

## ESTIMATION OF SOME GENETIC PARAMETERS USING LINE×TESTER ANALYSIS OF COMMON WHEAT (*TRITICUM AESTIVUM* L.)

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**Abstract.** Seven common wheat (*Triticum aestivum* L.) cultivars were crossed in a line×tester mating design. The 12 F<sub>1</sub> and their parents were evaluated using a Completely Randomized Block Design (CRBD) replicated three times in Kurdistan Reign-Iraq at two different locations, first Kanipanka in Sharazoor Valley, and the second was Qlyasan Agricultural Research Station, University of Sulaimani, during the winter season of 2017-2018. The Least Significant Differences Test (LSD) at (P≤0.05) was carried out to compare the means of the characters. The results confirmed that sufficient genetic variability was included with all traits studied. The cross Aras×Iba-95 at Kanipanka location and Klal×Cham-6 at Qlyasan location had better grain yield/plant mean than their parents. The cross Aras×Iba-95 and Klal×Cham-6 at both locations exhibited maximum positive heterosis for grain yield/plant and most of their components. Line parents Aras and Klal are good general combiners for grain yield/plant and most its components at both locations respectively. The cross Aras×Iba-95 is the better specific combiner to increase grain yield/plant at both sites. The superiority of non-additive type of gene actions in controlling the inheritance of these characters was confirmed.

**Keywords:** *heterosis, combining ability, heritability, gene action*

### Introduction

Bread wheat (*Triticum aestivum* L.) is the most important crop being one-fifth of the total calories for the population of the world (Sehgal et al., 2015). Wheat cultivation represents approximately 19% of global main cereal crop production (Todorovska et al., 2009). Considerable cultivated species of wheat include: *Triticum aestivum*, which is a hexaploid species and is widely seeded in the world (Moon, 2008). It has been imposed that the world population would increase to over 9 billion by the year 2050 (United Nations, Population Division, 2015). The population growth will increase the request for wheat crop by 60% compared with current years. To meet this demand, global annual yield increases have to rise from the current level of 1% per year to 1.6% per year until 2050 (Wheat, 2014). For this cause, the breeders have to share demanding need to increase yield potential of wheat by creating new wheat varieties with likable genetic makeup (Erkul et al., 2010). This could be reached by searching maximum genetic potential from available wheat germplasm (Khan et al., 2007). Common wheat is one of the earliest domesticated crops. It is a prime staple food for around 40% of the world's population (Kuzmanovic et al., 2014). Wheat provides about 20% of the calorific input for the world population and, for cereal crops has the third highest global production after maize and rice (FAO, 2014). Wheat is widely cultivated in various regions of the world, being well suited for growth in area between latitudes of 30° and 60° N and 27° and 40° S (Curtis, 2002). 349 million

tons of this crop was harvested in 2016, and more than 220 million hectare of the world was cultivated by wheat. Due to the raising of the world population, wheat plays a main role in the national economy of developing countries. Wheat is one of the major food grain crops in the world, as it provides 20% of the total energy and protein in the human diet (FAO, 2016). Most of wheat planted areas are located in arid or semi-arid regions where abiotic stresses, especially drought stress, are a main constraint for wheat production (Tahmasebi et al., 2014). Current wheat production does not meet global demand due to the declining arable land area, increasing global population, and the effects of climate condition change on the environment (Tester and Langridge, 2010; Altieri and Nicholls, 2017). To meet the need for population growth, the country's wheat requirement by 2030 has been estimated at 100 million metric tons and to reach this goal, wheat productivity has to be increased at the rate of <1% per annum and this can be fulfilled through horizontal approach i.e. by rising area under cultivation or through varietal/hybrid improvement, which is one of the substantial tools to take a volume jump in production and productivity under various agro-climatic conditions (Rahul, 2017). Developing hybrid wheat varieties with desirable traits require a thorough knowledge about the existing genetic variability (Maniee et al., 2009; Kahrizi et al., 2010a,b). The more the genetically diverse parents, the greater the chances of obtaining higher heterotic expression in F<sub>1</sub>s and broad spectrum of variability in segregating population (Shekhawat et al., 2001). The line × tester analysis method proposed by Kempthorne (1957) is one of the powerful tools available to evaluate the combining ability effects and aids in selecting desirable parents and crosses for exploitation in pedigree breeding (Basbag, 2007; Jain and Sastry, 2012; Rashid et al., 2013). Performances themselves do not necessarily reveal which parents are best or weak combiners. To get up this difficulty, it is necessary to collect information on the nature of gene effects. General combining ability is assigned to additive type of gene effects, while specific combining ability is attributed to non-additive gene works. Non-additive gene type of actions is not reliably fixable whereas additive type of gene effects or complementary type epistatic gene interactions is reliably fixable (Xiang and Li, 2001; Yan and Hunt, 2002; Iqbal et al., 2007). The objectives of this study are to estimate the combining ability, to estimate the nature and magnitude of gene actions, to evaluate heterosis and heritability for yield and yield related traits in a line × tester method in bread wheat.

## Materials and methods

This study was carried out at two different 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' 30.7"; N, Long 45° 21' 9.92"; E, 765 masl) 2 km North West of Sulaimani City, during 2017-2018. The experimental material comprises seven bread wheat (*Triticum aestivum* L.) genotypes. Four genotypes (Aras, Hasad, Kauz and Klal) were used as females, hereafter designated as lines, and three genotypes (Iba-95, Cham-6 and Saber beg) were used as males, fixed as testers. The seven parents were crossed to produce 12 F<sub>1</sub> crosses according to the line×tester mating design developed by Kempthorne (1957). F<sub>1</sub> seeds were sown in the field, along with their parents, in Complete Randomize Block Design (CRBD) with three replication. Each plot comprised one row of 2 m length with space

of 40 cm between rows and seeds were placed 15 cm apart. Five competitive plants (excluding border plants) were chosen and data were recorded for:

1-Evaluated 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) and effects, Specific Combining Ability (sca) and effects, Heterosis percentage as the  $F_1$ s deviation from average parental values, Heritability in Broad Sense, Heritability in Narrow Sense, Average Degree of Dominance ( $\bar{a}$ ).

3-Association analysis and path coefficient analysis.

The collected data were submitted to analysis of variance as proposed by Steel and Torrie (1980) to estimate significant differences among genotypes. Combining ability effects are very important genetic parameters in determining the next phase of breeding programs. They were computed according to the line×tester method (Singh and Chaudhary, 1985).

***Climate conditions of Sulaimani region***

The climate of Sulaimani governorate is semi-arid environment: wet and cold in winter dry and hot in summer; During July and August, the average temperature is between 39-43°C, and overwhelmingly amount to 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			
	Min Temp.(C°)	Max Temp.(C°)	Avg. Temp.(C°)	Rainfall (mm)	Min Temp.(C°)	Max 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***

The soil samples for both locations were taken from both sites in Sulaimani governorate in Kurdistan region, Iraq. It was obtain from surface (0-30 cm), and air dried which 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 <sup>-1</sup>	EC <sub>e</sub> g kg <sup>-1</sup>	OM Cmol <sub>c</sub> kg <sup>-1</sup>	CEC mg kg <sup>-1</sup>	Available P	CaCO <sub>3</sub> equivalent g kg <sup>-1</sup>	
						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 <sup>-1</sup>							
	Ca <sup>2+</sup>	Mg <sup>2+</sup>	Na <sup>+</sup>	K <sup>+</sup>	HCO <sub>3</sub> <sup>-</sup>	Cl <sup>-</sup>	SO <sub>4</sub> <sup>2-</sup>
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 <sup>-1</sup>							
	Zn		Cu		Fe		
Kanipanka	1.563		5.07		5.15		
Qlyasan	0.450		4.96		3.23		

## Results

The analysis of variance ratified highly significant genotype effect for all characters studied. This confirmed the presence of enough genetic variability among genotypes at both locations. The mean squares for parents was highly significant for number of spikes/plant, average spike weight, biological yield/plant and harvest index, but it was significant for spike length, number of grains/spike, weight of grains/spike and 1000-grain weight, while for other characters it was not significant at the first location. At the second location the mean squares for parents was highly significant for all characters except biological yield/plant, grain yield/plant and harvest index which was not significant. The mean squares due to crosses were highly significant for all characters at both locations with the exception of number of spikes/plant and average spike weight which was significant at the second location (*Table 3*).

The mean performance of parents and F<sub>1</sub>s crosses for all characters were represented in *Table 4*. At the first location the cross Aras×Iba-95 recorded the highest value for grain yield/plant 53.827 g, and some of its components such as number of spikes/plant, weight of spikes/plant and biological yield/plant with 30.176, 68.915 g and 157.762, respectively. The cross Kauz×Iba-95 exhibited maximum value for average spike weight, weight of grains/spike and harvest index 4.941 g, 3.695 g and 0.438, respectively. Regards to the parental performance at the same location the line parent Hasad produced the highest value for average spike weight, 1000-grain weight and harvest index 4.463 g, 53.468 g and 0.466, respectively, but the tester parent Saber beg produced the maximum weight for grain yield/plant 34.493 g and most its components such as number of spikes/plant, weight of spikes/plant, spike length and biological yield/plant 26.167, 53.748 g, 12.420 cm and 162.153 g, respectively. At the second location the cross Klal×Cham-6 produced the highest value for grain yield/plant and number of spikes/plant reached 23.422 g and 9.333 spikes, respectively. The cross Hasad×Iba-95 produced the highest amount for average spike weight, weight of grains/spike and harvest index reached 4.540 g, 3.439 g and 0.541, respectively. The

line parent Hasad showed maximum value for weight of spikes/plant, average spike weight, weight of grains/spike, 1000-grain weight and biological yield/plant with 34.018, 4.783, 3.627, 58.691 and 125.960 g, respectively. Maximum grain yield/plant recorded by the tester parent Cham-6 with 21.185 g.

**Table 3.** ANOVA table for the studied characters (1<sup>st</sup> location upper value and 2<sup>nd</sup> location lower value)

S.O.V	d.f	M.S									
		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	Grain yield/plant	Harvest index
blocks	2	0.070	10.306	0.215	0.345	127.753	0.128	2.240	307.184	63.330	0.005
		0.189	61.171	0.128	1.009	31.498	0.087	2.520	1214.901	6.308	0.003
Genotypes	18	93.041**	464.387**	1.408**	1.753**	334.113**	0.973**	76.626**	3192.694**	246.838**	0.019**
		7.504**	61.797**	0.834**	2.544**	199.325**	0.614**	198.271**	2232.995**	21.414**	0.038**
Parents	6	91.123**	277.571n.s	0.842**	0.9593*	234.524*	0.655*	66.086*	3462.575**	48.537n.s	0.030**
		14.540**	61.770**	1.132**	1.371**	278.275**	0.760**	188.862**	842.537n.s	3.422n.s	0.002n.s
P*C	1	1.320n.s	298.983n.s	0.238n.s	2.461**	0.541n.s	0.255n.s	123.451*	622.038n.s	111.556n.s	0.002n.s
		4.035n.s	22.784n.s	0.017n.s	1.264n.s	22.060n.s	0.080n.s	5.125n.s	11351.405**	16.808*	0.159**
Crosses	11	102.426**	581.323**	1.822**	2.121**	418.760**	1.212**	78.119**	3279.183**	367.301**	0.015**
		3.982*	65.358**	0.746*	3.300**	172.377**	0.583**	220.962**	2162.480**	31.646**	0.047**
Lines	3	146.488**	1530.861**	2.121*	4.120**	690.911*	1.160*	137.449*	10083.346**	994.871**	0.006n.s
		0.546n.s	56.173n.s	0.125n.s	3.701**	288.908*	0.035n.s	229.919*	2297.184n.s	34.161*	0.024n.s
Testers	2	67.000*	197.865n.s	4.721**	1.749*	711.784*	3.510**	110.988n.s	42.918n.s	280.862n.s	0.032*
		9.215*	80.703*	1.834*	2.724*	26.134n.s	1.438*	440.316*	3039.766n.s	35.245*	0.085**
L*T	6	92.204**	234.373n.s	0.707*	1.246**	185.010n.s	0.472n.s	37.497n.s	955.856n.s	82.330n.s	0.013**
		3.956*	64.835**	0.694*	3.291**	162.859*	0.571**	143.365*	1802.699*	29.189**	0.046**
Error	36	10.857	157.351	0.229	0.301	90.950	0.202	22.494	797.276	72.233	0.003
		1.508	13.375	0.278	0.331	51.654	0.147	44.161	673.454	3.901	0.004

Data in Table 5 illustrate the estimation of heterosis values determined as the percentage of F1s deviation from mid parental value. The cross Aras×Iba-95 showed maximum positive heterosis values for grain yield/plant 129.087% and some its components such as number of spikes/plant, weight of spikes/plant and biological yield/plant reached 129.114, 126.554 and 119.050% respectively, while the cross Kauz×Saber beg showed maximum negative heterosis value for grain yield/plant -54.917% and most its components such as weight of spikes/plant, average spike weight, spike length, number of grains/spike, weight of grains/spike and biological yield/plant reached -59.244, -35.415, -10.034, -44.598, -38.727 and -53.409% respectively at the first location, while at the second location maximum positive heterosis for grain yield/plant was 18.137% recorded by the cross Klal×Cham-6, but the cross Aras×Saber beg produced maximum positive heterosis for average spike weight, number of grains/spike and weight of grains/spike reached 19.432, 39.719 and 24.923%, respectively. The cross Hasad×Saber beg produced maximum negative value for grain yield/plant -41.316% and some its components such as weight of spikes/plant, average spike weight, weight of grains/spike and 1000-grain weight reached -51.048, -30.277, -34.955 and -23.423%, respectively.

**Table 4.** Averages of studied characters for parents and their  $F_1$  crosses (1<sup>st</sup> location upper value and 2<sup>nd</sup> location 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 5	30.167	68.915	4.545	12.433	67.867	3.378	49.851	157.762	53.827	0.362
	8.000	31.132	3.747	8.400	64.200	2.989	46.566	42.358	20.407	0.489
1 x 6	14.667	48.114	4.465	12.300	68.267	3.252	48.912	146.752	40.226	0.277
	9.000	26.958	3.405	9.367	50.533	2.584	51.102	79.728	15.782	0.202
1 x 7	15.000	44.165	4.011	13.100	68.867	2.886	41.912	121.195	33.655	0.312
	8.833	22.960	3.591	11.367	69.533	2.720	39.540	67.511	17.510	0.274
2 x 5	15.500	45.955	4.714	13.261	63.167	3.345	53.710	100.730	33.517	0.331
	6.833	19.775	4.540	9.367	59.867	3.439	57.385	48.059	16.983	0.541
2 x 6	15.500	54.517	4.789	13.200	59.000	3.547	61.422	116.190	41.957	0.358
	9.167	28.958	4.333	10.267	51.600	3.354	66.413	61.356	20.737	0.339
2 x 7	23.167	49.395	3.453	12.000	49.733	2.321	47.470	124.278	33.105	0.278
	8.167	15.612	2.667	10.400	49.400	1.818	36.963	67.733	12.207	0.198
3 x 5	10.167	31.282	4.941	12.200	67.800	3.695	54.415	56.940	24.360	0.438
	6.000	17.997	3.729	10.133	53.200	2.778	52.581	43.049	16.231	0.385
3 x 6	12.833	37.498	4.331	12.367	57.333	3.312	58.090	73.510	25.387	0.357
	9.333	24.983	3.980	10.933	64.867	3.056	47.225	116.105	22.735	0.196
3 x 7	11.167	17.980	2.537	10.700	32.133	1.727	53.629	65.773	14.285	0.217
	9.167	26.847	3.148	11.667	53.867	2.388	44.900	43.736	20.818	0.483
4 x 5	17.333	27.690	3.353	11.067	52.000	2.493	48.914	97.763	23.667	0.247
	9.000	26.582	3.648	11.633	68.267	2.592	38.076	115.053	20.943	0.230
4 x 6	12.167	29.710	3.542	12.033	51.067	2.511	49.971	61.643	23.797	0.372
	9.333	27.860	3.923	11.500	66.867	3.027	45.269	100.662	23.422	0.243
4 x 7	9.833	32.382	3.009	11.113	40.800	2.095	51.066	95.213	18.985	0.207
	6.833	22.897	3.538	9.833	65.333	2.593	41.114	67.688	18.512	0.273
Line 1	15.500	29.352	3.100	11.033	41.133	2.117	52.338	59.797	22.222	0.414
	8.500	22.738	3.148	10.100	47.600	2.392	50.764	97.788	20.060	0.210
Line 2	10.833	34.978	4.463	11.367	60.267	3.218	53.468	87.040	28.780	0.466
	8.167	34.018	4.783	10.900	62.200	3.627	58.691	125.960	20.572	0.175
Line 3	10.833	34.483	4.453	11.367	61.067	3.317	51.508	120.190	28.878	0.252
	6.000	21.937	3.461	9.767	51.533	2.613	50.665	82.145	18.703	0.248
Line 4	17.333	24.616	3.677	12.400	58.267	2.555	43.873	115.332	25.085	0.223
	9.000	22.447	3.706	11.167	64.867	2.778	42.848	77.243	18.467	0.243
Tester 5	10.833	31.486	4.165	11.367	69.533	3.088	44.944	84.245	24.771	0.293
	8.500	25.257	3.923	11.667	75.400	2.778	36.563	111.882	19.863	0.184
Tester 6	15.667	42.536	3.618	12.067	51.733	2.576	51.624	129.536	29.417	0.230
	8.500	23.673	3.675	11.100	56.000	2.753	49.100	104.700	21.185	0.202
Tester 7	26.167	53.748	3.404	12.420	54.933	2.319	42.182	162.153	34.493	0.218
	13.333	29.765	2.866	10.300	51.933	1.963	37.847	102.673	21.030	0.218
LSD (p≤0.05)	5.456	20.772	0.792	0.909	15.792	0.744	7.854	46.757	14.074	0.093
	6.056	0.874	0.953	11.901	0.634	11.004	42.973	3.270	0.105	2.034

**Table 5.** % Heterosis values for F1 crosses (1<sup>st</sup> location upper value and 2<sup>nd</sup> location 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	Grain yield/plant	Harvest index
1 x 5	129.114	126.554	25.124	11.012	22.651	29.790	2.488	119.050	129.087	2.499
	-5.882	29.729	5.997	-22.818	4.390	15.616	6.648	-59.595	2.229	148.223
1 x 6	-5.882	33.859	32.917	6.494	47.021	38.580	-5.905	55.020	55.799	-13.886
	5.882	16.171	-0.195	-11.635	-2.445	0.454	2.343	-21.251	-23.474	-1.859
1 x 7	-28.000	6.294	23.350	11.711	43.373	30.117	-11.317	9.209	18.681	-1.108
	-19.084	-12.539	19.432	11.438	39.719	24.923	-10.756	-32.644	-14.772	28.093
2 x 5	43.077	38.285	9.256	16.666	-2.671	6.094	9.153	17.617	25.177	-12.868
	-18.000	-33.277	4.296	-16.987	-12.984	7.390	20.489	-59.587	-15.997	201.578
2 x 6	16.981	40.663	18.528	12.660	5.357	22.441	16.891	7.297	44.189	2.972
	10.000	0.390	2.467	-6.667	-12.690	5.141	23.226	-46.800	-0.679	79.505
2 x 7	25.225	11.342	-12.228	0.897	-13.657	-16.176	-0.743	-0.256	4.641	-18.771
	-24.031	-51.048	-30.277	-1.887	-13.435	-34.955	-23.423	-40.749	-41.316	0.508
3 x 5	-6.154	-5.163	14.650	7.331	3.828	15.362	12.833	-44.295	-9.187	60.636
	-17.241	-23.729	1.011	-5.443	-16.176	3.054	20.562	-55.626	-15.831	78.378
3 x 6	-3.145	-2.627	7.310	5.548	1.655	12.398	12.651	-41.127	-12.903	48.374
	28.736	9.552	11.547	4.792	20.645	13.902	-5.328	24.279	13.993	-13.037
3 x 7	-39.640	-59.244	-35.415	-10.034	-44.598	-38.727	14.482	-53.409	-54.917	-7.660
	-5.172	3.852	-0.495	16.279	4.124	4.371	1.456	-52.671	4.790	107.439
4 x 5	23.077	-1.287	-14.481	-6.872	-18.623	-11.626	10.146	-2.029	-5.059	-4.393
	2.857	11.446	-4.361	1.898	-2.662	-6.695	-4.103	21.669	9.279	7.656
4 x 6	-26.263	-11.514	-2.892	-1.635	-7.152	-2.131	4.653	-49.652	-12.675	64.480
	6.667	20.815	6.296	3.293	10.645	9.474	-1.534	10.652	18.137	9.064
4 x 7	-46.847	-24.017	-20.504	-6.558	-34.440	-22.515	17.224	-22.716	-35.931	-19.035
	-37.405	-16.772	4.233	-10.470	2.618	9.408	10.507	-36.904	-9.464	35.543
S.E	13.844	13.677	6.152	2.771	7.986	7.080	3.357	14.339	14.425	9.266
	5.534	7.036	3.443	3.447	4.722	4.445	4.131	12.584	5.307	25.955

Table 6 clarified the general combining ability effect of parents. Combining ability plays important role in the estimation of inbred in terms of their breeding values, and this will help to decide efficient breeding method to be applied in segregating generation. Data in the same table revealed that the line parent Aras recorded significant and positive gca effect for grain yield and most its components viz. number of spikes/plant, weight of spikes/plant, number of grains/spike and biological yield/plant, while the tester parent Iba-95 gave significant and positive gca effect for average spike weight, weight of grains/spike and harvest index. Most negative gca effect values for the characters recorded by line parent Kauz and tester parent Saber beg at the first location. At the second location the highest positive and significant gca effect values for grain yield/plant and some its components such as spike length, number of grains/spike and biological yield/plant recorded by the line parent Klal, but the tester parent Cham-6 exhibited the highest positive and significant gca values for number of spikes/plant,

weight of spikes/plant and weight of grains/spike. Maximum negative gca effect values for most characters recorded by the line parent Hasad and the tester parent Saber beg.

**Table 6.** Estimation of gca effect for the parents (1<sup>st</sup> location upper value and 2<sup>nd</sup> location lower value)

Parents	No. of spikes/plant	Weight of spikes/plant	Average spike weight	Spike length	No. of grains/spike	Weight of grains/spike	1000-grain weight	Biological yield/plant	Grain yield/plant	Harvest index
1	4.319	13.098	0.366	0.463	11.831	0.292	-4.722	40.424	12.005	0.004
	0.306	2.637	-0.106	-0.694	1.628	-0.014	-1.525	-7.887	-0.958	0.001
2	2.431	9.322	0.344	0.672	0.797	0.191	2.587	12.254	5.629	0.009
	-0.250	-2.932	0.159	-0.394	-6.172	0.092	6.326	-12.037	-2.215	0.038
3	-4.236	-11.714	-0.038	-0.392	-4.081	0.031	3.765	-36.071	-9.220	0.024
	-0.139	-1.104	-0.068	0.506	-2.483	-0.038	0.974	-3.456	1.071	0.034
4	-2.514	-10.706	-0.673	-0.743	-8.547	-0.514	-1.630	-16.606	-8.414	-0.038
	0.083	1.399	0.015	0.583	7.028	-0.041	-5.775	23.381	2.102	-0.073
S.E lines	1.098	4.181	0.159	0.183	3.179	0.150	1.581	9.412	2.833	0.019
	0.409	1.219	0.176	0.192	2.396	0.128	2.215	8.650	0.658	0.021
5	2.667	2.827	0.414	0.092	6.206	0.348	0.109	1.820	3.279	0.031
	-0.847	-0.509	0.229	-0.522	1.589	0.171	1.391	-8.957	-0.216	0.090
6	-1.833	1.826	0.308	0.327	2.414	0.275	2.985	-1.955	2.278	0.028
	0.903	2.810	0.223	0.111	-1.328	0.227	5.241	18.376	1.812	-0.076
7	-0.833	-4.653	-0.722	-0.420	-8.619	-0.623	-3.094	0.136	-5.556	-0.060
	-0.056	-2.301	-0.451	0.411	-0.261	-0.398	-6.632	-9.419	-1.595	-0.014
S.E testers	0.951	3.621	0.138	0.158	2.753	0.130	1.369	8.151	2.453	0.016
	0.354	1.056	0.152	0.166	2.075	0.111	1.918	7.491	0.570	0.018

Data represent in *Table 7* explain the sca effect of the F<sub>1</sub> crosses at both locations, sca is mainly a function of dominance variance, it helps in the identification of superior cross combination of heterosis. At the first location the cross Aras×Iba-95 was the best specific combiner for number of spikes/plant, weight of spikes/plant, biological yield/plant and grain yield/plant, while the cross Kauz×Iba-95 was the better specific combiner for average spike weight, number of grains/spike, weight of grains/spike and harvest index. At the second location the cross Aras×Iba-95 was the best specific combiner for grain yield/plant, while the cross Hasad×Iba-95 was the best specific combiner for average spike weight, weight of grains/spike and harvest index. The cross Kauz×Cham-6 was the best specific combiner for number of grains/spike and biological yield/plant.

Some genetic parameters present in *Table 8* for both locations. At the first location the variance of sca effect was greater than those of gca effect for all characters except biological yield/plant and grain yield/plant, indicating to the importance of non additive gene effect in the inheritance of these characters, but for biological yield/plant and grain yield/plant the additive gene effect is more important in the inheritance of both. At the second location it was indicated that the magnitude of sca variance is larger than those of gca effect for all characters, confirming the importance of non additive gene effect in the inheritance of these characters. The average degree of dominance values are more than one for most characters at both locations.

**Table 7.** Estimation of sca effect for the F1 crosses (1<sup>st</sup> location upper value and 2<sup>nd</sup> location lower value)

Crosses	No. of spikes/plant	Weight of spikes/plant	Average spike weight	Spike length	No. of grains/spike	Weight of grains/spike	1000-grain weight	Biological yield/plant	Grain yield/plant	Harvest index
1 x 5	7.556	12.357	-0.209	-0.270	-6.672	-0.142	2.850	14.039	7.979	0.014
	0.236	4.624	-0.063	-0.789	1.189	0.053	-0.561	-11.884	2.723	0.077
1 x 6	-3.444	-7.444	-0.183	-0.638	-2.481	-0.195	-0.965	6.804	-4.621	-0.068
	-0.514	-2.868	-0.399	-0.456	-9.561	-0.407	0.125	-1.847	-3.929	-0.043
1 x 7	-4.111	-4.913	0.393	0.908	9.153	0.337	-1.886	-20.844	-3.358	0.055
	0.278	-1.755	0.462	1.244	8.372	0.354	0.436	13.731	1.206	-0.034
2 x 5	-5.222	-6.827	-0.019	0.348	-0.339	-0.074	-0.600	-14.822	-5.955	-0.023
	-0.375	-1.165	0.465	-0.122	4.656	0.398	2.407	-2.034	0.557	0.092
2 x 6	-0.722	2.735	0.163	0.053	-0.714	0.201	4.236	4.413	3.486	0.008
	0.208	4.700	0.264	0.144	-0.694	0.256	7.585	-16.070	2.283	0.056
2 x 7	5.944	4.093	-0.144	-0.401	1.053	-0.127	-3.636	10.410	2.469	0.015
	0.167	-3.535	-0.729	-0.022	-3.961	-0.654	-9.992	18.103	-2.840	-0.148
3 x 5	-3.889	-0.465	0.590	0.352	9.172	0.436	-1.072	-10.287	-0.263	0.069
	-1.319	-4.770	-0.119	-0.256	-5.700	-0.134	2.955	-15.624	-3.481	-0.060
3 x 6	3.278	6.752	0.087	0.284	2.497	0.126	-0.273	10.058	1.765	-0.008
	0.264	-1.102	0.138	-0.089	8.883	0.088	-6.252	30.099	0.995	-0.083
3 x 7	0.611	-6.287	-0.677	-0.636	-11.669	-0.561	1.345	0.230	-1.503	-0.061
	1.056	5.872	-0.020	0.344	-3.183	0.046	3.297	-14.474	2.486	0.143
4 x 5	1.556	-5.064	-0.362	-0.430	-2.161	-0.221	-1.178	11.070	-1.761	-0.060
	1.458	1.311	-0.284	1.167	-0.144	-0.317	-4.801	29.542	0.201	-0.109
4 x 6	0.889	-2.043	-0.067	0.302	0.697	-0.131	-2.998	-21.275	-0.630	0.069
	0.042	-0.729	-0.003	0.400	1.372	0.063	-1.459	-12.182	0.651	0.071
4 x 7	-2.444	7.108	0.429	0.128	1.464	0.352	4.177	10.204	2.392	-0.009
	-1.500	-0.581	0.287	-1.567	-1.228	0.254	6.260	-17.360	-0.852	0.038
S.E	1.902	7.242	0.276	0.317	5.506	0.259	2.738	16.302	4.907	0.032
	0.709	2.111	0.305	0.332	4.149	0.221	3.837	14.983	1.140	0.036

The simple correlation coefficient among studied characters represent in *Table 9* at both locations. At the first location the character number of spikes/plant recorded positive and highly significant correlation with weight of spikes/plant, biological yield/plant and grain yield/plant 0.721, 0.709 and 0.681, respectively. Weight of spikes/plant recorded positive and highly significant correlation with spike length, biological yield/plant and grain yield/plant 0.644, 0.760 and 0.939, respectively. Spike length exhibited positive and highly significant correlation with grain yield/plant 0.652, but it recorded positive and significant correlation with number of grains/spike and weight of grains/spike 0.597 and 0.549, respectively. Positive and highly significant correlation was recorded between number of grains/spike and each of grain weight/spike and grain yield/plant 0.849 and 0.609, respectively. Positive and significant correlation was recorded between weight of grains/spike and each of harvest index and grain yield/plant with 0.531 and 0.551, respectively. Positive and highly significant correlation was recorded between biological yield/plant and grain yield/plant

0.755. At the second location the character number of spikes/plant correlated positively and significantly with weight of spikes/plant 0.492, while weight of spikes/plant recorded positive and highly significant correlation with grain yield/plant 0.677. Positive and significant correlation recorded between spike length and biological yield/plant 0.487. Positive and highly significant correlation was recorded between weight of grains/spike and 1000-grain weight 0.691.

**Table 8.** Estimation of some genetic parameters (1<sup>st</sup> location upper value and 2<sup>nd</sup> location lower value)

Parameters	No. of spikes/plant	Weight of spikes/plant	Average spike weight	Spike length	No. of grains/spike	Weight of grains/spike	1000-grain weight	Biological yield/plant	Grain yield/plant	Harvest index
$\sigma^2_e$	10.857	157.351	0.229	0.301	90.950	0.202	22.494	797.261	72.233	0.003
	1.508	13.375	0.278	0.331	51.654	0.147	44.161	673.454	3.901	0.004
$\sigma^2_{gca}$	0.441	14.966	0.048	0.038	10.083	0.032	1.752	100.222	12.293	0.00007
	0.001	0.023	0.002	0.0004	0.411	0.0005	3.347	15.520	0.106	0.00005
$\sigma^2_{sca} = \sigma^2_D$	27.115	25.674	0.159	0.315	31.353	0.090	5.001	52.860	3.366	0.003
	0.816	17.153	0.139	0.987	37.068	0.142	33.068	376.415	8.429	0.014
$\sigma^2_{gca} / \sigma^2_{sca}$	0.016	0.583	0.302	0.120	0.322	0.354	0.350	1.896	3.653	0.023
	0.001	0.001	0.016	0.0004	0.011	0.003	0.101	0.041	0.013	0.003
$\sigma^2_A$	0.882	29.933	0.096	0.076	20.167	0.064	3.505	200.444	24.586	0.0001
	0.002	0.045	0.004	0.001	0.821	0.001	6.695	31.040	0.212	0.0001
$\bar{a}$	7.842	1.310	1.820	2.888	1.763	1.680	1.689	0.726	0.523	6.593
	26.816	27.576	7.870	51.017	9.502	16.988	3.143	4.925	8.918	16.989
$h^2_{b.s}$	0.721	0.261	0.528	0.564	0.362	0.433	0.274	0.241	0.279	0.520
	0.352	0.563	0.339	0.749	0.423	0.493	0.474	0.377	0.689	0.778
$h^2_{n.s}$	0.023	0.141	0.199	0.109	0.142	0.179	0.113	0.191	0.245	0.023
	0.001	0.001	0.011	0.001	0.009	0.003	0.080	0.029	0.017	0.005

**Table 9.** The simple correlation coefficient among all pairs of traits at both locations (1<sup>st</sup> location upper value and 2<sup>nd</sup> location 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)	0.721	1.000							
	0.492								
Spike length(cm)	0.345	0.644	1.000						
	0.312	0.047							
No. of grains/spike	0.120	0.467	0.597	1.000					
	-0.015	0.215	0.416						
Weight of grains/spike(g)	-0.071	0.424	0.550	0.850	1.000				
	-0.313	0.381	-0.061	0.372					
1000-grain weight (g)	-0.354	-0.020	0.008	-0.184	0.349	1.000			
	-0.311	0.203	-0.365	-0.401	0.691				
Biological yield/plant(g)	0.709	0.760	0.431	0.356	0.127	-0.415	1.000		
	0.384	0.358	0.487	0.278	0.052	-0.182			
Harvest index	-0.142	0.107	0.168	0.323	0.531	0.442	-0.431	1.000	
	-0.299	-0.061	-0.399	-0.067	0.261	0.300	-0.819		
Grain yield/plant(g)	0.681	0.939	0.652	0.609	0.551	-0.031	0.756	0.179	1.000
	0.400	0.677	0.351	0.335	0.357	0.097	0.479	-0.073	

Data represent in *Table 10* illustrate the path coefficient analysis, indicating to the direct and indirect effects on grain yield. At first location the highest positive direct effect was recorded by number of grains/spike reached 0.947 and followed by 1000-grain weight with 0.589, while the highest negative direct effect recorded by weight of grains/spike reached -0.735. The highest positive indirect effect was 0.805 recorded by number of grains/spike via weight of grains/spike and followed by number of grains/spike via spike length. The highest negative indirect effect in grain yield was -0.624 recorded by weight of grains/spike via number of grains/spike and followed by -0.403 for weight of grains/spike via spike length. At second location the highest positive direct effect in grain yield recorded by 1000-grain weight reached 1.425 and followed by number of grains/spike with 1.072, whilst only weight of grains/spike recorded negative direct effect reached -1.387. Maximum positive indirect effect was 0.984 recorded by 1000-grain weight via weight of grains/spike and the highest negative indirect effect was -0.958 recorded by weight of grains/spike via 1000-grain weight.

**Table 10.** Path coefficient analysis Illustrates direct effect (diagonal values) and indirect effect of studied characters in grain yield at both locations (1<sup>st</sup> location upper value and 2<sup>nd</sup> location 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	0.205	0.201	-0.006	0.113	0.052	-0.206	0.356	-0.031
	0.081	0.171	0.051	-0.017	0.434	-0.443	0.366	-0.244
Weight of spikes/plant (g)	0.148	0.279	-0.012	0.442	-0.311	-0.011	0.382	0.024
	0.040	0.349	0.008	0.230	-0.528	0.290	0.338	-0.050
Spike length(cm)	0.071	0.180	-0.018	0.565	-0.404	0.005	0.216	0.037
	0.025	0.016	0.164	0.446	0.085	-0.520	0.461	-0.327
No. of grains/spike	0.025	0.130	-0.011	0.947	-0.624	-0.108	0.179	0.071
	-0.001	0.075	0.068	1.072	-0.516	-0.571	0.263	-0.055
Weight of grains/spike(g)	-0.014	0.118	-0.010	0.805	-0.735	0.206	0.064	0.117
	-0.025	0.133	-0.010	0.399	-1.387	0.984	0.049	0.214
1000-grain weight (g)	-0.073	-0.005	-0.0001	-0.174	-0.256	0.589	-0.208	0.098
	-0.025	0.071	-0.060	-0.430	-0.958	1.425	-0.172	0.246
Biological yield/plant(g)	0.145	0.212	-0.008	0.337	-0.093	-0.245	0.502	-0.095
	0.031	0.125	0.080	0.298	-0.072	-0.259	0.947	-0.671
Harvest index	-0.029	0.030	-0.003	0.306	-0.390	0.260	-0.216	0.221
	-0.024	-0.021	-0.066	-0.072	-0.362	0.428	-0.776	0.818

## Discussion

The results confirmed that the data for all characters under the study can be analyzed further to estimate general and specific combining ability effects. Similar results 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; Singh et al., 2013; Rahul, 2017). Also similar results reported by Burungale et al. (2011), Mandal et al. (2016), and Nataša et al. (2017). Highly significant differences among genotypes were recorded for all characters, also significant differences were recorded among the mean performance of F<sub>1</sub>s crosses (Fellahi et al., 2013; Kalhor et al., 2015). Significant positive and negative heterosis for all characters were recorded, also significant positive

relative heterosis for grain yield recorded previously by Ajmal et al. (2004), Akram et al. (2004), Akbar et al. (2009), Ashadusjman et al. (2012), Devi et al. (2013), Anonymous (2015), and Rahul (2017). The gca effect is primarily function of additive genetic variance, which helps in the selection of suitable good general combiner parent for hybridization (Rahul, 2017). These results are in confirmation with Kumar et al. (2011), Kapoor 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). According to Kenga et al. (2004) cross-combinations with high means, appropriate sca estimates and involving at least one of the parents with high gca would likely enhance the concentration of desirable genes to improve target traits. Present findings are in confirmation with Kumar et al. (2011), Kapoor et al. (2011), Singh et al. (2013), Raj and Kandalkar (2013), Aslam et al. (2014), Kalhoro et al. (2015), and Kandil et al. (2016). The average degree of dominance values are more than one for most characters at both locations. Previous reports confirmed the importance of over dominance in the inheritance of the grain weight/ spike of wheat which was pointed out by Petrović et al. (2012) and Adel and Ali (2013). Obverse to these results, the importances of partial dominance in the inheritance of this trait were reported by Kohan and Heidari (2014). However, the selection in early generations for the trait grain weight/spike would be difficult due to over-dominance type of gene action which indicates that the selection for this trait in advanced segregating generations would be more efficient (Nazir et al., 2014; Yao et al., 2014; Shehzad et al., 2015). While, partial dominance effect was observed in the inheritance of this trait reported by Farooq et al. (2011) and Rashid et al. (2013). Similar results, which indicated the importance of the dominant component in the genetic variance and over-dominant inheritance of the grain weight/ spike, have been also pointed out by El-Hosary et al. (2015). Converse to these results, the high value of the additive component and partial dominance responsible for the inheritance of grain weight/spike was observed by Minhas (2012) and Kohan and Heidari (2014). Heterosis estimates, for different morphological and yield related characters, are attributed to both additive and non additive gene actions. Heritability gives information about genetic variation; it is important for predicting the response to selection in the superseding generations. Heritability is dependent upon the type of gene action (Swati and Ramesh, 2004; Hasnain et al., 2006; Chowdhary et al., 2007). At the first location heritability in broad sense was high for number of spikes/plant, average spike weight, spike length and harvest index, while for the other characters it was low to moderate. At the second location it was high for spike weight/plant, spike length, grain yield/plant and harvest index, but for the rest it was low to moderate. Heritability in narrow sense was found to be low for almost all character at both locations. High heritability accompanied with high genetic advance shows that the heritability is due to additive genetic control and selection may be effective in early generations for these traits (Jamil et al., 2017). Heritability estimates varied from 54.48 to 80.91%. Highest heritability 80.91% was observed for the cross combination Fareed 06×9242, While the lowest value of heritability 54.48% was estimated in cross combination Fareed 06×9317 (Waqas et al., 2014). Heritability for grain yield/plant was 0.68 in Kaleemullah et al. (2015), who said that this traits is greatly under genetic controlled and less influenced by environment. The estimates of heritability in narrow sense were medium to high reported by Yadav et al. (2011). Significant and positive correlation was recorded between grain yield and most its components. These results are harmony with those reported by Tofiq (2004), Hama-Ali (2006), Hama-Ameen (2008), Mohsin et al. (2009)

and Fellahi et al. (2013). Estimation of the correlation between yield and its components alone is not enough to tell as the importance of each one of these components in determining the grain yield (Bhutta et al., 2005; Bhutto et al., 2005; Anwar et al., 2009; Ali and Shakor, 2012). Similar results are agreement with a positive correlation of grain yield with number of grains/spike and 1000-grain weight, with support the present studies (Belay et al., 1993; Aycecik and Yildirim, 2006). Positive and highly significant correlations recorded between grain yield/plant and harvest index reported by Tawfiq et al. (2016). The path analysis is used to find the direct or indirect effects of some yield components on grain yield in relation to yield with other components. Many researchers have been done on wheat breeding in which both correlation and path analysis methods were simultaneously used. Positive and significant correlation between plant height and grain yield were reported in many studies (Khayatnezhad et al., 2010; Zakizadeh et al., 2010; Amri et al., 2011). It was shown that seed numbers/spike has a positive effect on grain yield (Taleei and Bahram-Nejad, 2003; Foroozanfar et al., 2011). Path analysis conducted by a large number of researchers, it has been observed that 1000-grain weight has a positive effect on yield, followed by spike length, while grains/spike had a negative direct effect on grain yield associated a positive direct effect and negative indirect effect on grain yield via harvest index, while biological yield had the highest direct effect on grain yield refers to followed by weight of main spike, they show that the biological yield and weight of main spike can be used as criteria for selection to improve the yield of wheat grain (Mohammadi et al., 2007; Mollasadeghi et al., 2011; Iftikhar et al., 2012; Ayer et al., 2017).

## Conclusion

Line parent Aras and tester parent Iba-95 was found to be a good general combiner for grain yield/plant at the first location, which produced a best specific combiner for this character, while at the second location the line parent Aras and the tester parent Iba-95 were poor general combiner for grain yield/plant, whilst they produced the best specific combiner for this character. Low ratio of  $\sigma^2_{gca}/\sigma^2_{sca}$  for most characters at the first location and for all characters at the second location and low estimates of heritability in narrow sense confirmed involvement of both additive and non additive gene effects with preponderance of non additive type of gene actions. The preponderance of non additive type of gene actions clearly indicated that selection of superior plants should be postponed to later generations.

Good general combine line parents like Aras and Klal for yield and most related components at both locations could be used in the development of high yielding varieties through selection for promising segregating cross generations. The crosses Aras×Iba-95 and Klal×Cham-6 was found high yielding which were very desirable for further breeding program.

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