

Combining Ability and Component Analysis in Bread Wheat (*Triticum aestivum* L.)

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ABSTRACT

In the present study a diallel set of 9×9 was attempted by crossing nine bread wheat genotypes in all possible combinations excluding reciprocals. The mean squares of nine diverse parents and 36F1s due to GCA and SCA component were significant for all the thirteen traits. These outcomes show the importance of additive variance in the inheritance of all the traits. The comparative importance of additive and non-additive components was revealed by checking the components of variance (s^2g and s^2s), heritability in broad-sense (Hb), narrow-sense (Hn) and gca/sca ratio. The magnitude of GCA component (s^2g) and gca/sca ratio was higher for plant height and peduncle length, indicating that these two traits were under the control of additive genetic variance and all the others traits were controlled by non-additive genetic component. Based on general combining ability effects and *per se* performance, parents WH1184, HD3086 and HD3059 were found the good general combiners for grain yield per plant. On the basis of *per se* performance and SCA effects the crosses viz., HD2967 \times WH1184 and HD3059 \times Raj3765 were found as

good specific cross combination. These crosses can be extensively used in further breeding programs to develop superior pure lines.

Keywords Bread wheat, Diallel, Combining ability, gene effects, grain yield.

INTRODUCTION

Wheat is known to be cultivated since prehistoric times and known as traditional crop of India (Kumar *et al.* 2017). It is nutritionally important cereal essential for the food security, poverty alleviation and is a cheap source of carbohydrates and proteins. It is widely cultivated as staple food crop among the cereals and is contributing about 30% to the food basket of the country. India is the second largest wheat producing country after China (Singh *et al.* 2018). In India, it is grown on an area 29.55 m hecter with total production 101.3 m tonnes and productivity 3.4 tones/ha (Anonymous 2019-20). In Haryana, wheat is grown on an area of 25.65 lakh ha with a production of 11.60 lakh tonnes and productivity of 4.6 tones/ha (Anonymous 2019-20).

The identification of superior parents and understanding of various characters are the important pre-requisites for launching efficient and effective breeding program. Since the phenotypically superior lines may yield poor so the assortment of parents is not only on the basis of their phenotypic performance. It is, therefore important that parents should be chosen on the basis of their genetic value. Advancement in the yield of bread wheat requires adequate infor-

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mation regarding the nature of combining ability of the parents to be used in the hybridization program and also the nature of gene actions involved in the expression of quantitative and qualitative traits of economic importance. Sprague and Tatum (1942) coined the terms “General combining ability” (GCA) and “Specific combining ability” (SCA), respectively. Griffing (1956) proposed its mathematical modelling in combination with diallel crosses in his classic article. Any population’s worth is determined by its inherent potential as well as its ability to combine in crosses (Vacaro *et al.* 2002). The effects of general combining ability (GCA) and specific combining ability (SCA) can be used to estimate the predominant genes that regulate adaptive traits (Dholariya *et al.* 2014, Masood *et al.* 2014). Several complex agronomic traits in wheat are regulated by both additive and nonadditive gene behavior, according to previous research (Adel and Ali 2013). Yield is a complex trait controlled by several components each influenced by polygenes with minor genetic effects (Farshadfar *et al.* 2014).

For the choice of suitable breeding methods and desirable genotypes from the segregating populations, the knowledge of nature and mode of actions of genes, their inheritance as well as the knowledge about both the types of combining abilities is very important.

Since the improvement in grain yield can be due to favorable combination of yield components and selection of genetically desirable parents after the analysis of various yield related traits are the preliminary breeding steps which can certify success in wheat breeding methods (Ilker *et al.* 2009). The diallel analysis is helpful to assess nicking ability of the parents and nature and magnitude of gene actions. Diallel mating design is one that allows the parents to be crossed in all possible combinations including reciprocals (Pospisilova 2010). The most frequently used method for parent selection and as an appropriate design to get genetic information of yield attributes in very short period of time is diallel analysis, which can be used for the estimation of genetic variance (Kohan and Heidari 2014, Jinks and Hayman 1953, Hayman 1954, Griffing 1956, Gardner and Eberhart 1966).

MATERIALS AND METHODS

Nine diverse wheat genotypes namely WH1105, HD2967, HD3086, HD3059, Raj3765 WH1124, WH283, WH711 and WH1184 were selected as parents on the basis of their origin, adaptability, diversity, yield potential, drought and heat tolerance traits. Pedigree and source of parents are given in Table 1. The nine parents along with 36 F₁s were evaluated in randomized Block Design with three replications under timely sown irrigated at wheat research area, Department of Genetics and Plant Breeding, CCS HAU, Hisar. Each entry was evaluated in single row of 2.5 meter length. Row to row and plant to plant distance was kept at 20 cm and 10 cm, respectively. All recommended agronomic practices were followed during the entire cropping season. Five irrigations were given during the entire crop period.

Five random plants were selected for the observations among the parents and F₁s of each row and the observations recorded for thirteen traits namely, days to heading, days to maturity, plant height, number of productive tillers per plant, spike length, grain weight per spike, main spike weight, number of grains per spike, 100 grain weight, biological yield per plant, grain yield per plant, harvest index. Parents and one set of F₁s without reciprocals were analyzed according to model-I (fixed effects) Griffing (1956) approach. Both the specific and general combining abilities were analyzed. The data will be subjected to statistical analysis suggested by Hayman (1954) and Griffing (1956).

RESULTS AND DISCUSSION

In the present investigation magnitude of GCA component (s^2_g) reported higher than SCA component (s^2_s) for plant height and peduncle length, indicating that these two traits were under the control of additive genetic variance. Similarly both these traits, plant height and peduncle length have more than one *gca/sca* ratio, indicating the preponderance of additive gene action, while the *gca/sca* ratio for all other traits was found less than unity, showed non additive genetic components play a role.

Heritability estimation adds to our understanding

Table 1. Pedigree and source of nine parents.

Parent	Pedigree	Source
WH1105	MILAN/S87230// BABAX	CCS HAU, Hisar
HD3059	KAUZ//ALTAR84// ADS/3/MILAN/ KAUZ/4/HUITES	IARI, New Delhi
WH1124	MUNIA/CHTO/ AMSEL	CCS HAU, Hisar
WH711	ALD'S/HUAC// HD2285/3/HFW17	CCS HAU, Hisar
HD2967	ALD/CUC//URES/ HD2160/HD2278	IARI, New Delhi
WH1184	HD2850/WH147	CCS HAU, Hisar
WH283	HD1981/Raj821	CCS HAU, Hisar
Raj3765	HD2402/VL639	RAU, Durgapura
HD3086	DBW14/HD2733// HUW468	IARI, New Delhi

of the function of genetic influences in total phenotypic variance. Out of thirteen traits, only three traits viz., plant height, number of grains per spike and peduncle length showed additive variance, while the remaining traits showed non additive variance. Combining ability analysis helps to determine the breeding values of genotypes. Thus based on the breeding potential or value, breeder can find out the superior general combiner and also identify best crosses for the further use in breeding programs.

Analyses of variance revealed mean squares GCA were found highly significant ($P \leq 0.01$) for all studied traits (Tables 1–6). Means squares for SCA were also highly significant ($P \leq 0.05$) for all the studied traits.

In bread wheat, pure line breeding and development of superior pure lines from the hybrids having high SCA effect as well as mean value is of great importance. Significant differences were found due to SCA and GCA for all the thirteen traits, indicating role of additive variance in the inheritance of these characters. The extent of s^2_g (GCA) component was higher than s^2_s (SCA) component for plant height and peduncle length, indicating that these two traits were under the control of additive genetic variance. All other traits were controlled by non additive genetic component. These results were also supported by earlier findings viz., Sharma *et al.* (2003), Khan *et*

al. (2007), Singh *et al.* (2012), Mandal and Madhuri (2016) and Ahmed *et al.* (2017).

For all the characters except plant height and peduncle length, the value of H_1 component was higher than that of D component indicating a more significant role of non-additive gene action in the inheritance of these characters. Net dominance component (h^2) was found significant for the traits plant height, spike length, main spike weight, grain weight per main spike, number of grain per main spike and 100 grain weight, whereas for rest of traits it was non-significant. Covariance of additive and non additive components (F) is used in parent population to find the virtual frequencies of dominant and recessive alleles. The significant and positive value of F was reported for the traits, days to heading, plant height, grain weight per main spike, peduncle length and biological yield per plant, signifying the presence of dominant genes in excess between the parents for these traits. For the rest of characters, F component was found non-significant sharing equal amount of dominant and recessive genes. The estimate of narrow-sense heritability was higher for the traits viz., plant height, peduncle length and number of grains per spike. Parents HD2967 and WH1184 were found good general combiner for the most of the traits. Verma *et al.* (2016) found the parents K9423, GW373, PBW343, K8962, Sonalika and HD2733 were best general combiners for grain yield and its component trait.

Based on GCA of parents, genotypes WH283, WH1105 and WH711 were considered as good general combiners for earliness. Six crosses, namely, WH1105 \times HD2967, WH1105 \times WH1124, HD2967 \times HD3086, HD2967 \times WH1184, HD3059 \times WH283 and WH283 \times WH711 showing significant negative specific combining ability effects and considered as better cross combinations for early flowering Mandal and Madhuri (2016), Ahmed *et al.* (2017) and Patel *et al.* (2018) recognized best crosses on the basis of these effects for days to heading and maturity.

The parents Raj 3765 and WH711 were found desirable for dwarfness on the basis of GCA effect. There was only one cross, namely, WH1105 \times WH1124 which showed negative and significant

Table 2. Analysis of variance for combining ability for thirteen traits in wheat (Griffing's Model I, Method 2). *,**significant at P=0.05 and 0.01, respectively.

Source	df	Days to heading	Days to maturity	Plant height (cm)	Number of tillers per plant	Spike length (cm)	Main spike weight (g)
GCA	8	7.45**	18.18**	101.11**	7.29**	1.13**	0.26**
SCA	6	8.67**	6.01**	8.34*	4.04**	0.40*	0.09**
Error	88	0.979	2.346	4.806	0.649	0.182	0.045

Table 2. Continued.

Source	df	Grain weight per main spike (g)	Number of grains per spike	Peduncle length (cm)	100 grain weight (g)	Grain yield per plant (g)	Biological yield per plant (g)	Harvest index (%)
GCA	8	0.19**	123.61**	25.99**	0.280**	33.54**	160.24**	63.90**
SCA	6	0.07**	28.15**	1.770**	0.082**	30.59**	110.41**	39.43**
Error	88	0.02	4.215	0.823	0.015	2.701	17.654	6.974

SCA effects indicating that it was good hybrid for dwarfness. Parents HD2967, HD3086, WH711 and WH1184 recorded significant positive general combining ability, indicating that these varieties were found good general combiner for productive tillers per plant. Significant positive SCA effects showed by crosses namely, WH1105 × WH711, HD2967 × WH283, HD3086 × HD3059 and HD3086 × WH711 and thus suggesting that these hybrids were good combiner for more number of productive tillers. Mandal and Madhuri (2016), Ahmed *et al.* (2017) and Patel *et al.* (2018) also identified good general combiner for number of productive tillers per plant

in wheat.

Significant positive general combining effects were recorded for the parents WH1105, HD2967, HD3086, HD3059, WH1124 and WH711 and found that these were good general combiner for spike length. The crosses namely, WH1105 × WH1124, WH1105 × WH711, HD2967 × WH283 and HD3086 × WH711 found significant positive specific combining ability effects for the trait spike length. Patel *et al.* (2018) also identified similar findings.

The parents Raj 3765, HD 2967, HD3086,

Table 3. Components of combining ability, heritability (narrow sence) and *gca/sca* ratio in diallel using Model I, Method 2 (Griffing 1956).

Components	Days to heading (no)	Days to maturity (no)	Plant height (cm)	Number of tillers per plant (no)	Spike length (cm)	Main spike weight (g)	Grain weight per main spike (g)	Number of grains per spike (no)	Peduncle length (cm)	100 grain weight (g)	Grain yield per plant (g)	Biological yield per plant (g)	Harvest index (%)
s ² _g	0.59	1.44	8.76	0.6	0.09	0.02	0.02	10.85	2.29	0.02	2.8	12.96	5.18
s ² _s	7.7	3.67	3.53	3.39	0.22	0.05	0.05	23.94	0.95	0.07	27.89	92.76	32.46
H _n	0.12	0.32	0.68	0.23	0.3	0.29	0.31	0.44	0.72	0.37	0.16	0.19	0.21
H _b	0.9	0.74	0.81	0.88	0.69	0.68	0.81	0.92	0.87	0.89	0.93	0.87	0.86
<i>gca/sca</i>	0.08	0.39	2.48	0.18	0.39	0.37	0.3	0.45	2.42	0.36	0.1	0.14	0.16

Table 4. Estimates of general combining ability (gca) effects (Griffing 1956). *,**significant at P=0.05 and 0.01, respectively.

Compo- nents	Days to head- ing (no)	Days to matu- rity (no)	Plant height (cm)	Num- ber of till- ers per plant (no)	Spike length (cm)	Main spike wei- ght (g)	Grain wei- ght per main spike (g)	Num- ber of grains per spike (no)	Ped- uncle len- gth (cm)	100 grain wei- ght (g)	Grain yield per plant (g)	Bio- logi- cal yield per plant (g)	Har- vest index (%)
WH1105	-0.13	-0.72	0.22	1.22*	-0.13	-0.08	-0.02	3.60*	0.35	-0.32*	1.19*	1.09*	0.37*
HD2967	0.93*	2.30*	1.80*	1.40*	-0.02	0.20*	0.09*	1.91*	-0.35	-0.01	2.24*	-0.65	3.43*
HD3086	0.09	-0.09	1.40*	0.60*	-0.26*	0.07	0.11*	1.21*	1.11*	0.06	1.06*	2.31	0.55
HD3059	0.99*	0.88*	0.71	-0.34	-0.34*	0	0.04	1.79*	-1.81*	-0.08*	1.32*	3.45*	3.64*
Raj3765	0.36	-0.6	-1.14	-0.96*	0.27*	-0.17*	-0.06	-2.26*	1.08*	0.14*	0.18	-1.25	1.12
WH1124	0.15	-0.82	0.05	-0.09	-0.25*	-0.04	-0.04	-0.85	0.76*	-0.08*	1.42*	0.49	1.56*
WH283	-1.36*	-2.11*	0.32	-0.13	0.25*	-0.14*	-0.26*	-5.66*	0.99*	-0.01	-0.01	6.80*	3.16*
WH711	-1.215*	1.03*	-7.19*	0.13	-0.15	-0.11	-0.06	-3.78*	-3.20*	0.23*	1.54*	2.49*	-1.28
WH1184	0.18	0.13	3.82*	0.620*	0.63*	0.27*	0.19*	4.03*	1.06*	0.07*	1.36*	4.32*	-0.37
SE (gi)	0.28	0.44	0.62	0.23	0.12	0.06	0.04	0.58	0.26	0.03	0.47	1.19	0.75
SE (gi-gj)	0.42	0.65	0.93	0.34	0.18	0.09	0.06	0.88	0.39	0.05	0.7	1.79	1.13
CD at 5% (gi-gj)	0.84	1.3	1.86	0.68	0.36	0.18	0.12	1.74	0.77	0.1	1.39	3.56	2.24

HD3059, WH1124 and WH1184 WH711 were found significant and positive general combining effects, indicates that these were good combiners for grain weight per main spike. The cross combinations, namely, WH1105 × Raj 3765, HD2967 × WH711, HD2967 × WH1184, HD3086 × HD3059, HD3086 × WH1124, HD3086 × WH283, HD3059 × WH711, WH283 × WH711 and WH711 × WH1184 exhibited significant and positive SCA effects for the trait grain weight per main spike. Thus these crosses were considered as good combiner for this trait.

The cultivars WH1105, HD3086, HD3059, WH1184 and HD 2967 showing significant positive general combining effects and considered the good general combiners for the trait number of grains per spike. The cross combination, namely, WH1105 × Raj3765, HD2967 × WH711, HD2967 × WH1184, HD3086 × HD3059, HD3086 × WH1124, HD3086 × WH283, HD3086 × WH1184, HD305 × WH1124, Raj3765 × WH283, WH1124 × WH711 WH283 × WH1184 and WH711 × WH1184 exhibited significant and positive SCA effects for the trait number of

Table 5. Estimates of components of genotypic variance and their ratios for studied traits. *,**significant at = 0.05 and 0.01, respectively.

Compo- nents	Days to head- ing (no)	Days to matu- rity (no)	Plant height (cm)	Num- ber of till- ers per plant (no)	Spike len- gth (cm)	Main spike wei- ght (g)	Grain weight per main spike (g)	Num- ber of grains per spike (no)	Ped- uncle len- gth (cm)	100 grain wei- ght (g)	Grain yield per plant (g)	Bio- logi- cal yield per plant (g)	Har- vest index (%)
D	12.78*	7.90*	52.62*	1.67	0.39*	0.08*	0.10*	70.60*	10.27*	0.03	8.36	162.97*	6.69
H ₁	40.82*	15.44*	23.82*	15.3*	1.08*	0.21*	0.24*	103.8*	6.01*	0.28*	130.6*	459.62*	155.8*
H ₂	27.43*	15.97*	18.24*	14.1*	0.90*	0.21*	0.19*	88.82*	4.32*	0.26*	106.4*	362.95*	129.5*
F	23.56*	1.85	25.43*	0.05	0.17	-0.01	0.08*	44.86	2.66*	-0.07	16.12	212.51*	3.61
h ²	0.86	25.63	14.13*	-0.27	2.14*	0.65*	0.25*	76.78*	0.3	0.22*	0.2	15.16	8.26
E	0.99	2.33*	4.94*	0.72	0.18*	0.05*	0.02*	4.18	0.91*	0.02	3.08	17.98	7.62

Table 6. Estimates of specific combining ability (sca) effects (Griffing 1956).

Components	Days to heading (no)	Days to maturity (no)	Plant height (cm)	Number of tillers per plant (no)	Spike length (cm)	Main spike weight (g)	Grain weight per main spike (g)	Number of grains per spike (no)	Peduncle length (cm)	100 grain weight (g)	Grain yield per plant (g)	Biological yield per plant (g)	Harvest index (%)
WH1105×HD2967	-4.05*	-4.35*	-0.73	-1.58*	-0.11	0.16	-0.07	1.38	0.52	0.09	-6.27*	-3.6	-7.50*
WH1105×HD3086	1.47*	-0.95	-0.93	-0.78	0.04	-0.09	-0.11	-2.59	0.56	0.18*	-6.56*	-12.65*	-3.45
WH1105×HD3059	-1.44*	1.41	0.16	-0.13	0.12	-0.03	-0.06	0.5	0.46	-0.1	6.12*	14.45*	1.19
WH1105×Raj3765	1.19	2.90*	4.68*	0.53	0.41	0.35*	0.51*	7.56*	-0.31	0.15	-6.41*	-9.38*	-5.75*
WH1105×WH1124	-3.59*	1.11	-4.12*	-1.91*	0.67*	0.14	-0.12	-1.53	-2.45*	-0.30*	-1.34	0.02	-2.17
WH1105×WH283	2.92*	0.08	-0.32	0.27	-0.4	-0.50*	-0.41*	-5.04*	0.48	-0.44*	2.04	0.99	2.63
WH1105×WH711	4.10*	1.26	2.46	4.10*	0.62*	0.04	-0.06	0.41	0.38	-0.15	6.39*	2.61	8.65*
WH1105×WH1184	0.71	4.50*	1.24	-2.20*	0.23	0.33*	0.18	0.59	0.84	0.25*	-1.26	-6.20*	1.73
HD2967×HD3086	-3.26*	-1.98	7.62*	-2.69*	-0.5	-0.27	-0.33*	-10.56*	1.23*	-0.24*	-4.49*	3.38	-8.06*
HD2967×HD3059	1.83*	1.38	-0.95	-0.13	0	-0.25	-0.14	-3.13*	-0.24	-0.25*	-2.53*	0.14	-3.42
HD2967×Raj3765	1.47*	-0.13	1.63	-2.13*	0.57	-0.02	-0.08	-2.07	0.19	0.07	7.32*	-10.40*	18.64*
HD2967×WH1124	3.68*	3.75*	0.84	-0.18	-0.03	0.42*	0	-1.83	0.77	0.26*	-4.16*	-7.52*	-2.45
HD2967×WH283	1.53*	2.38*	-0.16	4.37*	1.41*	0.26	0.05	-5.01*	-2.46*	0.62*	1.63	-0.45	1.92
HD2967×WH711	-0.62	2.23*	1.25	0.43	0.11	0.32*	0.45*	11.44*	0.61	0.11	7.02*	13.37*	2.4
HD2967×WH1184	-4.35*	-1.19	-1	4.85*	-0.81*	-0.07	0.28*	4.96*	2.14*	-0.15	9.82*	-0.64	13.49*
HD3086×HD3059	-1.66*	1.11	1.91	2.57*	0.59*	0.52*	0.19*	6.23*	-0.57	0.06	0.51	-4.04	2.87
HD3086×Raj3765	0.65	3.93*	-3.7	-0.03	-0.16	-0.23	0.07	1.96	0.86	0.11	3.32*	7.81*	1.06
HD3086×WH1124	1.19	0.81	-0.16	0.19	0.47	0.16	0.34*	7.20*	-0.83	-0.06	0.49	-11.98*	7.37*
HD3086×WH283	-0.96	3.78*	0.13	0.7	0.55	0.45*	0.39*	4.35*	-0.08	0.35*	1.86	4.26	0.54
HD3086×WH711	8.00*	-0.38	2.57	2.14*	0.69*	0.43*	-0.17	-1.53	1.77*	0.64*	7.67*	9.78*	5.19*
HD3086×WH1184	-0.17	-1.13	-1.87	-2.95*	-0.03	-0.14	-0.11	4.66*	-1.12	-0.26*	-5.71*	-21.26*	2.91
HD3059×Raj3765	1.41*	-2.71*	3.06*	2.38*	0.05	0.15	-0.17	-2.95*	1.53*	0.07	8.81*	1.74	11.20*
HD3059×WH1124	0.62	-1.16	2.87	-0.5	0.23	-0.02	0.12	4.96*	1.05	0.04	1.48	9.12*	-3.05
HD3059×WH283	-5.20*	0.14	-1	0.04	0.28	0.13	0.16	1.44	-1.95*	-0.03	4.95*	7.36*	2.22
HD3059×WH711	1.65*	2.32*	-0.35	-2.60*	-0.2	0.03	0.23*	-1.77	-0.67	0.28*	-8.73*	-15.02*	-4.44*
HD3059×WH1184	-2.75*	1.9	0.02	1.92*	0.02	0.01	0.01	-1.92	0.61	0.3	7.43*	19.60*	-0.38
Raj3765×WH1124	1.26	2.32*	-2.22	0.06	-0.85*	-0.18	-0.32*	-4.65*	-1.85*	-0.16*	1.82	15.44*	-4.86*
Raj3765×WH283	1.77*	0.96	1.11	-0.83	0.19	0.22	0.13	11.17*	1.51*	0.08	2.13	-2.85	3.74*
Raj3765×WH711	1.95*	0.81	-1.71	-1.99*	0.62*	0.07	0.07	-0.38	1.31*	-0.1	-6.96*	-14.39*	-3.38
Raj3765×WH1184	-1.78*	-0.95	1.61	-0.25	0.84*	0.11	0.20*	1.14	1.09	0.26*	-2.44*	6.96*	-6.52*
WH1124×WH283	-3.69*	-0.5	2.04	-1.31*	-0.34	0.16	0.1	-0.26	1.49*	0.44*	-2.79*	0.39	-3.85*
WH1124×WH711	1.50*	-1.32	-0.83	1.70*	-0.07	-0.1	-0.1	4.20*	-0.9	0.04	1.58	11.69*	-2.8
WH1124×WH1184	-1.90*	1.26	-2.79	-0.37	-0.29	0.1	0.11	0.05	-0.77	0.16*	-3.32*	-4.8	-2.58
WH283×WH711	-4.99*	-3.68*	5.86*	-1.59*	0.47	0.2	0.26*	0.02	-1.41*	-0.39*	-6.48*	-15.61*	-2.33
WH283×WH1184	-0.38	0.56	-1.62	-1.52*	0.73*	0.40*	0.08	2.87*	-0.37	-0.18*	-3.45*	-3.62	-2.58
WH711×WH1184	4.47*	0.41	-0.34	-1.15*	-0.1	0.06	0.33*	3.99*	-0.14	0.18*	-4.64*	-3.8	-4.60*
SE (S _{ii})	0.8	1.24	1.77	0.65	0.35	0.17	0.11	1.66	0.73	0.1	1.33	3.4	2.14
SE (S _{ij})	0.9	1.4	2	0.74	0.39	0.19	0.13	1.88	0.83	0.11	1.5	3.84	2.42
SE (S _{ii} -S _{ij})	1.12	1.73	2.47	0.91	0.48	0.24	0.16	2.32	1.02	0.14	1.85	4.74	2.98
SE (S _{ij} -S _{ik})	1.33	2.07	2.96	1.09	0.58	0.29	0.19	2.77	1.22	0.16	2.22	5.67	3.56
SE (S _{ij} -S _{kl})	1.27	1.96	2.8	1.03	0.55	0.27	0.18	2.63	1.16	0.15	2.1	5.37	3.38

grains per spike and revealed that these combinations were good combiner for this trait. Our results are in accord with the prior findings in wheat reported by Singh *et al.* (2012), Ahmed *et al.* (2017), and Patel *et al.* (2018).

The cultivars HD3059 and WH711 were found significant and having negative GCA effects for peduncle length. Significant and positive SCA effects were shown by the crosses, namely, HD2967 × HD3086, HD2967 × WH1184, HD3086 × WH711,

HD3059 × Raj3765, Raj3765 × WH283 Raj3765 × WH711 and WH1124 × WH283 and suggesting that these combination were the good for the peduncle length. Similarly cultivars viz, WH711, WH1184, HD2967, HD3086 and Raj 3765 were observed significant and positive GCA effects for 100 grain weight and ten cross combinations, namely, WH1105 × HD3086, WH1105 × WH1184, HD2967 × WH1124, HD2967 × WH283, HD3086 × WH283, HD3086 × WH711, HD3059 × WH711, WH1124 × WH283, WH1124 × WH711 and WH711 × WH1184 showed significant positive specific combining ability effects. The varieties HD 2967, HD3086, HD3059 and WH1184 were found to be the good general combiners for grain yield per plant. The positive significant SCA effects for grain yield per plant shown by three crosses viz., WH1105 × WH711, HD2967 × Raj3765 and HD2967 × WH711. Muhammad *et al.* (2009) found two crosses viz., Faisalabad 83 × PBW 502 and Faisalabad 85 × PBW 502 and found that these cross combinations were better for grain yield in bread wheat. Similar findings were reported by Singh *et al.* (2012), Ahmed *et al.* (2017) and Patel *et al.* (2018).

The cultivar WH283, HD3059 and WH1184 were considered as good general combiner for the trait biological yield per plant. Crosses, namely, WH1105 × HD3059, HD2967 × WH711, HD3086 × Raj3765, HD3086 × WH711, HD3059 × WH1124, HD3059 × WH 283 and Raj 3765 × WH1124 which expressed positive specific combining ability effects for biological yield per plant. The good general combiners for harvest index were HD2967 and HD3059 as they have significant positive general combining effects. Only the crosses, namely, WH1105 × WH711, HD2967 × Raj3765, HD2967 × WH1184, HD3086 × WH1124, HD 308 × WH711, HD 3059 × Raj 3765 and Raj3765 × WH283 represented positive and significant SCA effects for harvest index. Similar findings were prior observed by Kumar (2010), Singh *et al.* (2012), Ahmed *et al.* (2017) and Patel *et al.* (2018).

Out of thirteen traits, ten traits viz, Days to heading, days to maturity, plant height, spike length, main spike weight, grain weight per main spike, number of grains per main spike, peduncle length and biological yield per plant all had significant estimates of additive genetic variance (D) component. Dere and Yildirim

(2006) found that the additive variance component (D) was significant for spike height, plant height and 1000 kernel weight. Both H_1 and H_2 components were found significant for all the thirteen characters. Plant height and peduncle length have higher magnitude of D component than dominance components showing that these were under additive gene effects.

Except for plant height and peduncle length, all other characters have a higher H_1 component than D component, suggesting a greater contribution of non-additive gene action in the inheritance of these characters in subsequent generations. 9793 118 and Punjab-2011 108 were identified by Farooq *et al.* (2019) as the best unique combiners with substantial SCA effects.

sPlant height and peduncle length have a high GCA/SCA ratio, suggesting that additive gene effects predominate, whereas the remaining traits have a low GCA/SCA ratio, indicating that non additive genetic factors play a role in controlling these traits. Mandal and Madhuri (2016) found that all the studied traits were under non additive gene effects due to low gca/sca ratio i.e. less than one. The h^2 component was found to be significant for plant height, main spike weight, spike length, grain weight per main spike, number of grains per main spike and 100 grain weight, but not for the remaining seven traits. Similar results were previously recorded by Dere and Yildirim (2006).

CONCLUSION

An overall appraisal of GCA effects in present study, the genotypes WH1184, HD3086 and HD3059 were found significant and good general combiners for grain yield per plant. The crosses WH1105 × WH711, HD2967 × Raj3765, HD2967 × WH711, HD2967 × WH1184, HD3086 × Raj 3765, HD 3059 × Raj3765 and HD3059 × WH1184 showed significant positive SCA effects and high *per se* performance for grain yield per plant. Additive and additive × additive gene effects were related to high GCA effects that are due to the accumulation of favourable alleles. The occurrence of both additive and non-additive variances suggests the utilization of these parents and crosses for future breeding programme respectively. Hence,

use of diallel crosses with recurrent selection and pedigree selection could be suggested to exploit both additive and non additive component for the genetic enhancement in bread wheat.

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