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Combining ability analysis over environments in diallel crosses in bread wheat (*Triticum aestivum* L.)

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Abstract : Combining ability analysis was undertaken in a 12 x 12 half diallel progeny of bread wheat for grain yield and its component characters under timely (E_1) and late sown (E_2) conditions. The mean squares due to gca and sca showed highly significant differences for all the characters in both the environments, suggesting the importance of both additive and non-additive gene action. However, variances due to sca were higher in magnitude than gca for most of the traits except plant height and length of main spike in both the environments indicating the predominance of non-additive gene action. The low predictability ratios for most of the traits in both the sowing dates also confirm the results. However, the predictability ratios for plant height and length of main spike were near unity suggesting the importance of additive gene action in the inheritance of these characters. The estimates of gca effects of the parents revealed that GW 496 (in both the environments), GW 273, MACS 2496 and PBW 373 (in E_1) while J 24 and HUW 234 (in E_2) were observed to be good general combiners for grain yield and some contributing traits. The perusal of sca effects revealed that the crosses GW 496 x HD 2189, DL 788-2 x GW 173 and GW 496 x MACS 2496 were found to be good specific combiners with considerable *per se* performance in both the environments. The crosses GW 496 x PBW 373 in E_1 and GW 496 x HD 2189 in E_2 gave the highest sca effects as well as *per se* performance in respective generation. These crosses also showed desirable sca effects for the important yield contributing traits like number of tillers per plant, length of main spike, number of grains per plant, flag leaf area, biological yield per plant and harvest index. The crosses showing high sca effects for grain yield per plant involved high x high, high x low and low x low general combiners indicating the involvement of additive x additive, additive x dominance and dominance x dominance type of gene action in the inheritance of these characters. The simple pedigree selection in succeeding generations and non-conventional breeding methods like biparental mating coupled with few cycles of recurrent selection could be utilized for the exploitation of additive and non-additive gene action, respectively.

Key Words : Diallel analysis, gca, sca, Over environments, Bread wheat, Combining ability

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INTRODUCTION

Wheat (*Triticum aestivum* L.) is usually accorded a premier place among the cereals. It is grown over a range of latitudes and is known for its remarkable adaptation. There has been a steady and highly significant increase in wheat yields, largely due to the release of new varieties and improved production technologies. The success of any plant breeding programme mostly depends on the exact knowledge of the genetic architecture of the population being handled, the basic genetic mechanisms involved in generating variability and the selection of parents along with the information regarding nature and magnitude of gene action controlling various characters of agronomic importance. The concept of combining ability, which is a landmark in the adoption of appropriate breeding methods, is of great use for improving crop varieties. Generally, wheat is grown in the month of November but it is also grown after the harvesting of monsoon crops in the month of December. Hence, development of high yielding varieties under timely as well as late sowing are required. Therefore, the present study was carried out to estimate the combining ability of the 12 bread wheat varieties and their 66 crosses for

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12 quantitative characters under timely sown (E_1) and late sown (E_2) environments using diallel analysis.

MATERIALS AND METHODS

Twelve diverse varieties of bread wheat namely J 24, GW 273, GW 496, GW 322, HD 2189, MACS 2496, PBW 373, UP 2425, HUW 234, DL 788-2, Lok 1 and GW 173, along with their 66 F_1's produced by diallel mating system (without reciprocals) were grown in a randomized block design with three replications under two environments *viz.*, timely sown (E_1) and late sown (E_2) at the Wheat Research Station, Junagadh Agricultural University, Junagadh. Each cross/ parent was accommodated in each environment in a single row plot of 2.50 m length with a distance of 22.5 cm between rows and 10.0 cm between plants within rows. All the recommended cultural practices were followed for raising a healthy crop. The five competitive plants from parental lines and F_1s in each replication were selected randomly, excluding border plants, for recording the single plant observations on 12 characters *viz.*, days to flowering, days to maturity, plant height (cm), tillers per plant, length of main spike (cm), grains per spike, flag leaf area (cm^2), 1000-grain weight (g), protein content (%), biological yield per plant (g), harvest index (%) and grain yield per plant (g). The flag leaf area was measured by using leaf area meter (AM-100, ADC Bio-Scientifics Ltd., England). The mean values of the data recorded were subjected to the combining ability analysis following method 2 model I proposed by Griffing (1956). The predictability ratio ($2\sigma^2$gca / $2\sigma^2$gca + σ^2sca) was computed by following Baker (1978).

RESULTS AND DISCUSSION

The mean squares due to gca and sca were significant (Table 1) for all the characters in both the environments. This signified that the variances due to gca and sca had played an important role in the inheritance of different characters. Similar findings were reported by different workers (Patil *et al.*, 1995; Sharma *et al.*,2003; Joshi, *et al.*, 2004; Singh *et al.*, 2008). The magnitudes of sca variances were higher than gca variances indicating the predominance of non-additive gene action for different traits except plant height and length of main spike in both the environments. Further, the low predictability ratios for such traits in both the environments also confirmed non-

Table 1 : Analysis of variance for combining ability for 12 characters over environments in bread wheat

Source	d.f.	Mean squares											
		Days to flowering		Days to maturity		Plant height		Tillers per plant		Length of main spike		Grains per spike	
		E_1	E_2	E_1	E_2	E_1	E_2	E_1	E_2	E_1	E_2	E_1	E_2
Gca	11	227.86**	115.21**	33.18**	38.06**	162.07**	167.63**	5.19**	2.13**	6.79**	5.60**	194.94**	177.28**
Sca	66	16.87**	8.86**	11.04**	5.95**	7.38**	7.26**	3.47**	0.74**	0.22**	0.20**	15.40**	14.18**
Error	154	0.94	0.20	1.01	0.04	1.65	2.58	1.07	0.35	0.04	0.04	1.93	0.10
σ^2gca		15.07	7.60	1.58	2.29	11.05	11.46	0.12	0.10	0.47	0.39	12.82	11.65
σ^2sca		15.91	8.66	10.03	5.91	5.73	4.68	2.40	0.39	0.18	0.16	13.47	14.08
$2\sigma^2$gca / ($2\sigma^2$gca + σ^2sca)		0.67	0.64	0.31	0.44	0.80	0.83	0.19	0.32	0.84	0.83	0.67	0.62

Source	d.f.	Mean squares											
		Flag leaf area		1000-grain weight		Protein content		Biological yield per plant		Harvest index		Grain yield per plant	
		E_1	E_2	E_1	E_2	E_1	E_2	E_1	E_2	E_1	E_2	E_1	E_2
Gca	11	56.70**	35.49**	99.80**	70.17**	2.15**	2.16**	265.86**	68.91**	32.29**	52.48**	32.97**	4.62**
Sca	66	22.76**	14.29**	8.11**	5.53**	0.31**	0.31**	81.63**	14.10**	9.15**	6.50**	15.22**	2.00**
Error	154	0.23	0.36	0.09	0.21	0.02	0.03	16.77	4.73	0.48	1.86	3.54	0.70
σ^2gca		2.42	1.51	6.55	4.62	0.13	0.13	13.16	3.92	2.01	3.28	1.27	0.19
σ^2sca		22.53	13.93	8.02	5.32	0.29	0.28	64.86	9.37	8.67	4.64	11.68	1.30
$2\sigma^2$gca / ($2\sigma^2$gca + σ^2sca)		0.26	0.18	0.64	0.63	0.03	0.48	0.36	0.46	0.38	0.59	0.26	0.23

** Indicate significance of value at P=0.01

Table 2 : Estimates of gca effects of parents over environments in bread wheat

Parents	Days to flowering		Days to maturity		Plant height		Tillers per plant		Length of main spike		Grains per spike	
	E_1	E_2	E_1	E_2	E_1	E_2	E_1	E_2	E_1	E_2	E_1	E_2
J 24	-0.35	-0.06	-0.76**	0.91	3.83**	5.38**	0.35	0.61**	1.08**	1.13**	-0.88**	0.65**
GW 273	-0.41	0.16	1.45	-0.43**	1.32**	1.91**	0.44	-0.38	0.41**	0.49**	4.35**	2.39**
GW 496	2.41	1.41	1.57	0.35	-1.40	-1.72	1.17**	0.60**	0.22**	0.17**	-0.70	-0.84
GW 322	5.03	3.42	0.19	1.34	1.85**	1.00**	-0.02	-0.17	0.32**	0.00	3.15**	2.37**
HD 2189	0.68	0.70	0.33	1.25	5.60**	4.45**	-0.25	-0.13	0.47**	0.40**	3.02**	3.18**
MACS 2496	6.40	4.50	1.58	2.35	1.56**	1.97**	0.11	-0.28	0.65**	0.59**	5.87**	6.01**
PBW 373	4.98	3.51	2.48	1.38	1.74**	0.64	0.25	-0.39	0.39**	0.14**	2.85**	1.63**
UP 2425	-4.62**	-2.56**	-2.07**	-1.92**	-0.82	-0.38	-0.72	-0.54	-0.04	0.04	-4.19	-1.45
HUW 234	-1.19**	-1.00**	-0.52*	0.18	-2.42	-0.99	1.10**	0.45**	-0.85	-0.69	-1.04	0.78**
DL 788-2	-4.72**	-3.63**	-0.82**	-0.38**	-4.81	-5.59	0.51	0.14	-0.95	-0.92	-3.97	-3.52
Lok 1	-2.96**	-2.18**	-1.00**	-1.65**	-0.41	-0.46	-0.40	0.10	-0.77	-0.49	-3.39	-5.82
GW 173	-5.25**	-4.27**	-2.44**	-3.38**	-6.34	-6.21	-0.33	-0.02	-0.92	-0.88	-5.05	-5.38
S.E. (g_i) ±	0.25	0.11	0.26	0.05	0.33	0.41	0.26	0.15	0.05	0.05	0.36	0.08
S.E. $(g_i - g_j)$ ±	0.37	0.17	0.38	0.08	0.49	0.61	0.39	0.22	0.08	0.08	0.53	0.12

Parents	Flag leaf area		1000-grain weight		Protein content		Biological yield per plant		Harvest index		Grain yield per plant	
	E_1	E_2	E_1	E_2	E_1	E_2	E_1	E_2	E_1	E_2	E_1	E_2
J 24	2.23**	1.40**	0.04	0.65**	-0.23	-0.16	3.39**	5.32**	-3.03	-3.96	0.15	1.09**
GW 273	1.15**	1.14**	0.02	0.68**	0.05	0.14**	5.42**	-0.13	0.52**	0.64	2.61**	0.12
GW 496	0.99**	0.68**	-0.39	-0.02	0.30**	0.15**	1.67	1.58**	0.18	-0.76	0.96*	0.65**
GW 322	-1.16	-1.32	-1.94	-2.33	-0.82	-0.77	2.31*	-0.53	-1.32	-1.14	0.36	-0.68
HD 2189	-0.42	-0.17	-2.97	-2.61	-0.22	-0.11	0.95	0.31	-1.37	-0.59	-0.37	-0.04
MACS 2496	-0.14	-0.18	-3.16	-3.13	0.33**	0.36**	3.84**	0.79	-0.50	-0.66	1.40**	0.17
PBW 373	2.35**	1.65**	-0.90	-0.56	0.03	0.02	3.66**	-1.15	-0.79	-0.82	1.33**	-0.61
UP 2425	2.61**	2.69**	2.65**	1.94**	0.71**	0.66**	-4.50	-1.66	0.64**	0.41	-1.68	-0.52
HUW 234	-1.17	-0.77	-0.84	-1.05	-0.41	-0.65	-5.57	1.48**	0.18	0.32	-2.25	0.66**
DL 788-2	0.19	-0.35	2.16**	1.94**	0.09**	0.12*	-1.05	-1.57	0.63**	1.30**	-0.07	-0.32
Lok 1	-3.23	-2.78	6.42**	4.81**	0.19**	0.10	-1.37	-0.85	1.25**	0.89*	0.06	0.05
GW 173	-3.40	-2.00	1.10**	-0.32	-0.01	0.14**	-8.35	-3.58	3.59**	4.37**	-2.50	-0.58
S.E. (g_i) ±	0.12	0.15	0.08	0.12	0.03	0.05	1.05	0.56	0.18	0.35	0.48	0.21
S.E. $(g_i - g_j)$ ±	0.18	0.23	0.11	0.17	0.05	0.07	1.55	0.82	0.26	0.51	0.71	0.32

* and ** Indicate significance of value at P=0.05 and 0.01, respectivel

additive gene action. High predictability ratios for plant height and length of main spike in both environments suggested the importance of additive gene action in the inheritance of these characters. Similar results were also reported by Kant *et al.*, (2001), Dhayal and Sastry (2003), Sinha (2003), Sharma and Garg (2005), Kumar and Sharma (2008) and Seboka and Singh (2009) for most of the traits. In general, the results indicated that additive as well as non-additive gene action played an important role for the genetic control of different traits in both the environments.

The results of gca effects of the parents in E_1 and E_2 environments are presented in Table 2. The results revealed that GW 496 was found to be good general combiner for grain yield per plant, plant height, tillers per plant, length of main spike, flag leaf area and protein content in both the environments, while for biological yield per plant in E_2 environment only. GW 273, MACS 2496 and PBW 373 (in E_1) and J 24, GW 496 and HUW 234 (in E_2) were also observed to be good general combiners for grain yield per plant along with some other traits. GW 322 was found to be good general combiner for plant height, grains per spike; HD 2189 for plant height, length of main spike and grains per spike; UP 2425 for days to flowering, days to maturity, flag leaf area, 1000-grain weight and protein content; DL 788-2 for days to flowering, days to maturity, 1000-grain weight, protein content and harvest index; Lok 1 for days to flowering, days to maturity, 1000-grain weight and harvest index while GW 173 for days to flowering, days to maturity and harvest index in both the environments. The results indicated that these parents possess high concentration of desirable genes for important

Table 3 : Crosses showing significant sca effect for grain yield per plant, their *per se* performance and gca status of parents involved in the crosses in E_1 and E_2 in bread wheat

Sr. No.	Desirable crosses	sca effect	*Per se*	gca effect		Desirable sca effects for other traits
				P_1	P_2	
			E_1			
1.	GW 496 x PBW 373	8.67**	31.43	H (0.96*)	H (1.33**)	4,5,6,7,8,10
2.	GW 496 x HD 2189	7.86**	28.93	H (0.96*)	L (-0.37)	5,6,8,9,10,11
3.	GW 322 x Lok 1	7.30**	28.20	L (0.36)	L (0.06)	4,7,9,10,11
4.	DL 788-2 x GW 173	6.45**	24.37	L (-0.07)	L (-2.50**)	9,10
5.	MACS 2496 x HUW 234	6.20**	25.83	H (1.40**)	L (-2.25**)	1,2,8,10,11
6.	UP 2425 x DL 788-2	6.16**	24.90	L (-1.68**)	L (-0.07)	2,5
7.	GW 273 x MACS 2496	5.87**	30.37	H (2.61**)	H (1.40**)	4,7,10
8.	GW 273 x PBW 373	4.91**	29.33	H (2.61**)	H (1.33**)	1,2,4,5,7,8,11
9.	J 24 x DL 788-2	4.20*	24.77	L (0.15)	L (-0.07)	1,9,11
10.	GW 496 x Lok 1	4.04*	25.53	H (0.96**)	L (0.06)	4,7,9,10
11.	GW 496 x MACS 2496	3.79*	26.63	H (0.96**)	H (1.40**)	4,11
12.	GW 273 x HUW 234	3.55*	24.40	H (2.61**)	L (-2.25**)	1,4,6,9,10
13.	UP2425 x GW173	3.50*	19.80	L (-1.68**)	L (-2.50**)	8,10
			E_2			
1.	GW 496 x HD 2189	3.58**	13.57	L (0.12)	L (-0.04)	4,6,8,10
2.	GW 496 x MACS 2496	2.57**	12.77	L (0.12)	L (0.17)	1,3,8,10
3.	PBW 373 x DL 788-2	2.41**	10.87	L (-0.61**)	L (0.32)	1,4,8,9,10
4	J 24 x GW173	2.25**	12.13	H (1.09**)	L (-0.58**)	1,6,9
5.	DL 788-2 x GW 173	2.11**	10.37	L (-0.32)	L (-0.58**)	7
6.	MACS 2496 x DL 788-2	2.10**	11.33	L (0.17)	L (-0.32)	1,2,4,6,10
7.	J 24 x HUW 234	2.07**	13.20	H (1.09**)	H (0.66**)	1,2,5,6,8,10
8.	Lok 1 x GW 173	1.88*	10.73	L (0.05)	L (-0.58**)	6,8,9,10
9.	MACS 2496 x GW 173	1.67*	10.63	L (0.17)	L (-0.58**)	1,2,6,8
10.	GW 273 x HD 2189	1.62*	7.83	L (0.12)	L (-0.04)	2,3,7
11.	HUW 234 x GW 173	1.60*	11.07	H (0.66**)	L (-0.58**)	1,2,4,6

*and ** Indicate significance of value at P=0.05 and 0.01, respectively
1 = Days to flowering , 2 = Days to maturity, 3 = Plant height 4 = Tillers per plant 5 = Length of main spike 6 = Grains per spike
7 = Flag leaf area 8 = 1000- grain weight 9 = Protein content 10 = Biological yield per plant 11 = Harvest index 12 = Grain yield per plant
H = High, L= Low

yield contributing characters and could be used effectively in multiple crossing programme to isolate high yielding lines for timely as well as late sown conditions in bread wheat. The importance of such characters had also been emphasized by Singh and Paroda (1986), Singh and Yunus (1993), Sheikh and Singh (2000), Mahmood and Chowdhry (2000), Sharma *et al.*, (2003), Joshi and Sharma (2006), Dhadhal and Dobariya (2006) and Dhadhal *et al*. (2008).

Promising crosses on the basis of sca effect for grain yield per plant, *per se* performance alongwith gca status of the parents involved in these crosses are presented in Table 3. It was revealed that 13 and 11 crosses exhibited significant positive sca effects for grain yield per plant in E_1 and E_2, respectively. The best cross identified in E_1 was GW 496 x PBW 373 with the highest *per se* performance followed by GW 496 x HD 2189, GW 322 x Lok 1, DL 788-2 x GW 173, MACS 2496 x HUW 234, UP 2425 x DL 788-2, GW 273 x MACS 2496 and GW 273 x PBW 373. While, in E_2, the cross GW 496 x HD 2189 gave the highest sca effect and *per se* performance followed by GW 496 x MACS 2496, PBW 373 x DL 788-2, J 24 x GW 173, DL 788-2 x GW 173, MACS 2496 x DL 788-2 and J 24 x HUW 234. Three crosses *viz*., GW 496 x HD 2189, DL 788-2 x GW 173 and GW 496 x MACS 2496 were observed to be good specific combiners in both the environments with considerable *per se* performance. These crosses may be used for the development of varieties suitable for timely as well as late sown conditions. Crosses shown significant sca effects for grain yield involved parents with high x high, high x low and low x low gca effects, indicating the presence of additive x additive, additive x dominance of dominance x dominance type of non-allelic interactions. It appeared that high sca effect of a cross is not always dependent upon the high gca effects of the parents involved. The superiority of the crosses may be due to complementary type of gene interaction, which can be exploited in subsequent segregating generations.

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