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Heterosis study for yield and yield contributing character in barley (*H. vulgare* L.)

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Abstract
In present study crosses among the 11 genotypes (eight lines and three testers) were made in a line × tester fashion. The experimental material consisted of 11 parents and their resulting 24 F1's and check RD 2552, which were grown in a randomized block design with three replications under normal conditions during rabi 2020-21 at the Department of Seed Technology, Sardarkrushinagar Dantiwada Agricultural University, Sardarkrushinagar. Heterosis was found in all crosses for all measured barley traits. A wide range of variations in heterosis over a better parent and standard check was observed. For grain yield, the maximum percentage of heterosis over the standard check was observed when crossing UPB 1077 × DWRB 137. The cross UPB 1077 × DWRB 137 showed significant positive heterosis compared with the better parent, followed by DWRB203 × DWRB137. For the character number of grain per spike top auspicious crosses exhibiting the heterobeltiosis in order of merit were UPB 1077 × RD 2786, DWRB 203 × RD 2786 and DWRB 203 × BH 946, and for the economic heterosis top spectacular cross were UPB 1077 × RD 2786, DWRB 203 × RD 2786 and DWRB 203 × BH 946.

Keywords: Barley, heterosis, yield, lines testers

Introduction

Barley (*Hordeum vulgare* L.) is an important cereal crop grown throughout temperate and tropical regions of the world. It is the paramount cereal crop and is considered the first cereal domesticated for use by humans as food and feed (Potla *et al.*, 2013) [16]. Barley belongs to the family Poaceae (formerly called the Gramineae or grass family). It is a self-pollinated crop with a chromosome number of 14 (2n = 2x = 14). Barley has been cultivated since the Stone Age, making it one of the oldest domesticated plants in history (Salamini *et al.*, 2002) [17].

In addition, barley is a well-known model crop for plant breeding methodology, genetics, cytogenetics, pathology, virology, and biotechnology studies (Hockett and Nilan, 1985; Hagberg, 1987) [9, 7]. Aberg (1940) postulated that the six-rowed wild barley (*Hordeum vulgare* ssp. *agriocrithon*) found in Tibet is the progenitor of cultivated barley, and Harlan (1976) [8] suggested that barley was domesticated in southwest Asia from two-rowed wild barley (*H. vulgare* ssp. *spontaneum*) (Kumar *et al.*, 2014) [11]. The genus Hordeum has approximately 350 species, of which 32 are wild and cultivated. These 32 species were divided into two groups. *Hordeum sensu stricto*: It has two species *viz.*, *H. vulgare* L. and *H. bulbosum* L. The wild and cultivated forms of barley belong to *H. vulgare* subsp. *spontaneum* and *H. vulgare* subsp. *vulgare*, respectively (Ahlawat, 2012) [1].

Barley has been cultivated in India since ancient times, and is considered a sacred grain. Its Sanskrit name '*Yav'* is mentioned in '*Ved'* and the use of barley in religious ceremonies has been described. The major barley growing states in India are Rajasthan, Uttar Pradesh, Haryana, Punjab, Madhya Pradesh, Uttarakhand, Himachal Pradesh, Bihar, Jammu and Kashmir, West Bengal, Chhattisgarh and Sikkim.

The study of heterosis has a direct bearing on the breeding methodology to be employed for varietal improvement and also provides information about the usefulness of parents in breeding programs (Singh *et al.*, 2012) [19]. Grain yield is a complex metric trait that is the ultimate product of an action and the interaction between several component characters. However, grain yield and component characteristics are highly influenced by environmental fluctuations

Heterosis is recognized as one of the major landmarks in plant breeding. Heterosis has been proven to be the most important genetic tool for boosting the yield of self- and cross-pollinated species.

The phenomenon of vigor in artificial plant hybrids was first studied by Koelreuter in 1776. Bruce (1910) [5] explained heterosis as the combined action of favorable dominant or partial dominant factors. The term heterosis was first coined by Shull (1914) [18]. This refers to the phenomenon that the F_1 population obtained by crossing two genetically dissimilar individuals shows increased or decreased performance over the parents. Hybrid vigor is the manifested effect of heterosis. In self-pollinated crops, the utilization of heterosis depends mainly on the direction and magnitude of heterosis. Heterosis has a direct bearing on the breeding methodology employed for varietal improvement. The study of heterosis helps plant breeders to eliminate less productive crosses in early generations.

Therefore, in this context, the present investigation was conducted to study heterosis for yield and its component traits in barley.

Material and Methods

The present study was carried out at Sardarkrushinagar Dantiwada Agricultural University, Sardarkrushinagar, District: Banaskantha, Gujarat State. Sardarkrushinagar is situated at 24° 19' north latitude and 72° 19' east longitude, at an altitude of 175 m above sea level. The Sardarkrushinagar Dantiwada Agricultural University represents the typical climatic conditions of semi-arid regions with low rainfall. The soil was deep loamy sand and sandy loam.

Crosses among the 11 genotypes (eight lines and three testers) were made in a line × tester fashion, during rabi 2019-20 at Wheat Research Station, Sardarkrushinagar Dantiwada Agricultural University, Vijapur. A number of true-to-type plants selected from one parent were crossed with a number of true-to-type plants selected from another parent. All the resulting 24 F_1's were grown in a single row (2 m length) plot at the Department of Seed Technology, Sardarkrushinagar Dantiwada Agricultural University, Sardarkrushinagar, Dantiwada (Gujarat) during rabi 2020-21. The experimental material consisted of 11 parents and their resulting 24 F1's and check RD 2552, which were grown in a randomized block design with three replications under normal conditions during rabi 2020-21 at the Department of Seed Technology, Sardarkrushinagar Dantiwada Agricultural University, Sardarkrushinagar. Sowing was performed on the normal sowing date. The parents, F_1's and check were grown in a plot with a row-to-row distance of 22.5 cm and a plant-to-plant distance of 10 cm. All recommended cultural practices were adopted to raise good crops. In the crossing program, parents that were used as females (lines) were BH 1023, BH 1024, DWRB 203, NDB 1709, PL 906, RD 2991, UPB 1077, and UPB 1080. The parents that were used as male (testers) were RD 2786, BH 946, and DWRB 137.

Observations were recorded on five randomly selected plants in each of the parent, F_1's and check. The mean values of the selected plants were used for statistical analysis. Observations were recorded on five randomly selected plants in each replication for all the traits under study, except days to heading and days to maturity, where on-plot observations were recorded. Data on days to heading, days to maturity, plant height (cm), flag leaf area (cm^2), peduncle length (cm), and spike length (cm) were recorded on the tagged plants when the plants were in the field, while data for 1000-grain weight (g), number of grains per spike, biological yield per plant (g), grain yield per plant (g), and harvest index (%) were recorded after harvesting the randomly selected plants for yield.

For all the characteristics under study, the mean values of the plants were used for statistical analysis. The analysis of variance technique suggested by Panse and Sukhatme (1978) [15] for Randomized Block Design was used to test the differences among the genotypes for the characters under study.

Heterosis was estimated in terms of *the percent* increase or decrease of the hybrid over two parameters: the Magnitude of Heterosis expressed over a better parent, or heterobeltiosis or better parent heterosis (BH). Standard Heterosis (SH) was expressed over the check RD 2552.

Heterobeltiosis was calculated using the method described by Fonseca and Patterson (1968) [6]. It was measured as the proportion of deviation of the F_1 value from that of the better parent, expressed as a percentage. Standard heterosis was measured as the proportion of deviation of the F_1 value from the standard check, expressed as a percentage, as suggested by Meredith and Bridge (1972) [14].

$$BP\ \% = \frac{\bar{F}_1 - \overline{BP}}{\overline{BP}} \times 100$$

$$SH\ \% = \frac{\bar{F}1 - \overline{SH}}{\overline{SH}} \times 100$$

$\bar{F}_1$= mean value of F_1

$\overline{BP}$ = mean performance of better parent

$\overline{SH}$ = Mean performance of standard check

Result and Discussion

The experimental results obtained from the present investigation using a line × tester mating design for different characteristics are presented herein. The experimental materials (24 F_1s along with eight lines and three testers, including a standard check (RD 2552)) were tested for variance. The data for all quantitative traits were subjected to an analysis of variance (ANOVA). Treatment variations showed highly significant differences for all the characteristics studied (Table 1).

Heterosis was found in all crosses for all measured barley traits. A wide range of variations in heterosis over a better parent and standard check was observed. In the present investigation, the expression of heterosis, though varied with the crosses as well as yield-attributing traits.

For grain yield, the maximum percentage of heterosis over the standard check was observed when crossing UPB 1077 × DWRB 137. The cross UPB 1077 × DWRB 137 showed significant positive heterosis compared with the better parent, followed by DWRB203 × DWRB137. The superiority of hybrids over better parents is more suitable for the commercial exploitation of heterosis and indicates that the parental combination is capable of producing the highest level of transgressive segregants. These observations were also recorded by earlier researchers, such as Amer *et al.* (2012) [3], Mansour (2017) [13] and Lal *et al.* (2018) [12] and Potla *et al.* (2013) [16], and Bornare *et al.. al.* (2014) [4].

The present study showed that crosses showing heterosis in grain yield per plant were not heterotic for all other characteristics that contributed to the total yield. The yield is the end product of multiplicative interactions between various component characters. This implies that heterosis in a complex character, such as yield, can be registered by a single character or several characters.

For the character number of grain per spike top auspicious crosses exhibiting the heterobeltiosis in order of merit were UPB 1077 × RD 2786, DWRB 203 × RD 2786 and DWRB 203 × BH 946, and for the economic heterosis top spectacular cross were UPB 1077 × RD 2786, DWRB 203 × RD 2786 and DWRB 203 × BH 946. similarly

For the character flag leaf area, the best performing cross for heterobeltiosis was DWRB 203 × RD 2786, and for economic heterosis, the top spectacular cross of DWRB 203 × RD 2786 showed desirable standard heterosis followed by RD 2991 × RD 2786 and BH 1024 × DWRB 137.

For the peduncle length trait, cross combination PL 906 × RD 2786 showed highly significant positive heterosis over the better parent as well as over the standard check.

For character spike length, four crosses registered significant positive heterosis over their respective better parents. The cross RD 2991× BH 946 exhibited maximum heterobeltiosis, followed by BH 1024 × BH 946, and UPB 1077 × BH 946. For standard heterosis, only one hybrid showed significant positive heterosis compared with the check hybrid RD 2552. The most desirable standard heterosis was observed in crosses RD 2991 × BH 946. Similar findings were reported by Amer *et al.* (2012) [3], Abaas *et al.* (2016) [2] and Potla *et al.* (2013) [16].

The most promising hybrids for plant stature were BH 1023 × RD 2786, which exhibited desirable heterobeltiosis, followed by BH 1024 × RD 2786 and BH 1023 × DWRB 137. These crosses also showed desirable standard heterosis for plant height.

With regard to earliness based on the days to heading and days to maturity, cross combination RD 2991× BH 946 was found earlier than the other crosses. It also showed significant negative heterosis for heterobeltiosis and standard heterosis for character days to heading and days to maturity. Abaas *et al.* (2016) [2] and Jalata *et al.* (2019) [10] also reported similar findings.

Table 1: Analysis of variance for yield and yield component characters in barley

Source of variation	d.f.	Days to heading	Days to maturity	Flag leaf area (cm^2)	Peduncle length (cm)	Spike length (cm)	Plant height (cm)	Number of grain per spike	Grain yield per plant (g)	1000- grain weight (g)	Bio-logical yield per plant (g)	Harvest index (%)
Replications	2	1.231	3.527	7.786	0.033	0.204	35.041	2.190	3.170	0.275	8.7811	2.419
Genotype	35	58.764**	55.381**	68.978**	7.650**	1.400**	66.336**	91.681**	5.137**	28.573**	21.796**	27.977**
Error	70	2.755	5.108	3.539	0.211	0.273	11.658	12.275	1.008	1.885	4.641	6.078

Table 2: Better parent and standard heterosis for the character under study

Sr. No.	Hybrids	DH		DM		PL		SL		FLA		PH	
		BP	SH	BP	SH	BP	SH	BP	SH	BP	SH	BP	SH
1	BH 1024 × RD 2786	-5.41**	-1.87	0.00	-2.71	49.87**	18.03*	-13.32*	-18.19**	-21.81**	-10.95*	-9.75**	-7.19*
2	BH 1024 × BH 946	-15.32**	-12.15**	-5.88**	-8.43**	54.39**	21.59**	13.32*	6.96	-1.12	12.61**	-4.84	-2.14
3	BH 1024 × DWRB 137	-2.25	1.40	2.79	0.00	-10.56	-29.56**	7.83	1.77	2.61	16.86**	-3.78	-1.05
4	PL 906 × RD 2786	-5.14**	-5.14**	-1.86	-4.52**	164.42**	108.25**	9.34	3.20	-4.65	8.59	5.93	8.94**
5	PL 906 × BH 946	-0.46	1.40	2.48	-0.30	105.24**	61.64**	-2.20	-7.69	-22.01**	-11.18*	0.34	3.19
6	PL 906 × DWRB 137	-5.47**	-11.21**	-0.93	-3.61*	40.28**	10.48	-5.77	-11.06*	1.70	15.83**	-7.79*	-5.17
7	RD 2991 × RD 2786	-17.41**	-13.55**	-7.74**	-10.24**	93.52**	52.41**	11.26	5.01	6.31	21.07**	-2.27	0.51
8	RD 2991 × BH 946	-20.09**	-16.36**	-9.29**	-11.75**	85.54**	46.12**	25.82**	18.76**	0.91	14.92**	-1.10	1.71
9	RD 2991 × DWRB 137	-16.96**	-13.08**	-7.43**	-9.94**	59.89**	25.93**	-3.02	-8.47	-10.73*	1.67	-5.67	-2.99
10	UPB 1077 × RD 2786	1.40	1.40	0.62	-2.11	96.72**	54.93**	10.03	3.85	-8.87*	3.78	-1.44	1.36
11	UPB 1077 × BH 946	-4.59*	-2.80	0.31	-2.41	72.76**	36.06**	12.36*	6.05	0.72	14.71**	2.19	5.09
12	UPB 1077 × DWRB 137	0.00	-0.93	-1.24	-3.92*	46.14**	15.09	8.65	2.55	-12.20**	-0.01	0.68	3.54
13	UPB 1080 × RD 2786	-14.95**	-14.95**	-5.57**	-8.13**	72.23**	35.64**	10.58	4.36	-1.15	12.58*	-1.21	1.59
14	UPB 1080 × BH 946	-15.14**	-13.55**	-7.74**	-10.24**	37.62**	8.39	-16.21**	-20.92**	-26.20**	-15.95**	-5.44	-2.76
15	UPB 1080 ×DWRB 137	0.48	-2.80	1.24	-1.51	44.01**	13.42	-2.61	-8.08	-15.11**	-3.32	-6.24	-3.58
16	BH 1023 × RD 2786	-2.34	-2.34	1.24	-1.51	111.09**	66.25**	5.63	-0.30	-20.41**	-9.36	-10.66**	-8.12*
17	BH 1023 × BH 946	-1.38	0.47	0.93	-1.81	82.08**	43.40**	9.48	3.33	-12.12**	0.09	-0.83	1.98
18	BH 1023 × DWRB 137	5.82**	-6.54**	-2.17	-4.82**	46.94**	15.72*	-2.20	-7.69	-3.48	9.93*	-9.18**	-6.61*
19	DWRB 203 × RD 2786	0.47	0.93	2.17	-0.60	76.22**	38.78**	7.01	0.99	10.44*	25.78**	5.29	8.28*
20	DWRB 203 × BH 946	-6.88**	-5.14**	0.00	-2.71	71.16**	34.80**	-0.82	-6.40	-22.01**	-11.18*	-8.09*	-5.48
21	DWRB203 × DWRB 137	0.93	1.40	4.02*	1.20	-11.89	-30.61**	-6.87	-12.10*	-1.16	12.56*	-3.42	-0.68
22	NDB 1709 × RD 2786	0.47	0.47	3.72*	0.90	-2.31	-23.06**	4.74	-1.15	-1.56	12.11*	-2.34	0.43
23	NDB 1709 × BH 946	-1.83	0.00	-0.31	-3.01	-11.09	-29.98**	0.82	-4.84	-5.23	7.94	2.19	5.09
24	NDB 1709 × DWRB 137	6.12**	-2.80	0.00	-2.71	0.00	-21.24**	-0.00	-5.62	0.00	13.89**	0.00	2.84

Sr. No.	Hybrids	NGS		TGW		BYPP		GYPP		HI	
		BP	SH	BP	SH	BP	SH	BP	SH	BP	SH
1	BH 1024 × RD 2786	17.97**	1.34	-25.22**	-3.97	-6.20	-4.16	-4.26	-11.41*	2.04	-7.59
2	BH 1024 × BH 946	12.50*	-3.36	-15.44**	8.59*	-8.06	-6.05	-0.90	-8.30	8.02	-2.17
3	BH 1024 × DWRB 137	4.82	-9.96*	-13.31**	11.32**	-3.15	-1.04	-17.49**	-23.65**	-14.76**	-22.81**
4	PL 906 × RD 2786	21.74**	4.59	-9.22**	16.58**	-0.09	2.08	0.45	-7.05	0.38	-9.09*
5	PL 906 × BH 946	7.03	-8.05	-13.30**	11.33**	-4.26	-2.18	-13.68*	-20.12**	-9.62	-18.15**
6	PL 906 × DWRB 137	10.16	-5.37	-17.84**	5.51	1.76	3.97	-6.95	-13.90**	-8.55	-17.18**
7	RD 2991 × RD 2786	13.28*	-2.68	-5.08*	21.89**	8.70	11.07*	-2.47	-9.75	-10.03*	-18.52**
8	RD 2991 × BH 946	26.56**	8.72	-5.39*	21.49**	15.19**	17.69**	-2.47	-9.75	-14.54**	-22.60**
9	RD 2991 × DWRB 137	6.12	-8.84	-18.76**	4.33	-9.72	-7.76	-11.66*	-18.26**	-2.20	-11.43*
10	UPB 1077 × RD 2786	35.94**	16.78**	-23.83**	-2.18	1.67	3.88	4.26	-3.53	2.68	-7.01
11	UPB 1077 × BH 946	17.97**	1.34	-21.53**	0.77	-1.48	0.66	3.81	-3.94	5.36	-4.58
12	UPB 1077 × DWRB 137	31.25**	12.75**	-2.07	25.76**	8.24	10.60*	19.06**	10.17*	9.99*	-0.39
13	UPB 1080 × RD 2786	-2.47	-16.22**	-14.71**	9.52**	-6.76	-4.73	-4.26	-11.41*	3.24	-6.50
14	UPB 1080 × BH 946	2.67	-11.80*	-13.26**	11.39**	-26.39**	-24.79**	-30.49**	-35.68**	-5.46	-14.38**
15	UPB 1080 ×DWRB 137	4.49	-10.23*	-8.77**	17.16**	-3.80	-1.70	-5.61	-12.66*	-1.90	-11.16*
16	BH 1023 × RD 2786	2.47	-11.97*	0.06	28.49**	-1.11	1.04	-2.69	-9.96	-1.53	-10.82*
17	BH 1023 × BH 946	10.16	-5.37	-18.20**	5.05	1.94	4.16	6.50	-1.45	4.60	-5.27
18	BH 1023 × DWRB 137	14.06*	-2.01	-5.27*	21.65**	-10.46*	-8.51	-4.04	-11.20*	7.23	-2.89
19	DWRB 203 × RD 2786	32.03**	13.42**	-13.68**	10.84**	-0.83	1.32	-0.22	-7.68	0.77	-8.74*
20	DWRB 203 × BH 946	31.25**	12.75**	-13.97**	10.47**	-2.50	-0.38	-6.28	-13.28*	-3.89	-12.96**
21	DWRB203 × DWRB 137	4.69	-10.07*	0.91	29.59**	11.30*	13.72**	12.33*	3.94	1.09	-8.45
22	NDB 1709 × RD 2786	11.72*	-4.03	-18.68**	4.43	4.07	6.34	-4.04	-11.20*	-7.88	-16.57**
23	NDB 1709 × BH 946	26.56**	8.72	-3.43	24.01**	1.20	3.41	-2.02	-9.34	-3.19	-12.32**
24	NDB 1709 × DWRB 137	0.00	-14.09**	-0.00	28.42**	0.00	2.18	-3.46	-7.47	1.34	-9.44*

(DH: Days to heading, DM: Days to maturity, PL: Peduncle length, SL: Spike length, FLA: Flag leaf area, PH: Plant height, NGS: Number of grain per spike, TGW: 1000 grain weight, BYPP: Biological yield per plant, GYPP: Grain yield per plant, HI: Harvest Index)

Table 3: Top best cross combiation for some character

Character	Cross combination	
	HB	SH
Days to heading	RD 2991 × BH 946 RD 2991 × RD 2786 RD 2991 × DWRB 137	RD 2991 × BH 946 UPB 1080 × RD 2786 RD 2991 × DWRB 137
Days to maturity	RD 2991 × BH 946 RD 2991 × RD 2786 RD 2991 × DWRB 137	RD 2991 × BH 946 RD 2991 × RD 2786 RD 2991 × DWRB 137
Peduncle length	PL 906 × RD 2786 BH 1023 × RD 2786 PL 906 × BH 946	PL 906 × RD 2786 BH 1023 × RD 2786 PL 906 × BH 946
Spike length	RD 2991 × BH 946	RD 2991 × BH 946 BH 1024 × BH 946
Flag leaf area	DWRB 203 × RD 2786	DWRB 203 × RD 2786 RD 2991 × RD 2786 PL 906 × RD 2786
Plant height	BH 1023 × RD 2786 BH 1023 × DWRB 137 BH 1024 × RD 2786	BH 1023 × RD 2786 BH 1023 × DWRB 137 BH 1024 × RD 2786
Number of grain per spike	UPB 1077 × RD 2786 DWRB 203 × RD 2786 UPB 1077 × DWRB 137	UPB 1077 × RD 2786 DWRB 203 × RD 2786 UPB 1077 × DWRB 137
1000 Grain weight	-	DWRB203 × DWRB 137 BH 1023 × RD 2786 NDB 1709 × DWRB 137
Biological yield per plant	RD 2991 × BH 946 DWRB203 × DWRB 137	RD 2991 × BH 946 DWRB203 × DWRB 137 RD 2991 × RD 2786
Grain yield per plant	UPB 1077 × DWRB 137 DWRB203 × DWRB 137	UPB 1077 × DWRB 137

References

1. Ahlawat IPS. Agronomy: Rabi crops, lentils. Division of Agronomy Indian Agricultural Research Institute, New Delhi–110, 2012, 12(10).
2. Abaas SI, El-Shawy EE, Mansour M. Genetic parameters for yield and its components in barley. Egyptian Journal of Plant Breeding. 2016;20(1):135-149.
3. Amer KA, Eid AA, El-Sayed MMA, El-Akhdar AA. Estimation of some genetic parameters for yield and its components in some barley genotypes. Egyptian Journal of Agricultural Research. 2012;90(4):117-130.
4. Bornare SS, Prasad LC, Lal JP, Madakemohekar AH,

Prasad R, Singh J, Kumar S. Exploitation of heterosis and combining ability for yield and its contributing traits in crosses of two-row and six-row barley (*Hordeum vulgare* L.) under rainfed environment. Vegetos-An International Journal of Plant Research. 2014;27(3):40-46.

5. Bruce AB. The Mendelian theory of heredity and the augmentation of vigor. Science. 1910;32(827):627-628.
6. Fonseca S, Patterson FL. Hybrid vigor in a seven parent diallel cross in common winter wheat (*Triticum aestivum* L.). Crop Science. 1968;8(1):85-88.
7. Hagberg A. Barley as a model crop on plant genetic research. In: Yasuda S, Konishi T, editors. Proceedings of the 5th Int. Barley Genet. Symp; c1987.
8. Harlan JR, Dickson AD, Klingman DL, Moseman JG, Olien CR. Barley: origin, botany, culture, winter hardiness, genetics, utilization, pests-Revised edition; c1979.
9. Hockett EA, Nilan RA. Genetics. In: Rasmusson DC, editor. *Barley*. American Society of Agronomy–Crop Science Society of America–Soil Science Society of America, Madison, Wisconsin; c1985. p. 187–230.
10. Jalata Z, Mekbib F, Lakew B, Ahmed S. Gene action and combining ability test for some agro-morphological traits in barley. Journal of Applied Sciences. 2019;19(2):88-95.
11. Kumar V, Khippal A, Singh J, Selvakumar R, Malik R, Kumar D, Sharma I. Barley research in India: Retrospect and prospects. Journal of Wheat Research. 2014;6(1):1-20.
12. Lal C, Shekhawat AS, Singh J, Kumar V. Study of heterosis in six-rowed barley (*Hordeum vulgare* L.). Journal of Pharmacognosy and Phytochemistry. 2018;7(5):2287-2292.
13. Mansour M. Genetic analysis of earliness and yield component traits in five barley crosses. Journal of Sustainable Agricultural Sciences. 2017;43(3):165-173.
14. Meredith Jr WR, Bridge RR. Heterosis and gene action in cotton (*Gossypium hirsutum* L.). Crop Science. 1972;12(3):304-310.
15. Panse VG, Sukhatme PV. Statistical Methods for Agricultural Workers. New Delhi: Indian Council of Agricultural Research Publication; c1978. p. 87-89.
16. Potla KR, Bornare SS, Prasad LC, Prasad R, Madakemohekar AH. Study of heterosis and combining ability for yield and yield contributing traits in barley (*Hordeum vulgare* L.). The Bioscan. 2013;8(4):1231-1235.
17. Salamini F, Ozkan H, Brandolini A, Schäfer-Pregl R, Martin W. Genetics and geography of wild cereal domestication in the near east. Nature Reviews Genetics. 2002;3(6):429-441.
18. Shull GH. Hybridization methods in corn breeding. *American Breeder's Mav*. 1914;1:98-107.
19. Singh K, Sharma SN, Sharma Y, Tyagi BS. Combining ability for high temperature tolerance and yield contributing traits in bread wheat. Journal of Wheat Research. 2012;4(1):29-37.