Combining ability for high temperature tolerance and yield contributing traits in bread wheat

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Abstract

Combining ability analysis for high temperature tolerance in bread wheat (*Triticum aestivum* L. Em. Thell.) involving ten diverse parents and their 45 F_1 and F_2 progenies indicated significant differences among the parents for *gca* and crosses that of *sca* for all the characters studied. The *gca* and *sca* components of variance were significant for all the traits. The *gca/sca* variance ratio below unity in both the generations showed the preponderance of non-additive gene effects for all the characters. Based on general combining ability (*gca*) effects and *per se* performance, parents WH 789 and HD 2881 emerged as good general combiners for grain yield per plant and average to high combiners for most of the yield component characters in case of very late sown condition, it means, these genotypes probably possessed the desirable genes for high temperature tolerance during grain filling period. These genotype possessed desirable GCA effects for biological yield per plant, number of grains per spike, 1000 - grain weight, peduncle length, tillers per plant, days to heading and harvest index. On the basis of *per se* performance and SCA effects the crosses for grain yield were UP 2614 x HD 2851, WH 789 x PBW 520, HUW 468 x UP 2614 and HUW 468 x PBW 520 which emerged as good specific cross combinations. These crosses were the product of good x good, good x poor or poor x poor general combiners. Hybridization systems, such as multiple crossing and bi-parental mating could be useful in the genetic improvement for further amelioration of grain yield per plant in bread wheat.

Key words: Bread wheat, combining ability, gene effects, yield components

Introduction

Bread wheat (*Triticum aestivum* L. em. Thell.) is the second most important cereal crop after rice in the context to its antiquity and its use as source of food and energy in India. India is the second largest producer of wheat in the world with the production of around 93.9 million tons during 2011-12 that accounts for approximately 12 percent of world's wheat production (Anonymous, 2012). Clearly, wheat and its products play an increasingly important role in managing the country's food economy.

Continuous varietal improvement and their adoption have pushed the wheat productivity to new levels. Increase in productivity, however, has not been uniform all over the country and this indicates the opportunities and areas of increasing wheat production in future. Hence, there is need to develop varieties with early maturing and heat tolerant wheat varieties coupled with high yield. The success of a plant breeding programme largely depends upon the choice of desirable parents for hybridization of superior recombinants in the segregating generations on the basis of their heterotic performance and combining ability. Knowledge of gene action, heritability of the characters and genetic content of the parents is also needed.

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The isolation of superior and transgressive segregates in the advance generations equal or superior to the F_1 depends upon the type of gene action predominantly responsible for the expression of characters. The diallel analysis was developed in order to provide information on the genetic architecture of the breeding material, which helps in the identification of parents to be included in a future breeding programme for tangible advancement of bread wheat crop. The present investigation has, therefore, been intended to select parents for effective hybridization programme as well as to identify superior cross combination in very late sown condition for improving heat tolerance in wheat.

Material and methods

Ten diverse genotypes of bread wheat (*Triticum aestivum* L. em. Thell.) namely, HD 2881, HS 448, WH 789, HUW 468, UP 2614, NW 3015, PBW 520, K 209, HD 2851 and Raj 4063 were selected on the basis of a broad range of genetic diversity for major yield components, geographical origin and their suitability for different yield traits. The experiment was conducted during *rabi* 2010-11 at Research Farm of Agricultural Research Station, Durgapura, Jaipur. It is situated at 26^0 51'N latitude and 75^0 47' E longitude and an altitude of 300 meters above mean sea level in Rajasthan, India. Ten parents and their resulting 45 F_1s and 45 F_2s were grown in a randomized complete block design with three replications under normal (15th November) and very late (15th January) sown conditions. In each replication, parents and F_1s were sown by dibbling the seed in a plot of two rows of 4 m length while each F_2 plot consisted of six rows, with 30 cm spacing between rows and 10 cm between plants. Non experimental rows were planted all around the experimental plot to avoid border effects. All the recommended cultural practices including one weeding and hoeing and six supplementary irrigations were applied to raise a good crop. Twenty competitive plants in parents and F_1s while sixty plants in F_2 progenies were selected randomly from each replication for recording observation on fourteen morphological / agronomical parameters *viz*., days to heading, days to maturity, plant height (cm), number of tillers per plant, flag leaf area (cm^2), peduncle length (cm), spike length (cm), number of spikelets per spike, number of grains per spike, grain yield per spike (g), 1000-grain weight (g), biological yield per plant (g), harvest index (%) and grain yield per plant (g). The mean of each plot was used for statistical analysis. The data were first subjected to the usual analysis followed for a randomized block design for pooled (normal and very late) environments as well as for individual environment (Panse and Sukhatme, 1967). The combining ability analyses were carried out following Method II, Model I of Griffing (1956).

Results and discussion

The analysis of variance (ANOVA) indicated significant differences among the genotypes for all the characters. Similarly, the differences among F_1 hybrids and F_2 progenies were significant for all the characters, thus explained the fact that the characters exhibited the presence of adequate genetic variability among the parents. The differences between parent's vs F_1 were found significant for all the characters. Mean squares due to F_1s vs F_2s were found significant for all the characters except for days to heading, plant height, flag leaf area and harvest index (Table 1), indicated the presence of heterosis. Significant differences among genotypes for grain yield and its related traits in different sets of material were also reported by Manmohan *et al.* (2003), Shoran *et al.* (2005) and Prakash (2007). Analysis of variance for combining ability revealed that the variance due to general combining ability (*gca*) and specific combining ability (*sca*) were highly significant for all the traits studied in both F_1 and F_2 generations (Table 2). Thus, both kinds of gene effects figured important in controlling the inheritance of all the characters studied. The *gca/sca* variance ratio below unity in both the generations, except days to heading in F_1generation, showed the preponderance of non-additive gene effects in both the generations for all the characters studied. Similar results were earlier reported by Joshi *et al.* (2003), Desai *et al.* (2005) and Jag Shoran *et al.* (2005). Some differences in the reports occur because of the differences in the experimental material and conditions under which evaluation is done. It is thus, evident that grain yield and other characters are controlled by both additive and non-additive gene effects.

However, *sca* variance was more pronounced than *gca* variance for all the characters studied. The preponderance of non-additive genetic variance for all the characters indicated that the best cross combinations might be selected on the basis of *sca* for further tangible advancement in wheat.

On the basis of general combining ability (*gca*) effects and *per se* performance, it was revealed that among parents, WH 789 and HD 2881 emerged as good general combiners for grain yield and good to average combiner for most of the yield component characters (Table 3). However, rest of the parents were poor combiners for grain yield and average to poor general combiners for most of the yield contributing traits. The parent, HD 2851 was the best general combiners for early heading, early maturity, plant height, number of tillers per plant, peduncle length, spike length, number of spikelet per spike, number of grains per spike, grain yield per spike, 1000- grain weight, biological yield per plant, harvest index and grain yield per plant; WH 789 for early heading, early maturity, number of tillers per plant, peduncle length, number of grains per spike, grain yield per spike, 1000- grain weight, biological yield per plant, harvest index and grain yield per plant; HUW 468 for early heading, number of tillers per plant, flag leaf area, peduncle length, number of spikelet per spike, number of grains per spike, number of grains per spike, biological yield per plant and grain yield per plant; Raj 4063 for early heading, early maturity, flag leaf area, peduncle length, spike length, number of spikelet per spike, number of grains per spike, biological yield per plant and grain yield per plant; HS 448 for early heading, plant height, flag leaf area, spike length, 1000- grain weight, harvest index and grain yield per plant; UP 2614 for plant height, flag leaf area, spike length and number of spikelet per spike; HD 2881 for early maturity, plant height and harvest index; K 209 for early maturity, plant height and flag leaf area and NW 3015 for flag leaf area and spike length. Therefore, these parents have good potential and may be used in synthesizing a dynamic population with most of the favourable genes accumulated. Apparently, thus, there is still further scope for improving upon the combining ability for component traits, as none of high combiners for grain yield was a high combiner or at least an average combiner for all the desirable traits. In bread wheat, parents having good general combining ability have been reported by several workers (Joshi *et al*., 2003 and Desai *et al*., 2005).

Table 1. Analysis of variance showing mean squares for parents, F_1s and F_2s for different characters of bread wheat

Characteristics	Replication	Genotype	Parent	F_1	F_2	Ps vs. F_1	F_1 vs. F_2	Error
df	2	99	9	44	44	1	1	198
Days to heading	2.11	6.41**	9.51**	4.90**	7.46**	4.93*	0.03	0.9
Days to maturity	0.07	8.11**	3.86**	5.33**	10.08**	32.15**	80.03**	1.17
Plant height (cm)	4.62	55.36**	18.87**	51.61**	51.72**	712.86**	1.43	3.70
No. of tillers/ plant	0.17	0.68**	0.37**	0.65**	0.74**	2.95**	0.21**	0.02
Flag leaf area (cm^2)	0.32	16.17**	31.03**	17.82**	11.56**	27.80**	0.57	0.23
Peduncle length (cm)	1.45	22.35**	17.69**	17.50**	25.50**	61.42**	51.37**	0.59
Spike length (cm)	0.06	2.72**	1.57**	2.71**	2.11**	32.01**	23.98**	0.21
No. of spikelets/ spike	0.19	6.63**	0.78**	6.13**	6.93**	57.01**	39.37**	0.10
No. of grains/spike	0.15	82.64**	34.68**	91.75**	73.91**	498.39**	235.01**	0.81
Grain yield / spike	0.02	0.11**	0.06**	0.13**	0.10**	0.24**	0.37**	0.01
1000- grain weight (g)	0.18	47.20**	62.74**	45.81**	43.84**	12.13**	114.05**	0.74
Biological yield/plant	0.03	10.22**	5.58**	11.38**	9.37**	29.74**	32.99**	0.15
Harvest index (%)	3.13	30.60**	8.90*	35.23**	30.06**	76.43**	11.41	3.89
Grain yield/plant (g)	0.02	0.89**	0.45**	0.92**	0.88**	3.29**	2.58**	0.01

* ,** significant at 5 and 1 per cent level, respectively.

Table 2. Analysis of variance for combining ability for different characters of bread wheat

Characteristics	Source of variation						GCA/SCA variance	
	GCA (df = 9)		SCA (df = 45)		Error (df =108)			
	F_1	F_2	F_1	F_2	F_1	F_2	F_1	F_2
Days to heading	7.95**	8.48**	0.68**	1.40**	0.30	0.30	1.67	0.62
Days to maturity	2.34**	3.04**	1.76**	2.94**	0.40	0.40	0.12	0.09
Plant height (cm)	16.13**	19.77**	20.13**	19.16**	1.14	1.28	0.07	0.09
No. of tillers/ plant	0.48**	0.49**	0.16**	0.18**	0.01	0.007	0.26	0.23
Flag leaf area (cm^2)	18.40**	6.52**	4.40**	4.71**	0.07	0.07	0.35	0.12
Peduncle length (cm)	15.24**	21.27**	4.29**	6.33**	0.28	0.12	0.31	0.28
Spike length (cm)	2.24**	0.70**	0.78**	0.71**	0.07	0.08	0.26	0.08
No. of spikelets/ spike	2.62**	1.62**	1.95**	2.09**	0.04	0.03	0.11	0.06
No. of grains/spike	74.79**	46.41**	20.95**	18.39**	0.33	0.19	0.30	0.21
Grain yield / spike	0.14**	0.09**	0.02**	0.02**	0.001	0.001	0.51	0.45
1000- grain weight (g)	40.60**	36.80**	11.08**	13.72**	0.35	0.14	0.31	0.23
Biological yield/plant	12.15**	9.60**	1.87**	1.55**	0.06	0.04	0.56	0.53
Harvest index (%)	20.70**	17.55**	8.50**	7.10**	0.98	0.98	0.22	0.23
Grain yield/plant (g)	1.05**	0.95**	0.15**	0.13**	0.01	0.003	0.62	0.61

*, ** Significant at 5 and 1 per cent level of significance, respectively.

Table 3. Estimates of general combining ability effects for different characters of bread wheat

Parent	Days to heading		Days to maturity		Plant height		No. of tillers/ plant		Flag leaf area		Peduncle length		Spike length	
	F_1	F_2	F_1	F_2	F_1	F_2	F_1	F_2	F_1	F_2	F_1	F_2	F_1	F_2
HD 2881	0.28	0.044	-0.34*	0.28	-0.85**	-0.72*	-0.03	-0.05*	-1.45**	-0.60**	-0.65**	-0.98**	-0.53**	-0.22**
HS 448	-0.47**	-0.37*	0.43*	0.28	-0.49	-1.45**	0.02	-0.01	0.65**	0.46**	-1.11**	-0.39**	0.75**	0.29**
WH 789	-0.52**	-0.79**	-0.34*	0.28	0.15	0.68*	0.08	0.24**	-1.99**	-1.59**	0.59**	1.18**	-0.74**	-0.50**
HUW 468	-0.05	-0.43**	0.38*	0.12	2.07**	2.53**	0.12**	0.17**	0.84**	0.45**	1.88**	1.91**	-0.14	-0.02
UP 2614	0.62**	0.35*	-0.12	0.03	-0.94**	-0.06	-0.16**	-0.05*	1.57**	0.58**	-0.97**	0.12	0.17*	0.20**
NW 3015	0.51**	1.02**	0.43*	-0.49**	1.25**	0.99**	-0.22**	-0.25**	1.05**	0.67**	0.03	-0.68**	-0.01	0.18*
PBW 520	0.59**	0.82**	0.60**	0.73**	-0.21	0.94**	-0.11**	-0.22**	-0.55**	-0.56**	-0.48**	-0.89**	0.01	-0.07
K 209	1.14**	1.27**	0.04	-1.08**	-0.79**	-0.44	-0.16**	-0.16**	0.62**	0.59**	-1.51**	-2.39**	-0.15*	-0.13
HD 2851	-1.72**	-1.23**	-0.40*	-0.27	-1.46**	-1.56**	0.48**	0.37**	-1.39**	-0.25**	1.10**	1.60**	0.39**	0.23**
Raj 4063	-0.38*	-0.68**	-0.68**	0.12	1.27**	-0.92**	-0.02	-0.06*	0.64**	0.26**	1.11**	0.53**	0.25**	0.05
SE (g_i) ±	0.15	0.15	0.173	0.172	0.292	0.31	0.028	0.023	0.075	0.072	0.146	0.096	0.074	0.085
SE (g_i -g_j) ±	0.223	0.224	0.258	0.257	0.435	0.462	0.041	0.034	0.111	0.107	0.217	0.143	0.11	0.112

Parent	No. of spikelet / spike		No. of grains/spike		Grain yield / spike		1000- grain weight		Biological yield/ plant		Harvest index		Grain yield/ plant	
HD 2881	-0.83**	-0.38**	-4.22**	-2.59**	-0.14**	-0.08**	-1.95**	-0.86**	-1.32**	-0.84**	1.10**	1.33**	-0.29**	-0.18**
HS 448	-0.53**	-0.48**	-1.21**	-0.30*	-0.01	-0.01	0.93**	0.32**	-0.24**	-0.05	2.52**	0.81**	0.06*	0.02
WH 789	-0.24**	-0.32**	3.23**	1.83**	0.20**	0.11**	3.67**	2.51**	1.43**	1.41**	1.33**	0.58*	0.46**	0.4**
HUW 468	0.43**	0.68**	2.25**	1.48**	0.04**	0.02**	-0.62**	-0.43**	0.56**	0.34**	-0.56*	0.23	0.11**	0.09**
UP 2614	0.30**	0.33**	-1.26**	-1.03**	-0.06**	-0.05**	-1.65**	-1.18**	-0.62**	-0.33**	-1.25**	-0.98**	-0.22**	-0.11**
NW 3015	0.02	-0.26**	-1.00**	-0.63**	-0.04**	-0.04**	-0.67**	-0.90**	-0.39**	-0.38**	-1.23**	-1.79**	0.19**	-0.19**
PBW 520	-0.22**	0.06	-1.15**	-0.2	-0.06**	-0.01	-0.35*	0.04	-0.47**	-0.48**	-0.86**	-0.22	-0.14**	-0.14**
K 209	0.01	-0.05	-1.71**	-2.53**	-0.07**	-0.12**	-0.82**	-2.67**	-1.03**	-1.29**	-1.30**	-1.50**	-0.34**	-0.41**
HD 2851	0.37**	0.27**	3.47**	3.82**	0.16**	0.18**	2.59**	3.30**	1.75**	1.49**	0.56*	1.94**	0.50**	0.52**
Raj 4063	0.69**	0.13**	1.59**	0.15	-0.01	-0.01	-1.13**	-0.14	0.34**	0.13*	-0.3	-0.4	0.05*	-0.01
SE (gi) ±	0.056	0.046	0.158	0.119	0.009	0.008	0.162	0.102	0.07	0.053	0.271	0.272	0.02	0.015
SE (gi -gj) ±	0.083	0.069	0.235	0.178	0.013	0.012	0.242	0.152	0.104	0.079	0.404	0.405	0.029	0.023

* and ** Significant at 5 and 1 per cent level, respectively.

It was observed that top parents on the basis of high *per se* performance also have high general combining ability effects. Since *gca* effects are attributed to additive and additive x additive gene effects, the above mentioned parents for *gca* effects have good potential for respective characters and may be used in a multiple crossing programme to synthesize a dynamic population with most of the favourable genes amelioration of grain yield in barley (Griffing, 1956). It seems feasible, therefore, that the *gca* rank for grain yield is related to the *gca* for the useful yield components. It is, therefore, recommended that breeder should breed for superior combining ability for the component traits with an ultimate objective to improve the overall *gca* for grain yield in bread wheat.

Best parents having desirable *gca* effects for grain yield per plant in different environments revealed that the *gca* effect and *per se* performance were positively correlated in most of the best parents. Though, such pattern was not prevailed in all the cases. Parents, who showed desirable, *gca* effects for grain yield per plant, also exhibited desirable *gca* effects for one or more yield attributing traits. Present investigation indicated that parent HD 2851 and WH 789 emerged as good general combiner in case of very late sown condition, it means, they probably possessed the desirable genes for high temperature tolerance during grain filling period. These genotype possessed desirable GCA effects for biological yield per plant, number of grains per spike, 1000 - grain weight, peduncle length, tillers per plant, days to heading and harvest index. Shah (1998) reported that biological yield was the trait identified for selection with high temperature. The increase in productivity under late sown condition depends on the biomass attained by a genotype at the time of anthesis (Sharma, 1993). Blum *et al.* (1997) emphasized that selection for high biomass yield should bring about positive improvement in grain yield, effective tillers per plant and number of kernels per spike. Thus, selection for biomass yield is one of the ways to improve the productivity in bread wheat. The results of present investigation are in agreement with Guha Sarkar *et al.* (2001) and Nagarajan and Rane (2002). In all such cases where *gca* effect was more pronounced for particular trait indicating preponderance of additive gene action, so these genotypes should be involved in crosses to improve the specific trait in future breeding programme.

In order to synthesize a dynamic population with most of the favourable gene accumulated, it will be pertinent to make use of the aforesaid parents, which are good general combiner for several characters, in multiple crossing programmes. Apart from conventional breeding methods resting slowly upon additive or additive x additive type of gene action, population improvement appears to be hopeful alternative. Diallel selective mating system (Jensen 1970) sounds to be a good technique, which delays quick fixation of gene complexes, permit break down of linkage, general fostering of recombination and concentration of favorable genes / gene complexes, into central gene pool, by a series of multiple crosses.

Normally the *sca* effects do not contribute tangibly in the improvement of self-fertilizing crops, except where commercial exploitation of heterosis is feasible. The *sca* represent the dominance and epistatic interaction, which can be related with heterosis. High *sca* effect resulted from good x good general combiners reflects additive x additive type of gene interaction and superiority of favourable genes contributed by the parents, while those involving good x poor or poor x poor general combiners indicate interaction of additive x dominance or dominance x dominance, respectively. Thus, cross combinations involving good x good general combiner parents are of more relevance in self pollinated crops such as bread wheat because genes controlling these effects may be fixed in the end product of a breeding programme. However, in self-pollinated crops like bread wheat, the additive x additive type of interaction component is fixable in later generations. Breeder's interest, therefore, vests in obtaining transgressive segregants through crosses and producing more potent homozygous lines. Jinks and Jones (1958) emphasized that the superiority of the hybrids might not indicate there, ability to yield transgressive segregants, rather *sca* would provide satisfactory criteria.

The estimates of specific combining ability (*sca*) revealed that out of 45 crosses, 16 crosses in F_1 and 15 crosses in F_2 were good specific combiners for grain yield. It is noteworthy that seven crosses showed positive and significant *sca* effects for grain yield in both the F_1 and F_2 generations. The generation effects were also noticed in the *sca* effects of the crosses. The highest positive significant *sca* effect was exhibited by the cross UP 2614 x HD 2851. Other good combinations, which showed significant *sca* effects for grain yield and some other characters, are listed in Table 4. These crosses were generally higher yielding and, in most of the crosses, one of the parents involved was a good combiner indicating that such combinations may be expected to result in desirable transgressive segregants.

All the best crosses for grain yield also showed an average to high *sca* effects for most of the yield components. It is recommended that new materials should be used in future breeding programs for recombining the desirable traits in the envisaged elite genotypes. The result obtained in the study are in conformity with the earlier findings of (Muralia and Sastry, 2001; Dubey *et al.*, 2001 and Desai *et al.*, 2005).

Analysis of combining ability for different characters revealed that the good general combiners identified among the parents for grain yield also exhibited significant positive general combining ability effects for one or more effects also where crosses with significant specific combining ability effects for grain yield had significant *sca* effects for one or more yield components.

Table 4. Crosses showing significant high *sca* effects for yield and its component traits in bread wheat

S. No.	Cross	Character
1	HD 2881 x HS 448	3, 5, 9, 10, 11, 13
2	HD 2881 x WH 789	1, 4, 5, 6, 7, 9, 12,
3	HD 2881 x HD 2851	1, 2, 6, 10, 11, 12, 14
4	HS 448 x WH 789	4, 5, 9, 12, 14
5	HS 448 x K 209	2, 3, 7, 8, 12,
6	WH 789 x PBW 520	6, 9, 10, 11, 12, 14
7	WH 789 x HD 2851	8, 9, 10, 11, 13
8	HUW 468 x UP 2614	7, 8, 9, 10, 11, 12, 14
9	HUW 468 x PBW 520	4, 5, 7, 8, 9, 10, 12, 14
10	HUW 468 x HD 2851	2, 3, 4, 5, 10, 11,
11	HUW 468 x Raj 4063	2, 7, 9, 10, 12, 14
12	UP 2614 x HD 2851	4, 6, 7, 8, 9, 10, 12, 13, 14
13	NW 3015 x HD 2851	1, 2, 5, 7, 8, 11, 12, 14
14	NW 3015 x Raj 4063	1, 2, 6, 8, 9, 10, 12, 14
15	K 209 x HD 2851	1, 4, 5, 6, 7, 8, 9, 10, 11

Characters: 1 - Days to heading, 2 - Days to maturity, 3 - Plant height, 4 - No. of tillers/ plant, 5 - Flag leaf area, 6 - Peduncle length, 7 - Spike length, 8 - No. of spikelets/spike, 9 - No. of grains/spike, 10 - Grain yield/spike, 11 - 1000- grain weight, 12 - Biological yield/plant, 13 - Harvest index and 14 - Grain yield/plant.

Hence, it may be inferred that significant *gca* and *sca* effects for yield components generally result in significant combining ability effects for grain yield. However, in some of the crosses significant *sca* effects even for many yield components were not associated with significant *sca* effects for grain yield. Similarly, good general combiners for yield components among parents did not always exhibit high *gca* effect for grain yield. This could be due to yield component compensation and negative correlations, which arise in response to competition between developmentally flexible yield components (Adams, 1967) or component complementation between the two parents (Grafius *et al.,* 1976).

In self-pollinated crops like wheat, *sca* effects are not much important as they are mostly related to non-additive gene effects excepting those arising from complementary gene action or linkage effects they can not be fixed in the pure line or the end product inbred line. Jinks and Jones (1958) emphasized that the superiority of the hybrids might not indicate their ability to yield transgressive segregants, rather *sca* would provide satisfactory criteria. However, if a cross combination exhibiting high *sca* as well as high *per se* performance having at least one parent as good general combiner for a specific trait, it is expected to throw desirable transgressive segregants in later generations (Kathiria and Sharma, 1996). However, such combinations may not necessarily throw good segregants. Similarly, from a superior cross involving poor x poor combiners, very little gain is expected because high *sca* effects may be due to dominance and epistatic gene effects, which may dissipate with the advancement towards homozygosity. Those crosses involving good and poor general combiners indicate the additive x dominance interactions. This is one of the reasons why the discrepancy with regard to *sca* effects in F_1 and F_2 generations are observed.

None of the cross showed consistently high *sca* effects for all the characters. An overall appraisal of specific combining ability effects revealed that some crosses had significant *sca* effects for a few specific characters with varied magnitudes. For e.g., UP 2614 x HD 2851 for number of tillers per plant, peduncle length, spike length, number of spikelets per spike, number of grains per spike, grain yield per spike, biological yield per plant, harvest index and grain yield per plant; HUW 468 x UP 2614 for spike length, number of spikelets per spike, number of grains per spike, grain yield per spike, 1000-grain weight, biological yield per plant and grain yield per plant; HUW468 x PBW 520 for number of tillers per plant, flag leaf area, spike length, number of spikelets per spike, number of grains per spike, grain yield per spike, biological yield per plant and grain yield per plant; HD 2881 x HD 2851 for days to heading, days to maturity, peduncle length, grain yield per spike, 1000-grain weight, biological yield per plant and grain yield per plant; NW 3015 x HD 2851 for days to heading, days to maturity, flag leaf area, spike length, number of spikelets per spike, grain yield per spike, 1000- grain weight, biological yield per plant and grain yield per plant; NW 3015 x Raj 4063 for days to heading, days to maturity, peduncle length, number of spikelets per spike, number of grains per spike, grain yield per spike, biological yield per plant and grain yield per plant; K 209 x HD 2851 for days to heading, number of tillers per plant, flag leaf area, peduncle length, number of spikelets per spike, number of grains per spike, grain yield per spike and 1000-grain weight; HD 2881 x HUW 468 for days to heading, flag leaf area, peduncle length, number of spikelets per spike and 1000-grain weight; HUW 468 x Raj 4063 for days to maturity, spike length, number of grains per spike, grain yield per spike, biological yield per plant and grain yield per plant and grain yield per plant; HUW 468 x HD 2851 for days to maturity, plant height, number of tillers per plant, flag leaf area, grain yield per spike and 1000-grain weight; WH 789 x PBW 520 for peduncle length, number of grains per spike, grain yield per spike, 1000- grain weight, biological yield per plant and grain yield per plant; HD 2881 x WH 789 for days to heading, number of tillers per plant, flag leaf area, peduncle length, spike length, number of grains per spike and biological yield per plant; HD 2881 x HS 448 for plant height, flag leaf area, number of grains per spike, grain yield per spike, 1000-grain weight and harvest index; HS 448 x WH 789 for number of tillers per plant, flag leaf area, number of grains per spike, grain yield per spike, biological yield per plant and grain yield per plant; PBW 520 x Raj 4063 for days to heading, peduncle length, number of grains per spike and 1000-grain weight; HS 448 x K 209 for days to maturity, plant height, spike length, number of spikelets per spike and biological yield per plant; HS 448 x Raj 4063 for number of tillers per plant, peduncle length and biological yield per plant; WH 789 x HUW 468 for days to heading, peduncle length and number of grains per spike; WH 789 x HD 2851 for number of spikelets per spike, grain yield per spike, 1000-grain weight and harvest index; PBW 520 x HD 2851 for days to maturity, number of grains per spike and harvest index; HD 2851 x Raj 4063 for plant height, flag leaf area, 1000-grain weight and biological yield per plant; PBW 520 x K 209 for days to maturity, flag leaf area, peduncle length and number of spikelets per spike; HUW 468 x K 209 for flag leaf area, spike length and number of spikelets per spike; HD 2881 x NW 3015 for flag leaf area, peduncle length and number of spikelets per spike; HS 448 x PBW 520 for days to maturity, peduncle length and spike length; UP 2614 x PBW 520 for days to maturity, flag leaf area and spike length; NW 3015 x PBW 520 for number of tillers per plant, flag leaf area and spike length; NW 3015 x K 209 for days to maturity, plant height, grain yield per spike and 1000-grain weight.

It is noteworthy that the crosses, which exhibited consistently positive *sca* in both generations, also exhibited positive significant heterosis. Thus, the results of the present study indicated some relationship between *sca* effects and heterosis. It is, therefore, suggested that *sca* performance may be considered as a criterion for selecting the best crosses in bread wheat. It may also be worthwhile to attempt bi-parental mating in the segregating generation among selected crosses to permit superior recombination. All the important crosses involving parents with high x average, average x average and average x poor general combiners, indicated that non-additive type of gene actions, which are unfixable in nature, were involved in selected cross combinations.

The crosses, which showed desirable *sca* effects for grain yield per plant, also exhibited desirable *sca* effects for one or more yield contributing traits. The crosses UP 2614 x HD 2851, WH 789 x HUW 468 x UP 2614 and HUW 468 x PBW 520 emerged as good specific cross combinations for grain yield per plant. The parents WH 789, HD 2881, UP 2614, HD 2851 and PBW 520 involved in these crosses were good general combiners for grain yield and one or two yield contributing traits while the other parents were emerged as poor combiners. It is interesting to note that *sca* effects of best crosses and *gca* effects of their parents indicated that the good specific cross combinations were the result of good x good, good x poor or poor x poor combinations. Thus, it was evident that a good cross combination is not necessarily the result of good x good general combiners; rather it might occur from good x poor or poor x poor combiners as well. A number of studies also refer to such a situation (Muralia and Sastry, 2001; Dubey *et al.*, 2001 and Desai *et al.*, 2005).

The present study revealed that non-additive gene actions were found to be more propounded in the present investigation. Thus, it was concluded that an appreciable progress could be achieved through diallel selective mating (Jensen, 1970 and 1978) or biparental mating in early segregating generations or restricted recurrent selection by the way of inter-mating the most desirable segregants followed by selection (Joshi, 1979) or multiple crosses might prove to be effective alternative approach for further tangible advancement in grain yield in bread wheat. Inclusion of F_1 hybrids showing high *sca* and having parents with good *gca*, into multiple crosses, could also prove a worthwhile approach for tangible advancement of grain yield in bread wheat.

High *sca* effect due to good x good combiners reflect additive x additive type of gene interaction and superiority of favourable genes contributed by the parents, while those involving good x poor or poor x poor combiners indicate the interaction of additive x dominance or dominance x dominance, respectively. Biparental progeny selection suggested by Andrus (1963) may be used to get some transgressive segregants from crosses involving good x good and good x poor combiners.

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