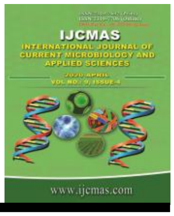
EXCELLENT PUBLISHERS

Int.J.Curr.Microbiol.App.Sci (2020) *9*(4): 2734-2747

International Journal of Current Microbiology and Applied Sciences
ISSN: 2319-7706 **Volume 9 Number 4 (2020)**
Journal homepage: http://www.ijcmas.com



Original Research Article https://doi.org/10.20546/ijcmas.2020.904.323

Estimation of Heterobeltiosis and Character Associations for Yield and Yield Attributing Traits in Bread Wheat (*Triticum aestivum* L.) Genotypes

Sameer Upadhyay*, Naveen Dubey, P. S.Yadav and V. K. Mishra

Department of Genetics and Plant Breeding, Institute of Agricultural Sciences, Banaras Hindu University, Varanasi-221005, India

**Corresponding author*

ABSTRACT

Keywords

Wheat (*Triticum aestivum* L), Heterobeltiosis, Correlation, Days to heading, Yield, biomass, Thousand grain yield

Article Info

Accepted:
22 March 2020
Available Online:
10 April 2020

The study involves 29 parents and their 92 F_{1s}laid out in RBD with three replications. ANNOVA for all the traits were found significantly variable at varying levels of significance. Highest heterobeltiosis of -10.22% for days to heading, 26.80% for grain yield and 25.46% for thousand grain weight were exhibited by BHU 31 × BHU 3, 6HPYT 416 × HUW 510 and HPVS 2 × BHU 3. Thus selection for these traits would be beneficial for indirect selection of grain yield. The crosses HPVS 1 × HUW 510, BHU 3 × BHU 6, 7HPAN 76 × BHU 3 and 6HPYT 407 × HD 3118 should be considered for the selection of homozygous lines in segregating generations with highest grain number per ear and biomass. Since these traits are controlled by additive genetic variance and biomass is significantly and positively associated with grain yield hence grain yield may improve. Grouping of top five cross combinations for five different yield contributing traits were made however; no F_1 alone gave satisfactory performance among all traits but it was observed that BHU 3, BHU 6 and BHU 35 were common parents which produced top F_{1s} for most of the traits.

Introduction

Wheat improvement programmes in collaboration with National Agricultural Research Centres and CIMMYT has made a significant progress but the production has hit the plateau since last few decades. Wheat is expected to suffer most among major crops from rising temperatures (particularly night time temperatures) in low-latitude countries (Ortiz *et al.*, 2008). Climate change may affect wheat production through heat stress, elevated carbon dioxide concentration and more variable precipitation resulting in altered crop development and a need to change farming practices (such as different sowing dates or more irrigation). With increasing drought incidences and water scarcity, wheat is likely to be grown increasingly under rainfed conditions, since among the major staple crops it is the most drought tolerant and water use efficient (Ortiz *et al.*, 2008). Utilization of heterosis is more attractive than conventional plant breeding methods, which obtain lower yield gain (1 % per year) in the north western plains zone - the bread bowl of India. Wheat consumption worldwide is estimated to cross 817million tonnes by 2030 and production would need to increase at 22.6-43.6% in different countries at the current production level to meet the demand (Zhang *et al.*, 2007) and one way to achieve this is through heterosis breeding. In this context, exploiting hybrid vigour at commercial level is considered as promising path that offer a significant means of overcoming food shortages because of yield heterosis (Singh *et al.*, 2004). To fulfil the increasing demand of world population, wheat production and productivity must be increased. In a self-pollinated crop like wheat, the utilization of heterosis depends mainly upon the direction and magnitude of heterosis. Studies of heterobeltiosis provide useful information about combining ability of the parents and their usefulness in breeding programmes (Sharma *et al.*, 1986; Borghi *et al.*, 1988). Keeping in view the above perspectives, the present investigation aims to estimate heterobeltiosis for yield contributing characters in wheat to suggest superior F_1 hybrids for varietal development, correlation analysis of various yield contributing characters.

Materials and Methods

The experiment was carried out at the Agricultural Research Farm, Institute of Agricultural Sciences, Banaras Hindu University, Varanasi during two Rabi seasons 2015 and 2016. For formulating valuable information 29 wheat (Table 1) germplasm lines were provided by the Department of Genetics and Plant Breeding, Institute of Agricultural Sciences, Banaras Hindu University for the study of heterosis and to carry out statistical analysis for yield contributing parameters. The experiment was performed in a randomised block design having three replications. The row length was 1 m with 2 rows. Row to row distance was maintained at 23 cm. Recommended agronomic practises were followed to raise the crop. Crosses were made among parents in 2015. F_{1s} crosses (Table.4) along with their parent were sown in 2016 crop season for evaluation. Observations were made on days to heading, canopy temperature, NDVI, SPAD, biomass, grain yield, grains per ear, thousand grains weight and plant height.

ANOVA was done for partitioning the total variation into variation due to treatment and replication as per Panse and Sukhatame (1967). It is worked out to test the significance of ‘F’ and ‘t’ test. It was carried out according to the procedure of Randomised Block Design for analysis of each character as per methodology of Fisher and Yates (1938). It facilitates in dividing the total variance into phenotypic, genotypic and environmental variance. Estimation of genetic parameters *viz.*, genetic variability (mean, range, component of variance, standard error, broad sense heritability and genetic advance was made followed by Correlation analysis and the amount of heterobeltiosis.

The Correlation analysis (as Correlation coefficient) and Heterobeltiosis was calculated as follow:

Correlation coefficient

It is represented as ‘r’ and was used to measure the association between two attributes and this was computed in terms of genotypic and phenotypic correlation coefficient based on variance and covariance which are given below:

Genotypic correlation coefficient

It was calculated by the formula as suggested by Robinson *et al.*, (1955)

$$r_g(x.y) = \frac{\text{Genotypic covariance of x and y}}{\sqrt{(\text{Genotypic var.(x).Genotypic var.(y)}}}$$

Where $r_g(x.y)$ = genotypic correlation coefficient between x and y.

Phenotypic correlation coefficient

$$r_p(x.y) = \frac{\text{Phenotypic covariance of x and y}}{\sqrt{(\text{Phenotypic var.(x).Phenotypic var.(y)}}}$$

Where $r_p(x.y)$ = phenotypic correlation coefficient between x and y.

Test of significance

The significance of correlation coefficient was tested with the help of 'r' value (statistical table by Fisher and Yates, 1963) at (n-2) df at 5% and 1% level of significance. If the calculated value of correlation coefficient is greater than the tabulated value of 'r' at (n-2) degree of freedom, the correlation was considered to be significant where 'n' is number of treatment.

$$\text{Heterobeltiosis} = \frac{(\overline{F_1}-\overline{BP})}{\overline{BP}} \text{ X } 100$$

Where, $\overline{BP}$ = mean of better parent

$\overline{F1}$ = mean of F_1 hybrid.

For testing the significance, Critical Difference (CD) was calculated using the formula:

CD (Heterobeltiosis) = SE $(\overline{F_1} - \overline{BP})$ x $t_{0.05}$

Where, SE = Standard Error formulated as

$$SE(\overline{F_1} - \overline{BP}) = \sqrt{\frac{2MSE}{r}}$$

MSR = Mean Sum of Error

r = number of replication

Results and Discussion

Presently, it is being felt that major wheat-producing zone of India has reached a sort of saturation level. In this context, exploiting hybrid vigour at commercial level through development of hybrid wheat is considered promising that offer a significant means of overcoming food shortages because of yield heterosis (Singh *et al.*, 2004). To fulfil the increasing demand of world population, wheat production and productivity must be increased and hence heterosis is an alternative approach to increase the productivity. Therefore the present research was planned to get information on various cross combinations made between various genotypes under following heads:

Analysis of variance

The analysis of variance (carried out through SAS version 9.2) showed highly significant variation for all the characters indicating the presence of considerable differences among genotypes undertaken in this experiment (Table.2) It also showed that the parental lines selected were quite variable, considerable amount of variability existed among the hybrids and presence of heterobeltiosis for most of the characters under study.

Variability

The development of an effective plant breeding is dependent upon the existence of genetic variability. The efficiency of selection largely depends upon the magnitude of genetic variability present in plant population. While dealing with variability an insight to the genotypic and phenotypic component of variability proves to be useful (*Table.2*) The phenotypic coefficient of variation was higher than the respective genotypic coefficient of variation (*Table.3*) for grain yield, biomass, thousand grain weight and indicated that apparent variation for the characters was not only due to genotype but also due to environment and selection may be misleading for such traits. The observation supported that there is a good scope of carrying out selection for these traits. The characters showing maximum phenotypic coefficient of variation should be considered while making selection in spite of environmental influence upto a certain extent. These reports were supported by findings of Kalimullah *et al.,* (2012), Baranwal*et al.,* (2012) Kumar *et al.,* (2014).

Heritability and genetic advance

Heritability in broad sense according to Lush (1949) is the ratio of total genotypic variance to phenotypic variance, expressed in percentage. The estimates of heritability are more advantageous when expressed in terms of genetic advance. Johnson *et al.,* (1955) suggested that without genetic advance the estimates of heritability will not be of practical value and he also emphasized the concurrent use of genetic advance along with heritability .The heritability estimates coupled with expected genetic advance as percent of mean indicate the mode of gene action in the expression of traits which helps in choosing an appropriate breeding methodology. High heritability and high genetic advance indicates predominance of additive genetic action (*Table.3*). High heritability with moderate genetic advance was shown by biomass (99.36; 43.31), grains per ear (99.12; 38.93) suggesting predominance of additive and non-additive gene action in the expression of these traits. Traits such as days to heading and NDVI 2 showed high heritability with poor genetic advance viz., 98.23; 9.33 and 95.25; 4.89 respectively suggesting the presence of non-additive gene action in expression of these traits. Grain yield showed moderate heritability followed by moderate genetic advance (76.42; 57.76) suggesting predominance of additive and non-additive gene action. These characters can be improved by mass selection and other breeding methods based on progeny testing. Very high heritability (broad sense) was noted in plant height (99.95%), biomass (99.364), grain per ear (99.12%), days to heading (98.23), NDVI 1(98.06%), CT1 (95.31%). Similar reports were published by Kalimulla *et al.,* (2009).

Correlation analysis

Correlation coefficient depicts the relationship between two variables. It is visualised that yield itself is a complex inheritance and is governed by several component characters which are generally positively associated with yield. Increase in yield through improvement in one or more particular set of characters may adversely affect simultaneous gain for other characters referred to as genetic slippage. Thus it become imperative to characterise the nature and magnitude of association among yield and yield components which may be helpful in assigning rational weight to different component characters during selection. Correlation may be either due to pleiotropic action of genes or due to linkage or more likely both. The information on correlation is of paramount importance for the plant breeder to bring about genetic improvement in one character by selecting the other characters that is generally correlated (*Table.4*).

Thousand grain weight (0.181), biomass (0.618) and plant height (0.246) showed positive and significant correlation with grain yield. This was observed that Days to heading showed significant positive correlations with NDVI 1 (0.226), NDVI 3 (0.255), SPAD 1(0.197), SPAD 2 (0.184), grains per ear (0.197) and plant height (0.234). Biomass exhibited significant positive correlation with SPAD 2(0.191). The grains per ear showed significant and positive correlation with days to heading (0.197) and NDVI 3 (0.257) whereas plant height showed significant positive correlation values with biomass (0.376), thousand grain weight (0.347) and grains per ear (0.219). This is supported by Aycicek and Yildirim (2006), Kumar *et al.*, (2012), Zeeshan *et al.*, (2014), Diyali*et al.*, (2015), Avinashe *et al.*, (2015). Hence, these characters should be given more weightage in selection programme of high yielding genotypes in wheat.

Heterobeltiosis

Heterobeltiosis is the increase or decrease in the mean value of F_1 over better parent in terms of yield, resistance or tolerance to insect pest and disease (Fonesca and Patterson, 1968). In the present experiment considerable amount of heterobeltiosis in all 15 traits under study was shown by F_{1s} (Table 5). Highest heterobeltiosis was of -10.22% shown by the F_1 (BHU 31 × BHU 3) with better parent as BHU 31 showing DH of 75 followed by F_1 (BHU 6 × BHU 3) giving heterobeltiosis of -7.66% with better parent as BHU 6 showing DH of 74. Highest positive heterosis of 22.58 % was shown by the F_1 (6HPYT 402 × BHU 3). Here we are considering negative heterobeltiosis because we need earliness in days to heading so F_1 should have less days to heading then its corresponding parents hence we require negative heterobeltiosis for this character exclusively. Maximum heterobeltiosis in biomass was shown by F_1 (7HPAN 76 x BHU 3) of 24.50 % with highest negative heterosis of -27.41 % was given by F_1 (BHU 31 x BHU 35). Under grain yield heterobeltiosis varies from highest of 26.80% of F_1 (6HPYT 416 x HUW 510) with maximum negative heterosis of -31.14% was shown by F_1 (BHU 3 x BHU 35). Maximum heterobeltiosis in thousand grain weight was exhibited by F_1 (HPVS 2 x BHU 3) which is 25.46% while highest heterobeltiosis was shown by F_1 (HPVS 1 x HUW 510) which is 32.27%. Heterosis for grain yield per ear contributed maximum towards yield heterosis (Singh *et al.,* 2004).

Table.1 Parents involved in constructing F_{1s}

S.No	Parents	S.No	Parents	S.No	Parents
1.	6HPYT 402	**11.**	BHU 35	**21.**	HPVS 5
2.	6HPYT 404	**12.**	HUW 234	**22.**	BAAZ
3.	6HPYT 407	**13.**	HUW 468	**23.**	HD 2733
4.	6HPYT 410	**14.**	HUW 510	**24.**	HD 2967
5.	6HPYT 415	**15.**	HUW 669	**25.**	HD 3118
6.	6HPYT 416	**16.**	HUW 712	**26.**	7HPAN 75
7.	BHU 3	**17.**	HPVS 1	**27.**	7HPAN 76
8.	BHU 6	**18.**	HPVS 2	**28.**	7HPAN 69
9.	BHU 28	**19.**	HPVS 3	**29.**	K 8027
10.	BHU 31	**20.**	HPVS 4		

Table.2 Analysis of variance for 15 characters of 121 genotypes of wheat

Source	df	DH	CT1	CT2	CT3	NDVI 1	NDVI 2	NDVI 3	SPAD 1	SPAD 2	SPAD 3	BM	GY	TGW	GPE	PH
Genotype	120	31.40**	3.53**	2.95**	3.65**	62.89**	42.99**	33.50**	6.72**	3.55**	4.51**	0.05**	11.67**	53.86**	257.61**	197.18**
Replication	2	0.52	0.28**	1.05**	0.26	2.33**	5.53**	9.47	1.19*	1**	0.606*	0.16*	2.00	0.15	1.42	0.16**
Error	240	0.19	0.06	0.15	0.19	0.41	0.70	3.20	0.37	0.15	0.14	0.021	1.09	0.32	0.76	0.033
Vg		10.40	1.16	0.93	1.15	20.83	14.10	10.10	2.12	1.13	1.46	0.016	3.53	17.85	85.62	65.716
Vp		10.59	1.22	1.08	1.35	21.24	14.80	13.30	2.49	1.29	1.60	0.016	4.62	18.17	86.38	66.100

* and ** denote 1% and 5% level of significance respectively.

df= degree of freedom, DH=days to heading, CT1, CT2, CT3= Canopy temperature readings at three different intervals , NDVI1, NDVI2, NDVI3 = Normalised difference vegetation (Green seeker) reading at three different intervals, SPAD1, SPAD2, SPAD3= Soil plant analysis development (Chlorophyll content) readings taken at three different intervals, BM= Biomass(g), GY=Grain yield(g), TGW= thousand grains weight(g), GPE= grains per ear, PH=plant height(cm).

Table.3 Estimation of Heritability, genetic advance, genetic advance as percent of mean, genotypic coefficient of variation, phenotypic coefficient of variation for 15 quantitative traits in wheat

	DH	**CT1**	**CT2**	**CT3**	**NDVI1**	**NDVI2**	**NDVI3**	**SPAD1**	**SPAD2**	**SPAD3**	**BM**	**GY**	**TGW**	**GPE**	**PH**
H	0.98	0.95	0.86	0.86	0.98	0.95	0.76	0.85	0.88	0.91	0.994	0.76	0.98	0.99	0.999
H in %	98.23	95.31	86.14	85.67	98.06	95.25	75.93	85.17	88.11	91.30	99.364	76.42	98.27	99.12	99.950
GA (5%)	6.59	2.17	1.85	2.05	9.31	7.55	5.70	2.77	2.06	2.38	0.257	3.38	8.63	18.98	16.695
GAM	9.33	11.84	8.55	8.21	5.96	4.89	5.88	13.32	12.18	9.94	43.31	57.76	20.73	38.93	16.43
GCV (%)	4.40	5.40	4.23	4.02	6.21	5.88	5.76	2.98	2.33	2.80	2.200	15.52	10.16	17.28	8.730
PCV (%)	4.50	5.60	4.56	4.34	6.27	6.03	6.61	3.23	2.49	2.98	2.210	17.72	10.25	17.36	8.761

H=heritability, H in %= heritability in percentage, GA= genetic advance, GAM = genetic advance as percent of mean, GCV=Genotypic coefficient of variation, PCV=Phenotypic coefficient of variation. DH=days to heading, CT1,CT2,CT3= Canopy temperature readings at three different intervals, NDVI1,NDVI2,NDVI3= Normalised difference vegetation index (Green seeker) reading at three different intervals, SPAD1, SPAD2, SPAD3= Soil plant analysis development (Chlorophyll content) readings taken at three different intervals, BM=Biomass (g),GY=Grain yield(g),TGW= thousand grains weight(g), GPE= grains per ear, PH=plant height(cm).

Table.4 Phenotypic correlation coefficient among 15 quantitative traits in Wheat

Parameters	CT1	CT2	CT3	NDVI1	NDVI2	NDVI3	SPAD1	SPAD2	SPAD3	BM	GY	TGW	GPE	PH
DH	-0.001	0.106	-0.017	0.226**	0.064	0.255**	0.197*	0.184*	0.052	0.077	0.094	0.071	0.197*	0.234**
CT1		0.14	0.008	-0.197*	-0.102	-0.240**	-0.296**	-0.007	0.338**	-0.022	0.082	0.058	-0.128	0
CT2			0.081	-0.029	-0.087	0.044	-0.022	0.075	0.228**	0.072	0.024	-0.049	0.048	0.089
CT3				-0.049	-0.013	-0.044	0.239**	0.049	0.002	0.021	0.08	0.128	-0.095	0.176*
NDVI1					0.573**	0.568**	0.313**	0.316**	0.008	-0.021	-0.154	-0.261**	0.117	0.101
NDVI2						0.475**	0.275**	0.312**	0.197*	-0.084	-0.239**	-0.079	0.128	0.006
NDVI3							0.470**	0.284**	-0.110	-0.054	-0.312**	-0.158	0.257**	0.136
SPAD1								0.436**	0.074	0.002	-0.162	-0.02	0.142	0.162
SPAD2									0.382**	0.191*	0.012	-0.079	0.051	0.15
SPAD3										0.056	0.066	0.045	-0.138	0.094
BM											0.618**	0.149	0.197*	0.376**
GY												0.181*	0.017	0.246**
TGW													-0.121	0.347**
GPE														0.219**

* and ** depicts significant value at 5% and 1% level of significance respectively.

DH=days to heading, CT1,CT2,CT3= Canopy temperature readings at three different intervals , NDVI1,NDVI2,NDVI3 = Normalised difference vegetation index (Green seeker) reading at three different intervals, SPAD1,SPAD2,SPAD3= Soil plant analysis development (Chlorophyll content) readings taken at three different intervals, BM= biomass(g), GY=Grain yield(g), TGW= thousand grains weight(g), GPE= grains per ear, PH=plant height(cm).

Table.5 Estimation of heterobeltiosis (%) for 5 yield contributing traits in 92 F_{1s}

S.No.	F_1	HB (DH)	HB (BM)	HB (GY)	HB (TGW)	HB (GPE)
1	6HPYT 404 × BAAZ	11.29	10.99	6.83	2.30	-17.75
2	6HPYT 404 × BHU 3	15.05	-14.75	-13.26	-3.30	26.02
3	6HPYT 404 × 7HPAN 75	17.74	-22.41	-27.96	-7.96	-23.31
4	6HPYT 404 × HUW 234	12.37	0.00	-2.93	-7.81	15.51
5	6HPYT 402 × 6HPYT 404	19.35	6.49	-16.52	-3.92	-12.50
6	6HPYT 402 × HUW 234	10.45	5.09	24.93	-6.15	-10.12
7	6HPYT 402 × BHU 3	22.58	-5.45	-1.53	10.07	-8.93
8	6HPYT 402 × 7HPAN 75	12.90	0.00	-9.74	15.22	-30.63
9	6HPYT 415 × HUW 234	-1.37	7.98	-1.45	-17.48	-0.72
10	6HPYT 415 × BAAZ	0.49	9.70	-8.76	-11.46	-7.69
11	6HPYT 415 × 6HPYT 404	17.74	-21.61	-23.75	2.08	-22.03
12	6HPYT 407 × HD 3118	0.47	24.24	18.05	-10.85	13.69
13	6HPYT 407 × HUW 712	-5.97	5.42	0.33	-8.63	-16.57
14	6HPYT 407 × HUW 510	6.04	-3.56	-14.41	-17.81	11.55
15	6HPYT 407 × HUW 234	3.11	-7.11	-8.56	-5.89	24.63
16	6HPYT 407 × BAAZ	-0.48	-16.29	-18.31	-20.29	-12.42
17	6HPYT 415 × HD 3118	0.47	-19.20	-2.99	-12.31	13.01
18	6HPYT 416 × HUW 712	7.10	18.53	7.98	-0.09	0.58
19	6HPYT 416 × HUW 510	15.22	-4.38	26.80	-6.04	17.89
20	6HPYT 416 × BAAZ	9.13	22.75	-16.82	-9.78	1.78
21	6HPYT 416 × BHU 3	11.16	18.17	-17.06	-0.46	25.77
22	6HPYT 416 × HUW 234	17.25	13.43	5.47	-9.01	25.20
23	7HPAN 76 × HUW 510	13.07	-16.13	19.82	-8.12	-19.13
24	7HPAN 76 × HUW 712	-2.88	-4.13	-4.08	-22.62	-27.39
25	7HPAN 76 × HUW 234	0.00	20.04	26.59	-26.95	-7.83
26	7HPAN 76 × 7HPAN 75	0.00	-4.47	-3.29	-24.92	-20.00

27	7HPAN 76 × BHU 3	6.74	24.50	-30.22	-13.51	-30.74
28	7HPAN 76 × HUW 669	11.06	-11.87	-18.00	-11.50	-29.13
29	7HPAN 69 × BAAZ	0.00	25.62	-13.74	-24.19	20.72
30	7HPAN 69 × HUW 669	8.08	-18.75	-6.95	-15.75	-24.09
31	6HPYT 410 × HUW 234	5.96	-7.66	-34.06	-5.23	0.61
32	6HPYT 410 × BAAZ	5.29	22.63	-27.35	-14.02	9.47
33	6HPYT 410 × HUW 712	-5.05	16.37	-26.00	-21.07	-4.57
34	6HPYT 410 × BHU 3	-0.92	18.13	-15.14	-22.50	16.36
35	6HPYT 410 × 6HPYT 404	12.90	4.14	-30.97	-10.23	-4.24
36	6HPYT 410 × K 8027	9.45	7.13	-28.03	-0.71	-20.00
37	HUW 669 × BHU 35	-2.38	-20.99	-17.49	-29.76	-27.15
38	HUW 669 × BAAZ	6.74	22.56	1.26	8.28	2.96
39	HUW 669 × HUW 510	13.07	19.33	-7.90	3.32	3.02
40	HUW 669 × HUW 234	5.24	-21.22	-23.13	7.10	-24.69
41	HUW 669 × BHU 6	-0.95	0.00	-21.20	-23.71	-6.62
42	HPVS 1 × HUW 234	-1.84	17.82	20.54	-1.95	25.69
43	HPVS 1 × HUW 510	8.55	-0.75	0.28	0.80	22.27
44	HPVS 1 × BHU 28	7.51	-19.02	-26.89	3.83	-18.93
45	HPVS 2 × BHU 28	0.00	-12.23	-12.27	-4.03	2.37
46	HPVS 2 × BHU 3	1.93	19.77	-12.80	25.46	8.85
47	HPVS 2 × BHU 35	17.68	7.25	7.84	-17.57	12.94
48	HPVS 3 × HPVS 1	0.00	1.42	-0.55	9.52	22.32
49	HPVS 3 × BHU 3	2.78	-15.87	-22.66	-8.73	23.09
50	HPVS 3 × BHU 35	-5.09	-13.21	-26.26	-17.07	-19.82
51	HPVS 3 × HUW 510	9.55	-3.59	-12.89	2.16	22.32
52	HPVS 4 × HUW 234	6.59	-19.74	-66.50	-24.89	15.28
53	HPVS 4 × HUW 510	14.21	-3.05	3.36	-0.58	4.86
54	HPVS 4 × BHU 35	12.68	-20.86	21.57	-31.95	-30.00
55	HPVS 5 × BHU 35	10.21	21.58	10.18	-15.29	-21.55

56	HPVS 5 × HUW 510	16.33	4.85	-18.18	-3.74	1.93
57	HPVS 5 × HUW 234	4.09	-14.77	-21.06	-9.53	-9.68
58	HPVS 5 × BHU 3	6.13	0.33	-24.99	-6.51	-5.17
59	BHU 35 × BHU 28	2.82	-1.88	-13.15	-4.26	-24.48
60	BHU 35 × BHU 31	1.81	-10.84	-22.19	-9.72	-19.82
61	BHU 35 × BHU 6	4.07	18.18	-3.43	-18.04	-19.39
62	BHU 35 × BHU 3	3.16	-23.67	-23.37	-12.19	-17.67
63	BHU 35 × HUW 234	-4.98	-1.40	-9.25	-8.84	-21.55
64	BHU 28 × BHU 35	4.23	-1.70	-5.27	-6.47	-13.36
65	BHU 28 × BHU 31	-1.88	-26.47	-27.08	-9.77	9.47
66	BHU 28 × BHU 6	5.63	-2.27	-28.28	-14.35	10.07
67	BHU 28 × BHU 3	-4.23	3.93	-19.77	9.31	-26.62
68	BHU 28 × HUW 234	3.29	-0.96	18.06	-5.64	-9.46
69	BHU 31 × BHU 35	0.45	-27.41	-23.24	-25.24	-17.67
70	BHU 31 × BHU 28	-1.41	-4.62	-17.33	14.34	14.80
71	BHU 31 × BHU 6	-5.86	13.39	-3.97	-10.86	18.59
72	BHU 31 × BHU 3	-10.22	15.11	-12.44	4.51	4.49
73	BHU 31 × HUW 234	0.00	-12.04	-29.28	-9.72	9.62
74	BHU 6 × BHU 35	5.88	25.78	23.45	-6.98	-26.29
75	BHU 6 × BHU 31	2.70	-2.78	-20.19	-7.25	9.62
76	BHU 6 × BHU 28	5.63	17.11	19.13	-7.05	-2.36
77	BHU 6 × HUW 234	-0.90	4.86	8.60	-7.73	27.92
78	BHU 6 × BHU 3	-7.66	5.07	-25.30	-4.71	24.83
79	BHU 3 × BHU 35	-3.17	-4.37	-21.14	-6.65	-24.48
80	BHU 3 × BHU 28	7.04	12.72	-22.10	6.65	6.52
81	BHU 3 × BHU 31	-2.67	3.65	-22.61	5.13	4.49
82	BHU 3 × BHU 6	0.90	-9.66	-20.12	2.78	30.12
83	BHU 3 × HUW 234	-4.00	11.40	-4.27	-4.71	28.78
84	HUW 510 × HD 2967	5.53	-4.17	-25.16	15.31	3.72

85	HUW 510 × HD 2733	4.03	1.27	-11.16	-25.47	26.30
86	HUW 510 × HUW 468	4.03	-25.37	-21.37	-2.03	29.67
87	HUW 510 × HUW 669	8.55	-26.47	-23.94	-19.81	6.03
88	HUW 510 × HUW 234	13.07	-7.06	-7.11	-20.78	23.95
89	HD 2733 × HUW 468	1.45	-25.91	-28.55	-30.04	24.69
90	HD 2733 × HUW 510	9.55	-24.79	-19.92	-35.99	25.66
91	HD 2733 × BAAZ	0.00	-20.23	-23.29	-34.77	-2.95
92	HD 2733 × HUW 234	7.38	-13.21	-22.23	-32.79	12.11

HB (DH) = heterobeltiosis for days to heading, HB (BM) = heterobeltiosis for biomass, HB (GY) = heterobeltiosis for grain yield, HB (TGW) = heterobeltiosis for thousand grain weight, HB (GPE) = heterobeltiosis for grains per ear.

Table.6 Top 5 crosses for five yield contributing traits

S.No	**DH**	**BM**	**GY**	**TGW**	**GPE**
1	BHU 31× BHU 3	7HPAN 69 × BAAZ	6HPYT 416 × HUW 510	HPVS 2 × BHU 3	BHU 3 × BHU 6
2	BHU 6 × BHU 3	BHU 6 × BHU 35	7HPAN 76 × HUW 234	HUW 510 × HD 2967	HUW 510 × HUW 468
3	6HPYT 407 × HUW 712	7HPAN 76 × BHU 3	6HPYT 402 × HUW 234	6HPYT 402× 7HPAN 75	BHU 3 × HUW 234
4	BHU 31 × BHU 6	6HPYT 407 × HD 3118	BHU 6 × BHU 35	BHU 31 × BHU 28	HUW 510 × HD 2733
5	HPVS 3 × BHU 35	6HPYT 410 × BAAZ	HPVS 4 × BHU 35	HPVS 3 × HPVS 1	6HPYT 404 × BHU 3

DH =days to heading, BM=Biomass, GY grain yield, TGW= thousand grain weight, GPE=Grains per ear

Highly significant differences among the tested entries were detected for different traits, indicating wide genetic variability among studied genotypes for all traits supported by Saad *et al.*, (2010), Balkan *et al.*, (2012).

Grouping of top five cross combination under five different yield contributing traits was made (Table 6). After analysis it was concluded that there is no F_{1s} which is giving satisfactory performance among all the selected yield contributing traits. But it was observed that BHU 3, BHU 6 and BHU 35 were the common parents which produced top F1s for most of the traits.

References

Avinashe, H. A., Shukla, R. S., Dubey, N., and Jaiwar, S. (2015). Correlation and path analysis for yield and yield contributing characters in bread wheat (*Triticum aestivum* L.). *Electronic Journal of Plant Breeding*, 6(2): 555-559.

Aycicek, M. E. H. M. E. T., and Yildirim, T. (2006).Path coefficient analysis of yield and yield components in bread wheat (*Triticum aestivum* L.)Genotypes. *Pakistan Journal of Botany*, 38(2): 417.

Balkan, A. (2012). Heterotic and heterobeltiotic potentials of bread wheat (*Triticum aestivum* L.) hybrids for yield and yield components. *JOTAF/TekirdağZiraatFakültesiDergisi* 8(2): 104

Baranwal, D. K., Mishra, V. K., Vishwakarma, M. K., Yadav, P. S., and Arun, B. (2012). Studies on genetic variability, correlation and path analysis for yield and yield contributing traits in wheat (*T. aestivum* L. emThell.).*Plant Arch*, 12: 99-104.

Borghi, B., Perenzin, M., and Nash, R. J. (1988). Agronomic and qualitative characteristics of ten bread wheat hybrids produced using a chemical hybridizing agent. Euphytica, 39(2), 185-194.

Devi, L., Goel, S. P., Singh, M. A. M. T. A., and Jaiswal, J. P. (2013). Heterosis studies for yield and yield contributing traits in bread wheat (*Triticum aestivum* L.). *The Bioscan*, 8(3): 905-909.

Diyali, S., Priya, B., and Mukherjee, S. (2015, January). Character association and path coefficient analysis among yield attributing traits in bread wheat. In *Compendium of abstracts of the 2nd international conference on bio-resource and stress management*, ANGRAU and PJTSAU, Hyderabad, India (pp. 7-10).

Fisher, R. A. and Yates, F. (1938). Statistical tables for biological, Agricultural and Medical Research. Edinburgh: Oliver and Boyd.

Fisher, R. A. (1963). Yates. Statistical Tables for Biological, Agricultural and Medical research (Oliver and Boyd, London, 1957), 42.

Fonseca, A. and Patterson, F. L. (1968). Hybrid vigour in a seven parent diallel cross in common winter wheat (*T. aestivum* L.). Crop Sci. 8: 85-88.

Johnson, H. W., Robinson, H. F. and Comstock, R. E. 1955.Estimates of genetic and environmental variability in soybean. Agronomy J. 47: 314-18.

Kalimullah, S. J., Khan, J., Irfaq, M., and Rahman, H. U. (2012).Genetic variability, correlation and diversity studies in bread wheat (*Triticum aestivum* L.) germplasm. *J.Anim. Plant Sci*, 22(2): 330-333.

Kumar, A., Kerkhi, S. A., Kumar, S., Chand, P., and Gangwar, L. K. (2012). Correlation and path coefficient analysis for different morphological and biochemical traits in bread wheat (*Triticum aestivum* L.). *Environment* *and Ecology*, 30(3B): 930-934.

Kumar, Y., Lamba, R. A. S., and Saharan, R. P. (2014). Genetic variability for different biometric traits in wheat (*Triticum aestivum* L.) under medium fertility conditions. *Electronic Journal of Plant Breeding*, 5(1): 71-76.

Lush, J. L. 1949. Intra-sire correlation on regression of off-spring on dams as a method of estimating heritability of characters. In: Proceedings of American Society of Animal Production, 33: 292-301.

Ortiz, R., Sayre, K. D., Govaerts, B., Gupta, R., Subbarao, G. V., Ban, T. and Reynolds, M. (2008). Climate change: can wheat beat the heat? Agriculture, Ecosystems and Environment, 126(1-2), 46-58.

Panse, V.G. and Sukhatme, P.V. 1967. Statistical Methods for Agricultural Workers. Indian Council of Agricultural Research, New Delhi, p.381

Saad, F. F., Abo-Hegazy, S. R. E., EL-Sayed, E. A. M., and Suleiman, H. S.(2010) Heterosis and combining ability for yield and its components in diallel crosses among seven bread wheat genotypes. *Egypt. J. Plant Breed*. 14 (3): 7 – 22

Sharma, S. K., SINGH, I., and Singh, K. P. (1986). Heterosis and combining ability in wheat (*T. aestivum* L.).

Singh, H., Sharma, S. N., and Sain, R. S. (2004). Heterosis studies for yield and its components in bread wheat over environments. Hereditas, 141(2), 106-114.

Zeeshan, M., Arshad, W., Khan, M. I., Ali, S., and Tariq, M. (2014). Character association and casual effects of polygenic traits in spring wheat (*Triticum aestivum* L.) genotypes. *International Journal of Agriculture, Forestry and Fisheries*, 2(1): 16.

Zhang, W., Liu, G., and Bai, C. (2007). A forecast analysis on global production of staple crops.

How to cite this article:

Sameer Upadhyay, Naveen Dubey, P. S. Yadav and Mishra, V. K. 2020. Estimation of Heterobeltiosis and Character Associations for Yield and Yield Attributing Traits in Bread Wheat (*Triticum aestivum* L.) Genotypes. *Int.J.Curr.Microbiol.App.Sci.* 9(04): 2734-2747.
doi: https://doi.org/10.20546/ijcmas.2020.904.323