatest specialized combiner to the characters grains weight spike^{-1} and 1000 grains weight recording 3.360 and 7.259 respectively. The best seven crosses out of the 78 in this study were chosen based on significant and desired SCA effects for increased grain yield as well as for other yield components in both the F1 and F2 generations. (33).

Table 9. Estimation that of specific combining abilities effect of the reciprocal crosses ($\acute{r}_{ij}$) for grain yield and its components at Qlyasan location

$\acute{r}_{ij}$	Spikes no. plant^{-1}	Spikes weight plant^{-1} (g)	Grains weight spike-1(g)	1000-grain weight (g)	Grain weight plant^{-1} (g)
2 x 1	-0.155	2.477	-0.076	-0.827	-0.698
3 x 1	1.467	-3.248	0.219	2.920	-2.149
4 x 1	0.483	1.892	0.025	-0.833	1.528
5 x 1	0.733	7.628	0.053	1.493	-7.370
3 x 2	0.667	1.228	0.381	-0.493	-1.226
4 x 2	-1.062	2.927	-0.086	-3.303	-0.583
5 x 2	0.533	-9.675	0.159	4.433	-1.992
4 x 3	0.098	1.430	0.275	-3.583	-0.416
5 x 3	0.292	2.280	0.099	1.142	-1.402
5 x 4	-1.367	-4.830	0.050	0.220	0.552
C.D. (0.05) Critical Difference	0.853	4.107	0.232	3.311	2.790

The estimation of sca effects of the reciprocal crosses for studied characters in Qlyasan location illustrated in table (9). The reciprocal crosses 3x1, 5x1, 3x2, 5x2, and 4x1 were the most effective particular combiner regarding the characters spikes quantity /plant, spike weight/plant, grains weight/spike, 1000-grains weight, and grains weight/plant, recordings 1.467, 7.628, 0.381, 4.433 and 1.528 respectively.

Table 10. Estimation of some genetic parameters for the grain yield and its components at Qlyasan location

Parameters	Spikes no. plant-1	Spikes weight plant-1 (g)	Grains weight spike-1 (g)	1000-grain weight (g)	Grain weight plant-1 (g)
Mse¯	0.727	16.864	0.054	10.964	7.782
σ^2gca	0.772	1.346	0.020	2.563	0.035
σ^2sca =σ^2D	4.030	50.192	0.097	29.470	25.236
σ^2gca / σ^2sca	0.191	0.027	0.211	0.087	0.001
σ^2A	1.543	2.691	0.041	5.126	0.070
σ^2Dr	0.313	12.839	0.005	0.232	3.110
$\bar{A}$	2.286	6.107	2.178	3.391	26.944
h^2 b.s	0.885	0.758	0.719	0.759	0.765
h^2 n.s	0.245	0.039	0.213	0.113	0.002
$\bar{a}$ r	0.637	3.089	0.511	0.301	9.459
h^2 bsr	0.718	0.479	0.462	0.328	0.290
h^2 nsr	0.597	0.083	0.409	0.314	0.006

The estimates of some genetic parameters as a result of the features under study in Qlyasan location present in Table (10). The magnitude of σ^2_{sca} was more than σ^2_{gca} for all characters, this causes it to value the ratio σ^2_{gca} / σ^2_{sca} less than one and $\bar{a}$ be multiples for every character, showing the role that non-additive gene effects play in regulating these traits' inheritance. While for the reciprocal crosses, it was found that the average degree of dominance was less than one for the characters spikes number/plant, grains weight/ spike, and 1000-grains weight. All characters have strong heritability in the wide meaning of diallel crosses, but poor heritability in the narrow sense. regarding to reciprocal crosses, heritability in broad sense was high for spike number/plant only and it was low for the other traits, while in narrow sense it was high for the same character only. For the majority of traits, heritability was low to moderate in the narrow meaning and moderate to high in the broad sense (19, 20). The ratios of GCA to SCA, and average degree of dominance were smaller and greater than unity, respectively, which revealed that non-additive gene effects governed all the traits. These results were in good agreement with those published by (19, 20, 23).

Table 11. Mean squares of variance analysis for grain yield characters at Koya locations

S.O.V	d.f	M.S				
		Spikes no. plant^{-1}	Spikes weight plant^{-1} (g)	Grains weight spike^{-1} (g)	1000-grain weight (g)	Grain weight plant^{-1} (g)
Blocks	2	172.459	0.270	0.292	156.943	609.769
Genotypes	24	21.897**	0.530**	0.353**	93.621**	123.581**
gca	4	21.112**	0.095**	0.410**	98.583**	83.664**
sca	10	4.628$^{N.S}$	0.181$^{N.S}$	0.056$^{N.S}$	12.163$^{N.S}$	38.354*
rcs	10	4.445$^{N.S}$	0.205$^{N.S}$	0.062$^{N.S}$	23.301*	27.045$^{N.S}$
Exp. Error	48	9.109	0.267	0.134	27.054	52.994
MSe¯		3.036	0.089	0.045	9.018	17.665

The mean squares of data analysis for studied characters in Koya location present in table (11). The mean squares of genotypes and gca were highly significant for every character, while for sca it was significant for only grains weight/plant and not significant for the other characters. Only the 1000-grain weight showed a significant mean square for rca; the other characters did not show any significant mean square. Except for spike weight/plant, which was the sole relevant character, the mean squares for rca were not statistically significantt for any character. That mean the performance of hybrids were greater than parents for all characters, these results were in a good agreement with those reported by (32, 27, 28). Significant differences among genotypes for the studied characters were reported by (25, 26). Significant variations were discovered between the genotypes. for all traits, indicating a relatively high magnitude of genetic variability in these genotypes (8, 9, 11).

Table 12. Analysis of mean squares of the related genotype's variance of wheat for grain yield and its components at Koya location

Crosses and parents	Spikes no. plant^{-1}	Spikes weight plant^{-1} (g)	Grains weight spike^{-1}(g)	1000-grain weight (g)	Grain weight plant^{-1} (g)
1 x 2	12.800	73.953	1.609	44.240	24.953
1 x 3	10.467	70.330	1.490	37.813	24.721
1 x 4	7.267	45.360	1.400	37.560	22.195
1 x 5	10.800	70.407	1.819	39.787	25.011
2 x 3	8.067	81.433	2.275	44.040	25.343
2 x 4	14.267	91.707	1.837	36.653	32.393
2 x 5	15.533	110.627	1.938	40.080	37.356
3 x 4	12.400	83.633	1.949	32.533	30.137
3 x 5	8.533	68.917	1.827	32.507	40.520
4 x 5	13.267	83.120	1.854	36.507	28.090
2 x 1	8.867	71.833	2.042	45.520	40.941
3 x 1	6.933	51.653	1.975	32.627	25.593
4 x 1	8.867	49.247	1.437	34.280	17.337
5 x 1	14.200	76.850	1.548	26.213	30.283
3 x 2	10.867	90.250	2.713	40.133	31.795
4 x 2	13.933	78.667	1.672	33.453	29.863
5 x 2	12.867	78.490	1.983	26.747	30.286
4 x 3	12.600	57.367	1.279	32.800	24.426
5 x 3	14.133	70.223	1.593	29.173	30.925
5 x 4	13.867	83.190	1.748	31.213	31.321
1	8.267	49.040	1.236	38.533	17.273
2	9.200	65.127	2.022	42.267	24.108
3	6.533	55.280	2.146	37.813	17.607
4	11.200	49.640	1.255	28.867	19.866
5	13.467	77.723	1.792	27.627	29.247
LSD$_{(p\leq0.05)}$	8.762	0.257	0.130	26.026	50.981

The mean performance of the crosses and their parents for studied characters in Koya location presents in table (12). The highest values for spike number/plant and spike weight/plant is illustrated by the cross 2x5, recording 15.533 spike and 110.627 g respectively. While the cross 2x1 showed the highest weight of 1000 grains and grain weight/plant, recording 45.520 and 40.941g respectively. Maximum grains weight/spike was 2.713 g recorded by the cross 3x2. Parent 3 gave minimum number of spikes/plant, recording 6.533 spikes, while the cross 1x4 recorded minimum weight of spikes/plant, which was 45.360 g. The lowest weight of grains/spike and grain weight/plant were 1.236 and 17.273 g as evidenced by the cross parent 1. The lowest weight of 1000 grains was 26.213 g showed at the cross 5 x1.

Table 13. The percentage of heterosis in F$_2$ diallel and reciprocal crosses grain yield and its components at Koya location

Crosses	Spikes no. plant^{-1}	Spikes weight plant^{-1} (g)	Grains weight spike^{-1}(g)	1000-grain weight (g)	Grain weight plant^{-1} (g)
1 x 2	**46.565**	**29.553**	**-1.248**	**9.505**	**20.604**
1 x 3	**41.441**	**34.835**	**-11.889**	**-0.943**	**41.751**
1 x 4	**-25.342**	**-8.066**	**12.378**	**11.454**	**19.523**
1 x 5	**-0.613**	**11.084**	**20.137**	**20.274**	**7.528**
2 x 3	**2.542**	**35.264**	**9.181**	**9.990**	**21.503**
2 x 4	**39.869**	**59.814**	**12.072**	**3.055**	**47.329**
2 x 5	**37.059**	**54.885**	**1.617**	**14.689**	**40.029**
3 x 4	**39.850**	**59.423**	**14.633**	**-2.420**	**60.847**
3 x 5	**-14.667**	**3.631**	**-7.204**	**-0.652**	**72.963**
4 x 5	**7.568**	**30.524**	**21.680**	**29.242**	**14.390**
S.E Diallel Crosses	**8.381**	**7.390**	**3.592**	**3.219**	**6.782**
2 x 1	**1.527**	**25.839**	**25.373**	**12.673**	**97.873**
3 x 1	**-6.306**	**-0.971**	**16.818**	**-14.530**	**46.747**
4 x 1	**-8.904**	**-0.189**	**15.349**	**1.721**	**-6.638**
5 x 1	**30.675**	**21.250**	**2.279**	**-20.758**	**30.197**
3 x 2	**38.136**	**49.909**	**30.166**	**0.233**	**52.440**
4 x 2	**36.601**	**37.090**	**2.003**	**-5.942**	**35.823**
5 x 2	**13.529**	**9.891**	**3.994**	**-23.464**	**13.527**
4 x 3	**42.105**	**9.353**	**-24.767**	**-1.620**	**30.365**
5 x 3	**41.333**	**5.596**	**-19.089**	**-10.839**	**32.004**
5 x 4	**12.432**	**30.634**	**14.701**	**10.503**	**27.549**
S.E Reciprocal Crosses	**6.351**	**5.367**	**5.622**	**3.875**	**8.622**

The estimates of heterosis for diallel and reciprocal crosses in Koya location present in table (13). Regarding to the diallel crosses, Maximum positive heterosis for spikes number and weight/plant were 46.565 and 59.814% recorded by the crosses 1x2 and 2x4 respectively, while maximum heterosis values for grains weight/spike and 1000-grains weight were 21.680 and 29.242% recorded by the cross 4x5. Maximum positive heterosis for grains weight/plant was 72.963% recorded beside the cross 3x5. Concerning to the reciprocal crosses the highest positive heterosis for spikes number/plant was 42.105% recorded by the cross 4x2, while for spike weight/plant and grains weight/spike, it was 49.909 and 30.166% showed by the cross 3x2. The cross 5x4 gave maximum positive heterosis for 1000 -grains weight reached 10.503%, while the cross 2x1 showed maximum positive heterosis for grains weight/plant reached 97.873%. Both positive and negative heterosis values were present for every character. At the first location, the maximum positive heterosis value for grain yield/plant was 7.425% for the Klal×Kauz cross. while the cross Hasad×Iba-95 in the second place recorded the highest positive heterosis for some components for weight of grains/spike at 71.402%. Every character had displayed a significant degree of heterosis over middle parents (19, 20).

Table 14. Reciprocal effect values of reciprocal crosses about the grain crop and its constituents for Koya location

Reciprocal crosses	Spikes no. plant^{-1}	Spikes weight plant^{-1} (g)	Grains weight spike^{-1} (g)	1000-grain weight (g)	Grain weight plant^{-1} (g)
2 x 1	-30.729	-2.867	26.958	2.893	64.069
3 x 1	-33.758	-26.556	32.580	-13.717	3.525
4 x 1	22.018	8.568	2.643	-8.733	-21.888
5 x 1	31.481	9.152	-14.864	-34.115	21.082
3 x 2	34.711	10.827	19.221	-8.871	25.462
4 x 2	-2.336	-14.219	-8.984	-8.730	-7.810
5 x 2	-17.167	-29.050	2.339	-33.267	-18.926
4 x 3	1.613	-31.407	-34.371	0.820	-18.951
5 x 3	65.625	1.896	-12.808	-10.254	-23.680
5 x 4	4.523	0.084	-5.735	-14.500	11.504
S.E	10.217	5.796	6.540	5.787	8.920

The reciprocal effect values of reciprocal crosses for studied characters in Koya location present in table (14). A maximum positive effect of spikes number/plant and maximum negative effect of grains weight/plant were 65.625 and -23.680% respectively recorded by the cross 5x3, while maximum positive effect of spikes weight/plant was 10.827% recorded by the cross 3x2. The highest positive effect of grains weight /spike and maximum negative effect of spikes number/plant were 32.580 and -33.758% respectively shown by the cross 3x1. The highest positive effect of 1000 grains weight and grains weight/plant were 2.893 and 64.069% showed opposite the cross 2x1. Maximum negative effect of spikes weight/plant and grains weight/spike were -31.407 and -34.371% recorded by the cross 4x3. The highest negative reciprocal effect of 1000 grains weight was -34.115% recorded by the cross 5x1.

Table 15. Estimating the effect of parents' general capacity to combine grain output and its constituent parts at Koya location

$\hat{g}_{ii}$	Spikes no. plant^{-1}	Spikes weight plant^{-1} (g)	Grains weight spike^{-1} (g)	1000-grain weight (g)	Grain weight plant^{-1} (g)
1	-1.495	-10.591	-0.198	1.951	-3.106
2	0.392	9.359	0.234	3.981	2.451
3	-1.461	-2.926	0.162	0.166	-0.796
4	0.719	-4.206	-0.209	-2.286	-2.114
5	1.845	8.364	0.012	-3.811	3.565
C.D. (0.05) Critical Differences	0.779	4.662	0.095	1.343	1.880

The estimates of general combining ability of parents for studied characters in Koya location present in table (15). Parent 5 was the best general combiner for spikes number/plant and grains weight/plant recording 1.845 and 3.365 respectively, while parent 2 was the most effective general combiner, recording 9.359, 0.243, and 3.981 for spike weight/plant, grain weight/plant, and grain weight/spike, respectively. Regarding the GCA effects of parents, all parents had a positive GCA effect for one or more yield components under examination in both the F1 and F2 generations, but none of the parents was shown to be a good general combiner for all 11 features. (33).

Table 16. Determining the impact of particular skill combinations for diallel crossings for grain yield and its components for Koya location

$\hat{s}_{ij}$	Spikes no. plant^{-1}	Spikes weight plant^{-1} (g)	Grains weight spike^{-1} (g)	1000-grain weight (g)	Grain weight plant^{-1} (g)
1 x 2	0.768	2.763	0.013	3.389	5.938
1 x 3	-0.579	-3.953	0.041	-5.751	-0.054
1 x 4	-2.325	-9.262	0.048	0.695	-2.678
1 x 5	0.981	4.493	0.093	-0.699	-0.476
2 x 3	-0.632	8.046	0.321	2.381	-0.750
2 x 4	1.821	8.671	-0.048	-2.201	3.128
2 x 5	0.795	5.473	-0.063	-2.315	0.141
3 x 4	2.075	6.269	-0.116	-0.773	2.528
3 x 5	-0.219	-7.231	-0.241	-1.074	5.290
4 x 5	-0.165	7.634	0.220	4.398	0.591
C.D. (0.05) Critical Differences	1.559	9.323	0.189	2.686	3.759

The estimates of specific combining ability effect of the diallel crosses for studied characters in Koya location present in table (16). The cross 3x4 was the best specific combiner for spikes number/plant recording 2.075, while the cross 2x4 was the best specific combiner for spikes weight/plant recording 8.671. The crosses 1x5, 4x5, and 1x2 were the best specific combiner for the characters grains weight/spike, 1000-grains weight, and grains weight/plant recording 0.321, 4.398, and 5.938 respectively. The best seven crosses out of the 78 in this study were chosen based on significant and desired SCA effects for increased grain yield as well as for another yield component in the F1 and F2 generations (33).

Table 17. Evaluation of the reciprocal crossings' effect on particular combining abilities ($\acute{r}_{ij}$) about grain production and its constituents at Koya location

$\acute{r}_{ij}$	Spikes no. plant^{-1}	Spikes weight plant^{-1} (g)	Grains weight spike^{-1} (g)	1000-grain weight (g)	Grain weight plant^{-1} (g)
2 x 1	1.967	1.060	-0.217	-0.640	-7.994
3 x 1	1.767	9.338	-0.243	2.593	-0.436
4 x 1	-0.800	-1.943	-0.019	1.640	2.429
5 x 1	-1.700	-3.222	0.135	6.787	-2.636
3 x 2	-1.400	-4.408	-0.219	1.953	-3.226
4 x 2	0.167	6.520	0.082	1.600	1.265
5 x 2	1.333	16.068	-0.023	6.667	3.535
4 x 3	-0.100	13.133	0.335	-0.133	2.856
5 x 3	-2.800	-0.653	0.117	1.667	4.798
5 x 4	-0.300	-0.035	0.053	2.647	-1.616
C.D. (0.05) Critical Deference	1.743	10.424	0.211	3.003	4.203

The estimates of specific combining abilities effect of reciprocal crosses for studied characters in Koya location present in table (17). The reciprocal crosses 2x1, 5x2, 4x3, 5x1, and 5x3 were the best combiner for the studied characters, recording 1.967, 16.068, 0.335, 6.787, and 4.798 respectively.

Table 18. Estimation of some genetic parameters for the grain yield and its components at Koya location

Parameters	Spikes no. plant^{-1}	Spikes weight plant^{-1} (g)	Grains weight spike-1(g)	1000-grain weight (g)	Grain weight plant^{-1} (g)
Mse¯	3.036	108.659	0.045	9.018	17.665
σ^2_{gca}	1.200	41.395	0.028	7.153	3.067
$\sigma^2_{sca} = \sigma^2_D$	4.628	189.982	0.056	12.163	38.354
$\sigma^2_{gca} / \sigma^2_{sca}$	0.259	0.218	0.489	0.588	0.080
σ^2_A	2.401	82.791	0.055	14.306	6.134
σ^2_{Dr}	0.704	5.224	0.008	7.141	4.690
ā	1.964	2.142	1.430	1.304	3.536
$h^2_{b.s}$	0.698	0.715	0.714	0.746	0.716
$h^2_{n.s}$	0.239	0.217	0.353	0.403	0.099
ā r	0.766	0.355	0.555	0.999	1.237
h^2_{bsr}	0.506	0.448	0.588	0.704	0.380
h^2_{nsr}	0.391	0.421	0.509	0.470	0.215

The estimates of some genetic parameter for studied characters in Koya location present in table (18). As shown in this table the magnitude of σ^2_{SCA} was larger than σ^2_{gca} for all characters, indicating that the ratio of $\sigma^2_{gca} / \sigma^2_{sca}$ was less than one for all characters, and For diallel crosses, the average degree of dominance was greater than one, whereas for reciprocal crosses, the average degree of dominance was greater than one for the weight/plant of only grains. For diallel crosses, it was found that all characters had high heritability in the broad sense, while all characters had low heritability in the narrow sense. Similarly, for reciprocal crosses, only the 1000-grain weight had high heritability in the broad sense, while the other characters had low heritability and the spike number/plant and grains weight/spike had moderate heritability in the narrow sense. For the majority of traits, heritability was low to moderate in the narrow meaning and moderate to high in the broad sense (19, 20). The values of broad sense heritability ranged between 44.44% and 93.27% for grain weight per spike (5). All the attributes were governed by non-additive gene effects, as seen by the ratios of GCA to SCA and the average degree of dominance, which were both greater than unity. These results were in a good agreement with those reported by (19, 20, 23). The SCA mean squares were larger than the GCA means squares, and the GCA/SCA ratio was smaller than unity, indicating a stronger significance of non-additive gene effects over additive gene effects in the expression of these wheat features (29). The presents of highly significant mean squares for genotypes due to every studied traits affirmed the essentiality of genetic analysis, which separated the mean squares of genotypes to gca, sca, and rca components. Significant positive and negative heterosis was showed up as a result of the diallel and reciprocal crossings between parents. The reciprocal effect was appearing for all characters due to the distinctions between reciprocal and diallel crosses. Parent Kauz and Ipa-95 were the good general combiner for grain weight plant at both locations respectively, while the crosses Aras×Ipa-95 and Aras×Hasad were the best specific combiner for diallel crosses due to grain weight plant at both locations respectively, but the reciprocal crosses Ipa-95×Aras and Hasad×Aras were the good specific combiner for reciprocal crosses since this character. The variance component due to sca was greater than the variance component for almost all characters in both locations, while the ratio of $\sigma^2_{gca} / \sigma^2_{sca}$ value was less than unity for all characters at both locations, confirming the importance of non-additive gene effect in controlling the inheritance of these characters. Heritability in narrow sense was found to be low for studied characters as a result of controlling non-additive variance over additive variance.

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