Estimation Heterosis and Combining Ability for Yield and Yield Contributing Traits in Two -Rowed Barley Using Line X Tester

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Article info	Abstract
	Five diverse genotypes of tow-rowed barley were crossed with a line × tester fashion. Combining ability for grain yield and yield related in tow-rowed barley was investigated in a set of two female lines, three male testers and their six F1's hybrids. Analysis of variance detected highly significant differences for all of the quantitative traits studied among the genotypes, among the parents for GCA, among the crosses for SCA, while most traits among Parents x crosses and among Lines x Testers. The parent GOB (line) had a positive and significant effect for grain yield plant^{-1} only. Two crosses were found to be well enough specific combiners for grain yield plant^{-1} with maximum SCA effect in cross GOB x MSEL. The estimated value of σ2A was greater than its $σ^2D$ for grains spike^{-1}, thousand grain weight and plant height, which pointed out the predominance of additive gene action as the ratio of $σ^2A/σ^2D$ was more than unity, whereas the rest of the traits *viz.,* spike plant^{-1}, spike length, harvest index biological yield plant^{-1} and grain yield plant^{-1} appeared overbalance of non-additive gene action. The average degree of dominance values for spike length and 1000- grain weight indicated partial dominance while rest of the traits showed over-dominance. All the crosses, excluding CANELA x MSEL, showed good positive and significant heterosis for grain yield plant^{-1}.

Introduction

Barley is a major cereal grain, a member of the poaceae family grown in temperate climates globally. It serves as a major animal fodder, as a rule malt, and as components of diverse health foods. Also used human food of diverse cultures *[1]* and *[2].* In a 2014 ranking of cereal crops in the world, barley was fourth both in terms of quantity produced (144.5 million tons) and in area of cultivation (49.4million hectare). Iraq area harvested was 1.146 million hectare and production was 1.278 million ton in 2014 *[3]*. Barley is a self-pollinating and diploid species with 14 chromosomes., *Hordeum vulgare* subsp. Spontaneum, which is the wild ancestor of domesticated barley and abundant in grasslands throughout the Fertile Crescent. To formulate an efficient breeding program for development of superior genotypes, it is also essential to understand the inheritance's mode, gene effect's magnitude and its interaction *[4]*. Allard (1960) *[5]* explanted that the parents transmit genes, not genotypes, to their progenies. Therefore, the value of parent is estimated by the mean performance of its progeny and progeny selection is a key step of plant breeding. Breeding programs based on selection of hybrids demand predictable level of heterosis as well as the specific combining ability . In breeding varieties with high yielding of crop plant, the breeders and researchers often be faced with the trouble of selecting parents and crosses. Combining ability analysis is available powerful tools to estimate the combining ability effects and assists to select the eligible parents and crosses for the utilization of heterosis *[6, 7, 8]*. Presence of heterosis and SCA effects for yield and its related traits in barley are reported by *[7, 9, 10]*. Combining ability analysis assists in the identification of parents with excess general combining ability (gca) effects and cross combinations with high – specific combining effects (sca) for commercial exploitation of heterosis and isolation of pure lines among the offspring's of the

heterotic hybrids. Thence the present consideration has been proceeded to determine the combining ability, gene action for yield and its related components and to improve grain yield using line x tester mating design for two-rowed barley under rain-fed conditions in Kurdistan- Iraq Region.

Materials and Methods

The present investigation was carried out at Qilyasan Agricultural Research Station, University of Sulaimani (35° 34′ 307″ N, 45° 21′ 992″ E and elevation 765 meters above sea level) during the 2013/2014 and 2014/2015 cropping seasons. The soil of the experimental site is silty clay, with Available phosphate, $CaCO_3$ and organic matter contents of 4.49 ppm, 23% and 2.13%, respectively. The total rainfall for 2014/2015 cropping seasons about 604.2 mm(Agro-meteorological station at Bakrajo).The experimental material comprises five two-rowed barley (*Hordeum distichum* L.) genotypes presented in Table 1. Local – Abide Sulaimany cultivar is a genealogical selection from a land race and widely adapted to the Kurdistan-Iraq Region at guaranteed rainfall secure zone (>500 mm). Acsad 60 was released and or adopted as cultivar in the eighties in many Arab countries like Syria, Jordan, Morocco, Algeria and Iraq, this variety had highly biotic and abiotic Stress-Tolerant and highly Productive yield **[11]**. The five parents were crossed to generate 6 F1 hybrids relying on the line × tester mating design developed by Kempthorne (1957) **[12]**. Six F1and the five parents seeds were sown in the field experiment, in a randomized complete block design(RCBD) with three replications. Each plot encompassed two row of 2.0m length with space of 40 cm between rows and seeds were placed 10 cm apart. Recommended cultural practices like sowing time, fertilization, and weeds control were followed to get the best crop. Five competitive plants were tagged before spiking date and data were recorded for the plant height (cm) PH, spike length (cm) SL, number of spike plant^{-1} SP, number of grains spike^{-1} GS, 1000-kernel weight (g) TKW, harvest index (0.00) HI, biological yield plant^{-1} (g) BY and grain yield plant^{-1}(g) GY. Data for the traits representing significant difference were furthermore analyzed for line x tester relying on Singh & Chaudhry (1985) **[13]**.

Table 1: List of two barley lines and three Testers crossed in line × tester fashion

No	Genotypes	Source
	Lines	
1	*GOB/ALELI//CANELA/3/BICHY2000/4/GUENZA CBSS99M00280T-AD-1M-2Y-1M-0Y* (GOB)	*Center Research of Sulaimany*
2	*CANELA/ZHEDAR#2//LIMON/3/MSEL CBSS98M00077T-0TOPY-0M-1Y-1M-1Y-1M-0Y(CANELA)*	*Center Research of Sulaimany*
	Testers	
3	*Local –Abide Sulaimany (Abide)*	*Center Research of Sulaimany*
4	*MSEL/GOB67DH/3/ARUPO/K8755//MORA CBSS98Y00303T-D-0Y-0M-1Y-2M-1Y-0M (MSEL)*	*Center Research of Sulaimany*
5	*Acsad 60*	*Center Research of Abo-Graib*
	F1 hybrids	
6	*GOB × Abide*	
7	*GOB × MSEL*	
8	*GOB × Acsad60*	
9	*CANELA × Abide*	
10	*CANELA × MSEL*	
11	*CANELA × Acsad 60*	

Results and Discussion

Analysis of variance and Gene action

The Table 2 showed highly significant (P ≤ 0.01) differences among two-rowed barley genotypes for all the traits studied pointing out presence of adequate genetic variability in the breeding substance used in this study. Sum of squares of two-rowed barley genotypes for these traits were moreover distributed into cross, parents and parents vs crosses, whose detected highly significant differences through themselves. Similar results were reported by Amer et al. (2012) *[14]*. As well highly significant due to crosses indicating altering performance of cross combinations for the traits under studying and hence, selection is possible to identify the best desired cross. The sum of squares calculated for two-rowed barley crosses were moreover distributed into lines, testers and line x tester components. Highly significant (P ≤ 0.01) differences were offered among line x tester interaction for all the traits indicated the significance of non-additive variance. Significant differences among two-rowed barley genotypes and theirs F1 hybrids for yield related traits have also been recorded earlier by Eshghi & Akhundova (2009) *[15]*, and Patial et al. (2016) *[16]*. While, among lines and testers had non-significant differences occurred for all most traits with excepting of spike length and 1000- grain weight, which gave significant and highly significant, respectively for testers. Patial et al. (2016) *[16]* reported similar results. Significant differences among parents *vs.* crosses for plant height, spike plant[-1], 1000- kernel weight, harvest index, biological yield plant[-1] and grain yield plant[-1] indicated that the F1 hybrids differ so much from parents and hence great heterosis was reflected in the hybrid which may be active role in the development of great yielding two-rowed barley genotypes. The ratio of GCA and SCA variances was less than one for the traits studied e.g. plant height (0.80), spike plant[-1](0.01), grain spike[-] (0.54), harvest index (0.069), biological yield plant[-1] (0.12) and grain yield plant[-1](0.06) that revealed the preponderance of non-additive gene action (dominant, overdominance and epistasis) over the additive gene action. Hence, the heterosis should be exploit through, selection of eminent plants, in terms of yield related traits should be put off to later generation by selections among the recombinants within the segregating populations. These results agreed with the results of Fatieh (17) and Potla et al (9). However, the traits e.g. spike length (-8.51) and 1000- kernel weight (-14.93) that revealed the GCA variances were greater than SCA variances, so preponderance of additive gene action over the non-additive gene action. These results agreed with the results of *[9]* and *[18]*.

Table 2: Estimates of mean sum of squares for lines, testers, line x tester as well as some genetic parameters in 11 F1 hybrids and their parents of two-rowed barley.

Source of Variation	df		Plant height (cm)	No of Spike Plant[-1]	Spike length cm	No of Grain spike[-1]	1000 grain weight g	HI	Biological yield Plant[-1] g	Grain yield Plant[-1] g
Replicates	r-1	2	6.76	1.48	0.54	0.87	0.55	0.000	5.99	0.89
Genotypes	g-1	10	170.70**	12.52**	4.52**	21.87**	79.41**	0.006**	86.72**	34.22**
Parents	p-1	4	253.27**	14.81**	10.07**	33.74**	93.45**	0.004**	58.23**	23.72**
Crosses	c-1	5	131.26**	12.62**	0.94**	16.69**	59.95**	0.001**	123.47**	30.98**
Parents x crosses	1	1	37.63**	2.80	0.24	0.28	120.60**	0.039**	16.93*	92.39**
Lines	l-1	1	522.72	28.54	0.04	19.64	2.28	0.001	427.62	104.67
Testers	t-1	2	35.72	5.30	2.18*	26.43	148.54**	0.002	11.79	0.55
Lines x Testers	(l-1)(t-1)	2	31.06**	11.97**	0.14	5.48**	0.20	0.001**	83.06**	24.56**
Error	(g-1)(r-1)	20	1.22	0.75	0.16	0.51	1.15	0.00004	2.70	0.46
Total	gr-1	32								
Estimation of some genetic parameters										
$\sigma^2 gca$ (Line)			54.63	1.84	-0.01	1.57	0.23	-0.0004	38.28	8.90

$\sigma^2 gca$ (Tester)	0.78	-1.11	0.34	3.49	24.72	0.00017	-11.88	-4.00
$\sigma^2 gca$ (Average)	7.95	0.05	0.06	0.89	4.74	0.00003	3.21	0.51
$\sigma^2 sca = \sigma^2 D$	9.94	3.74	-0.01	1.66	-0.32	0.00038	26.79	8.03
$\sigma^2 gca / \sigma^2 sca$	0.80	0.01	-8.51	0.54	-14.93	0.069	0.12	0.06
$\sigma^2 A$	15.91	0.10	0.13	1.78	9.49	0.00005	6.41	1.02
$\bar{a}$	1.12	8.53	-0.33	1.37	-0.26	3.816	2.89	3.97
$h^2 b.s$	0.96	0.84	0.49	0.87	0.90	0.91	0.93	0.95
$h^2 n.s$	0.59	0.02	0.47	0.45	0.87	0.11	0.18	0.11

*p=0.05, **p=0.01 and ns=non-significant., $\sigma^2 A$: additive genetic variance, $\sigma^2 D$: dominance genetic variance, $h^2 b.s$: broad sense heritability $h^2 n.s$: narrow sense heritability, $\sigma^2 gca$: estimate of GCA variance, $\sigma^2 sca$: estimate of SCA variance, $\sigma^2 gca /\sigma^2 sca$ ratio and $\bar{a}$: average degree of dominance.

Genetic parameters estimates

The $\sigma^2 A$ estimated value was higher than its $\sigma^2 D$ for the traits plant height, no of spike plant^{-1}, no of grain spike^{-1} and 1000- grain weight indicating the predominance of additive gene action accordingly the ratio of $\sigma^2 A/\sigma^2 D$ was more than unity, while spike length, harvest index, biological yield plant^{-1} and grain yield plant^{-1} traits showed preponderance of non-additive gene action. The value of $\bar{a}$ (average degree of dominance) of plant height, number of spike plant^{-1}, number of grain spike^{-1}and 1000- grain weight indicated partial dominance while rest of the traits *viz.,* Spike length, harvest index, biological yield Plant^{-1} and grain yield Plant^{-1} traits indicated over dominance (Table: 2). These results were in harmony with that of **[19]** for plant height and 1000- grain weight, spike length, number of spike plant^{-1}, number of grain spike^{-1} harvest index, and grain yield Plant^{-1}, **[9]** for spike length, grain spike^{-1}, 1000- grain weight and grain yield Plant^{-1} and **[15]** for number of grain spike^{-1}.

The estimates of heritability are essential demand to plant breeders either in broad or in narrow sense to judge in the expected improvement through programs of selection. Broad sense heritability (h^{2}b.s) values were obtained to be high in quantity for all eight traits under realization with exception of spike length which was moderate. High h^{2}b.s ranged from 0.49 for spike length to 0.96 for plant height. Narrow sense heritability (h^{2}n.s) in general was low to moderate with exception of 1000-grain weight which was moderate and ranged from 0.11 for grain yield plant^{-1} to 0.87 for 1000--grain weight. The high difference between h^{2}b.s and h^{2}n.s estimates which was obtained for the most traits studied was an expected due to more effective role of non-additive genes in the inheritance of these traits as it mentioned before (Table: 2). These results were in accordance with **[14]** and **[20]**.

Means performance of the measured traits

The differences between the extreme mean values for the measured traits were 35.66 cm, 7.33 spike, 3.88 cm, 8.57 grains, 12.92 g, 0.15,16.73 g and 11.90 g for plant height, spike plant^{-1}, spike length, grains spike^{-1}, 1000- grain weight, harvest index biological yield plant^{-1} and grain yield plant^{-1}, respectively. These differences were 5 to 19 times higher than the LSD0.05 values (excepting of harvest index). Parents and crosses presented significant effects for all traits (Table 2). The differences between overall mean of hybrids and that of parents indicated that hybrids were 2.14 cm taller and had more 1000- grain weight and a grain yield plant^{-1} advantage of 4.36 g. Parents and hybrids showed similar averages for spike plant^{-1}, spike length and grains spike^{-1} (Table: 3). Among lines, the differences between the extreme mean values for the measured traits, were 10.33 cm, 4.33 spike, 1.56 cm, 3.97 grains, 0.66 g, 0.08, 3.50 g and 4.06 g for plant height, Spike Plant^{-1}, spike length, grains spike^{-1}, 1000- grain weight, harvest index biological yield plant^{-1} and grain yield plant^{-1}, respectively (Table 3). The best grain yielding line was GOB which was the tallest and had also the highest average for the rest traits with excepting of thousand grain weight. CANELA had the most thousand grain weight (Table: 3). Among testers, the differences, between the extreme mean values for the traits studied, 13.33 cm, 1.33 spike, 1.82 cm, 6.33 grains, 21.81 g, 0.02, 5.18 g and 4.16 g for plant height, Spike Plant^{-1}, spike length, grains spike^{-1}, 1000- grain weight, harvest index biological yield plant^{-1}

and grain yield plant[-1], respectively (Table: 3). The best grain yielding tester was MSEL (18.80 g) which exhibited also the best yield related traits vis, Spike Plant[-1](18.33 spike), grains spike[-1](28.20 grain) and harvest index (0.40). Acsad 60 had the most thousand grain weight(53,08 g), the longest spike (11.18 cm) and the heaviest biological yield (39.94 g), while Abide was the shortest with 66.67 cm (Table: 3). The interaction lines × testers were significant for all traits suggesting that hybrids perform better than the parents for these traits (Table: 2). Mean values of the hybrids were within the limits of the means of the parents for spike plant[-1], spike length, grains spike[-1] and biological yield plant[-1]. For grain yield plant[-1], GOB × MSEL, GOB- × Abide and GOB- × Acsad 60 cross-combinations offered higher mean values than the their parents (Table: 3). Genetic variability and performance of the mean for hybrids and parents are important criteria for genotypic evaluation, however, the parents with high mean value may do not transmit this traits to their hybrids. In programs of hybrid barley both agronomic and grains yield traits are very important **[21]**.

Table 3: Means of the measured traits for 5 two-rowed barley parents and their 6 F1 hybrids.

Traits / Genotypes	PHT	SP	SL	GS	TKW	HI	BY	GY
Lines								
GOB-	92.33a	20.00a	7.86e	23.50ef	41.70e	0.39h	38.88cd	15.00f
CANELA	82.00c	16.67d	6.30f	19.53h	42.36e	0.31j	35.38de	10.94h
Testers								
Abide	66.67g	16.89d	9.38b	26.43c	41.27e	0.39h	35.23de	14.64f
MSEL	78.00e	18.33bc	9.36b	28.20a	50.53c	0.40f	34.76e	18.80cd
Acsad 60	80.00d	14.00e	11.18a	22.87g	53.08b	0.38i	39.94c	15.711e
Lines × testers								
GOB- x Abide	88.00b	17.78bcd	8.87cd	27.40b	44.16d	0.44e	45.82b	20.35b
GOB- x MSEL	86.67b	18.44b	8.95c	24.43d	49.95c	0.44d	51.49a	22.84a
GOB- x Acsad 60	87.33b	17.33cd	7.97e	23.07fg	53.71b	0.46a	41.87c	19.18c
CANELA- x Abide	80.33cd	17.00d	8.71d	23.97de	44.45d	0.45c	35.23d	15.85e
CANELA- x MSEL	78.00e	12.67f	9.38b	24.53d	50.87c	0.40g	34.76e	13.82g
CANELA- x Acsad60	71.33f	16.33d	7.99e	20.13h	54.62a	0.46b	39.94c	18.23d
Over all mean	80.97	16.86	8.722	24.006	47.882	0.410	40.865	16.851
LSD0.05	1.702	1.046	0.224	0.708	1.599	0.000	3.747	0.633

PHT: plant height (cm),SP: number of Spike Plant[-1], SL: spike length (cm), GS: number of Grain spike[-1], TKW: 1000-grain weight (g) HI: harvest index, BY: Biological yield, and GY: grain yield (g). Means within each column followed by the same letter are not significantly different from each other based on the 0.05 probability level of LSD.

General combining ability analysis

In general combining ability effects was estimated among lines and testers for eight traits of two-rowed barley to distinguish the preferable parent for pediment desired transgressive segregants. For plant height trait negative GCA effects, while for the rest traits positive GCA effects are eligible. Ashort plant height is desired to keep the plants or and crop from lodging. The estimates of GCA ability effects detected that the line CANELA had the best combining ability with highly negative and significant effect for reduced plant height(-5.39**). The line GOB was found to be the best parent combiner for grain yield plant[-1] with positive and highly significant effect (2.41**) along with the grain contributing trait like spike plant[-1] (1.26*) and biological yield plant[-1] (4.87**) , while it was a good combiner with positive and significant effect for grains spike[-1] (1.26*) and harvest index (0.01*) (Table: 4). Hence, it can be a potential parent which can share in next development of hybrid with superfat yield , spike plant[-1] and biological yield.

Among testers Acsad 60 was a good combiner for plant height and it was the best parent combiner with positive and highly significant effect for 1000- grain weight (4.54**) and harvest index (0.02**), while the tester Abide was the best parent combiner with positive and significant effect for grains spike[-1] (1.26*). These 4 parents (GOB, Acsad 60, Abide and CANELA) have good potential and may be utilized in composition a dynamic population with combination of more favorable genes. Number of different parents with good general combining ability for barley have as well been recorded by several researchers **[10, 16, 22]**.

Table 4: General combining ability (gi) effects for traits in two-rowed barley parents.

Traits Genotypes	PHT	SP	SL	GS	TKW	HI	BY	GY
Lines								
GOB	5.39**	1.26*	-0.05	1.04**	-0.36	0.01*	4.87**	2.41**
CANELA	-5.39**	-1.26*	0.05	-1.04**	0.36	-0.01*	-4.87**	-2.41**
SE (gl)	0.522	0.409	0.189	0.336	0.506	0.003	0.774	0.318
Testers								
Abide	2.22**	0.80	0.14	1.76**	-5.32**	0.01	-0.99	-0.28
MSEL	0.39	-1.04	0.52*	0.56	0.78	-0.02**	1.60	-0.05
Acsad 60	-2.61**	0.24	-0.66**	-2.32**	4.54**	0.02**	-0.61	0.32
SE (gt)	0.639	0.501	0.232	0.412	0.619	0.004	0.948	0.390

SE (gl): standard error for GCA effects for line, SE (gt): standard error for GCA effects for tester, ns, and * and **: non significant and significant effect at 0.05 and 0.01 probability.

Specific combining ability analysis

SCA effect is an indicator to define the advantage of a special cross combination in the utilization of heterosis. Because of that yield is a complex trait with low heritability, *per se*, selection for it is predominately mysterious and leads to hard predictable outcomes. Indirect selection by using simple inherited traits have been followed for yield improvement since ancient time **[23]**. While selecting the preferable particular combination for yield, it would be significant to give effective role to the related traits for yield. Grafius (1959) **[24]** had already proposed that yield is an end product of multiplicative interaction among several yield components. In the same direction, Allard (1960) **[5]** pointed that the capability of parents to combine will be based on complex interaction among genes for interest trait which cannot be regulated just by yield and yield adaptation of the parents which were advocated by varies researchers in several crops**[18, 35, 26, 27, 28, 29]**. The cross GOB x MSEL showed positive and significant SCA effects for grain yield plant[-1] (2.10**) and yield contributing traits (spike plant[-1] (1.63**), harvest index (0.02**) and biological yield plant[-1](3.49*). Therefore, this cross could be utilized for increasing grain yield/plant following approach of gene accumulation for these traits as it mentioned before. While the cross CANELA x MSEL showed positive and significant SCA effects for grains spike[-1](1.09**) was found to be good which may also contribute to grain yield *via.* number of grains spike[-1], as well CANELA x Acsad60 for grain yield plant[-1] (1.94**) along with harvest index (0.01**), biological yield plant[-1](3.91*) and desired negative and significant SCA effects for plant height (Table: 5) indicating, that; non-additive gene effects were predominant in these particular combinations of two-rowed barley hybrids for these traits due to the existence of great inter and intra-allelic interactions.. Zhang et al. (2013) **[21]** reported that in spite of the low SCAs of hybrid, high GCA of two parents always showed better F1s hybrids performance and the parents selection should fundamentally be depended on their GSAs. Many researchers have distinguished the potential cross combinations for varies traits in different crops**[9, 28, 30, 31]**.

Table 5: Specific combining ability (sij) effects for characters two-rowed barley hybrids.

traits genotypes	PHT	SP	SL	GS	TKW	HI	BY	GY
Lines × testers								
GOB x Abide	-1.56	-0.87	0.13	0.67	0.21	-0.01**	0.42	-0.63
GOB x MSEL	-1.06	1.63**	-0.17	-1.09**	-0.11	0.02**	3.49*	2.10**
GOB x Acsad 60	2.61**	-0.76	0.04	0.42	-0.10	-0.01**	-3.91*	-1.9**
CANELA x Abide	1.56	0.87	-0.13	-0.67	-0.21	0.01**	-0.42	0.16
CANELA x MSEL	1.06	-1.63**	0.17	1.09**	0.11	-0.02**	-3.49*	-2.1**
CANELA x Acsad60	-2.61**	0.76	-0.04	-0.42	0.10	0.01**	3.91*	1.94**
SE (sij)	0.816	0.501	0.107	0.340	0.767	0.000	1.796	0.304

SE (sij): standard error for SCA effects for crosses, , ns, and * and **: nonsignificant and significant effect at 0.05 and 0.01 probability.

Heterosis estimates

Estimates the values of heterosis over mid-parent for the studied combinations for two-rowed barley hybrids are showed in Table 6. Heterosis**:** Percent heterosis was calculated for eight traits. The heterosis degree changed from cross to cross and from trait to trait. Khoshnaw (2013) **[10]** in two-rowed barley observed the varying degree of heterosis for these traits. A negative heterosis was desirable for plant height but for rest of the traits positive heterosis was eligible. Positive heterosis ranges from 1.35-10.69%; 1.33-6.52%; 2.86-19.80%; 2.79-9.75%; 6.31- 14.47%; 12.32-32.24%; 4.65-19.85% and 23.99-37.31% for plant height, number of spike plant[-1], spike length, number of Grain spike[-1], 1000-kernel weight, harvest index, biological yield and grain yield. Eid (2010) **[32]**, Amer et al. (2012) **[14]**, Khoshnaw (2013) **[10]** and Potla et al. (2013) **[9]** found high heterosis for grain yield and its components in two and six-rowed barley. However, through six crosses, significant and desirable heterosis was observed in 2 crosses for plant height, 4 for number of spike plant[-1], 4 for spike length, 3 for number of grain spike[-1], 6 for 1000-grain weight and harvest index, 4 for biological yield Plant[-1], and 5 for grain yield Plant[-1]. In general, heterosis for grain yield Plant[-1] was large and positive. The cross GOB x Abide exhibited the largeest heterosis for grain yield (37.31%). Similarly, CANELA-x Acsad60 and , GOB x MSEL produced the second and third largest effects for grain yield Plant[-1], respectively. Conclusive target of breeding is to profit the heterotics yield linked with other heterotic traits. Yield is a complex traits; so those 6 crosses may be investigated for further study of combining ability.

Table 6: Significant mid-parent heterosis (%) for eight traits in two-rowed barley genotypes.

Traits Crosses	PHT	SP	SL	GS	TKW	HI	BY	GY
GOB x Abide	10.69**	-3.61**	2.86**	9.75**	6.45**	14.99**	19.26**	37.31**
GOB x MSEL	1.76*	-3.77**	3.91**	-5.48**	8.31**	12.86**	19.85**	35.13**
GOB- x Acsad 60	1.35	1.96**	-16.23**	-0.50	13.33**	19.41**	4.65*	24.87**
CANELA x Abide	8.07*	1.33*	11.05**	4.28**	6.31**	29.66**	-3.92*	23.99**
CANELA x MSEL	-2.50*	-27.62**	19.80**	2.79**	9.53**	12.32**	-15.67**	-7.054*
CANELA x Acsad60	-11.93**	6.52**	-8.53**	-5.03**	14.47**	32.24**	4.42*	36.81**
S.E	0.816	0.501	0.107	0.340	0.767	0.0000	1.796	0.304

Proportion contribution

The lines were contributed by a high proportion for plant height (79.65), biological yield Plant[-1] (69.27), grain yield Plant[-1] (67.579) and number of spike plant[-1] (45.245) while, tester the high contributed proportion for 1000-grain weight (99.107),spike length (93.148)and number of grain spike[-1] (63.33) and harvest index (57,81). For line x tester interaction were less considerable (Table: 7). Madic et al. (2014) **[22]** and Patial et al. (2016) **[16]** in barley traits found major contribution of line x tester.

Table 7: Proportional (%) contribution of lines, testers, and lines × testers to total hybrids variation in in two-rowed barley.

Traits Crosses	PHT	SP	SL	GS	TKW	HI	BY	GY
Lines (L)	79.650	45.245	0.919	23.528	0.762	10.883	69.271	67.579
Testers (T)	10.886	16.810	93.148	63.331	99.107	57.809	3.819	0.715
L × T	9.464	37.945	5.933	13.142	0.132	31.309	26.910	31.706

Conclusion

This research appeared the rewarding parents and crosses of two-rowed barley that can exploited by the plant breeders to launch active breeding strategies. The breeding material experimented had sufficient genetic variability and may be further exploited in breeding programs. In ANOVA the SCA and GCA proposed that 5 *viz.,* spike plant^{-1}, spike length, harvest index biological yield plant^{-1} and grain yield plant^{-1} of the 8 quantitative traits studied were controlling by non-additive gene action consequently proposing that selection of excellent plants should be postponed to later generation. Among the lines, GOB among testers Acsad 60 showed maximum GCA effects and were looked to be good general combiner for most of the quantitative traits studied and thence, for furthermore breeding programs in two-rowed barley it can be exploited. cross GOB x MSEL showed excellent SCA performance for the yield and most yield related traits under search and can be exploited effectively to gain segregates in order to transfer a population with high potential for yield.

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