COMBINING ABILITY AND GENE ACTION FOR DIFFERENT CHARACTERS IN BREAD WHEAT (*TRITICUM AESTIVUM* L.)

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ABSTRACT
Combining ability analysis was studied in a 10 × 10 diallel cross of spring wheat (*Triticumaestivum*L.). The genotypes GAW-4, GAW-5 and GAW-8 were considered as the best general combiners, while 18 hybrids including GW-322 × LOK-1, GAW-4 × LOK-1, GAW-1 × GAW-4, GAW-2 × GW-366, GAW-2 × GW-173, GAW-5 × GAW-13, GAW-13 × LOK-1, GAW-8 × LOK-1, GAW-4 × GAW-13, GAW-8 × GAW-13 and GAW-1 × GW-366 as good specific combinations for grain yield and other yield contributing traits. The promising parents namely GAW-4 (1.15), GAW-5 (0.72) and GAW-8 (0.78) which are having high gca effects in desirable direction for yield contributing traits may be incorporated in crossing programme to have high yielding genotypes. The crosses GW-322 × LOK-1 (6.44), GAW-4 × LOK-1 (6.31), GAW-1 × GAW-4 (5.33), GAW-2 × GW-366 (5.02) and GAW-2 × GW-173 (4.87) which showed good sca effects for yield components characters. In conclusion, those parents and hybrids may be exploited for higher yield by exploiting them through heterosis breeding or involving them in multiple cross breeding programme for obtaining transgressive segregants and broad genetic base population in wheat for improvement in yield.

INTRODUCTION

The choice of suitable parents for evolving better varieties/ hybrids is a matter of concern to the plant breeders. For these purpose, the combining ability is a powerful tool to discriminate good as well as poor combiners for choosing appropriate parental materials for a particular character in the plant breeding programme (Lyngdoh *et al.*, 2011). At the same time, it also provides information about the nature of gene action involved in the inheritance of grain yield and its component characters. In a systematic breeding programme, selection of parents with desirable characteristics having good general combining ability effects for grain yield and its components and high estimates of specific combining ability effects are essential (Baloch *et al.*, 2001). The present investigation was, therefore, planned to study combining ability and genetic architecture of grain yield and its components in bread wheat crosses obtained from 10 x 10 half diallel mating design (Ashutosh *et al.*, 2011).These estimates will help in formulating sound, efficient and effective breeding procedure to bring about rapid and purposeful improvement in this crop. Therefore, the paper deals with combining ability and gene action for different characters in bread wheat (*Triticumaestivum*).

MATERIALS AND METHODS

The basic material for the present investigation comprised of ten wheat genotypes/varieties namely GAW-1, GAW-2, GAW-4, GAW-5, GAW-8, GAW-13, GW-173, GW-322, GW-366 and LOK-1 was obtained from Regional Research Station, Anand Agricultural University, Anand. The genotypes were used for crossing programme in a half diallel fashion (10 ×

10) during crop season 2013-2014. Field plot was well prepared for sowing of the experimental material (55 genotypes-comprising 10 parents and 45 F_1s seeds). The experiment was conducted in a Randomized Complete Block Design with three replications during *rabi* season 2014-2015. Seeds of each of the parental lines and crosses were sown by hand dibbling method in one rows plot. The length of row was 5 m long by maintaining 25 cm row to row and 10 cm plant to plant distance. All the recommended agronomic inputs and practices were applied to the crop during the season. The data were recorded on five randomly selected competitive plants in each of three replications and thirteen different characters namely days to 50% flowering, days to maturity, plant height, number of effective tillers per plant, length of main spike (cm), peduncle length (cm), number of grains per main spike, grain yield of main spike (g), grain yield per plant (g), test weight (g), biological yield per plant (g), harvest index and protein content (%). The mean data on these traits were subjected to statistical analysis. Combining ability analysis according to (Griffing, 1956) model I and method 2 was conducted using the statistical software package of SPAR-1.

RESULTS AND DISCUSSION

The analysis of variance for combining ability partitioning the total genetic variance into variance due to general combining ability representing additive type of gene action and variance due to specific combining ability regarded as measure of non-additive gene action. (Kumar *et al.*, 2013).The analysis of variance for combining ability presented in Table 1 revealed that mean squares due to general combining ability were highly

significant for all the characters except grain yield of main spike and protein content, while due to specific combining ability were highly significant for all the characters except length of main spike, grain yield of main spike and protein content. The results indicated the importance of both additive and non additive gene action in the inheritance of all characters except length of main spike, grain yield of main spike and protein content, whereas only additive gene action was important for length of main spike.

The ratio of gca to sca variance ($\acute{o}^2_{gca} / \acute{o}^2_{sca}$) was found high for days to maturity, plant height, length of main spike, peduncle length and number of grains per main spike which indicated that additive gene actions were found predominant in the expression of these characters. The characters, days to 50 per cent flowering, number of effective tillers per plant, grain yield of main spike, grain yield per plant, test weight, biological yield per plant, harvest index, in which the ratio of gca to sca variance ($\acute{o}^2_{gca} / \acute{o}^2_{sca}$) was found low indicated the preponderance of non additive gene actions for these characters. The results, in general, are in accordance with the findings of Mohla*et al.*(2000), Sheikh and Singh (2000), Hamada *et al.*(2002), Dhayal and Sastry (2003), Mavi*et al.*(2003), Sharma and Garg (2005) and Zahid *et al.* (2011).

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The estimate of GCA effects (Table 2) revealed that parents *viz.,* GAW-4, GAW-5 and GAW-8, were good general combiners for grain yield per plant. Parent GAW-1 was found good general combiner for the characters like length of main spike, number of grains per main spike, grain yield of main spike, test weight, biological yield per plant and protein content.

Parent GAW-1 was good general combiner for length of main spike, number of grains per main spike, grain yield of main spike, test weight, biological yield per plant and protein content. GAW-2 was good general combiner for plant height, number of effective tillers per plant, peduncle length, and biological yield per plant. GAW-4 was found good general combiner for the characters like length of main spike, number of grains per main spike, grain yield of main spike, grain yield per plant and protein content. In order to achieve earliness and dwarfness selection of parents become important. GAW-13, GW-173 and LOK-1 were found good general combiner for days to 50% flowering, days to maturity and plant height.

The best three hybrids with significant desirable sca effects for days to 50% flowering were GAW-4 x GAW-5 (-4.11), GAW-2 x GAW-4 (-3.66) and GAW-8 x GW-366 (-3.44). Significant and negative (desirable) sca effects were possessed by 8 hybrids. The hybrid GAW-13 x GW-366 (-3.70) depicted highest significant desirable sca effect for days to maturity followed by GAW-8 x GW-322 (-3.18), GAW-5 x GW-173 (-2.73) and GAW-4 x GAW-13 (-2.23). Hence, they were considered as good cross combinations for exploiting early maturity. The estimates of sca effects revealed that 9 out of 45 crosses exhibited significant negative sca effects for plant height. The highest negative sca effect in case of the character plant height was manifested by GAW-2 x GAW-13 (-7.23) followed by GAW-1 x GW-366 (-5.80) GAW-1 x GAW-5 (-4.97) and GAW-2 x GAW-4 (-4.95). Out of 45 hybrids evaluated only four hybrids depicted significant positive sca effects for number of effective tillers per plant *viz.,* GAW-2 x GW-173 (6.69), GW-173 x GW-322 (2.08), GAW-5 x GAW-13 (2.03) and GAW-2x GW-366 (1.88).

Perusal of sca effects revealed that seven crosses recorded significant positive sca effects for length of main spike. The cross combinations, GAW-1 x GAW-4 (1.23) followed by GAW-2 x GW-366 (0.86) and GAW-2 x GW-173 (0.81) were the best specific combinations for length of main spike. The hybrids viz., GAW-2 x GAW-4 (–3.72), GAW-1 x GAW-2 (-3.01), GAW-4 x GAW-5 (-2.71) and GAW-5 x GAW-8 (-2.35)

Table 1: Analysis of variance for combining ability for various characters

Source of variation	d.f.	DaysTo50 %flowering	Days to maturity	Plant height	No. of effective tillers per plant	Length of main spike	Peduncle length	No. of grainsper mainspike
GCA	9	60.12**	45.05**	406.98**	11.74**	8.24**	99.48**	56.15**
SCA	45	6.40**	3.13**	19.48**	3.25**	0.28	5.57**	5.66**
Error	108	0.45	0.84	3.14	1.04	0.07	1.68	1.58
$\acute{o}^2$gca		4.97**	3.68**	33.65**	0.89**	0.68**	8.14**	4.55**
$\acute{o}^2$sca		5.95**	2.28**	16.34**	2.21**	0.21	3.88**	4.08**
$\acute{o}^2$gca/$\acute{o}^2$sca		0.83	1.61	2.06	0.40	3.23	2.09	1.11

Source of variation	d.f.	Grain yield of main spike	Grain yield per plant	Test weight	Biological yield per plant	Harvest index	Protein content
GCA	9	0.21	8.32**	98.49**	113.53**	200.13**	0.42
SCA	45	0.14	14.79**	26.75**	45.51**	116.79**	0.64
Error	108	0.01	0.79	0.78	4.93	15.95	0.02
$\acute{o}^2$gca		0.02	0.63**	8.14**	9.05**	15.35**	0.03
$\acute{o}^2$sca		0.15	13.99**	25.97**	40.57**	100.84**	0.62
$\acute{o}^2$gca/$\acute{o}^2$sca		0.13	0.04	0.31	0.22	0.15	0.05

*, ** Significant at 5% and 1% levels of probability, respectively.

Table 2: Estimates of general combining ability (gca) effects of parents for various characters

Sr. No.	Parents	Days to 50% flowering	Days to maturity	Plant height	No. of effective tillers per plant	Length of main spike	Peduncle length
1	GAW-1	0.70**	-0.27	4.69**	-0.76**	0.21**	2.51**
2	GAW-2	1.89**	0.09	-7.99**	1.20**	-0.30**	-4.08**
3	GAW-4	-0.22	0.28	7.01**	0.51	1.21**	4.48**
4	GAW-5	-1.47**	-0.44	2.82**	-0.91**	-0.25**	1.55**
5	GAW-8	1.89**	2.23**	1.35**	-1.33**	1.65**	0.21
6	GAW-13	-1.91**	0.12	-11.32**	0.98**	-0.78**	-5.25**
7	GW-173	-3.08**	-4.44**	-3.95**	-0.88**	-0.88**	-0.27
8	GW-322	4.34**	2.87**	3.20**	-0.62*	-0.1	-0.58
9	GW-366	-0.38*	0.26	2.10**	0.57*	-0.63**	0.96**
10	LOK-1	-1.77**	-0.69*	1.98**	1.23**	-0.12	0.49
	SE (gi)	0.17	0.24	0.47	0.28	0.08	0.34
	SE(gi-gj)	0.26	0.37	0.72	0.41	0.36	0.52

Sr. No.	No. of grains per main spike	Grain yield of main spike	Grain yield per plant	Test weight	Biological yield per plant	Havest index	Protein content
1	1.58**	0.14**	-0.55*	1.84**	5.25**	-8.23**	0.18**
2	-0.5	-0.11**	-0.08	-7.24**	1.42*	-2.59*	-0.22**
3	2.49**	0.15**	1.15**	0.39	4.17**	-1.96	0.22**
4	0.13	0.03**	0.72**	1.14**	-2.21**	4.32**	-0.10*
5	3.08**	0.15**	0.78**	0.83**	-0.45	2.63*	0.14**
6	-1.61**	-0.07**	-0.05	1.13**	-2.03**	2.55*	0.21**
7	-3.76**	-0.19**	-1.06**	2.19**	-5.17**	4.14**	0.04
8	1.57**	0	0.1	-2.61**	-1.47*	2.28*	-0.05
9	-1.41**	0.09**	-1.47**	0.70**	0.23	-4.06**	-0.31**
10	-1.57**	-0.19**	0.46	1.61**	0.26	0.92	-0.11**
	0.33	0	0.24	0.24	0.6	1.09	0.03
	0.5	0.55	0.36	0.36	0.9	1.62	0..06

*, ** Significant at 5% and 1% levels of probability, respectively.

recorded significant negative sca effects and therefore, they were spotted out as good specific combinations for reduced peduncle length.

Best five hybrids with respect to grain yield per plant based on significant positive sca effects were GW-322 x LOK-1 (6.44), GAW-4 x LOK-1 (6.31),GAW-1 x GAW-4 (5.33),GAW-2 x GW-366 (5.02) and GAW-2 x GW-173 (4.87). Seventeen crosses showed significant positive sca effects for test weight. Among them, GW-366 x LOK-1 (10.79) recorded highest estimates of sca effects followed by GAW-1 x GW-322 (9.35) and GW-322 x LOK-1 (7.44). For biological yield per plant, hybrid GAW-2 x GW-173 (19.51) exhibited maximum estimates of sca effect followed by GAW-1 x GW-366 (12.39), GAW-4 x GAW-13 (11.58) and GAW-5 x GAW-13 (10.69), hence these hybrids were best specific combiners for this trait. The number of hybrids depicted highest significant SCA effects in positive direction were GAW-8 x LOK-1 (23.28) followed by GAW-8 x GAW-13 (22.40), GAW-4 x GW-173 (15.45) and GAW-1 x GAW-5 (12.57) for the character harvest index. The hybrid GW-322 x GW-366 (2.12) exhibited highest estimates of sca effect followed by GAW-5 x GAW-8 (1.65) and GAW-8 x GAW-13 (1.19), hence these hybrids were best specific combinations for the trait protein content.

In majority of cases, the best specific combinations for different characters were either good x poor, average x average, average x good and *vice versa* general combiners. This sug-gested that information on GCA effects should be supplemented by SCA effects and hybrid performance of cross combinations to predict the transgressive type possibly made available in segregating generations. The GCA effects of the parents and SCA effect of their crosses indicated that the crosses between two high general combiners were not always best specific combiners (Jaiswal *et al.*, 2013)

A comparison between mean performance of parents and their gca effects (Table 3) revealed that high *per se* performance of parents was related with their significant gca effects in majority of characters studied. For example, out of best three parents, at least two parents were common for the characters like days to 50%, flowering, days to maturity, plant height, length of main spike, number of grains per main spike, grain yield per plant, biological yield per plant and harvest index. Whereas in case of high *per se* performance of crosses was not related with their significant SCA effects in this study

It can be concluded that information on GCA effects should be supplemented by SCA effects and hybrid performance of cross combinations to predict the transgressive type possibly made available in segregating generations. Seed yield is complex, polygenically controlled quantitative character and due to predominance of non-additive gene action, it would be worthwhile to resort to breeding methodologies, such as bi-parental mating, recurrent selection and diallel selective mating than to use of conventional pedigree or backcross techniques.

Table 3: Top 3 parents and F₁S for *per se* performance, best general combiners and specific combiners

Sr. No.	Characters	Per se performance Parents	Hybrids	Best performing parents	Best specific crosses
1	Days to 50% flowering	LOK-1	GAW-13 x LOK-1	GW-173	GAW-4 x GAW-5
		GW-173	GAW-5 x GAW-13	GAW-13	GAW-2 x GAW-4
		GAW-5	GAW-5 x GW-173	LOK-1	GAW-8 x GW-366
2	Days to maturity	GW-173	GAW-5 x GW-173	GW-173	GAW-13 x GW-366
		LOK-1	GW-173 x LOK-1	LOK-1	GAW-8 x GW-322
		GAW-5	GAW-8 x GW-173	GAW-5	GAW-5 x GW-173
3	Plant height	GAW-13	GAW-2 x GAW-13	GAW-13	GAW-2 x GAW-13
		GAW-2	GAW-13 x GW-173	GAW-2	GAW-1 x GW-366
		GW-173	GAW-2 x GAW-8	GW-173	GAW-1 x GAW-5
4	No. of effective tillers per plant	LOK-1	GAW-2 x GAW-13	LOK-1	GAW-2 x GW-173
		GW-173	GAW-2 x LOK-1	GAW-2	GAW-1 x GW-366
		GAW-5	GAW-13 x LOK-1	GAW-13	GW-173 x GW-322
5	Length of main spike	GAW-8	GAW-4 x GAW-8	GAW-8	GAW-1 x GAW-4
		GAW-4	GAW-8 x LOK-1	GAW-4	GAW-2 x GW-366
		GAW-1	GAW-1 x GAW-4	GAW-1	GAW-2 x GW-173
6	Peduncle length	GAW-13	GAW-2 x GAW-13	GAW-13	GAW-2 x GAW-4
		GAW-4	GAW-2 x GW-322	GAW-2	GAW-1 x GAW-2
		GW-322	GAW-13 x GW-173	GW-173	GAW-4 x GAW-5
7	No. of grains per main spike	GAW-8	GAW-8 x GW-322	GAW-8	GAW-5 x GAW-8
		GAW-5	GAW-4 x GAW-8	GAW-4	GAW-1 x GAW-4
		GAW-4	GAW-2 x GAW-4	GAW-1	GW-366 x LOK-1
8	Grain yield of main spike	GAW-4	GAW-1 x GAW-2	GAW-8	GAW-1 x GAW-4
		GAW-5	GAW-8 x GAW-13	GAW-4	GAW-8 x GW-173
		GW-366	GW-322 x GW-366	GAW-1	GAW-2 x GAW-8
9	Grain yield per plant	GAW-8	GAW-4 x LOK-1	GAW-4	GW-322 x LOK-1
		GAW-5	GW-322 x LOK-1	GAW-8	GAW-4 x LOK-1
		GW-173	GAW-4 x GAW-8	GAW-5	GAW-1 x GAW-4
10	Test weight	GAW-1	GAW-1 x GW-173	GW-173	GW-366 x LOK-1
		GAW-5	GW-366 x LOK-1	GAW-1	GAW-1 x GW-322
		GAW-8	GAW-4 x LOK-1	LOK-1	GW-322 x LOK-1
11	Biological yield per plant	GAW-4	GAW-2 x GAW-13	GAW-1	GAW-2 x GW-173
		GAW-1	GAW-1 x GW-366	GAW-4	GAW-1 x GW-366
		GW-366	GAW-4 x GAW-8	GAW-2	GAW-4 x GAW-13
12	Harvest index	GAW-8	GAW-8 x LOK-1	GAW-5	GAW-8 x LOK-1
		GAW-13	GW-322 x GW-366	GAW-8	GAW-4 x GW-173
		GAW-5	GAW-4 x GAW-13	GAW-13	GAW-1 x GAW-5
13	Protein content	GW-322	GAW-1 x LOK-1	GAW-13	GW-322 x GW-366
		GAW-5	GAW-13 x GW-173	GAW-4	GAW-5 x GAW-8
		GAW-13	GAW-4 x GW-322	GAW-1	GAW-8 x GAW-13

REFERENCES

Ashutosh, K., Mishra, V. K., Vyas, R. P. and Singh, V. 2011. Heterosis and combining ability analysis in bread wheat (*Triticumaestivum* L.). *J. Pl. Breeding and Crop Sc.* **3(10):** 209-217.

Baloch, M. Z., Ansari, B. A., Memon, N., Kumbhar, M. B. and Soomoro, A. 2001. Combining ability and heterotic performance of some agronomic traits in bread wheat (*Triricumaestivum*). *Pakistan J. Biological Sciences.* **4(2):** 138-140.

Dhayal, L. S. and Sastry, E. V. D. 2003. Combining ability in bread wheat under salinity and normal conditions. *Indian J. Genet.* **63:** 69-70.

Griffing, B. 1956. Concept of general and specific combining ability in relation to diallel crossing systems. *Aust. J. Biol. Sci.* **9:** 463-493.

Hamada, A. A., El-seidy, E. H. and Hendawy, H. I. 2002. Breeding measurements for heading date, yield and yield components in wheat using line x tester analysis. *Annal. Agric. Sci. Cairo.* **47:** 587-609.

Jaiswal, K. K., Marker, S. and Kumar, B. 2013. combining ability analysis in diallel crosses of wheat(*Triticumaestivum*L.).*The Bioscan*. **8(4):** 1557-1560.

Kumar, P., Lamba, A., Yadav, R. K., Singh, L. and Singh, M. 2013. Analysis of yield and its components based on heterosis and combiningability in indian mustard (brassica juncea l. Czern and coss). *The Bioscan.* **8(4):** 1497-1502.

Lyngdoh, Y. A., Mulge, R. and Shadap A. 2011. Heterosis andcombining ability studies in near homozygous lines of okra(Abelmoschusesculentus (L.) Moench) for growth parameters. *The Bioscan.* **8(4):** 1275-1279.

Mavi, G. S., Nanda, G. S., Sahu, V. S., Sharma, S. and Kaur, S. 2003. Combining ability analysis for yield and its components in bread wheat (*Triticumaestivum*L.) in two nitrogen regimes. *Crop Improv.* **30:** 50-57.

Mohla, B. S., Sharma, S. C. and Hooda, J. S. 2000. Gene action for certain quantitative traits in wheat. *Ann. Biology (Ludhiana).* **16(1):** 95-100.

Sharma, A. K. and Garg, D. K. 2005. Combining ability over environments in bread wheat (*Triticumaestivum* L.). *J. Maharashtra Agric.Univ.* **30:** 153-156.

Sheikh, S. and Singh, I. 2000. Combining ability analysis in wheat plant characters and harvest index. *International J. Tropical Agric.* **18(1):** 29-37.

Zahid, A. U. A., Saif, S. K. Khalid, Rahmatullah and Muhammad. 2011. Combining ability estimates of some yield and quality related traits in spring wheat (*Triticumaestivum*L.). *PakistanJournal of Botany* **43(1):** 221-231.