INHERITANCE OF GRAIN YIELD AND ITS RELATED CHARACTERS FOR 5×5 DIALLEL CROSS OF F1 BREAD WHEAT

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Abstract. A full Diallel cross among five cultivars of common wheat (*Triticum aestivum* L.) with their twenty F_1 progeny were evaluated at Kurdistan Reign-Iraq at two different locations, Kanipanka and Qlyasan, during the winter season of 2017-2018 using Completely Randomized Block Design (CRBD) with three replications. The mean squares of genotypes were highly significant for all studied characters. Parent Iba-95 at Kanipanka location produced highest value for grain yield/plant, while at Qlyasan location the highest value was provided by the Kauz parent. Maximum heterosis value for grain yield/plant at Kanipanka location produced by the reciprocal cross Klal×Kauz was 7.425%, while at Qlyasan location the diallel cross Hasad×Iba-95 reached 71.402%. Klal parent at both locations was the best general combiner for grain yield/plant and some yield components. The cross Aras×Iba-95 was found to be the best specific combiner for most characters at both locations. The inheritance of most characters is controlled by non-additive gene effect. Heritability in broad sense for most characters was moderate to high, while for narrow sense it was low to moderate. Grain yield/plant exhibited positive and significant correlation with most its important components at both locations. Maximum positive direct effect in grain yield recorded by weight of spikes/plant and biological yield/plant at both locations respectively.
Keywords: *common wheat, genetic analysis, combining ability, heterosis, heritability*

Introduction

Wheat species of the genus *Triticum* L. are members of the *Triticeae* Dum. Tribe of the Poaceae Barn family and represent the world's most important monocotyledenous cereals (Anonymous, 2015). The *aestivum* species is one of the most important crops all over the world. Increasing production per unit area seems to be one of the great factors for narrowing the hole between wheat production and consumption (Ismail, 2015). Bread wheat is the most important food crop in our country and is the main source of protein and energy. Among the cereals, bread wheat is commonly identified as a species with a higher requirement of nutrients (Al-Naggar et al., 2015). According to the FAO statistics, 349 million tons of wheat was produced in 2016 and more than 220 million hectare of the world farmlands were under wheat cultivation (FAO, 2016). Due to the persistent increase of the world population, wheat plays a key role in the national economy of developing countries. Wheat production can be increased either by bringing more area under cultivation or vertically by increasing per unit yield. It is not possible horizontally to increase area under wheat due to other competing crops and shortage of irrigation water. Therefore, the only alternative left is to increase yield/ha, which is possible by introducing genetically superior new high yielding cultivars that are adapted to a wider range of environments. Wheat breeders, all over the world, have been utilizing the existing genetic resources to modify the wheat varieties in order to meet the requirement of an ever increasing population (Sprague and Tatum, 1942). Most of the

wheat planted areas are located in arid or semi-arid regions where a biotic stresses, especially drought stress, are a major constraint for crop production (Tahmasebi et al., 2014). Wheat breeding in the semi-arid region aims to develop new cultivars combining high productivity and good a biotic stress tolerance. Thus, it is important to understand the genetic control of these traits (Zine El Abidine et al., 2017). Genetic improvement of wheat yield is the trait breeders aim to achieve the most to promote wheat production and face the request of a continuous population expansion. This goal can be achieved either directly by selecting for high yield or indirectly by improving yield components and morphological traits (Hannachi et al., 2013). Knowledge of the genetic control of these traits related to wheat grain yield is requisite in a breeding program to design a selection strategy and manage the progeny. Several authors have attempted to impose the genetic basis of traits interested in yield determination. The results are often inconsistent and scarce; however, a predominance of additive gene action has been noticed with dominance effects for most traits studied (Saad et al., 2010; Rashid et al., 2012; Nazir et al., 2014). The diallel cross designs are frequently used in plant breeding research to obtain information about genetic properties of parental lines or estimates of general and specific combining abilities and heritability (Baker, 1978; EL-Maghraby et al., 2005; Iqbal et al., 2007). In addition, the diallel cross technique was laid to supply early genetic information in the first generation (Chowdhry et al., 1992; Topal et al., 2004; Ataei et al., 2017). Understanding and knowing about gene action in breeding programs could improve the accuracy of selection and decrease the breeding cost and time. Therefore, the aims of this study were to investigate combining ability, gene action, heritability of some quantitative traits, correlation and path analysis in bread wheat.

Materials and methods

The current study was carried out at two locations in Kurdistan Region-Iraq. First Kanipanka Nursery Station (Lat 35° 22'; N, Long 45° 43'; E, 550 masl) in Sharazoor Valley 35 km East of Sulaimani City, and second was at Qlyasan Agricultural Research Station, College of Agricultural Sciences-University of Sulaimani located (Lat 35° 34' 307"; N, Long 45° 21' 992"; E, 765 masl) 2 km North West of Sulaimani City. Five varieties of common wheat (*Triticum aestivum* L.) were used namely (Aras, Hasad, Kauz, Klal and Iba-95). The varieties were selected according to the prior experience on some of them regarding the efficiency of these varieties and their suitability to the prevailing environmental conditions in the region and creating new combinations with other varieties that have not yet been tested in the region.

Name, pedigree and origin of parental genotypes

No.	Genotypes	Pedigree	Origin
1	Aras	(Sonora 64×Lerma Rojo 64) × Sentaelena	Mexico
2	Hasad	SNB//CMH79A955/3*CNO79/3/ATTILA	Iraq
3	Kauz	PVN/5*SUPER KAUZ	CIMMYT-Veery
4	Klal	KLEIN RECORD/38 MA//KLEIN PALANTELEN	CIMMYT
5	Iba-95	Veery "S"	Iraq

All possible crosses including reciprocals were perfected from April 24 to May 8, 2017 to generate the 20 F₁s crosses at Qlyasan location. Seeds of 20 F₁s with their parents were sown on December 12, 2017 at Kanipanka location and on December 6, 2017 at Qlyasan location, according to Complete Randomize Block Design with three replications. Each treatment was one row of 2 m long, 40 cm between rows and 15 cm between plants within row. Five competitive plants (excluding border plants) were tagged, and data were recorded for:

1. Morphological traits:

Number of spikes/plant, Weight of spikes/plant (g), Average spike weight (g), Spike length (cm), Number of grains/spike, Weight of grains/spike (g), 1000-grain weight (g), Biological yield/plant, Grain yield/plant and Harvest index.

2. Genetic parameters:

General Combining Ability (gca) variances and effects, Specific Combining Ability (sca) variances and effects, Heterosis % as a deviation of F₁s from their mid parents, Broad Sense Heritability, Narrow Sense Heritability, Average Degree of Dominance (ā).

3. Association analysis and path coefficient analysis.

Statistical analysis

Combining ability analysis

The (gca) and (sca) were estimated using the general linear model for the analysis which takes the formula of (Singh and Chaudhary, 2007).

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

where:
Y_{ijk}: observed value of the experimental unit,
μ: populations mean,
g_i: general combining ability (gca) effect for the ith parent,
g_j: general combining ability (gca) for the jth parent,
s_{ij}: specific combining ability (sca) for the diallel crosses involving parent i and j,
R_{ij}: specific combining ability (rca) for the reciprocal crosses involving parent i and j,
r_k: replication (block) effect, and
$\frac{1}{bc}\sum\sum \varepsilon_{ijk}$: means error effect.

Estimation of general, specific combining ability and reciprocal effects

$$gi = \frac{1}{2p}\left(Yi + Yj\right) - \frac{1}{p^2}Y..$$

$$si = \frac{1}{2}(Yij + Yji) - \frac{1}{2p}\left(Yi + Yi + Yj + Yj\right) + \frac{1}{p^2}Y..$$

$$ri = \frac{1}{2}\left(Yij - Yji\right)$$

where:

gi: effect of expected general combining ability for parents I,

si: effect of expected specific combining ability for single diall crosses ij when $i = j$,

ri: effect of expected specific combining ability for reciprocal crosses ij when $I = j$,

Yij: F1s mean as a result of crossing parent i with parent j,

$Y..$: sum of the means of all parents and F1s hybrids, and

P: parents number

Estimation of heterosis

The percent increase (+) or decrease (-) of F1 cross over mid- parent was calculated to determined heterotic values for all characters (AGB301, 2004).

$$\text{Heterosis}\ (H)\ \% \ = \ [\frac{F'1 - M.P}{M.P}] \times 100 \qquad M.P = \frac{(P1 + P2)}{2}$$

where:

F'1: mean of hybrid,

P1: parent one, and

P2: parent two.

Estimation of heritability

The term heritability has been further divided into broad sense and narrow sense, broad sense heritability was calculated by dividing genotypic variance by total variance and narrow-sense heritability was calculated by dividing additive genetic variance by total variance (Singh and Chaudhary, 1985).

$$h^2b.s \ = \ \frac{\sigma^2 G}{\sigma^2 P} = \frac{\sigma^2 A + \sigma^2 D}{\sigma^2 A + \sigma^2 D + \sigma^2 e} = \frac{2\sigma^2 gca + \sigma^2 sca}{2\sigma^2 gca + \sigma^2 sca + \sigma^2 e}$$

$$h^2n.s \ = \ \frac{\sigma^2 A}{\sigma^2 P} = \frac{\sigma^2 A}{\sigma^2 A + \sigma^2 D + \sigma^2 e} = \frac{2\sigma^2 gca}{2\sigma^2 gca + \sigma^2 sca + \sigma^2 e}$$

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 epistasis) genetic variance,

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

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

Estimation of average degree of dominance

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

If:

$\bar{a}$ = *zero* denote no dominance,

$\bar{a}$ < 1 denote partial dominance,

$\bar{a}$ = 1 denote complete dominance,

$\bar{a}$ > 1 denote over dominance.

Analysis of variance for full diallel cross according to (Griffing, 1956b), Method I, Model II (parents + diallel crosses + reciprocal crosses)

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

Climate conditions of Sulaimani Governorate

The climate of Sulaimani governorate is semi-arid environment: hot and dry in summer; cold and wet in winter. During July and August, the average temperature is between 39-43 °C, and often reaching nearly 50 °C. Autumn means high temperatures are 20-30 °C in October, cooling slightly in November. Precipitation is limited to winter and spring months, and the overall average annual rainfall of 550-700 mm was at Sulaimani city. An overview of experimental conditions is given in (*Table 1*).

Table 1. The meteorological data of the two locations

Month	Kanipanka location				Qlyasan location			
	Mini. Temp.(°C)	Maxi. Temp.(°C)	Avg. Temp.(°C)	Rainfall (mm)	Mini. Temp.(°C)	Maxi. Temp.(°C)	Avg. Temp.(°C)	Rainfall (mm)
October	22.6	30.0	15.1	-	10.4	33.1	21.2	10.0
November	14.4	20.0	8.8	71	7.6	23.9	14.2	114.6
December	10.2	16.1	4.4	18.5	-2.5	17.8	7.0	22.2
January	7.8	12.5	3.1	60	1.4	15.6	7.8	72.4
February	10.3	14.9	6.1	281	-2.3	20.9	8.7	323.0
March	14.7	21.3	8.1	19	1.0	24.4	13.0	44.6
April	17.1	24	10.5	90.5	2.2	31.6	17.4	98.6
May	22.2	29.5	15.0	68	13.0	38.1	24.7	70.4
Total rainfall				608				755.8

Soil analysis

Soil samples belonging to both locations were taken from experimental sites in Sulaimani governorate in Kurdistan region, Iraq. The samples were taken from surface (0-30 cm), the soil samples were air dried and ground to pass through a 2-mm sieve prior to analysis, shown in (*Table 2*).

Table 2. *Some physicochemical properties of the soil samples for locations of the experiment*

Location	Physical properties of the studied soil Particle size distribution (PSD) (g/kg)			
	Sand	**Silt**	**Clay**	**Texture class**
Kanipanka	214.00	540.00	246.00	Salty loam
Qlyasan	90.40	508.40	401.20	Salty clay
	Chemical properties of the studied soil						
	pH (dS m^{-1})	**EC$_e$ (g kg^{-1})**	**OM (Cmol$_c$ kg^{-1})**	**CEC (mg kg^{-1})**	**Available P**	**CaCO$_3$ equivalent (g kg^{-1})**	
						Total	**Active**
Kanipanka	8.05	0.16	22.03	22.10	7.44	195.00	100.00
Qlyasan	7.80	0.38	16.06	29.76	9.61	230.00	117.00
	Soluble ions (mmol L^{-1})						
	Ca^{2+}	**Mg^{2+}**	**Na$^+$**	**K$^+$**	**HCO$_3^-$**	**Cl$^-$**	**SO$_4^{2-}$**
Kanipanka	1.20	1.05	0.19	0.05	3.20	0.90	0.91
Qlyasan	2.20	1.80	0.10	0.13	2.34	0.80	0.88
	Available micronutrients (mg kg^{-1})		
	Zn	**Cu**	**Fe**
Kanipanka	1.563	5.07	5.15
Qlyasan	0.450	4.96	3.23

Results

The analysis of variance represent in *Table 3* was carried out according to Fisher (1918) to estimate the significant differences among genotypes. General and specific combining ability variances and effects were determined. The analysis of variance revealed highly significant differences among the genotypes for all characters. This signified the presence of wide diversity among the genotypes at both locations. The estimates of gca and sca variances represented in the same table, confirmed that both additive and non additive gene effects were important for the inheritance of different characters. The mean squares for gca were highly significant for all characters except weight of spikes/plant, and grain yield/plant which were significant, and not significant for spike length, biological yield/plant and harvest index at first location, but at second location were highly significant for all characters except spike length and biological yield/plant which were significant and it was not significant for weight of spikes/plant and grain yield/plant. The mean squares for sca was highly significant for weight of spikes/plant, grain yield/plant and harvest index, and it is significant for spike length, and biological yield/plant at first location, while at second location it was highly significant for weight of spikes/plant, biological yield/plant and grain yield/plant, but it was significant for spike length, and harvest index.

Table 3. *Mean squares of variance analysis in common wheat genotype for studied characters at both locations (Kanipanka upper value and Qlyasan lower value)*

S.O.V	d.f	No. of spikes/plant	Weight of spikes/plant (g)	Average spike weight (g)	Spike length (cm)	No. of grains/spike	Weight of grains/spike (g)	1000-grain weight (g)	Biological yield/plant (g)	Grain yield/plant (g)	Harvest index
Blocks	2	47.284	51.486	0.032	0.968	13.117	0.193	29.528	221.224	54.650	0.004
		1.040	30.225	0.109	3.011	98.436	0.169	31.004	2437.631	16.342	0.003
Genotypes	24	16.458**	241.469**	0.657**	1.589**	242.121**	0.438**	164.082**	1493.674**	102.266**	0.008**
		19.803**	108.637**	1.263**	1.172**	181.974**	0.926**	132.428**	2554.647**	87.388**	0.020**
gca	4	16.257**	115.806*	0.756**	0.533$^{N.S}$	168.977**	0.435**	168.998**	462.408$^{N.S}$	43.154*	0.001$^{N.S}$
		18.175**	17.142$^{N.S}$	1.123**	0.475*	115.406**	0.641**	117.569**	1247.252*	29.534$^{N.S}$	0.013**
sca	10	3.808$^{N.S}$	99.349**	0.094$^{N.S}$	0.567*	43.078$^{N.S}$	0.073$^{N.S}$	25.904$^{N.S}$	569.758*	42.352**	0.004**
		3.433$^{N.S}$	43.350**	0.196$^{N.S}$	0.326*	52.450$^{N.S}$	0.191$^{N.S}$	15.128$^{N.S}$	1165.362**	41.366**	0.006*
rcs	10	2.855$^{N.S}$	47.504$^{N.S}$	0.129$^{N.S}$	0.491*	83.028**	0.103$^{N.S}$	37.763$^{N.S}$	440.218*	22.199$^{N.S}$	0.003**
		5.140**	36.703**	0.365*	0.422**	46.967$^{N.S}$	0.293**	43.787**	379.455$^{N.S}$	16.730$^{N.S}$	0.004$^{N.S}$
Exp. Error	48	6.917	103.188	0.254	0.697	79.763	0.194	59.967	641.146	42.442	0.003
		5.660	37.696	0.494	0.412	81.289	0.287	33.381	1136.154	35.093	0.008
$\overline{MSe}$		2.306	34.396	0.085	0.232	26.588	0.065	19.989	213.715	14.147	0.001
		1.887	12.565	0.165	0.137	27.096	0.096	11.127	378.718	11.698	0.003

Data in *Table 4* illustrate the performance of the genotypes at both locations. At the first location the cross Hasad×Aras produced maximum grain yield/plant reached 51.852 g, but for biological yield/plant it was 161.159 produced by the cross Iba-95×Klal. Iba-95 parent showed the best value for grain yield/plant 60.724 g, and some components such as weight of spikes/plant, number of grains/spike, and biological yield/plant reached 86.160, 80.733 and 170.901 g respectively. At the second location maximum grain yield/plant was 38.962 g recorded by the cross Hasad×Aras, and maximum weight of 1000-grain was 59.403 g produced by the same cross. Kauz parent at the same location produce the highest value for grain yield/plant, harvest index and weight of spikes/plant reached 33.902 g, 0.384 and 43.252 respectively.

The estimation of heterosis value represent in *Table 5* determined as the percentage of F_1s deviation from mid parental value. For all characters positive and negative heterosis values were present. Maximum positive heterosis value for the grain yield/plant was 7.425% recorded by the cross Klal×Kauz at the first location, while at the second location reached 71.402% for the cross Hasad×Iba-95, which recorded the highest positive heterosis for some components such as average spike weight and weight of grains/spike. All characters had shown considerable amount of heterosis over mid parents.

Table 6 illustrates the general combining ability effect of parents. Klal parent was the best general combiner for grain yield/plant and number of spikes/plant, while Hasad parent and Iba-95 was the best combiner for most components at the first location. At the second location Klal was the best general combiner for grain yield/plant, number of spikes/plant and weight of spikes/plant, while Hasad parent was the best general combiner for average spike weight, weight of grains/spike, 1000-grain weight and biological yield/plant. Present findings are in confirmation with Kumar et al. (2011), Singh et al. (2013), Raj and Kandalkar (2013), Aslam et al. (2014), Ismail (2015), Kalhoro et al. (2015) and Kandil et al. (2016); they found high positive value due to gca for these characters.

Table 4. *The mean values of studied characters for F₁ diallel, F₁ reciprocal crosses and parents at both locations (Kanipanka upper value and Qlyasan lower value)*

Crosses and parents	No. of spikes/plant	Weight of spikes/plant (g)	Average spike weight (g)	Spike length (cm)	No. of grains/spike	Weight of grains/spike (g)	1000-grain weight (g)	Biological yield/plant (g)	Grain yield/plant (g)	Harvest index
1 x 2	19.666	59.596	4.274	11.500	51.067	3.027	59.318	112.599	44.941	0.438
	10.222	34.019	3.410	9.533	47.100	2.371	50.403	113.788	27.400	0.209
1 x 3	14.889	50.877	4.441	11.900	62.467	3.315	53.441	126.058	42.692	0.343
	8.778	31.545	5.040	11.367	64.333	3.524	54.685	95.562	24.839	0.259
1 x 4	16.667	58.492	4.484	12.700	60.600	3.270	53.718	103.250	44.257	0.428
	11.889	34.126	3.760	11.133	54.467	2.879	52.838	92.327	26.460	0.302
1 x 5	15.000	51.079	4.357	11.100	65.667	3.333	50.530	128.945	37.617	0.293
	8.000	26.848	4.091	10.833	59.400	2.935	50.295	96.009	20.754	0.213
2 x 3	19.778	59.383	3.883	11.333	58.933	2.863	47.109	140.202	40.110	0.367
	11.778	36.113	4.165	11.100	67.533	3.195	47.847	109.226	26.040	0.240
2 x 4	19.222	55.395	3.969	11.720	76.533	3.148	43.460	104.553	42.956	0.445
	14.444	49.852	4.447	12.067	78.867	3.537	44.826	140.021	36.413	0.290
2 x 5	15.667	54.476	5.057	13.400	75.400	3.979	52.981	102.906	43.124	0.446
	12.778	42.841	3.939	11.667	63.400	3.154	49.609	138.604	32.231	0.240
3 x 4	16.111	51.150	4.555	12.767	82.200	3.283	39.952	104.458	39.819	0.496
	12.111	43.454	4.433	12.700	78.267	3.153	40.087	149.018	32.904	0.235
3 x 5	16.000	61.627	4.548	12.800	63.467	3.341	52.936	149.095	46.659	0.312
	9.778	38.168	5.479	11.833	71.467	4.134	58.403	119.730	29.387	0.243
4 x 5	14.555	50.805	5.618	12.800	76.133	4.352	57.093	118.479	47.978	0.418
	11.444	39.752	4.041	10.600	64.200	3.015	47.247	132.275	29.841	0.231
2 x 1	17.445	63.583	4.866	12.300	61.733	3.557	57.533	154.662	51.852	0.354
	13.222	38.171	4.767	11.933	61.933	3.523	59.403	154.194	38.962	0.255
3 x 1	21.000	60.014	4.531	13.000	69.433	3.355	48.318	141.322	44.034	0.368
	16.111	41.122	4.222	11.567	74.600	3.201	42.910	185.791	36.180	0.197
4 x 1	15.222	53.967	4.985	12.600	64.400	3.595	56.165	120.627	38.772	0.364
	10.111	44.181	5.843	11.400	75.200	4.534	54.852	96.908	34.502	0.366
5 x 1	17.111	61.796	4.346	13.733	91.133	3.362	40.245	136.119	42.877	0.325
	12.333	42.437	4.826	12.000	75.933	3.053	39.476	123.645	31.998	0.259
3 x 2	18.667	53.242	4.583	11.387	71.067	3.415	47.960	119.454	48.534	0.403
	17.555	42.795	4.193	10.800	72.733	3.244	44.592	69.486	33.985	0.568
4 x 2	18.222	65.807	4.628	12.967	74.067	3.389	45.588	143.652	50.111	0.348
	11.889	29.316	4.125	10.885	67.350	2.865	42.603	81.353	28.900	0.365
5 x 2	15.222	60.208	5.082	11.833	65.267	3.785	57.935	140.471	46.352	0.336
	9.889	35.662	4.476	11.167	67.733	3.702	54.880	83.053	30.105	0.375
4 x 3	17.778	66.105	4.931	12.500	78.133	3.525	45.423	153.638	47.878	0.317
	12.333	38.984	4.188	12.140	67.400	2.979	45.168	126.621	28.289	0.231
5 x 3	16.000	46.294	4.038	12.278	66.678	3.042	45.839	93.517	34.396	0.378
	15.999	45.983	4.267	11.767	69.000	3.134	46.810	143.065	33.559	0.251
5 x 4	18.445	66.502	4.805	13.633	73.000	3.516	48.947	161.159	51.463	0.324
	11.111	29.283	3.413	11.667	63.933	2.684	42.340	95.348	21.557	0.240
1	19.889	56.031	3.942	11.633	59.600	2.923	49.350	151.563	41.829	0.283
	8.889	30.507	3.583	11.567	56.067	2.591	46.744	93.904	24.160	0.262
2	15.667	76.871	5.522	12.033	63.067	4.071	64.525	164.526	53.585	0.316
	7.222	35.093	5.756	11.533	74.533	4.653	62.230	124.757	22.689	0.194
3	14.000	49.221	5.140	12.600	61.533	3.991	67.306	112.131	41.088	0.365
	10.111	43.252	4.895	11.300	65.600	3.823	58.428	87.180	33.902	0.384
4	22.667	67.503	4.045	12.333	66.133	2.884	43.286	155.342	52.208	0.372
	13.778	41.162	3.991	11.000	68.933	3.019	44.090	105.669	31.690	0.304
5	21.111	86.160	4.471	11.533	80.733	3.137	39.120	170.901	60.724	0.366
	9.445	30.351	4.016	11.633	75.600	2.948	39.122	62.808	17.570	0.300
LSD(p≤0.05)	4.318	16.676	0.828	1.371	14.662	0.724	12.713	41.569	10.695	0.089
	3.906	10.079	1.154	1.054	14.801	0.879	9.485	55.336	9.725	0.146

Table 5. *Heterosis percentage of F₁ diallel and reciprocal crosses for studied characters at both locations (Kanipanka upper value and Qlyasan lower value)*

Crosses	No. of spikes/plant	Weight of spikes/plant (g)	Average spike weight (g)	Spike length (cm)	No. of grains/spike	Weight of grains/spike (g)	1000-grain weight (g)	Biological yield/plant (g)	Grain yield/plant (g)	Harvest index
1 x 2	10.624	-10.317	-9.679	-2.817	-16.739	-13.458	4.180	-28.755	-5.798	46.132
	26.899	3.716	-26.970	-17.460	-27.871	-34.530	-7.496	4.077	16.971	-8.254
1 x 3	-1.639	11.147	-1.255	4.814	0.055	-5.418	-7.902	-21.690	6.749	31.860
	25.144	-7.467	-11.293	-2.624	-10.466	-10.217	0.479	1.971	-8.857	-6.502
1 x 4	-7.050	-3.859	-2.763	-5.424	-6.257	-1.389	1.709	-8.635	-14.693	12.049
	3.922	0.779	9.990	-1.625	8.053	13.916	5.350	9.459	-6.751	-15.362
1 x 5	-23.577	-23.377	20.222	15.683	7.458	31.295	19.772	-36.175	-15.899	37.339
	39.394	40.790	3.667	0.575	-3.696	13.890	15.551	76.890	54.473	-14.692
2 x 3	7.863	-2.251	-14.688	3.924	1.873	-17.132	-19.691	7.783	-1.432	-8.370
	12.821	-2.565	2.892	3.650	1.998	-2.462	-3.193	12.986	3.856	-15.868
2 x 4	-8.984	-11.919	1.721	0.958	-4.438	2.291	6.728	-3.296	-1.975	3.004
	25.927	0.114	-2.195	5.917	-13.662	-8.176	11.743	33.834	43.298	2.410
2 x 5	-17.222	-33.796	-0.240	6.931	-10.431	-0.250	8.378	-28.076	-32.162	6.849
	21.336	35.019	19.593	-1.583	0.178	19.295	8.241	3.332	71.402	48.213
3 x 4	1.818	-8.772	-0.218	-8.663	11.332	-0.669	-13.266	-10.679	4.043	9.263
	46.974	1.394	-5.619	-3.139	8.127	-5.183	-13.008	-27.938	3.626	65.293
3 x 5	-13.292	-11.054	5.750	-1.934	-8.247	6.182	8.874	-0.738	-8.945	-8.162
	1.137	-3.096	0.464	-2.616	-4.060	9.343	12.517	10.746	16.974	9.552
4 x 5	-26.903	-39.747	-5.166	2.885	-9.200	1.041	11.252	-42.671	-39.086	2.349
	37.788	28.600	6.586	3.976	-4.520	5.039	12.508	69.834	36.253	-16.823
S.E Diallel crosses	4.014	4.791	2.956	2.189	2.725	4.123	3.827	5.255	4.737	5.978
	4.745	5.627	3.999	2.043	3.412	5.020	3.060	10.170	8.586	9.160
2 x 1	16.249-	23.438-	6.157-	0.563	1.848	5.204-	6.140-	20.239-	10.512-	14.636
	8.965	3.825-	7.938	1.587-	1.480-	2.706-	0.364	12.593-	6.038	13.367
3 x 1	11.473-	2.940-	4.045-	8.391-	8.420	3.606-	13.369-	2.201-	9.266-	9.764-
	15.789-	27.200-	3.492-	5.248-	2.356-	8.492-	4.357-	6.038	28.511-	34.056-
4 x 1	9.660-	10.316-	0.626-	2.197-	21.739	8.415	6.171-	31.866-	8.641-	35.841
	27.448	39.117	17.437	6.942	26.187	26.108	1.301-	40.321	30.396	2.295
5 x 1	21.409-	28.055-	8.288	10.216	17.150	8.327	9.682-	35.213-	22.345-	52.851
	32.121	42.806	16.687	9.483	18.886	13.842	6.628-	90.180	57.700	16.469-
3 x 2	1.874-	19.416-	5.384	3.924	22.204	7.954	13.384-	14.350-	1.354	22.663
	32.053	1.479	24.111-	7.153-	8.373-	28.871-	21.685-	24.825	5.461	19.908-
4 x 2	9.565	16.863-	5.275-	6.703	7.482	3.537-	10.365-	11.637-	16.754-	7.074
	53.438	7.853	13.371-	2.663	3.996	16.570-	19.282-	61.259	33.066	20.884-
5 x 2	6.947-	24.192-	13.029	16.549	26.750	6.723-	22.342-	18.839-	24.981-	4.501-
	48.000	29.687	1.228-	3.597	1.155	19.663-	22.101-	31.842	58.961	4.922
4 x 3	0.607-	12.756	0.769	4.011	16.031	1.406-	17.557-	7.414	7.425	5.648-
	0.465-	30.542-	7.165-	2.377-	0.124	16.251-	16.887-	15.630-	11.880-	6.253
5 x 3	1.266	2.343-	2.615	3.591	9.841	1.094-	14.640-	8.566	5.948-	13.269-
	26.136	5.929	6.000-	5.872	4.533-	12.002-	7.394-	68.842	9.919	32.554-
5 x 4	15.735-	13.444-	12.830	14.246	0.590-	16.785	18.794	1.203-	8.859-	12.105-
	4.309-	18.104-	14.761-	3.093	11.531-	10.044-	1.763	15.630-	12.478-	20.684-
S.E Reciprocal crosses	2.992	3.947	2.408	2.366	2.881	2.464	3.512	4.791	3.118	7.114
	7.222	8.256	4.276	1.718	3.715	5.163	2.958	68.842	9.361	5.388

Table 6. *Estimation of general combining abilities effect of parents for studied characters at both locations ($\hat{g}_{ii}$) (Kanipanka upper value and Qlyasan lower value)*

$\hat{g}_{ii}$	No. of spikes/plant	Weight of spikes/plant (g)	Average spike weight (g)	Spike length (cm)	No. of grains/spike	Weight of grains/spike (g)	1000-grain weight (g)	Biological yield/plant (g)	Grain yield/plant (g)	Harvest index
1	0.238	-4.196	-0.314	-0.367	-3.531	-0.212	-0.802	-9.775	-3.517	0.014
	-0.871	-1.820	-0.330	-0.054	-4.873	-0.281	-0.388	-0.577	-1.836	-0.029
2	-0.718	2.153	0.261	0.135	-2.141	0.186	4.687	6.416	1.263	-0.013
	-1.004	0.157	0.539	-0.078	0.960	0.392	4.388	14.327	0.476	-0.040
3	-1.429	-2.867	0.247	-0.007	-0.991	0.221	3.856	-4.261	-0.278	-0.010
	-0.349	-0.585	0.040	-0.209	-1.828	0.066	2.493	-15.292	0.180	0.049
4	1.971	1.075	-0.265	-0.007	-0.367	-0.213	-3.590	4.536	1.353	0.005
	2.318	1.695	-0.216	-0.029	1.958	-0.132	-2.844	6.168	2.525	0.021
5	-0.062	3.834	0.070	0.246	7.030	0.018	-4.150	3.084	1.179	0.003
	-0.093	0.552	-0.033	0.370	3.783	-0.045	-3.649	-4.626	-1.344	-0.001
S.E	0.679	2.623	0.130	0.216	2.306	0.114	1.999	6.538	1.682	0.014
	0.614	1.585	0.181	0.166	2.328	0.138	1.492	8.703	1.530	0.023

Data represent in *Table 7* illustrate the estimation of sca effects for crosses. The cross Kauz×Klal was the best specific combiner for grain yield/plant, but the cross Aras×Iba-95 was the best specific combiner for most traits including average spike weight, spike length, number of grains/spike, weight of grains/spike and harvest index in the first location. At the second location the cross Aras×Iba-95 was the best specific combiner for grain yield/plant, number of spikes/plant, weight of spikes/plant and spike length, while the cross Aras×Klal recorded the best specific combiner for average spike weight, number of grains/spike and weight of grains/spike, similar results reported previously by Kapoor et al. (2011), Singh et al. (2013), Raj and Kandalkar (2013), Desale et al. (2014) and Kandil et al. (2016).

Table 7. *Estimation of specific combining abilities effect for the diallel crosses at both locations ($\hat{s}_{ij}$) (Kanipanka upper value and Qlyasan lower value)*

$\hat{s}_{ij}$	No. of spikes/plant	Weight of spikes/plant (g)	Average spike weight (g)	Spike length (cm)	No. of grains/spike	Weight of grains/spike (g)	1000-grain weight (g)	Biological yield/plant (g)	Grain yield/plant (g)	Harvest index
1 x 2	0.318	-2.168	-0.194	-0.403	-6.299	-0.222	1.772	-9.697	0.636	0.021
	-0.273	-3.356	-0.359	-0.826	-7.793	-0.437	-0.252	-21.888	-1.893	0.023
1 x 3	-0.593	-1.836	-0.075	-0.253	1.371	-0.026	-2.031	-11.801	-1.902	0.0002
	0.304	-4.794	-0.678	-0.498	-5.568	-0.517	-2.747	-15.091	-4.288	0.003
1 x 4	-0.149	1.063	-0.100	-0.435	2.893	0.012	-1.046	-4.767	-1.737	0.019
	0.016	5.306	0.478	0.259	8.692	0.505	0.773	6.218	1.165	-0.007
1 x 5	-1.727	-6.272	0.446	0.869	6.563	0.406	0.696	-22.012	-1.625	0.085
	1.760	6.614	0.174	0.460	4.500	0.205	0.089	36.201	6.376	-0.013
2 x 3	-0.016	-2.518	-0.029	0.337	4.194	0.021	-4.251	-0.754	0.899	0.019
	0.316	1.587	-0.193	0.095	1.278	-0.158	-2.852	14.154	-0.415	-0.053
2 x 4	0.529	-0.877	0.098	0.187	-0.647	0.064	1.106	4.655	-0.107	0.001
	1.705	-0.007	-0.203	0.449	-2.075	-0.173	0.817	36.683	5.197	-0.036
2 x 5	-0.493	-7.554	-0.270	0.451	4.140	-0.144	-3.055	-13.513	-7.052	-0.014
	0.671	4.799	0.454	0.0003	3.400	0.173	-2.371	-12.239	4.746	0.073
3 x 4	0.462	1.868	0.019	-0.145	5.187	-0.024	-4.215	-1.107	2.813	0.012
	1.105	-2.855	-0.039	-0.328	2.488	-0.153	-4.846	-28.270	-0.635	0.116
3 x 5	0.551	2.741	0.085	-0.408	-3.077	-0.002	1.250	15.846	0.780	-0.036
	-0.095	-0.445	-0.049	0.084	-1.812	0.046	2.385	11.942	0.989	-0.026
4 x 5	-2.127	-7.959	0.012	0.381	-5.562	0.056	4.411	-12.667	-5.036	-0.026
	-0.318	-2.415	-0.285	-0.032	-6.698	-0.188	2.273	4.850	-2.996	-0.055
S.E	1.358	5.246	0.260	0.431	4.612	0.228	3.999	13.076	3.364	0.028
	1.229	3.171	0.363	0.332	4.656	0.277	2.984	17.406	3.059	0.046

The estimation of specific combining abilities for reciprocal crosses represent in *Table 8*. At first location the cross KauzxAras produced maximum rca value for grain yield/plant, spike length and harvest index, while at second location the reciprocal cross Iba-95xKlal exhibited the highest rca value for grain yield/plant, weight of spikes/plant and biological yield/plant, while the cross KauzxHasad was the best specific combiner for average spike weight, spike length and number of grains/spike.

Table 8. Estimation of specific combining abilities effect for the reciprocal crosses at both locations (ŕ$_{ij}$) (Kanipanka upper value and Qlyasan lower value)

ŝ$_{ij}$	No. of spikes/plant	Weight of spikes/plant (g)	Average spike weight (g)	Spike length (cm)	No. of grains/spike	Weight of grains/spike (g)	1000-grain weight (g)	Biological yield/plant (g)	Grain yield/plant (g)	Harvest index
2 x 1	2.389	4.360	0.083-	0.200-	5.700-	0.144-	2.938	6.729-	1.125	0.047
	0.722	1.237	0.815-	0.917-	8.617-	0.576-	2.141-	9.113	1.281	0.025-
3 x 1	0.833	3.707	0.063	0.800	2.533-	0.031-	1.594	12.847-	3.320	0.068
	1.944	3.639	0.165-	0.150	2.467-	0.028-	1.272	1.841-	2.853	0.045
4 x 1	0.278	1.994	0.043-	0.193-	8.800-	0.142-	1.825	17.825	1.423-	0.039-
	1.333-	6.869-	0.141-	0.483-	5.667-	0.171-	1.510	15.398-	5.187-	0.025-
5 x 1	0.222-	1.663	0.251	0.317	3.400-	0.348	6.515	0.776-	1.653	0.025-
	0.333	0.307-	0.247-	0.517-	7.433-	0.001	4.761	5.207-	0.337-	0.003
3 x 2	0.722	5.411	0.535-	0.000	6.333-	0.506-	2.079-	15.308	0.659-	0.053-
	0.833-	0.792-	0.719	0.617	3.633	0.560	5.578	6.273-	0.227-	0.006
4 x 2	1.778-	1.784	0.167	0.350-	3.850-	0.101	4.607	6.670	3.909	0.007-
	1.444-	1.476-	0.272	0.183	6.333-	0.161	8.246	15.798-	1.391	0.029
5 x 2	0.945-	3.914-	0.320	0.567-	13.367-	0.117	7.960	7.746-	2.052-	0.019
	1.111-	0.872	0.509	0.300-	0.367-	0.740	7.688	13.369-	1.252	0.054
4 x 3	0.222	6.282-	0.023-	0.790-	1.500-	0.013	1.186	12.099-	0.789-	0.028
	2.833	6.740	0.034	0.043-	2.692	0.189	0.994	5.934-	2.543	0.102
5 x 3	1.278-	2.949-	0.075	0.333-	6.433-	0.130	6.256	6.584-	0.763-	0.009
	1.222-	1.661-	0.144	0.487-	0.167	0.361	4.856	21.784-	0.908	0.072
5 x 4	1.222-	10.104-	0.383-	0.678-	3.161-	0.237-	1.554-	33.821-	8.534-	0.027
	2.444	8.350	0.427	0.050	2.533	0.225	2.235	23.859	6.001	0.006
S.E	1.519	5.865	0.291	0.482	5.156	0.255	4.471	14.619	3.761	0.0313
	1.374	3.545	0.406	0.371	5.205	0.309	3.336	19.461	3.420	0.051

Data in *Table 9* revealed that both additive and non additive gene effects were most important in the inheritance of different characters at both locations. The estimated value of σ²gca for the characters average spike weight, weight of grains/spike and 1000-grain weight was higher than its σ²sca, which indicates the predominance of additive gene effect as the ratio of σ²gca/σ²sca was more than unity, while the rest showed the predominance of non-additive gene action at first location. At the second location the estimated value of σ²gca was higher than its σ²sca for number of spikes/plant, average spike weight and 1000-grain weight. The average degree of dominance value for the characters average spike weight, weight of grains/spike and 1000-grain weight indicated partial dominance, and the rest showed over dominance at the first location, while at the second location the characters number of spikes/plant, average spike weight and 1000-grain weight showed partial dominance. The estimation of heritability in broad sense represent in the same table was found to be moderate to high for almost all characters, while in narrow sense it was found to be low to moderate for all characters at both locations except number of spikes/plant, average spike weight and 1000-grain weight at the first location which was found to be high.

Table 9. *Estimation of some genetic parameters for the studied characters at both locations (Kanipanka upper value and Qlyasan lower value)*

Parameters	No. of spikes/plant	Weight of spikes/plant (g)	Average spike weight (g)	Spike length (cm)	No. of grains/spike	Weight of grains/spike (g)	1000-grain weight (g)	Biological yield/plant (g)	Grain yield/plant (g)	Harvest index
Mse^-	2.306	34.396	0.085	0.232	26.588	0.065	19.989	213.715	14.147	0.001
	1.887	12.565	0.165	0.137	27.096	0.096	11.127	378.718	11.698	0.003
$\sigma^2 gca$	1.395	8.141	0.067	0.030	14.239	0.037	14.901	24.869	2.901	0.00003
	1.629	0.458	0.096	0.034	8.831	0.055	10.644	86.853	1.784	0.001
$\sigma^2 sca = \sigma^2 D$	1.502	64.953	0.009	0.334	16.490	0.008	5.915	356.043	28.204	0.003
	1.546	30.784	0.031	0.188	25.354	0.096	4.001	786.644	29.669	0.003
$\sigma^2 gca / \sigma^2 sca$	0.929	0.125	7.485	0.090	0.863	4.446	2.519	0.070	0.103	0.010
	1.053	0.015	3.089	0.179	0.348	0.570	2.660	0.110	0.060	0.306
$\sigma^2 A$	2.790	16.282	0.134	0.060	28.478	0.074	29.802	49.738	5.801	0.0001
	3.258	0.915	0.192	0.067	17.662	0.109	21.288	173.707	3.567	0.002
$\sigma^2 Dr$	0.275	6.554	0.022	0.129	28.220	0.019	8.887	113.251	4.026	0.001
	1.627	12.069	0.100	0.142	9.935	0.099	16.330	0.368	2.516	0.001
$\bar{A}$	1.038	2.825	0.366	3.337	1.076	0.474	0.630	3.784	3.118	10.004
	0.974	8.202	0.569	2.363	1.694	1.324	0.613	3.010	4.078	1.808
$h^2 b.s$	0.651	0.703	0.628	0.629	0.628	0.560	0.641	0.655	0.706	0.729
	0.718	0.716	0.575	0.651	0.614	0.682	0.694	0.717	0.740	0.679
$h^2 n.s$	0.423	0.141	0.589	0.096	0.398	0.503	0.535	0.080	0.120	0.014
	0.487	0.021	0.495	0.172	0.252	0.363	0.585	0.130	0.079	0.258
$\bar{A}r$	0.444	0.897	0.574	2.076	1.408	0.720	0.772	2.134	1.178	5.847
	0.999	5.135	1.023	2.052	1.061	1.346	1.239	0.065	1.188	0.939
$h^2 bsr$	0.571	0.399	0.649	0.449	0.681	0.590	0.659	0.433	0.410	0.488
	0.721	0.508	0.639	0.604	0.505	0.685	0.772	0.315	0.342	0.537
$h^2 nsr$	0.520	0.284	0.557	0.142	0.342	0.469	0.508	0.132	0.242	0.027
	0.481	0.036	0.420	0.194	0.323	0.359	0.437	0.314	0.201	0.372

The simple correlation coefficient among studied characters for both locations represent in *Table 10*. At first location number of spikes/plant correlated positively and significantly with weight of spikes/plant, biological yield/plant and grain yield/plant 0.498, 0.416 and 0.407 respectively, while it correlated negatively and high significantly with weight of grains/spike -0.670, but negative and highly significant correlation was recorded between number of spikes/plant and 1000-grain weight -0.543. Positive and highly significant correlation was recorded between weight of spikes/plant with biological yield/plant and grain yield/plant 0.802, 0.853 respectively. Spike length correlated positively and significantly with number of grains/spike 0.477. Number of grains/spike showed negative and highly significant with 1000-grain weight -0.644, but weight of grain/spike associated positively and high significantly with 1000-grain weight 0.610. Biological yield/plant recorded negative and highly significant correlation with harvest index -0.691, whilst it correlated positively and highly significant correlation with grain yield/plant. At second location number of spikes/plant showed positive and highly significant correlation with weight of spikes/plant and grain yield/plant 0.618 and 0.675 respectively, but it correlated negatively and significantly with 1000-grain weight -0.444. Weight of spikes/plant recorded positive and highly significant correlation with number of grains/spike and grain yield/plant 0.538 and 0.820 respectively, whilst it correlated positively and significantly with biological yield/plant 0.508. Number of grains/spike recorded positive and significant correlation with weight of grains/spike 0.417. Weight of grains/spike recorded positive and highly significant correlation with biological yield/plant 0.731. Negative and highly significant

correlation was recorded between biological yield/plant and harvest index -0.616, while positive and highly significant correlation was recorded between biological yield/plant and grain yield/plant 0.543. Previously it could be noticed that harvest index was significantly and positively correlated with number of spikes/plant, plant height, spike length, 1000-grain weight and grain weight/spike. Number of spikes/plant was significantly and positively correlated only with plant height, while it was negatively associated with spike length and1000-grain weight as well as positively correlated with grain weight/spike. Moreover, plant height was significantly and positively correlated with 1000-grain weight and grain weight/spike. In the same time, spike Length was significantly and positively correlated with 1000-grain weight and grain weight per spike.1000-grain weight were significantly and positively correlated with grain weight/spike (Mohsin et al., 2009; Fellahi et al., 2013; Motawea, 2017).

Table 10. *The simple correlation coefficient among all pairs of traits at both locations (Kanipanka upper value and Qlyasan lower value)*

Characters	No. of spikes/plant	Weight of spikes/plant (g)	Spike length (cm)	No. of grains/spike	Weight of grains/spike (g)	1000-grain weight (g)	Biological yield/plant (g)	Harvest index	Grain yield/plant (g)
No. of spikes/plant	1.000								
Weight of spikes/plant (g)	0.498	1.000							
	0.624								
Spike length (cm)	-0.190	-0.001	1.000						
	0.137	0.356							
No. of grains/spike	0.021	0.167	0.477	1.000					
	0.280	0.517	0.610						
Weight of grains/spike (g)	-0.670	-0.070	0.374	0.170	1.000				
	-0.226	0.342	0.275	0.513					
1000-grain weight (g)	-0.543	-0.177	-0.069	-0.644	0.610	1.000			
	-0.447	-0.047	-0.149	-0.268	0.669				
Biological yield/plant (g)	0.416	0.802	-0.035	0.033	-0.056	-0.092	1.000		
	0.392	0.503	0.395	0.195	0.074	-0.019			
Harvest index	0.024	-0.298	0.081	0.156	0.020	-0.115	-0.691	1.000	
	0.316	0.193	-0.187	0.187	0.148	-0.025	-0.607		
Grain yield/plant (g)	0.407	0.853	0.031	0.178	0.159	-0.041	0.712	-0.141	1.000
	0.677	0.820	0.223	0.291	0.257	0.072	0.543	0.266	

Data in *Table 11* illustrate the direct and indirect effects of grain yield components in grain yield/plant at both locations. At first location maximum positive direct effect recorded by weight of spikes/plant 0.504 and followed by biological yield/plant 0.493, while maximum negative direct effect was -0.079 recorded by spike length. Maximum positive indirect effect in grain yield/plant was 0.405 recorded by weight of spikes/plant via biological yield/plant, and followed by 0.395 for biological yield/plant via weight of spikes/plant. At second location biological yield/plant recoded maximum positive direct effect in grain yield/plant 1.094 and followed by harvest index 0.983. Maximum negative direct effect was -0.252 recorded by number of grains/spike and followed by -0.208 for number of spikes/plant. Maximum positive indirect effect in grain yield/plant was 0.551 recorded by biological yield/plant via weight of spikes/plant, and followed by 0.433 for biological yield/plant via spike length. Maximum negative indirect effect was -0.664 recorded by biological yield/plant via harvest index, and followed by -0.597 for harvest index via biological yield/plant.

Table 11. *Path coefficient analysis illustrates direct effect (diagonal values) and indirect effect of studied characters in grain yield at both locations (Kanipanka upper value and Qlyasan lower value)*

Characters	No. of spikes/plant	Weight of spikes/plant (g)	Spike length (cm)	No. of grains/spike	Weight of grains/spike (g)	1000-grain weight (g)	Biological yield/plant (g)	Harvest index
No. of spikes/plant	0.164	0.251	0.015	-0.001	-0.262	0.026	0.205	0.008
	-0.208	0.200	0.004	-0.070	-0.004	0.016	0.429	0.311
Weight of spikes/plant (g)	0.082	0.504	0.0001	-0.007	-0.028	0.008	0.395	-0.103
	-0.130	0.321	0.011	-0.131	0.006	0.002	0.551	0.190
Spike length (cm)	-0.031	-0.001	-0.079	-0.019	0.146	0.003	-0.017	0.028
	-0.029	0.114	0.032	-0.154	0.005	0.005	0.433	-0.184
No. of grains/spike	0.003	0.084	-0.038	-0.040	0.067	0.031	0.016	0.054
	-0.058	0.167	0.020	-0.252	0.009	0.010	0.213	0.183
Weight of grains/spike (g)	-0.110	-0.036	-0.030	-0.007	0.391	-0.029	-0.028	0.007
	0.047	0.110	0.009	-0.129	0.018	-0.024	0.081	0.145
1000-grain weight (g)	-0.089	-0.089	0.005	0.026	0.239	-0.048	-0.045	-0.040
	0.093	-0.015	-0.005	0.068	0.012	-0.036	-0.021	-0.024
Biological yield/plant (g)	0.068	0.405	0.003	-0.001	-0.022	0.004	0.493	-0.238
	-0.082	0.162	0.013	-0.049	0.001	0.001	1.094	-0.597
Harvest index	0.004	-0.150	-0.006	-0.006	0.008	0.006	-0.340	0.345
	-0.066	0.062	-0.006	-0.047	0.003	0.001	-0.664	0.983

Discussion

The analysis of variance confirmed highly significant genotype effect for all characters under the study. This provides evidence of the presence of sufficient genetic variability among genotypes at both locations. The mean squares due to genotypes were highly significant for all characters at both locations except number of spikes/plant and average spike weight which was significant at the second location. The results indicated that the data for all traits studied can be analyzed further to estimate general and specific combining ability effects. Similar results reported previously confirmed that both gca and sca variances were significant for most of the characters indicating importance of both additive as well as non-additive components of genetic variance in the control of these traits (Kumar et al., 2011; Burungale et al., 2011; Singh et al., 2013; Mandal et al., 2016; Rahul, 2017; Ljubičić et al., 2017). Combining ability describes the breeding value of parental lines to produce crosses (Romanus et al., 2008). The general combining ability has been equated with additive gene action and specific combining ability with non-additive gene action (Griffing, 1956b).

All characters had shown considerable amount of heterosis over mid parents. These results are in confirmation with Devi et al. (2013) and Rahul and Kandalkar (2018). To improve any character, plant breeders heavily rely on the availability of genetic variability generated from different matting designs. It is also well known phenomena that in a hybridization program, certain crosses pass on more favorable genes than the others. Thus, some cross associations may be superior as compared to their parents for improving any economic traits (Baloch et al., 2016).

Combining ability plays a major role for estimation of inbred in terms of their breeding value, which help to decide suitable breeding method to be used in segregating generation. The gca is primarily a function of additive genetic variance it helps in the selection of good general combiner parents for hybridization (Rahul and Kandalkar, 2018).

The estimation of sca effects for crosses is mainly a function of dominance variance, helps in the identification of superior cross combination for commercial exploitation of heterosis.

The non-additive gene effect controlled the inheritance of most characters. Several researchers reported the predominance of non-additive gene effect (Bhowmik et al., 1991; Khan et al., 1995; Ajmal et al., 2000; Subhani and Chowdhry, 2000; Singh, 2003; Chaman et al., 2005; Heidari et al., 2006; Kumar et al., 2011; Singh et al., 2012a, b), while some workers exhibited the importance of additive type of gene action (Rhahman and Krons, 1991; Bhutta et al., 1997; and Tawfiq et al., 2008).

Beche et al. (2013) and Baloch et al. (2016) reported high values of heritability for grain yield/plant. Grain yield/plant is the prime objective of plant breeders. High estimates of variability and heritability for this trait would be helpful for the breeders to select for the best combinations and to reach at the desirable level of yield potential.

Grain yield/plant exhibited positive and significant correlation with most its important components at both locations. These results are agreement with those reported by Tofiq (2004), Hama-Ali (2006), Hama-Ameen (2008), Mohsin et al. (2009) and Fellahi et al. (2013). Previous researches indicated the positive correlation between grain yield and yield component traits in wheat such as spike number/plant (Mondal and Khajuria, 2001), grains number/spike (Kashif and Khaliq, 2004), 1000-grain weight and biological yield/plant (Akbar et al., 1995). Estimation of the correlation between yield and its components alone is not sufficient to understand the importance of each one of these components in determining the grain yield reported by Bhutta et al. (2005), Anwar et al. (2009) and Ali and Shakor (2012).

Unlike the correlation coefficient, which measures the extent of the relationship, the path coefficient measures the magnitude of direct and indirect contribution of a component character to a complex character and it has been defined as a standardized regression coefficient which splits the correlation coefficient into direct and indirect effects (Arbuckle, 2009). Path coefficients have been used to develop selection criteria for complex traits in several crop species of economic importance such as wheat (Larik, 1979; Aydin et al., 2010). Path analysis grains/spike followed by 1000-grain weight, spikes/plant and harvest index had positive direct effects on grain yield of bread wheat obtained from Majumder et al. (2008). The path coefficient analysis provides more information among variables than do correlation coefficients since this analysis provides the direct effects of specific yield components on yield and indirect effects via other yield components (Arshad et al., 2006). In agricultural, path analysis has been used by plant breeders to assist in identifying traits that are useful as selection criteria to improve crop yield (Dewey and Lu, 1959; Milligan et al., 1990). In a study of path analysis it was indicated that 1000-grain weight had the highest positive direct effect on yield followed by spike length, while plant height and grains/spike had a negative direct effect on yield (Iftikhar, 2012).

Conclusion

It can be stated that enough genetic variation existed among the studied genotypes for most of the studied traits. Additive and non-additive gene effects were involved in the expression of all traits. Thereafter, it is recommended that breeding methods, which make the best use of additive effects such as direct selection, are applied for those traits where dominant effects are negligible. However, using hybrid vigor will be more

efficient than selection for those traits that show high levels of dominant effects. Proportion of variances due to sca confirmed the predominance of dominant genes in the expression of majority of the traits. Among the parents, the Klal parent at both locations were the best general combiner for grain yield and some of its components, and thus can reliably be used in a hybridization program so as to select the desirable plants from segregating populations. So, it is concluded that this parent may be used in breeding program to develop high yielding wheat varieties. The cross Kauz×Klal was the best specific combiner for grain yield/ plant, but the cross Aras×Iba-95 was the best specific combiner for most grain yield components at the first location, while at the second location the cross Aras×Iba-95 was the best specific combiner for grain yield and most its components that can be used in developing cross varieties. The characters with high estimates of heritability indicated the presence of additive genes effect in their inheritance, and suggested reliable wheat improvement through selection.

Recommendation

Klal parent was a good general combiner for grain yield/plant, biological yield/plant, number of spikes/plant, weight of spikes/plant and number of grains/spike, which could be used in the development of high-yielding varieties using selection from promising segregating cross generations.

It was recommended to conduct a favourable selection method to the cross Aras×Iba-95 in the future to develop new common wheat variety.

The varieties should be tested at different locations along with growth seasons to evaluate these traits, so that these traits are more inconsistent in different growth seasons.

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