RESEARCH ARTICLE

Heterosis and Combining Ability Estimation in Hexaploid Wheat (*Triticum aestivum* L.) with the Feasibility of Developing F1 Hybrid in Half Diallel Mating Design

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Abstract

During 2019-20, and 2020-21 present study was carried out at Mata Gujri College, Fatehgarh Sahib's Experimental Farm, Department of Agriculture. Experimental materials comprising 15 F_1s using half diallel mating design involving six parents(HD 1981, PBW 343, CPAN 3004, RAJ 2184, PBW 154, and PBW 65) collected from IIWBR (Indian Institute of Wheat and Barley Research) New Delhi, India and one check (HD 2967) was grown in RBD. The variance due to parents was highly significant for most of the traits. Variances due to crosses were significant for all the traits. Estimation of heterosis, PBW 343 x CPAN 3004 was cross found to be most promising for grain yield/ plant. General combing ability (GCA) effects revealed that PBW 65 followed by CPAN 3004 having significant and positive GCA effects and PBW 65 was observed as the best combiner for yielding characters as no. of grain/plant and on the basis of Specific combining ability (SCA), PBW 154 x PBW 65, PBW 343 x CPAN 3004 and HD 1981 x PBW 65 were recorded best specific combinations for higher yield. The above parents and crosses can be used in hybridization and heterosis breeding.

Keywords: Heterosis, Specific combining ability, Hybridization, Half diallel, Variance.

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Introduction

Bread wheat (*Triticum aestivum* L.) is also known as hexaploid wheat. It belongs to family Poaceae (Sharma *et al.,* 2016). Wheat crop was domesticated at least 12000 years ago. Wheat has evolved from wild grasses. Primary origin of the wheat is South West Asia. Bread wheat is allohexaploid wheat originated by crossing between *Triticum turgidum* and *Aegilops tauschii* (wild relative). Bread wheat contains three genomes namely A, B and D. Wheat was cultivated over an area of about 215 mha with production 756 mt and productivity 4477 kg/ha of wheat in the year 2018-19. Among the wheat growing countries, China has the largest area followed by India, Russia Federation, USA, Australia and France.

In India, Uttar Pradesh stands first followed by Madhya Pradesh and Punjab. In India, area, production and average yield of wheat is 29 mha, 106.21 mt and 3500 kg/ha respectively (Anonymous, 2019).

To fulfil projected demand of the world population for food grains, it is essential that production and productivity of wheat must be increased (Birchler *et al.,* 2003). The productivity of wheat increased by using hybrid varieties of wheat it is an alternative approach and another useful technique is to selection of suitable individual with high general (*gca*) and specific (*sca*) combining ability for grain yield and used that as parent than exploited heterosis. Combinations aims in breeding programmes to get maximum yield associated with best quality. General combing ability (GCA) effects indicated fixable gene action and specific combing ability (SCA) effects indicated non-fixable gene action. To understand the gene action and combining ability the material in which breeding program is undertaken based on half diallel mating design. In hybrid combinations to knowing the performance of genotypes and gene action's nature involved in the expression of quantitative traits, half diallel mating design used. The half diallel mating design used in both self as well as cross pollinated crops. In this crosses are made in all possible combinations in one direction. It also provides information about components of variance and *gca* and *sca* variance and their effects. Therefore, it helps in the detection of suitable individual used as parent for hybridization and in selection of appropriate breeding procedure by Hayman, (1954) and Griffing, (1956).

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Materials And Methods

Panse and Sukhatme, (1967) gave the procedure of RBD, the data pertaining to various traits were analyzed as per this procedure. Griffing (1956) suggested method for the combing ability analysis, was performed for half diallel mating design. Kempthorne, (1957) described the following method to calculate heterosis over superior parent (heterobeltiosis) and over the standard variety, *i.e.*, check (economic heterosis). Data were analyzed by Indo stat, Hyderabad.

Heterosis over the mid parent, superior parent and over the standard variety was calculated in %, as given below:

Average heterosis or mid-parent heterosis

$$= \frac{F_1 - MP}{MP} \times 100$$

Better parent heterosis or heterobeltiosis

$$= \frac{F_1 - BP}{BP} \times 100$$

Useful or standard check heterosis

$$= \frac{F_1 - SC}{SC} \times 100$$

Where,

MP= Mid Parent

BP= Better Parent

SC= Standard Check

The test of significance of heterosis was accomplished by the't' test, as given below:

$$t, = \frac{\bar{F}_1 - \overline{SP}}{\text{S.E. of heterosis over superior parent}}$$

Where,

$$\text{S. E. of heterosis over superior parent} = \sqrt{s_1^2\left(\frac{1}{r}+\frac{1}{r}\right)}$$

s_1^2 = Error variance obtained by using F1s and parents together

r = Number of replications.

The calculated 't' value was compared with table value of 't' at error degrees of freedom at P = 0.05 and P = 0.01. The difference of two estimates was tested against C.D.

C.D. = S.E. difference ×t 5% at error d.f.

$$\text{Here, S. E. difference will be} = \sqrt{\left(\frac{s_1^2}{r}+\frac{3}{2}\right)}$$

Where, s_1^2= Error variance obtained by using F_1s and parents together;

r = Number of replications.

The combining ability analysis was carried out by the procedure given by Griffing (1956) calculated as given below:-

General combining ability (g.c.a.) effects of ith parent was calculated as:

$$\hat{g}_i = \frac{1}{p+2}\left(Y_{io} + Y_{oi} - \frac{2}{p}Y_{oo}\right.$$

Specific combining ability (s.c.a.) effects of ijth cross was calculated as

$$\hat{S}_{ij} = \frac{1}{p+2}(Y_{io} + Y_{oi} + Y_{jo} + Y_{oj}) + \frac{2}{(p+1)(p+2)}Y_{oo}$$

The component analysis of the diallel crosses was done following Hayman's approach (Hayman, 1954). Under this procedure it is possible to measure additive and dominance variations in order to describe the relative dominance properties of the parental lines and to detect the non-allelic gene interaction. The following genetic components of variation were calculated

$\hat{D} = 4\sum uvd^2$ = Component of variation due to additive effects of the genes.

If; u = v = 0.5; D = d^2

Where,

u= Proportion of positive alleles in the parents;

v = Proportion of negative alleles in the parents;

d = Additive effect and u + v = 1.

$\hat{H}_1 = 4\sum uvh^2$ =Component of variation due to dominance effects of the genes.

$\hat{H}_2 = H_1[1-(u-v)^2] = 16\sum u^2v^2h^2$ = Proportion of dominance variance due to the positive (u) and the negative (v) effects of the alleles.

$\hat{h}^2$= Net dominance effect (the algebric sum of overall loci in heterozygous phase in all crosses);

$\hat{F}r$ = The covariation of additive and dominance effects in a single array;

$\hat{F}$ = The mean of Fr over the arrays.

The aforementioned components of variance were derived by constructing a set of equations based on the following parameters derived from the diallel table:-

V_{OLO} = V_p = Variance of the parent array;

V_r = Variance of the rth array;

V_1L_1 = V_r = Mean of the array variance;

W_r= Covariance between the parents and their offspring in one Array (rth array);

$W_{OLO\,1}$=Wr = Mean covariance between the parents and their offspring of all the arrays;

$V_{OL\,1}$ = Vm = Variance of array means

$M_{L\,1}$ - $M_{L\,0}$= Difference between the mean of the parents and the mean of their progenies;

E = Expected environmental component of variation, which is observed from analysis of variance for this design;

M_e' = Error variance / Number of replications.

The expected values of these components of variation were calculated by substituting the values of these equations:-

$$V_{OLO} = V_p = \hat{D} + \hat{E}\ ;$$

$$V_1L_1 = \bar{V}r = \frac{1}{4}\hat{D} + \frac{1}{4}\hat{H}_1 - \frac{1}{4}\hat{F} + \frac{p+1}{2n}\hat{E}$$

$$W_{OLO\,1} = \bar{W}r = \frac{1}{2}\hat{D} - \frac{1}{4}\hat{F} + \frac{1}{p}\hat{E}$$

$$V_{OL\,1} = V_m = \frac{1}{4}\hat{D} + \frac{1}{4}\hat{H}_1 - \frac{1}{4}\hat{H}_2 - \frac{1}{4}\hat{F} + \frac{1}{2p}\hat{E}$$

Where,

$\hat{E} = V_E = M_e$;

p= Number of parents;

D= $W_{OLO} - \hat{E}$;

$$\hat{H}_1 = V_{OLO} - 4W_{OLO\,1} + 4V_{1L1} - (3p-2)\frac{\hat{E}}{p}\ ;$$

$$\hat{H}_2 = 4V_{1L1} - 4V_{OL\,1} - 2\hat{E};$$

$$\hat{h}^2 = 4(M_{L1} - M_{Lo})^2 - 4(n-1)\hat{E}/p^2;$$

$$\hat{F}_r = 2(V_{OLO} - W_{OLO1} + V_{1L1} - W_r - V_r) - 2(n-2)\hat{E}/p^2;$$

$$\hat{F} = 2V_{OLO} - 4W_{OLO1} - 2(p-2)E/p^2.$$

Results And Discussion

ANOVA for Combining Ability

Source of variation for all the yield traits: days to booting, days to heading, days to anthesis, days to maturity, number of

Table 1: Mean performance of parents and hybrids

S.No.	Genotypes	Days to booting	Days to heading	Days to anthesis	Days to maturity	No.of productive tillers	Plant height (cm)	Peduncle length (cm)	Spike length (cm)	No.of spikelet/ spike	No.of grain/ spike	No. of grain per plant	Test weight (g)	Biological yield/plant (g)	Harvest index	Grain yield/ plant (g)
1	HD 1981 (PRATAP)	86.61	97.90	105.17	130.57	11.07	99.93	31.34	10.17	17.73	41.77	490.20	38.06	51.37	36.19	18.60
2	PBW 343	83.27	98.13	104.50	131.83	9.07	98.30	37.17	9.37	19.77	39.33	369.20	40.86	45.40	33.26	15.09
3	CPAN 3004 (SANGAM)	86.40	101.67	104.50	129.79	10.20	105.00	35.23	9.63	19.00	36.67	373.07	42.17	49.92	32.30	16.10
4	RAJ 2184	85.34	97.77	102.37	132.00	9.20	99.73	33.24	11.20	20.17	42.33	415.87	41.13	51.13	33.45	17.10
5	PBW 154	83.47	93.17	103.53	130.73	10.57	112.07	36.80	10.73	23.00	43.33	456.45	38.17	56.62	30.81	17.44
6	PBW 65	88.00	99.53	102.07	133.23	8.57	97.30	37.08	11.50	17.90	48.80	417.50	38.67	53.07	30.39	16.13
7	HD 2967 (Check)	84.57	95.37	101.23	127.23	12.00	103.73	35.23	10.10	19.13	43.97	469.83	40.90	49.81	34.87	17.36
8	HD 1981xPBW343	81.30	94.20	99.47	124.43	8.80	99.03	37.31	8.73	20.10	50.13	440.11	40.68	47.73	45.24	21.58
9	HD 1981xCPAN 3004	85.03	94.67	102.10	131.93	11.33	104.50	30.77	11.87	19.83	43.23	489.69	39.81	58.50	35.63	20.83
10	HD 1981xRAJ 2184	81.80	97.50	100.40	127.52	9.33	98.83	38.40	11.90	21.92	46.73	435.24	48.08	56.97	36.77	20.92
11	HD 1981xPBW 154	84.64	95.23	102.53	128.08	9.67	111.73	37.23	9.67	24.27	47.60	458.49	37.04	54.47	31.18	16.97
12	HD 1981xPBW 65	85.30	95.93	104.27	132.10	13.07	98.90	36.88	10.23	19.03	44.57	580.60	44.13	67.40	38.01	25.62
13	PBW 343xCPAN 3004	84.70	93.34	98.57	124.60	13.30	101.23	37.31	11.93	20.43	48.00	637.70	39.92	61.53	41.37	25.46
14	PBW 343xRAJ 2184	84.93	97.83	102.17	126.73	11.07	98.20	38.14	11.80	21.99	50.53	557.94	43.06	64.17	37.46	24.05
15	PBW 343xPBW 154	86.69	96.13	99.87	131.57	11.16	100.47	36.57	10.97	24.17	46.32	516.75	47.43	62.93	39.00	24.52
16	PBW 343xPBW 65	83.60	96.37	104.80	129.67	9.39	99.50	32.70	10.70	19.43	49.47	463.36	39.27	55.03	33.04	18.18
17	CPAN 3004xRAJ 2184	85.10	98.43	102.20	128.37	13.43	107.87	37.17	11.57	19.23	48.70	652.14	43.35	63.40	37.93	24.03
18	CPAN 3004xPBW 154	85.27	95.91	99.73	130.00	13.30	111.53	33.60	11.33	21.87	37.00	491.08	42.61	66.09	29.32	19.39
19	CPAN 3004xPBW 65	83.43	98.23	105.10	127.33	11.56	98.83	34.57	10.97	19.37	47.40	546.97	37.77	45.79	45.22	20.66
20	RAJ 2184xPBW 154	83.40	92.43	101.63	124.73	8.63	111.50	37.00	11.43	22.40	45.15	362.54	47.17	43.62	39.29	17.09
21	RAJ 2184xPBW 65	84.23	94.60	104.10	132.07	13.17	100.13	37.83	11.30	18.33	44.63	539.65	44.54	57.52	41.87	24.05
22	PBW 154xPBW 65	84.07	97.13	104.27	127.50	11.47	105.23	32.77	11.63	20.93	50.70	581.09	45.90	69.77	38.22	26.67
	Mean	84.60	96.43	102.48	129.18	10.88	102.89	35.65	10.85	20.45	45.29	488.43	41.85	56.01	36.40	20.36
	Min	81.30	92.43	98.57	124.43	8.57	97.30	30.77	8.73	17.73	36.67	362.54	37.04	43.62	29.32	15.09
	Max	88.00	101.67	105.17	133.23	13.43	112.07	38.40	11.93	24.27	50.70	652.14	48.08	69.77	45.24	26.67
	SE(d)	0.80	0.75	1.19	1.04	0.61	1.24	1.20	0.54	0.98	1.54	10.28	1.54	1.65	1.73	0.95
	C.D. at 5%	1.61	1.52	2.40	2.11	1.23	2.52	2.44	1.09	1.99	3.11	20.82	3.12	3.33	3.51	1.92
	C.V. (%)	1.15	0.95	1.42	0.99	6.86	1.48	4.14	6.06	5.87	4.15	2.58	4.51	3.60	5.83	5.70

Table 2: Analysis of variance for parent and hybrids

Sourced of variation	*df*	*Days to booting*	*Days to heading*	*Days to anthesis*	*Days to maturity*	*No.of productive tillers*	*Plant height (cm)*	*Peduncle length (cm)*	*Spike length (cm)*
REP	2	1.75	0.06	0.77	1.21	1.56	1.80	1.89	0.05
PAR	5	10.46**	23.51**	4.74**	4.58**	2.87**	93.30**	17.20**	2.20**
F1	14	5.74**	9.65**	13.50**	22.07**	9.18**	79.75**	16.81**	2.51**
PVF1	1	21.16**	60.23**	33.32**	109.33**	27.67**	15.90**	6.99**	5.19**
ERROR	40	0.94	0.84	2.19	1.67	0.51	2.36	2.23	0.44

Sourced of variation	*df*	*No.of spikelet/ spike*	*No.of grain/ spike*	*No. of grain per plant*	*Test weight (g)*	*Biological yield/ plant (g)*	*Harvest index*	*Grain yield/plant (g)*
REP	2	1.01	6.13	491.78	2.44	2.14	0.21	0.31
PAR	5	11.19**	50.24**	6637.62**	9.29**	40.89**	13.24**	4.55**
F1	14	10.02**	37.42**	18908.59**	37.69**	188.29**	61.60**	30.23**
PVF1	1	21.48**	276.68**	119751.57**	106.31**	643.68**	352.55**	355.59**
ERROR	40	1.50	3.71	164.29	3.65	4.10	4.64	1.38

*, ** significant at 5 and 1% level, respectively

productive tillers per plant, plant height, spike length, number of spikelets per spike, number of grains per spike, number of grains per plant, biological yield per plant, grain yield per plant, harvest index and test weight showed positive significance results in Table 2. Similar findings recorded (Hassan *et al.,* 2007; Hamouda *et al.,* 2016).

General Combining Ability (Gca) and Specific Combining Ability (Sca) Analysis

In Table 3 results of effects due to general combining ability are given. For the selection of outstanding parents with favourable alleles for different component traits GCA effects useful. PBW 65 among the parents as male parent could be screened as superior donor for most of the yield traits except no. of tillers per plant, peduncle and spike length, number of grain/ spike and test weight. Many earlier studies have determined good combiners with significant *gca* effects for yield and its contributing components (Yadav *et al.,* 2017 and Seboka *et al.,* 2009). Results of specific combining ability (*sca*) effects are given in Table 4. Two crosses namely PBW 343 X CPAN 3004 and PBW 154 X PBW 65 were associated with highly significant SCA value of grain yield/plant. Similar observations are reported by Joshi and Sharma, (2004) and Yadav *et al.* (2017).

Heterosis Estimation

Without evaluating the performance of the combinations to that of respective better parent and with check variety practical utility of desirable SCA effects may not be effective. According to new concept, heterosis is combined effect of favourable genes due to interaction between alleles, (Adhikari *et al.,* 2019). From heterotic data information about extent of genetic diversity in parents of a cross also taken and exploit hybrid vigour by choosing the parents for superior F_1's (Noorka *et al.,* 2013). The heterotic effect in F_1generation over superior parent and check variety presented in Table 5a, 5b, 5c & 5d.

For days to booting negative heterosis is useful. Due to earliness in booting stages provides best results for earliness in heading stage, anthesis and maturity stage. In days to booting, one cross combination found to be significant positive (PBW 343 X PBW 154) and nine cross combinations analyzed for significant negative over better parent. One cross combination found to be significant positive (PBW 343 X PBW 154) and two cross combinations significant negative over standard check. Similar results for days to booting are also reported by Samier and Ismail, (2015).

For days to heading negative heterosis is useful. In days to heading, none of the cross combination exhibited positively significant and nine crosses showed negatively significant better parent heterosis. Three crosses showed positively significant and significant negative heterosis showed by two crosses over standard check. Similar findings for this trait are reported by Samier and Ismail, (2015).

For days to anthesis negative heterosis is useful. In days to anthesis, none of the cross combination exhibited positively significant and significant negative heterosis showed by six crosses over better parent. Five cross combinations exhibited significant positive and one cross (PBW 343 X CPAN 3004) showed significant negative heterosis over standard check. Murugan and Kannan (2017) observed similar findings.

For maturity days negative heterosis is useful. In days to maturity, none of the cross combination exhibited positively significant and negatively significant heterosis showed by ten cross combinations over superior parent. Significant positive results exhibited by six cross combinations and three crosses showed significant negative heterosis over standard check. These findings showed similar results with Farooq *et al.* (2019).

For tillers/plant, positive heterosis is useful. Due to increase in number of tillers no. of spikes, spikelets increases it ultimately increases the grain yield. In this trait, nine cross combinations exhibited positively significant heterosis, three combinations of crosses how significantly negative heterbeltiosis. One cross combination (CPAN 3004 X RAJ 2184) exhibited significant positive and significantly negative heterosis over check showed by five crosses. Noorka *et al* (2013) and Chowdhry *et al* (2005) reported similar results.

For both growth and vigour of plants height of plant is useful measure. For plant height also negative heterosis is useful. Four cross combinations show significant positive and significantly

Table 3: General combining ability (GCA) effects for parents

Sourced of variation	*Days to booting*	*Days to heading*	*Days to anthesis*	*Days to maturity*	*No productive tillers*	*Plant height (cm)*	*Peduncle length (cm)*	*Spike length (cm)*	*No.of spikelet/ spike*	*No.of grain/ spike*	*No. of grain per plant*	*Test weight (g)*	*Biological yield/plant (g)*	*Harvest index*	*Grain yield/ plant (g)*
HD 1981	-0.11	-0.25	0.17	0.03	-0.18	-0.88 **	-0.80 **	-0.43 **	-0.38	-0.21	-5.08 *	-0.93 *	-0.79 *	0.49	-0.05
PBW 343	-0.55 **	-0.15	-0.49	-0.53 *	-0.49 **	-3.11 **	0.83 **	-0.42 **	0.25	0.71	-8.87 **	-0.15	-1.49 **	0.91 *	0.06
CPAN 3004	0.52 **	1.07 **	-0.13	-0.39	0.94 **	1.75 **	-0.73 *	0.09	-0.61 **	-2.47 **	17.31 **	-0.69	0.13	-0.16	-0.11
RAJ 2184	-0.26	0.12	-0.32	-0.19	-0.22	-0.49	0.67 *	0.52 **	0.07	0.37	-5.75 *	1.90 **	-0.78 *	0.61	0.11
PBW 154	-0.15	-1.52 **	-0.33	-0.20	-0.05	5.58 **	0.13	0.04	2.00 **	-0.50	-12.79 **	0.40	2.00 **	-2.08 **	-0.50 *
PBW 65	0.56 **	0.74 **	1.11 **	1.28 **	0.00	-2.84 **	-0.10	0.20	-1.34 **	2.11 **	15.18 **	-0.54	0.94 *	0.23	0.49 *
SE (gi)	0.18	0.17	0.28	0.24	0.13	0.29	0.28	0.12	0.23	0.36	2.39	0.36	0.38	0.40	0.22

*, ** significant at 5% and 1% level, respectively

Table 4: Specific combining ability (sca) for hybrids

S.No.		*Days to booting*	*Days to heading*	*Days to anthesis*	*Days to maturity*	*No productive tillers*	*Plant height (cm)*	*Peduncle length (cm)*	*Spike length (cm)*	*No.of spikelet/ spike*	*No.of grain/ spike*	*No. of grain per plant*	*Test weight (g)*	*Biological yield/ plant (g)*	*Harvest index*	*Grain yield/ plant (g)*
1	HD 1981XPBW343	-2.63 **	-1.87 **	-2.75 **	-4.34 **	-1.35 **	0.18	1.61 **	-1.30 **	-0.30	4.28 **	-35.25 **	-0.14	-6.29 **	7.37 **	1.07 **
2	HD 1981XCPAN 3004	0.03	-2.63 **	-0.47	3.01 **	-0.26	0.78 *	-3.37 **	1.32 **	0.30	0.56	-11.86 **	-0.48	2.86 **	-1.18 *	0.49
3	HD 1981XRAJ 2184	-2.43 **	1.15 **	-1.99 **	-1.60 **	-1.09 **	-2.64 **	2.87 **	0.92 **	1.70 **	1.22 *	-43.24 **	5.21 **	2.23 **	-0.80	0.36
4	HD 1981XPBW 154	0.30	0.53 *	0.16	-1.03 **	-0.93 **	4.19 **	2.23 **	-0.82 **	2.12 **	2.96 **	-12.94 **	-4.33 **	-3.04 **	-3.69 **	-2.98 **
5	HD 1981XPBW 65	0.26	-1.04 **	0.45	1.51 **	2.42 **	-0.22	2.11 **	-0.42 *	0.23	-2.69 **	81.19 **	3.70 **	10.95 **	0.82	4.68 **
6	PBW 343XCPAN 3004	0.14	-4.06 **	-3.35 **	-3.75 **	2.02 **	-0.25	1.53 **	1.37 **	0.27	4.42 **	139.94 **	-1.14 *	6.59 **	4.14 **	5.02 **
7	PBW 343XRAJ 2184	1.14 **	1.39 **	0.43	-1.82 **	0.95 **	-1.04 **	0.97 *	0.81 **	1.14 **	4.11 **	83.24 **	-0.58	10.13 **	-0.54	3.39 **
8	PBW 343XPBW 154	2.80 **	1.33 **	-1.85 **	3.02 **	0.88 **	-4.85 **	-0.06	0.46 **	1.39 **	0.77	49.09 **	5.29 **	6.12 **	3.70 **	4.46 **
9	PBW 343XPBW 65	-1.00 **	-0.70 **	1.64 **	-0.35	-0.94 **	2.61 **	-3.71 **	0.03	0.00	1.30 **	-32.27 **	-1.94 **	-0.72	-4.58 **	-2.87 **
10	CPAN 3004XRAJ 2184	0.24	0.76 **	0.11	-0.33	1.88 **	3.76 **	1.56 **	0.07	-0.75 *	5.45 **	151.26 **	0.24	7.74 **	1.00	3.54 **
11	CPAN 3004XPBW 154	0.30	-0.12	-2.34 **	1.31 **	1.59 **	1.35 **	-1.48 **	0.32	-0.04	-5.37 **	-2.75	0.99 *	7.66 **	-4.91 **	-0.50
12	CPAN 3004XPBW 65	-2.24 **	-0.06	1.58 **	-2.83 **	-0.21	-2.93 **	-0.28	-0.21	0.80 **	2.41 **	25.15 **	-2.90 **	-11.58 **	8.68 **	-0.22
13	RAJ 2184XPBW 154	-0.79 **	-2.65 **	-0.25	-4.16 **	-1.92 **	3.56 **	0.53	-0.01	-0.19	-0.07	-108.23 **	2.97 **	-13.91 **	4.29 **	-3.02 **
14	RAJ 2184XPBW 65	-0.66 **	-2.75 **	0.77 *	1.70 **	2.56 **	0.62	1.60 **	-0.31	-0.92 **	-3.20 **	40.90 **	1.29 **	1.05 *	4.56 **	2.95 **
15	PBW 154XPBW 65	-0.94 **	1.43 **	0.95 *	-2.85 **	0.69 **	-0.35	-2.94 **	0.51 **	-0.25	3.74 **	89.39 **	4.14 **	10.52 **	3.60 **	6.17 **
	SE (sij)	0.50	0.47	0.76	0.66	0.37	0.78	0.76	0.34	0.63	0.99	6.56	0.98	1.04	1.10	0.60
	SE (sij-sik)	0.24	0.22	0.36	0.31	0.17	0.37	0.36	0.16	0.30	0.47	3.13	0.47	0.49	0.53	0.29

*, ** significant at 5% and 1% level, respectively

Table 5a: Heterosis for hybrids

S. no.	Hybrids	*Days to booting*			*Days to heading*			*Days to anthesis*			*Days to maturity*		
		MP	*BP*	*SC*	*MP*	*BP*	*SC*	*MP*	*BP*	*SC*	*MP*	*BP*	*SC*
1	HD 1981xPBW343	-6.13 **	-4.29 **	-3.86**	-4.01 **	-3.89 **	-1.22	-5.42 **	-5.12 **	-1.74	-5.61 **	-5.16 **	-2.20**
2	HD 1981xCPAN 3004	-1.82	-1.70 *	0.55	-6.89 **	-5.13 **	-0.73	-2.92 *	-2.61 *	0.86	1.05	1.35	3.69**
3	HD 1981xRAJ 2184	-5.55 **	-4.85 **	-3.27**	-0.41	-0.34	2.24	-4.53 **	-3.24 **	-0.82	-3.39 **	-2.86 **	0.23
4	HD 1981xPBW 154	-2.28 *	-0.47	0.08	-2.72 **	-0.32	-0.14	-2.50 *	-1.74	1.28	-2.03 *	-1.97 **	0.67
5	HD 1981xPBW 65	-3.07 **	-2.30 **	0.87	-3.61 **	-2.82 **	0.59	-0.86	0.63	3.00**	-0.85	0.15	3.83**
6	PBW 343xCPAN 3004	-1.96 *	-0.16	0.16	-8.19 **	-6.57 **	-2.13**	-5.68 **	-5.68 **	-2.63*	-5.49 **	-4.75 **	-2.07*
7	PBW 343xRAJ 2184	-0.48	0.74	0.43	-0.31	-0.12	2.59**	-2.23	-1.22	0.92	-3.99 **	-3.93 **	-0.39
8	PBW 343xPBW 154	3.87 **	3.99 **	2.51*	-2.04 *	0.50	0.80	-4.43 **	-3.99 **	-1.35	-0.20	0.22	3.41**
9	PBW 343xPBW 65	-5.00 **	-2.38 **	-1.14	-3.18 **	-2.49 **	1.05	0.29	1.47	3.52**	-2.68 **	-2.16 **	1.91*
10	CPAN 3004xRAJ 2184	-1.50	-0.89	0.63	-3.18 **	-1.29	3.21**	-2.20	-1.19	0.96	-2.75 **	-1.93 **	0.89
11	CPAN 3004xPBW 154	-1.31	0.39	0.83	-5.66 **	-1.55 *	0.57	-4.56 **	-4.12 **	-1.48	-0.56	-0.20	2.17*
12	CPAN 3004xPBW 65	-5.19 **	-4.32 **	-1.34	-3.38 **	-2.35 **	3.01**	0.57	1.76	3.82**	-4.43 **	-3.18 **	0.08
13	RAJ 2184xPBW 154	-2.27 *	-1.19	-1.38	-5.46 **	-3.18 **	-3.08**	-1.84	-1.28	0.40	-5.51 **	-5.05 **	-1.96*
14	RAJ 2184xPBW 65	-4.28 **	-2.81 **	-0.39	-4.95 **	-4.10 **	-0.80	1.69	1.84	2.83**	-0.88	-0.41	3.80**
15	PBW 154xPBW 65	-4.47 **	-1.95 *	-0.59	-2.40 **	0.81	1.85	0.71	1.43	3.00**	-4.30 **	-3.40 **	0.21
	SE ±	0.79	0.69		0.75	0.65		1.21	1.04		1.05	0.91	
	CD at 5%	1.69	1.46		1.59	1.38		2.57	2.23		2.24	1.94	

*, ** significant at 5% and 1% level, respectively

Table 5b: Heterosis for hybrids

S. no.	Hybrids	No productive tillers			Plant height (cm)			Peduncle length (cm)			Spike length (cm)		
		MP	BP	SC	MP	BP	SC	MP	BP	SC	MP	BP	SC
1	HD 1981xPBW343	-20.51 **	-12.60 *	-26.67**	-0.90	-0.08	-4.53**	0.36	8.90 **	5.89*	-14.10 *	-10.58 *	-13.53**
2	HD 1981xCPAN 3004	2.38	6.57	-5.56	-0.48	1.98	0.74	-12.68 **	-7.58 *	-12.68**	16.72 **	19.87 **	17.50**
3	HD 1981xRAJ 2184	-15.69 **	-7.91	-22.23**	-1.10	-1.00	-4.72**	15.51 **	18.91 **	8.99**	6.25	11.39 *	17.82**
4	HD 1981xPBW 154	-12.68 *	-10.65 *	-19.44**	-0.30	5.41 **	7.71**	1.18	9.28 **	5.67*	-9.94	-7.50	-4.29
5	HD 1981xPBW 65	18.04 **	33.08 **	8.89	-1.03	0.29	-4.66**	-0.54	7.80 *	4.67*	-11.01 *	-5.54	1.32
6	PBW 343xCPAN 3004	30.39 **	38.06 **	10.83	-3.59 **	-0.41	-2.41	0.36	3.05	5.89*	23.88 **	25.61 **	18.15**
7	PBW 343xRAJ 2184	20.29 **	21.17 **	-7.78	-1.54	-0.82	-5.33**	2.60	8.33 **	8.25**	5.36	14.75 **	16.83**
8	PBW 343xPBW 154	5.62	13.68 *	-7.00	-10.35 **	-4.48 **	-3.15*	-1.61	-1.11	3.80	2.17	9.12	8.58
9	PBW 343xPBW 65	3.57	6.50	-21.75**	1.22	1.74	-4.08*	-12.03 **	-11.92 **	-7.19**	-6.96	2.56	5.94
10	CPAN 3004xRAJ 2184	31.70 **	38.49 **	11.94*	2.73 *	5.37 **	3.99*	5.49	8.55 **	5.49*	3.27	11.04 *	14.52**
11	CPAN 3004xPBW 154	25.90 **	28.12 **	10.86	-0.48	2.76 **	7.52**	-8.69 *	-6.71 *	-4.63*	5.59	11.29 *	12.21*
12	CPAN 3004xPBW 65	13.33 *	23.20 **	-3.67	-5.87 **	-2.29 *	-4.72**	-6.78 *	-4.40	-1.89	-4.64	3.79	8.58
13	RAJ 2184xPBW 154	-18.30 **	-12.65 *	-28.06**	-0.51	5.29 **	7.49**	0.55	5.65	5.02*	2.08	4.26	13.20**
14	RAJ 2184xPBW 65	43.12 **	48.22 **	9.73	0.40	1.64	-3.47*	2.03	7.60 *	7.38**	-1.74	-0.44	11.88*
15	PBW 154xPBW 65	8.52	19.86 **	-4.44	-6.10 **	0.53	1.45	-11.63 **	-11.29 **	-7.00**	1.16	4.65	15.18**
	SE ±	0.59	0.51		1.25	1.08		1.22	1.06		0.54	0.47	
	CD at 5%	1.25	1.08		2.67	2.31		2.60	2.25		1.15	1.00	

*, ** significant at 5% and 1% level, respectively

negative heterosis showed by two crosses for heterobeltiosis. Four crosses show positively significant and eight cross combinations show negative heterosis over standard check. Lal *et al*. (2013) and Kumar and Kerkhi, (2014) observed similar results for plant height.

Due to decrease in plant height peduncle length of plant is ultimately decreases. Significant positive heterobeltiosis for peduncle length was exhibited by seven crosses from and significant negativel to be found by four crosses. Positively significant heterosis over check variety was shown by nine crosses and significant negative for four crosses. Farooq *et al.* (2019) Mehmood *et al.* (2006) and Chowdhry *et al.* (2005) observed similar results.

Significantly positive results shown by six crosses for spike length and one combination of cross show significantly negative heterobeltiosis. Nine cross combinations from show significant positive and one cross combination (HD 1981 X PBW 343) show significant negative heterosis over standard check. Patil *et al.*

Table 5c: Heterosis for hybrids

S. no.	Hybrids	No.of spikelet/spike			No.of grain/spike			No. of grain per plant			Test weight (g)		
		MP	BP	SC	MP	BP	SC	MP	BP	SC	MP	BP	SC
1	HD 1981xPBW343	1.69	7.20	5.05	20.03 **	23.63 **	14.02**	-10.22 **	2.42	-6.32	-0.42	3.10	-0.53
2	HD 1981xCPAN 3004	4.39	7.99	3.66	3.51	10.24 **	-1.67	-0.10	13.45 **	4.23	-5.60	-0.76	-2.67
3	HD 1981xRAJ 2184	8.69	15.67 **	14.57**	10.39 **	11.14 **	6.29	-11.21 **	-3.93	-7.36	16.90 **	21.43 **	17.56**
4	HD 1981xPBW 154	5.51	19.15 **	26.83**	9.85 **	11.87 **	8.26*	-6.47 **	-3.13	-2.41	-2.95	-2.82	-9.44*
5	HD 1981xPBW 65	6.33	6.83	-0.52	-8.67 **	-1.58	1.36	18.44 **	27.93 **	23.58**	14.14 **	15.04 **	7.90
6	PBW 343xCPAN 3004	3.37	5.42	6.79	22.03 **	26.32 **	9.17**	70.93 **	71.83 **	35.73**	-5.33	-3.83	-2.39
7	PBW 343xRAJ 2184	9.02	10.12 *	14.92**	19.37 **	23.76 **	14.93**	34.16 **	42.14 **	18.75**	4.69	5.05	5.29
8	PBW 343xPBW 154	5.07	13.02 **	26.31**	6.89	12.06 **	5.35	13.21 **	25.17 **	9.99**	16.10 **	20.05 **	15.97**
9	PBW 343xPBW 65	-1.69	3.19	1.57	1.37	12.25 **	12.51**	10.99 **	17.80 **	-1.38	-3.89	-1.24	-3.99
10	CPAN 3004xRAJ 2184	-4.63	-1.79	0.52	15.04 **	23.29 **	10.76**	56.81 **	65.32 **	38.80**	2.79	4.07	5.98
11	CPAN 3004xPBW 154	-4.93	4.13	14.29**	-14.62 **	-7.50 *	-15.85**	7.59 **	18.40 **	4.52	1.04	6.07	4.17
12	CPAN 3004xPBW 65	1.93	4.97	1.22	-2.87	10.92 **	7.81*	31.01 **	38.37 **	16.42**	-10.44 **	-6.56	-7.66
13	RAJ 2184xPBW 154	-2.61	3.78	17.08**	4.18	5.40	2.68	-20.57 **	-16.88 **	-22.83**	14.67 **	18.96 **	15.32**
14	RAJ 2184xPBW 65	-9.09	-3.68	-4.18	-8.54 *	-2.05	1.51	29.26 **	29.51 **	14.86**	8.29 *	11.64 **	8.91*
15	PBW 154xPBW 65	-8.99 *	2.36	9.41*	3.89	10.06 **	15.31**	27.31 **	32.98 **	23.68**	18.71 **	19.48 **	12.22**
	SE ±	1.00	0.87		1.57	1.36		10.47	9.06		1.56	1.35	
	CD at 5%	2.13	1.84		3.35	2.90		22.30	19.32		3.32	2.88	

*, ** significant at 5% and 1% level, respectively

Table 5d: Heterosis for hybrids

S. no.	Hybrids	Biological yield/plant (g)			Harvest index			Grain yield/plant (g)		
		MP	BP	SC	MP	BP	SC	MP	BP	SC
1	HD 1981xPBW343	-7.09 *	-1.36	-4.19	25.02 **	30.29 **	29.75**	16.02 **	28.11 **	24.27**
2	HD 1981xCPAN 3004	13.89 **	15.51 **	17.44**	-1.55	4.04	2.19	12.01 *	20.07 **	19.97**
3	HD 1981xRAJ 2184	10.90 **	11.15 **	14.36**	1.61	5.61	5.47	12.49 *	17.20 **	20.49**
4	HD 1981xPBW 154	-3.81	0.87	9.34*	-13.83 **	-6.92	-10.56*	-8.75	-5.82	-2.26
5	HD 1981xPBW 65	27.01 **	29.08 **	35.31**	5.03	14.17 **	9.01*	37.77 **	47.55 **	47.57**
6	PBW 343xCPAN 3004	23.26 **	29.10 **	23.52**	24.38 **	26.21 **	18.67**	58.18 **	63.32 **	46.66**
7	PBW 343xRAJ 2184	25.49 **	32.94 **	28.82**	12.00 *	12.31 **	7.45	40.64 **	49.45 **	38.52**
8	PBW 343xPBW 154	11.14 **	23.37 **	26.34**	17.26 **	21.74 **	11.85*	40.58 **	50.75 **	41.21**
9	PBW 343xPBW 65	3.71	11.78 **	10.48**	-0.66	3.81	-5.23	12.73 *	16.50 **	4.72
10	CPAN 3004xRAJ 2184	23.99 **	25.48 **	27.28**	13.39 *	15.37 **	8.78*	40.52 **	44.76 **	38.42**
11	CPAN 3004xPBW 154	16.72 **	24.06 **	32.68**	-9.22	-7.08	-15.90**	11.16 *	15.60 **	11.67**
12	CPAN 3004xPBW 65	-13.71 **	-11.07 **	-8.07*	40.02 **	44.28 **	29.71**	28.08 **	28.20 **	19.00**
13	RAJ 2184xPBW 154	-22.96 **	-19.03 **	-12.43**	17.46 **	22.27 **	12.68**	-1.99	-1.03	-1.55
14	RAJ 2184xPBW 65	8.39 **	10.40 **	15.47**	25.18 **	31.17 **	20.08**	40.62 **	44.73 **	38.52**
15	PBW 154xPBW 65	23.21 **	27.21 **	40.06**	24.03 **	24.88 **	9.62*	52.91 **	58.87 **	53.59**
	SE ±	1.65	1.43		1.76	1.52		0.96	0.83	
	CD at 5%	3.52	3.05		3.75	3.25		2.05	1.77	

*, ** significant at 5% and 1% level, respectively

(2011) Wajad *et al.* (2011) and Noorka *et al.* (2013) observed similar findings for spike length. It is useful trait for grain yield.

Four cross combinations exhibited significant positive heterobeltiosis for spikelets/spike and negatively significant effect for heterobeltiosis not shown by any none of the cross combination. For standard heterosisseven crosses exhibited significant positive and for negatively significant results none of the cross combinations were exhibited. The present study agrees with findings of Noorka *et al.* (2013) and Baloch, (2016). Due to spike length this trait is effective.

Eleven cross combinations exhibited significant positive and one cross combination (CPAN 3004 X PBW 154) show significant negative heterosis over better parent. Eight cross combinations from exhibited significant positive and one cross combination (CPAN 3004 XPBW 154) show negative heterosis over standard checkfor number of grains per spike. The present study corresponds with the findings reported (Bhagwan *et al.,* 2014; Baloch, 2016).

The number of grains/plant is an important trait. For heterobeltiosis, eleven crosses from expressed significant positive and one cross combination (RAJ 2184 X PBW 154) show significant negative heterosis over better parent. Eight cross combinations from show significant positive and one cross combination (RAJ 2184 X PBW 154) show significant negative heterosis over standard check. The present study corresponds with the findings reported with Mehmood *et al*. (2006), Chowdhry *et al*. (2005) and Ribadia *et al.* (2007).

Six crosses showed positively significant and none of the cross show negatively significant results. Five cross combinations show significant positive and one cross combination (HD 1981 X PBW 154) show significant negative heterosis over standard check for test weight. The present study agrees with reporting's of Murugan and Kannan, (2017), Mehmood *et al*. (2006) and Tosun *et al*. (2015).

Out of eleven crosses, (PBW 343 X RAJ 2184) expressed highest significant positive heterosis over better parent. Due to best performance of its parents. Two crosses show significantly negative heterobeltiosis. Twelve cross combinations showed positively significant and two cross combinations show significant negative heterosis over standard check for biological yield/plant. The results of this study are in agreement with Rajput and Kandalkar, (2018) and Nagar, (2019).

In the present investigation the grain yield per plant increased mainly due to increase in average no. of tillers/plant and no. of spikelets/spike. Significantly positive results showed by thirteen cross combinationsand significantly negative results for heterobeltiosis not showed by any cross combination. Twelve cross combination showed positively significant and significantly negative heterosis over commercial checks not showed by any trait. Similar findings are reported (Rajput and Kandalkar, 2018; Kumar *et al.,* 2017) for grain yield.

Harvest index is one of the important components. Ten crosses show significant positive and none of cross combinations show significant negative heterosis over better parent. Nine cross combination exhibited significant positive and two cross combinations show negative heterosis over standard check. These findings are in accordance with the results reported (Desale *et al.,* 2013).

Conclusion

In combining ability analysis, cross combinations PBW 343 X CPAN 3004 and PBW 154 X PBW 65 exhibited good SCA effect due to non-fixable gene action. And parent PBW 65 shows good GCA effect due to additive gene action for most of the traits especially for number of grain/plant. So, considered as good tester. In heterosis, cross combinations PBW 343 X CPAN 3004, HD 1981 X RAJ 2184, PBW 343 X PBW 154 and CPAN 3004 X PBW 65 showed significant results for maximum traits, due to interaction of different alleles these cross combinations showed non-additive gene action. Therefore, such combinations were evaluated further for exploitation of heterosis and used in further hybridization programmes to take desired and superior genotypes.

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