

SELECTION OF SUPERIOR GENOTYPES IN SPRING WHEAT (*Triticum aestivum* L.) THROUGH COMBINING ABILITY ANALYSIS

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Received: July 13, 2015; Revised: September 03, 2015; Accepted: September 07, 2015

Abstract- Combining ability analysis was studied in a diallel mating design of spring wheat (*Triticum aestivum* L.). The analysis of variance for combining revealed that the variance due to *gca* and *sca* were highly significant for all the characters indicated that both the additive and non-additive gene actions were involved in the expression of the traits. The genotypes HW 5206, HD 2964 and PBW 373 were considered as the best general combiners, while hybrids HW 5207 x RT, PBW 550 x PBW 373, COW (W) 1 x PBW 373, HW 5206 x HD 2964, HD 2964 x PBW 373, HD 2833 x HD 2687, HD 2964 x WH 711, COW (W) 1 x PBW 550, HD 2833 x HW 5207, HD 2687 x WH 711 and COW (W) 1 x HW 5206 as good specific combiners for grain yield and other yield contributing and quality traits. The promising parents namely PBW 373, HD 2964 and HW 5206 which are having high *gca* effects in desirable direction for yield components and for quality traits may be incorporated in cross-ing programme to have better genotypes for yield better and quality. The crosses PBW 550 x PBW 373, COW (W) 1 x PBW 373, HW 5206 x HD 2964, COW (W) 1 x PBW 550 and HD 2833 x HW 5207 exhibited good *sca* effects for major yield and more than six yield contributing characters. They were also found to be superior for gluten content, ash content and showed low reaction of phenol on the grains. This may be exploited for better yield and *chapati* quality either by exploiting them through heterosis breeding or involving them in multiple cross breeding programme.

Keywords- analysis, combining ability, diallel analysis, gene action, quality traits, wheat

Citation: Baghyalakshmi K., et al. (2015) Selection of Superior Genotypes in Spring Wheat (*Triticum aestivum* L.) through Combining Ability Analysis. International Journal of Agriculture Sciences, ISSN: 0975-3710 & E-ISSN: 0975-9107, Volume 7, Issue 7, pp.-559-564.

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Introduction

Among the cereals, spring wheat (Triticum aestivum L.) was the first crop to be domesticated and constitutes as the major staple food crop for about 35% of the world population. Now the wheat productivity has reached a ceiling in yield. To overcome the yield barriers and quality improvement, the combining ability analysis is a powerful tool to discriminate good as well as poor combiners. This helps in choosing appropriate parental materials for particular traits in the wheat improvement programme. Therefore, wheat improvement for quality depends intensive on hybridization using quality and high yielding commercial parental lines. To evolve an effective hybridization programme combining ability analysis is used to test the performance of genotypes in different cross combinations and characterize the nature and magnitude of gene effects in the expression of various yield and quality parameters. However, breeding of yield contributing and quality resistance genotypes requires selection of parents based on their combining ability of the traits. In view of this, objective of present study was to identify the best combining parents on the basis of their general and specific combining ability for various traits for further yield components and quality improvement in spring wheat.

Materials and Method

The basic material for the present investigation comprised of ten wheat genotypes/varieties namely COW (W) 1, PBW 550, HW 5206, HD 2964, PBW 373, HD 2833, HW 5207, HD 2687, RT and WH 711- was obtained from IARI-Regional Station, Wellington. The genotypes were used for crossing programme in a diallel half fashion (10 × 10). Field plot was well prepared for sowing of the experimental material (55 genotypes- comprising 10 parents and 45 F1's seeds). The experiment was conducted in a Randomized Complete Block Design with three replications. Seeds of each of the parental lines and crosses were sown by hand dibbling method in two rows plot. The length of row was 3m long by maintaining 25cm row to row and 10cm plant to plant distance. All the recommended agronomic inputs and practices were applied to the crop during the season. The data were recorded on ten randomly selected competitive plants in each of three replications and fifteen different characters namely days to 50% flowering, days to maturity, number of productive tillers per plant, plant height, flag leaf area (cm2), spike length (cm), spikelets per spike, grains per spike, 1000-grain weight (g), biological yield per plant (g), grain yield per plant (g), harvest index, ash content (%), gluten content (%) and phenol colour reaction

(grading). The mean data on these traits except phenol colour reaction were subjected to statistical and biometrical analysis. Combining ability analysis according to [1] model I and method 2 was conducted using the statistical software package of INDOSTAT.

Result and Discussion

The analysis of variance for combining ability [Table-1] revealed that the variance due to general combining ability (GCA) and specific combining ability (SCA) were highly significant for all the characters indicating that both additive and non-additive gene action were involved in expression of these traits. Almost similar trend of involvement of both additive and non-additive gene actions has been earlier reported by [2-6]. The variance component for σ^2 s were less than estimates of $\sigma^2 g$ for all the traits except for days to 50% flowering, days to maturity, plant height, 1000-grain weight and biological yield. Similar findings were also reported by [2,7]. The ratio of $\sigma^2 g$ / σ^2 s being less than unity indicated the involvement of the nonadditive gene action for nine characters viz; number of productive tillers per plant, flag leaf area, spike length, spikelets per spike, grains per spike, grain yield per plant, harvest index, ash content and gluten content, which indicated more involvement of nonadditive type of gene action for these traits. The findings are in conformity with [2,4,5,8]. However this ratio was more than unity for five traits namely days to 50% flowering, days to maturity, plant height, 1000-grain weight and biological yield per plant which indicated additive type of gene action for these traits. The results of this study were in agreement with [8]. The mean degree of dominance ($\sigma 2s$ / σ 2g).5 was found greater than unity for nine characters namely number of productive tillers/ plant, flag leaf area, spike length, spikelets per spike, grains per spike, grain yield per plant, harvest index, ash content and gluten content indicating the involvement of over dominance. Such types of findings were also reported by [7]. However, it was less than one for five characters namely days to 50% flowering, days to maturity, plant height, 1000-grain weight and biological yield per plant, indicated the involvement of partial dominance. In earlier studies role of non-additive genetic variance were reported by [2,4]. The estimate of gca effects, along with range and mean performance of 10 parents for all the 14 attributes have been presented in [Table-2]. Based on the combining ability effects, the parents values were categorized in three groups as good (G), average (A) and poor (P) general combiners. The parents with significant qca effects towards desirable direction were considered as good general combiners (G), with positive gca effects were considered as average general combiners (A) basis of good general combiner was taken as significance gca and desirable per se performance and the parents with negative *gca* effects were designated as poor general combiners (P).

Parent COW (W) 1 was found to be significant and good general combiner for days to 50% flowering, days to maturity, number of productive tillers per plant, spikelets per spike, grains per spike and harvest index, Similarly, parent PBW 550 was found to be good general combiner for days to 50% flowering, days to maturity, flag leaf area, spikelets per spike and grains per spike. Parent, HW 5206 was found to be good general combiner for days to 50% flowering, days to maturity, plant height, spike length, spikelets per spike, grains per spike, ash content and gluten content. Parent, HD 2964 was found to be good general combiner for number of productive tillers per plant and spike length. Parent, PBW 373 was found to be good general combiner for days to 50% flowering, flag leaf area, spike length, grain per spike, 1000-grain weight, biological yield per plant and grain yield per plant. Genotype, HD 2833 was found to be good general combiner for flag leaf area and grain yield per plant. Parent HW 5207 was found to be good general combiner for 1000-grain weight, Variety, HD 2687 was found to be good general combiner for days to maturity, flag leaf area, spikelets per spike and gluten content. Parent, RT was found to be good general combiner for plant height and gluten content. Genotype, WH 711 was found to be good general combiner for plant height, flag leaf area, spike length, 1000-grain weight, harvest index and gluten content. A close examination of the result revealed that the parent HW 5206 combined well for the highest number of eight characters followed by PBW 373 for seven characters, COW (W) 1 for six characters, PBW 550 for five characters, HD 2687 and WH 711 for four characters each and the parent, HD 2833, PBW590 and RT for two characters and HW 5207 was good general combiner for one character. The good combiners on the basis of per se performance and significant gca effects in desirable direction were observed in PBW 550, COW (W) 1, PBW 373 and HW 5206 for days to 50% flowering; PBW 550, COW (W) 1, HW 5206 and HD 2687 for days to maturity; HD 2964 and COW (W) 1 for number of tillers per plant; WH 711, HW 5206 and RT plant height; HD 2833, PBW 373, WH 711, PBW 550 and HD 2687 for flag leaf area; PBW 373, HD 2964 and HW 5206 for spike length; COW (W) 1, HD 2687, HW 5206 and PBW 550 for spikelets per spike; COW (W) 1, HW 5206, PBW 550 and PBW 373 for grain number per spike; PBW 373, HW 5207, and WH 711 for 1000 grain weight; PBW 373 for biological yield per plant ; PBW 373 and HD 2833 for grain yield per plant; COW (W) 1 for harvest index; HW 5206 for ash content and WH 711, HD 2687, RT and HW 5206 for gluten content.

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Parents & hybrids variation	DF	Days to 50% Flowering	Days to maturity	No of productive tillers/ plant	Plant height (cm)	Flag leaf area (cm)	Spike length (cm)	Spikelets / spike	Grains / spike	1000 grain weight (g)	Biological yield/ plant (g)	Grain yield/ plant (g)	Harvest index	Ash content	Gluten content
GCA	9	51.46**	10.50**	1.80**	196.92**	139.11**	1.18**	0.74**	85.86**	25.41**	121.87**	32.52**	8.72**	0.018**	0.34**
SCA	45	2.10**	0.97**	0.60**	8.53**	14.67**	0.18**	0.33**	10.42**	2.78**	9.14**	3.23**	9.30***	0.017**	0.06**
Error	108	0.29	0.25	0.13	0.55	1.11	0.03	0.03	1.31	1.52	0.87	0.5	2.89	0.004	0.01
Estimated v	varianc	es due to													
δ2 ġ		4.26	0.85	0.14	16.36	11.5	0.1	0.06	7.05	1.99	10.08	2.67	0.49	0.001	0.03
δ2 ġ		4.26	0.85	0.14	16.36	11.5	0.1	0.06	7.05	1.99	10.08	2.67	0.49	0.001	0.03
δ2 ġ/ δ2 s		2.35	1.19	0.29	2.05	0.85	0.65	0.2	0.77	1.58	1.22	0.98	0.08	0.081	0.59
(δ2 s/ δġ)½		0.65	0.91	1.82	0.7	1.09	1.22	2.19	1.14	0.79	0.9	1.01	3.62	3.449	1.29

Table 1- Analysis of variance for combing ability for 14 characters in wheat

International Journal of Agriculture Sciences ISSN: 0975-3710 & E-ISSN: 0975-9107, Volume 7, Issue 7, 2015

Table 2- Estimates of gca effects along with mean	performance of parents for gra	ain vield and its components traits in wheat
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Genotypes (Parents)	Days to 50% Flowering				No. of productive tillers/plant Plant height (cm)			Flag leaf a	area (cm2)	Spike length (cm)		Spikelets/ spike			
(Parents)	gca	Mean	gca	Mean	gca	Mean	gca Mean		gca	Mean	gca	Mean	gca	Mean	
COW (W) 1	-2.62**	82.66	-0.89**	136.66	-0.89**	136.66	4.01**	103.66	-4.28**	28.78	-0.08	8.27	0.38**	20.56	
PBW 550	-3.46**	83.66	-1.89**	135.33	-1.89**	135.33	1.11**	95.76	0.84**	35.96	-0.03	8.59	0.17**	20.3	
HW 5206	-0.62**	92	-0.44**	139.33	-0.44**	139.33	-5.82**	78.53	-3.25**	32.58	0.18**	9.3	0.19**	19.86	
HD 2964	-0.26	91.66	0.25	140	0.25	140	-0.25	93	-2.30**	35.64	0.25**	9.68	-0.43**	17.3	
PBW 373	-1.26**	90	0.47**	141.33	0.47**	141.33	4.17**	101.43	4.74**	47.86	0.68**	10.28	-0.15**	17.7	
HD 2833	-0.04	91.66	0.67**	141.33	0.67**	141.33	4.16**	100.5	5.99**	49.3	-0.31**	8.45	-0.27**	18.33	
HW 5207	1.54**	94	0.36**	140.66	0.36**	140.66	1.99**	97.26	-0.47	42.19	-0.06	8.91	-0.13*	18.7	
HD 2687	2.10**	96	-0.28*	139.66	-0.28*	139.66	1.19**	93.03	0.66*	41.32	0	9.45	0.22**	20	
RT	1.93**	95.66	0.22	141	0.22	141	-4.65**	79.1	-3.03**	31.21	-0.19**	8.75	-0.02	19.53	
WH711	2.68**	96.66	1.53**	142	1.53**	142	-5.90**	76.93	1.11**	36.08	-0.43**	8.14	0.03	19.5	
Mean	91.4 139.73		9.73	139.73		91.92		38	38.09		8.98		19.18		
Range	82.66-	96.66	135.33- 142.00		135.33- 142.00		76.93- 103.66		28.78-49.30		8.14- 10.28		17.30-20.56		
S.E.	0.4	42	0.	44	0.44		0.36		0.1	0.74		0.11		0.21	
SE (Gi)	0.33		0.	31	0.31		0.46		0.0	65	0.	.1	0.1	12	
SE (Gi-Gj)	0.	.5	0.	46	0.46		0.68		0.9	0.97		0.15		17	
Genotypes	Grains	ins / spike 1000 grain weight (g)		Biological yield/ plant (g)		Grain yield per plant (g)		Harvest index (%)		Ash content		Gluten content			
	gca	Mean	gca	Mean	gca	Mean	gca	Mean	gca	Mean	gca	Mean	gca	Mean	
COW (W) 1	4.35**	62.7	0.41	42.24	-0.66*	38.43	0.34	17.9	1.71**	46.57	0.028	1.655	-0.26**	8.41	
PBW 550	2.40**	63.3	-0.76*	39.23	-0.33	35.76	-0.11	16.2	-0.01	45.29	0.032	1.177	-0.26**	8.18	
HW 5206	2.93**	61.3	0.53	42.62	-0.11	38.9	0.1	18.6	0.33	47.86	0.064**	1.577	0.07*	8.76	
HD 2964	-2.18**	48.1	-0.05	39.64	-0.46	38.76	-0.31	17.06	-0.24	44.06	-0.036*	1.288	0.01	8.68	
PBW 373	1.94**	52.43	2.28**	46.82	8.56**	50.23	4.22**	28.3	-0.2	56.32	0.03	1.532	-0.05	8.73	
HD 2833	-2.46**	47.9	0.42	40.82	0.5	39.66	0.52**	21.8	0.85	55.38	-0.025	1.444	0	8.8	
HW 5207	-1.82**	50.53	0.81*	43.46	-0.92**	34.66	-0.84**	16.7	-0.87	48.13	-0.058**	1.377	-0.02	8.5	
HD 2687	-0.06	52.76	-3.18**	35.58	-1.68**	35.03	-1.36**	14.76	-1.31**	42.15	-0.003	1.566	0.15**	9	
RT	-2.89**	49.56	-1.18**	37.86	-1.56**	36.66	-0.97**	16.86	-0.43	46.01	-0.034*	1.488	0.08*	8.75	
WH711	-2.20**	49.13	0.71*	40.14	-3.32**	35.96	-1.60**	16.7	0.17	46.42	0.002	1.533	0.29**	9.35	
Mean	53.77		40.84		38	.41	18	.49	47	47.81		64	8.7	72	
Range	47.90	-63.30	35.58-	46.82	34.66	50.23-	14.76-	28.30	42.14-56.32		1.180- 1.653		8.18- 9.35		
	1.08		1.0)24	0	.6	0	.9	2.64		0.077		0.09		
S.E.	1.1			0.71 0.76		0.58		0.44		1.05		0.038		0.07	
S.E. SE (Gi)			0.	76	0.	58	0.4	44	1.	05	0.0	38	0.0	07	

The estimates of gca effects of the parental lines for different characters revealed that none of the parental lines excelled in gca effects for all the characters studied. However parent HW 5206, PBW 373 and COW (W) 1 showed significant gca effect with good per se for 6-8 characters related to productivity. These may be used for exploiting additive type genetic variability which is fixable type and selection may be effective in segregating population for development of better genotype with regards to yield. However parents PBW 550, HD 2833, RT, PBW 373 and HW 5206 which showed significant gca effect and good per se performance may be used for multiple parent participation through multiple crossing to effect substantial improvement having for broad genetic base population. Similar results were reported by [9] for spikelets per spike, 1000grain weight and harvest index and Adel et al. [4] for number of spikes/plant, spikes weight/plant and grain yield/plant. The sca effects represent the non-additive gene action which is non-fixable [Table-3]. The estimation of specific combining ability (sca) effects for 45 hybrids along with mean performance for all the fourteen characters are presented in [Table-3], significant positive or negative sca effects were observed in F1 generation for yield and vari-

ous yields attributing traits. In the present investigation, none of the crosses expressed good specific combining ability effect for all the traits under study. Out of 45 crosses, ten for days to 50 per cent flowering; six for days to maturity; nine for number of tillers per plant; sixteen for plant height; seven for flag leaf area; fourteen for Spike length; fourteen for Spikelets per spike; twelve for Grains per spike; thirteen for biological yield per plant; four for harvest index; nine for ash content, seven for gluten content and 11 crosses showed significant and positive sca effect for grain yield per plant. The cross combinations viz; HW 5207 x RT, PBW 550 x PBW 373, COW (W) 1 x PBW 373, HW 5206 x HD 2964, HD 2964 x PBW 373, HD 2833 x HD 2687, HD 2964 x WH 711, COW (W) 1 x PBW 550, HD 2833 x HW 5207, HD 2687 x WH 711 and COW (W) 1 x HW 5206 which showed significant and positive sca effects with good per se performance for grain yield per plant, also showed significant sca effects for other important yield component traits. However, the best cross negative and positive desirable direction highest significant sca effects yield and yield contributing traits [Table-4].

Table 3- Estimates of sca effects along with mean performance of crosses for grain yield and its components traits in wheat

0	Days to 50% Flowering		Days to maturity		No of productive tillers/plant		Plant height (cm)		Flag leaf area (cm2)		Spike length (cm)		Spikelets/ spike	
Crosses	sca	Mean	sca	Mean	sca	Mean	sca	Mean	sca	Mean	sca	Mean	sca	Mean
COW (W) 1xPBW 550	-1.90**	84	-0.19	136.66	1.03**	10.2	1.97**	98.1	2.57*	40.39	0.47**	9.61	0.43*	20.8
COW (W) 1xHW 5206	1.26*	90	-0.3	138	0.94**	9.9	-1.54*	87.66	-0.85	32.87	0.54**	9.88	0.31	20.7
COW (W) 1xHD 2964	0.57	89.66	-2.33**	136.66	-0.47	9.4	-1.77*	93	-4.50**	30.17	0.44**	9.86	0.40*	20.16
COW (W) 1xPBW 373	1.23*	89.33	0.45	139.66	0.45	9.47	-1.26	97.93	3.29**	45	0.35*	10.2	0.12	20.16
COW (W) 1xHD 2833	0.01	89.33	0.92	140.33	0.33	9.17	-1.20	97.96	2.10*	45.07	-0.08	8.78	-0.53**	19.4
COW (W) 1xHW 5207	3.10**	94	1.89**	141	-0.35	8.17	-3.28**	93.73	-0.14	36.37	0.34*	9.45	-0.24	19.83
COW (W) 1xHD 2687	2.87**	94.33	0.2	138.66	-0.32	8.47	-2.28**	93.93	3.76**	41.39	-0.1	9.06	-0.24	20.2
COW (W) 1xRT	1.71**	93	2.03**	141	-0.52	8.03	-2.20	89.83	-1.23	32.72	-0.01	8.96	-0.22	19.86
COW (W) 1xWH 711	-0.71	91.33	-0.28	141	-0.3 0.24	9.2	-0.34 0.64	89.76	2.83**	40.91	-0.01	8.4	-0.32 0.07	20.3
PBW 550xHW 5206	-1.90**	86	-0.20	136.33	0.24	9.2 9.1	2.96**	89.26	-4.49**	34.35	-0.34 0.33*	9.73	0.07	20.3
PBW 550xHD 2964	-1.90		-0.97	138.66	0.70*	9.1 10.53			-4.49 -4.24**	35.56			0.2 0.68**	
		87					-0.11	91.76			0.17	9.65		20.23
PBW 550xPBW 373	-1.27*	86	1.11*	139.33	-0.08	8.9 0.5	-3.96**	92.33	6.18**	53.02	-0.47**	9.43	0.17	20
PBW 550xHD 2833	1.85**	90.33	-0.41	138	-0.3	8.5	-1.42*	94.86	1.89	49.98	0.25	9.16	-0.22	19.5
PBW 550xHW 5207	1.93**	92	0.22	138.33	-0.08	8.4	-0.92	93.2	1.55	43.18	0.47**	9.63	-0.05	19.8
PBW 550xHD 2687	2.37**	93	-1.47**	136	-0.25	8.5	-1.55*	91.76	4.28**	47.05	0.45**	9.66	-0.44*	19.76
PBW 550xRT	1.21*	91.66	-0.3	137.66	0.2	8.7	1.22	88.7	4.92**	44	-0.15	8.88	-0.77**	19.2
PBW 550xWH 711	1.79**	93	2.39**	141.66	-0.15	8.77	-3.26**	82.96	1.29	44.5	-0.31*	8.48	-0.31	19.7
HW 5206xHD 2964	-0.1	91	-0.44	139	0.84*	10.47	-8.41**	76.53	-1.63	34.07	0.33*	10.01	0.66**	20.23
HW 5206xPBW 373	0.23	90.33	0	139.66	0.02	8.8	3.07**	92.43	2.07*	44.81	0.13	10.23	-0.12	19.73
HW 5206xHD 2833	-0.99	90.33	0.81	140.66	0.07	8.67	0.91	90.26	6.12**	50.12	-0.14	8.98	-0.1	19.63
HW 5206xHW 5207	-0.9	92	-0.22	139.33	0.19	8.47	5.18**	92.36	-1.25	36.29	0.28	9.65	-0.04	19.83
HW 5206xHD 2687	0.21	93.66	0.09	139	0.09	8.63	2.99**	89.36	2.46*	41.12	0.24	9.66	-0.32	19.9
HW 5206xRT	0.71	94	-0.08	139.33	0.27	8.57	-1.65*	78.9	-0.16	34.81	-0.33*	8.9	0.18	20.16
HW 5206xWH 711	-1.04*	93	-0.05	140.66	-0.15	8.57	-1.83*	77.46	2.08*	41.19	-0.76**	8.23	-0.13	19.9
HD 2964xPBW 373	0.54	91	0.64	141	0.95**	10.63	0.34	95.26	4.16**	47.87	-0.02	10.16	0.33	19.56
HD 2964xHD 2833	0.65	92.33	0.78	141.33	-0.57	8.93	1.25	96.16	-1.27	43.67	-0.02	9.18	0.51**	19.63
HD 2964xHW 5207	-0.6	92.66	0.09	140.33	0.32	9.5	0.18	92.93	1.52	40.01	-0.3	9.15	0.68**	19.93
HD 2964xHD 2687	-0.82	93	0.72	140.33	-0.01	9.43	0.85	92.8	6.47**	46.09	-0.37*	9.13	0.09	19.7
HD 2964xRT	0.01	93.66	0.22	140.33	0.5	9.7	5.05**	91.16	3.17**	39.1	-0.06	9.25	0.06	19.43
HD 2964xWH 711	0.6	95	-0.08	141.33	0.05	9.67	-2.36**	82.5	-1.67	38.4	-0.02	9.05	-0.12	19.3
PBW 373xHD 2833	-1.02*	89.66	-1.44**	139.33	-0.05	8.6	-0.38	98.96	1.17	53.16	0.11	9.73	0.77**	20.16
PBW 373xHW 5207	-0.27	92	0.2	140.66	0.3	8.63	-4.28**	92.9	-6.94**	38.59	0.13	10	0.53**	20.06
PBW 373xHD 2687	-0.82	92	-0.16	139.66	-0.23	8.37	-2.80**	93.56	-5.87**	40.78	-0.73**	9.2	0.68**	20.56
PBW 373xRT	-1.32*	91.33	-1.66**	138.66	0.42	8.77	-0.37	90.16	-1.64	41.33	0.71**	10.45	0.69***	20.33
PBW 373xWH 711	1.60**	95	-0.64	141	-0.17	8.6	5.48**	94.76	3.35**	50.46	0.43**	9.93	0.44*	20.13
HD 2833xHW 5207	-0.15	93.33	-0.33	140.33	0.79*	8.93	-3.96**	93.2	0.16	46.94	-0.64**	8.25	0.41*	19.83
HD 2833xHD 2687	0.62	94.66	-0.36	139.66	0.22	8.63	-0.33	96.03	-3.02**	44.88	0.48**	9.41	0.2	19.96
HD 2833xRT	-0.88	93	0.14	140.66	0.3	8.47	0.31	90.83	1.2	45.42	0.15	8.9	0.53**	20.06
HD 2833xWH 711	0.37	95	-0.83	141	0.71*	9.3	2.49**	91.76	-0.48	47.88	0.25	8.76	0.32	19.9
HW 5207xHD 2687	-1.96**	93.67	-0.39	139.33	1.87**	9.97	-0.66	93.53	-2.46*	38.99	-0.66**	8.53	0.06	19.96
HW 5207xRT	0.54	96	-1.55**	138.66	0.55	8.4	0.54	88.9	-1.3	36.46	0.15	9.15	0.2	19.86
HW 5207xWH 711	0.46	96.67	-0.53	141	0.5	8.77	2.66**	89.76	5.15**	47.05	0.66**	9.41	0.18	19.9
HD 2687xRT	-1.02*	95	-0.91	138.66	0.85*	8.97	2.21**	89.76	-1.17	37.72	-0.27	8.78	0.05	20.06
HD 2687xWH 711	-1.10*	95.67	1.11*	142	0.57	9.1	2.27**	88.56	-1.93	41.11	0.55**	9.36	0.43*	20.5
RTxWH 711	-0.6	96	0.28	141.66	0.28	8.57	-1.53*	78.93	4.19**	43.53	0.04	8.66	-0.13	19.7
Mean	92	.11	139.61		9.01		90.81		41.96		9.31		19.95	
range	84.00	-96.67	136.00	-142.00	8.03-	10.63	76.53	-98.96	30.17-53.15		8.23-10.45		19.20-20.80	
S.E.	0.	56	0.	52	0.34		0.	78	1.1		0.17		0.	18
SE (Sij)		1	0.	93	0.	66	1.3	37	1.	95	0.31		0.	35
SE (Sij-Sik)	1.	47	1.	37	0.	98	2.	02	2.	87	0.	45	0.	51

International Journal of Agriculture Sciences ISSN: 0975-3710 & E-ISSN: 0975-9107, Volume 7, Issue 7, 2015

Table 3- Continue ..

Crosses	Grains / spike		1000 grain weight (g)		Biological yield per plant (g)		Grain yield per plant (g)		Harvest index		Ash content		Gluten content	
	sca	Mean	sca	Mean	sca	Mean	sca	Mean	sca	Mean	sca	Mean	sca	Mean
COW (W) 1xPBW 550	4.19**	64.9	0.23	39.05	3.92**	43.83	1.79**	22.53	-0.51	51.39	0.066	1.666	0.29**	8.71
COW (W) 1xHW 5206	1.62	62.86	1.12	41.22	3.54**	43.66	1.48*	22.43	-0.89	51.35	0.097	1.733	0.2	8.94
COW (W) 1xHD 2964	2.43*	58.56	-0.28	39.25	-1.28	38.5	-0.95	19.6	-0.79	50.88	0.153**	1.688	0.04	8.73
COW (W) 1xPBW 373	-1.33	58.93	2.06	43.91	3.80**	52.6	2.22**	27.3	0.19	51.9	-0.256**	1.344	-0.07	8.56
COW (W) 1xHD 2833	-3.79**	52.06	-1.22	38.77	-1.17	39.56	0.36	21.73	2.22	54.98	-0.254**	1.288	0.01	8.68
COW (W) 1xHW 5207	0.07	56.56	-1.01	39.38	-1.38	37.93	-0.05	19.96	1.61	52.65	-0.044	1.466	0.07	8.73
COW (W) 1xHD 2687	-0.75	57.5	-1.84	34.55	-3.29**	35.26	0.2	19.7	5.27**	55.86	0.088	1.655	-0.04	8.78
COW (W) 1xRT	-5.12**	50.3	-3.55**	34.85	-2.08*	36.6	0.25	20.13	3.78*	55.26	-0.002	1.533	-0.05	8.71
COW (W) 1xWH 711	2.62*	58.73	0	40.29	0.25	37.16	1.28	20.53	3.22*	55.29	0.039	1.61	-0.44**	8.54
PBW 550xHW 5206	1.55	60.83	-1.8	37.14	0.11	40.56	0.39	20.9	0.99	51.51	0.001	1.632	-0.38**	8.36
PBW 550xHD 2964	3.69**	57.86	0.81	39.17	0.88	41	1.07	21.16	1.62	51.57	0.173**	1.71	0.48**	9.16
PBW 550xPBW 373	-0.24	58.06	-1.1	39.58	5.20**	54.33	3.23**	27.86	1.29	51.28	0.151**	1.755	-0.22*	8.4
PBW 550xHD 2833	-1.1	52.8	-0.95	37.88	1.13	42.2	0.37	21.3	-0.57	50.47	0.11	1.655	-0.19	8.48
PBW 550xHW 5207	-4.14**	50.4	-0.05	39.16	-1.55	38.1	-0.1	19.46	1.8	51.13	0.129*	1.644	0.06	8.71
PBW 550xHD 2687	-5.30**	51	-2.11	33.12	-0.32	38.56	0.58	19.63	2.04	50.91	0.231***	1.799	-0.33**	8.49
PBW 550xRT	-4.57**	48.9	1.24	38.47	-1.81*	37.2	-0.17	19.26	2.03	51.79	-0.039	1.499	0.64**	9.39
PBW 550xWH 711	-3.16**	51	0.57	39.69	1.38	38.63	1.05	19.86	1.08	51.43	0.025	1.599	0.11	9.08
HW 5206xHD 2964	3.56**	58.26	-0.69	38.95	3.27**	43.6	2.19**	22.5	1.33	51.61	0.021	1.588	-0.05	8.97
HW 5206xPBW 373	2.67*	61.5	0.1	42.07	-1.15	48.2	-0.28	24.56	0.65	50.97	0.002	1.632	0.16	9.1
HW 5206xHD 2833	-4.53**	49.9	-2.33*	37.78	-0.78	40.5	-0.03	21.1	0.67	52.04	-0.146*	1.433	0.22*	9.22
HW 5206xHW 5207	-3.83**	51.23	0.91	41.4	1.73*	41.6	1.02	20.8	0.38	50.04	0.007	1.555	0.04	9.02
HW 5206xHD 2687	-1.66	55.16	-1.74	34.77	-1.14	37.96	0.34	19.6	2.41	51.62	-0.011	1.588	0.03	9.18
HW 5206xRT	0.57	54.56	-0.44	38.07	-0.09	39.13	0.25	19.9	0.75	50.85	0.096	1.666	0.33**	9.41
HW 5206xWH 711	-2.92**	51.76	0.07	40.48	-1.93*	35.53	-1.12	17.9	-0.32	50.37	0.116*	1.722	0.06	9.36
HD 2964xPBW 373	-4.72**	49	-1.08	40.32	3.53**	52.53	2.10**	26.53	0.76	50.52	0.055	1.588	0.02	8.91
HD 2964xHD 2833	1.35	50.66	1.62	38.9	-1.31	39.63	-0.79	19.93	-0.5	50.31	0.153**	1.633	-0.13	8.82
HD 2964xHW 5207	3.18**	53.13	-1.03	36.68	-1.02	38.5	0.07	19.43	1.44	50.53	0.11	1.555	0.35**	9.28
HD 2964xHD 2687	-2.25*	49.46	0.74	38.56	-0.16	38.6	0.49	19.33	1.44	50.09	-0.168**	1.333	0.13	9.23
HD 2964xRT	-1.12	47.76	0.62	37.98	-2.08*	36.8	-0.5	18.73	1.39	50.91	-0.038	1.433	-0.36**	8.66
HD 2964xWH 711	-3.11**	46.46	-1.85	40.76	0.61	37.73	-0.5 1.99**	20.6	4.63**	54.75	-0.094	1.435	0.08	9.32
PBW 373xHD 2833	4.95**	58.4	-1.1	39.67	0.08	50.03	-2.52**	22.73	-5.35**	45.5	0.068	1.61	0.00	9.02
PBW 373xHW 5207	1.35	55.43	-2.58*	36.99	1.47	50.05	-1.50*	22.75	-3.33 -4.33**	44.8	0.000	1.555	0.01	8.87
PBW 373xHD 2687	1.29	57.13	-2.50	39.12	2.39**	50.16	-0.78	22.4	-3.58*	45.11	0.113	1.677	0.14	9.17
PBW 373xRT	4.72***	57.73	-1.27	42.08	-1.23	46.66	-0.76	22.0	-3.30	45.11	-0.071	1.466	0.14	8.96
PBW 373xWH 711	4.72 2.13*	55.83	-0.07	42.00	1.47	40.00	0.29	22.33	-0.95	49.22	0.023	1.400	0.02	9.19
HD 2833xHW 5207	0.19	49.86	-0.07	36.09	4.29**	44.76	1.71*	21.9	-1.28	48.9	0.122*	1.535	-0.02	8.9
HD 2833xHD 2687	3.63**	49.00 55.06	-0.31	37.47	4.29 3.98**	44.70	2.03**	21.5	-0.06	40.9 49.67	-0.092	1.422	0.12	9.2
HD 2833xRT	2.09	50.7	-0.93	41.89	2.13*	41.96	2.03 0.47	20.53	-0.00	49.07	-0.092 0.151**	1.633	-0.12	9.2 8.82
HD 2833xWH 711														
	-0.5 1.42	48.8 53.5	1.59 1.86	34.93 38.77	-3.91**	34.16 38.36	-2.10**	17.33 18.8	-0.42	50.79	-0.018	1.499	0.26*	9.49 9.26
HW 5207xHD 2687	1.42	53.5	-1.86	38.77 38.07	0.07 8.08**	38.36 46 5	0.48 3.03**	18.8 22.63	0.98	49 48.66	-0.093 0.116*	1.388	0.21	9.26 8.08
HW 5207xRT	1.85	51.1 49.4	-0.02	38.97 36.15	8.08** 2.02**	46.5 33.73	3.93**	22.63 16.8	-0.24	48.66	-0.116*	1.333	-0.01	8.98 0.26
HW 5207xWH 711	-0.54	49.4 50.1	-1.72	36.15	-2.92**	33.73 20.22	-1.28	16.8	0.28	49.78	-0.062	1.422	0.06	9.26
HD 2687xRT	-0.91	50.1	1.34	38.2	0.58	38.23	1.11	19.3	2.01	50.46	-0.07	1.433	0.15	9.31
HD 2687xWH 711	6.67**	58.36	1.5	39.51	2.90**	38.8	1.61*	19.16	0.34	49.39	-0.063	1.477	0.04	9.41
RTxWH 711	-0.3	48.56	0.81	38.9	-1.28	34.73	-0.48	17.46	0.37	50.31	0.057	1.566	0.15	9.46
Mean		4	38.79		41.45 33.73- 54.33		20.96		50.72		1.557		8.98 8.36- 9.49	
Range	46.46		33.12-				16.80- 27.86		44.80- 55.86		1.290- 1.800			
S.E.		15		28		99		65	1.4		0.057			11
SE (Sij)		12		29		74	1.			15	0.1			21
SE (Sij-Sik)	3.	12	3.	36	2.	55	1.	92	4.	64	0.166		0.3	

International Journal of Agriculture Sciences ISSN: 0975-3710 & E-ISSN: 0975-9107, Volume 7, Issue 7, 2015

Characters	Best cross on basis of negative and positive desirable direction highest significant sca effects
Days to 50% Flowering	HW 5207 x HD 2687, COW (W) 1 x PBW550, PBW550 x HW 5206, PBW 373 x RT, PBW550 x HD 2964
Days to maturity	COW (W) 1 x HD 2964, PBW 373 x RT, HW 5207 x RT, PBW550 x HD 2687, PBW 373 x HD 2833
Number of tillers per plant	HW 5207 x HD 2967, COW (W) 1 x PBW550, HD 2964 x PBW 373, COW (W) 1 x HW 5206, HD 2687 x HW 5207
Plant height (cm)	HW 5206 x HD 2964, PBW 373 x HW 5207, PBW550 x PBW 373, HD 2833 x HW 5207, COW (W) 1 x HW 5207
Flag leaf area (cm2)	HD 2964 x HD 2687, PBW550 x PBW 373, HW 5206 x HD 2833, HW 5207 x WH 711, PBW550 x RT
Spike length (cm)	PBW 373 x RT, HW 5207 x WH 711, RT x WH 711, COW (W) 1 x HW 5206, HD 2833 x HD 2687
Spikelets per spike	PBW 373 x HD 2833, PBW 373 x RT, HD 2964 x HW 5207, PBW 373 x HD 2687, PBW550 x HD 2964
Grains per spike	HD 2687 x WH 711, PBW 373 x HD 2833, PBW 373 x RT, COW (W) 1 x PBW 550, PBW550 x HD 2964
1000 grain weight (g)	COW (W) 1 x PBW373, HD 2964 x HD 2833, HD 2833 x WH711, HD2687 x WH711, HD2687 x RT
Biological yield per plant (g)	HW 5207 x RT, PBW550 x PBW 373, HD 2833 x HW 5207, HD 2833 x HD 2687, COW (W) 1 x PBW 550
Grain yield per plant (g)	HW 5207 x RT, PBW550 x PBW 373, COW (W) 1 x PBW 373, HW 5206 x HD 2964, HD 2964 x PBW 373
Harvest index	COW (W) 1 x HD 2687, HD 2964 x WH 711, COW (W) 1 x RT, COW (W) 1 x WH 711
Ash content	PBW550 x HD 2687, PBW550 x HD 2964, COW (W) 1 x HD 2964, HD 2964 x HD 2833, PBW550 x PBW 373
Gluten content	PBW550 x RT, PBW550 x HD 2964, HD 2964 x HW 5207, HW 5206 x RT, COW (W) 1 x PBW550

These individual crosses or their multiple cross combinations may be exploited developing broad genetic base population. Out of these 11 crosses, the cross PBW 550 x PBW 373 and COW (W) 1 x PBW 373 which showed significant sca effect with good per se performance for grain yield may be used in cross breeding programme and might be expected to give transgressive segregants in F2 as these two crosses are having the parents with low x high and high x high gca effect. On the other hand, the crosses viz., PBW 550 x PBW 373, COW (W) 1 x PBW 373, HW 5206 x HD 2964, COW (W) 1 x PBW 550 and HD 2833 x HW 5207 with good per se performance and significant gca effect were common for gluten content, ash content and grain yield per plant. These crosses also showed light colouration on grains when tested with phenol solution (1%). Hence these crosses may be exploited for developing hybrid/ genotypes with better yield and quality including chapati quality. These cross combinations may be exploited in heterosis breeding programme for developing genotype having broad genetic base by multiple crossing programme.

Conclusion

The good specific combiners involved all the three possible combinations of the parents with high and low gca effects viz; high x high, high x low and low x low, indicated additive and non additive type of gene action. Similar results were reported by [2] for number of tillers per plant, number of grains per plant, flag leaf area and biological yield per plant [3,4,10] for grain yield/ plant. Both additive and nonadditive components of genetic variation appeared important in the expression of almost all the traits in present set of material. For exploitation of both the additive and non-additive component of variation, material may be handled though pedigree method, reciprocal recurrent selection or biparental mating for obtaining superior segregants and genotypes. The promising parents namely PBW 373, HD 2964 and HW 5206 which are having high gca effects in desirable direction for yield and yield components and for quality traits may be incorporated in crossing programme to have better genotypes for better and quality. The crosses PBW 550 x PBW 373, COW (W) 1 x PBW 373, HW 5206 x HD 2964, COW (W) 1 x PBW 550 and HD 2833 x HW 5207 which showed good sca effects for major yield and 6-8 yield components were also found superior for gluten content, ash content and showed low reaction of phenol on

the grains, may be exploited for better yield and *chapati* quality either 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.

Conflicts of Interests: None declared.

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