



Research Article

GENETIC CHARACTERIZATION FOR ECONOMIC AND BIOCHEMICAL TRAITS IN BREAD WHEAT (*Triticum aestivum* L.) GENOTYPES OVER THE GENERATION

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Abstract- Eight parental genotypes along with their 28 F₁ hybrids and 28 F₂ generations of wheat were evaluated to study the combining ability in a randomized complete block design with three replications during 2016-17 at SKUAST-Jammu, India. Mean sum of squares due to GCA and SCA were found to be highly significant for all the traits studied in both generations except number of effective tillers per plant in F₂ generation for GCA, indicating that both additive and non-additive genes were controlling these traits. The magnitude of SCA variance were greater than GCA variance for most of the traits in both the generations indicated that non-additive type of gene effects were more pronounced than those of additive gene effect showed significant GCA effects for grain yield per plant. In F₁ generation three crosses with both parent as poor combiners; five crosses with one parent as good combiner and one cross with both parent as good combiners and in F₂ generation six crosses with both parent as poor combiners; four crosses with one parent as good combiner and one cross with both parent as good combiners were found to be desirable crosses for grain yield per plant and biochemical traits.

Key words- Bread wheat, Combining ability, GCA, SCA, Additive, Non-additive

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Introduction

Wheat (*Triticum aestivum* L.) is an important and strategic cereal crop for majority of world populations [1]. Wheat is mainly used as a staple food providing more protein than any other cereal crop. Wheat is the most widely grown cereal grain, occupying 17 percent of the total cultivated land in the world, which accounts for 21.8 percent of the total area under food grains [2]. Wheat production accounts for 36.04 percent of total food grain production which is next only to corn which accounts for approximately 50.19 percent of total food grain production. Wheat contributes ~16 percent and 26 percent of total dietary calories in the developing and developed countries, respectively [2]. In India, wheat is cultivated on over an area of about 43.388 million hectares with a production of 93.50 million tonnes and productivity of 3093 kg/ha [3]. India ranks second in terms of wheat production and consumption after China. It shares 12.98 percent of global wheat production in 2016-17. During the last three decades, wheat production has been continued to increase at the rate of about 1-2 percent per annum, at national level but it is negligible at state level. The existing yield gap has to be reduced to achieve enhanced wheat productivity through diversification of wheat breeding programmes by developing new set of high yielding wheat varieties. Further adequate advancement in the wheat yields requires information regarding the combining ability of the parents available in a wide array of genetic material to be used in the hybridization programs. A number of biometrical procedures have been put forward by different investigators to study the combining ability of the genotypes. The diallel method of genetic analysis has been widely used to assess the combining ability of parents and hybrids [4-6]. The analysis of diallel cross [7] partitioning the total genetic variation into general combining ability (GCA) of the

parents and specific combining ability (SCA) of the crosses have been widely used. Knowledge of general and specific combining abilities influencing yield and its components has become increasingly important for plant breeders in making choice of suitable parents for developing potential possessing varieties in many crop plants [8,9]. In many studies, GCA effects for parents and SCA effects for crosses were estimated in wheat [10,11,12]. Hence, the present investigation was undertaken with the objectives to study the combining ability of wheat genotypes.

Material and Methods

The experimental material of the present study was comprised of eight true breeding lines of bread wheat viz., HD2967, WH1105, PBW343, Raj3077, RSP561, WH1080, DPW621-50 and PBW550, were planted at research farm of Division of Plant Breeding and Genetics, Faculty of Agriculture, Sher-e-Kashmir University of Agricultural Sciences & Technology of Jammu for hybridization in diallel mating design during Rabi 2015-16 for developing 28 F₁'s (one way). F₁'s were advanced to F₂'s generation through off-season nursery at IIWBR, Lahaul-Spiti (H.P.). All the F₁'s their F₂'s and parents were evaluated in Randomized Block Design with three replications during Rabi 2016-17. Seeds of 64 genotypes (8 parents + 28F₁'s + 28F₂'s seeds = 64 genotypes) were sown by hand dibbling method and the length of each row was kept 3m long by maintaining row to row and plant to plant distances of 30 cm and 15 cm, respectively at Research Farm of Division of Plant Breeding and Genetics, Faculty of Agriculture. Recommended doses of fertilizers (@ 120 kg N + 60 kg P₂O₅ + 40 kg K₂O/ha) were applied in the experimental field along with irrigations at all critical stages and other agronomic input and practices to raise a healthy crop.

Table-1 Mean squares from diallel analysis for economic and biochemical traits in F₁ and F₂ generations

Source of variation →		Replications	Genotypes	Parents	Hybrids	Parents vs hybrids	GCA	SCA	Error
Traits↓	d f	2	35	7	27	1	7	28	70
Days to 50% flowering	F ₁	0.26	289.73**	233.14**	7.47**	8306.84**	29.27**	113.40**	1.72
	F ₂	0.48	312.34**	233.14**	8.38**	9073.82**	33.20**	121.84**	1.57
Flag leaf area	F ₁	0.81	103.40**	113.72**	81.71**	616.83**	22.88**	37.36**	0.74
	F ₂	0.60	58.42**	113.72**	40.99**	141.78**	27.81**	17.39**	0.21
Days to maturity	F ₁	0.70	228.73**	157.66**	1.49*	6861.67**	21.47**	89.94**	0.93
	F ₂	2.06	227.22**	157.66**	1.42*	6810.64**	24.07**	88.66**	0.81
Plant height	F ₁	4.24	62.96**	65.95**	63.60**	24.97	16.46**	22.12**	6.91
	F ₂	0.14	41.01**	65.95**	28.88**	193.93**	30.40**	9.49**	9.54
No. of effective tillers per plant	F ₁	1.42	3.00**	0.47	1.86**	51.65**	0.41*	1.15**	0.51
	F ₂	0.01	1.24**	0.47	0.83*	17.64**	0.25	0.45**	0.40
Spike length	F ₁	0.68	3.40**	3.46**	2.32**	32.32**	0.75**	1.23**	0.43
	F ₂	0.06	3.09**	3.46**	2.62**	13.16**	1.57**	0.89**	0.62
No. of spikelet/ spike	F ₁	0.82	6.30**	4.00**	3.01**	111.22**	1.38**	2.28**	1.09
	F ₂	1.25	9.61**	4.00**	5.98**	146.90**	3.23**	3.20**	2.39
No. of grains /spike	F ₁	1.27	99.09**	38.96**	83.56**	939.36**	45.70**	29.86**	6.88
	F ₂	1.26	153.64**	38.96**	111.15**	2103.97**	42.92**	53.29**	8.63
1000-grain weight	F ₁	0.75	11.38**	18.44**	9.49**	12.93**	7.86**	2.78**	0.73
	F ₂	0.66	10.42**	18.44**	8.70**	0.70	5.77**	2.90**	0.90
Grain yield / plant	F ₁	0.90	8.22**	2.16**	9.89**	7.77**	4.00**	2.42**	0.41
	F ₂	0.01	13.83**	2.16**	15.22**	58.18**	2.00**	5.26**	0.61
Biological yield/ plant	F ₁	3.21	81.11**	4.14**	101.78**	61.82**	22.01**	28.29**	1.19
	F ₂	0.08	114.32**	4.14**	120.10**	729.75**	16.33**	43.55**	2.58
Harvest index	F ₁	0.93	13.96**	5.55**	15.45**	32.82**	6.27**	4.25**	1.04
	F ₂	0.34	15.25**	5.55**	17.92**	0.37**	3.83**	5.39**	1.44
Total Protein content	F ₁	1.45	1.69**	3.35**	1.22**	2.58**	0.70**	0.53**	0.03
	F ₂	3.01	2.39**	3.35**	2.07**	0.25	1.39**	0.65**	0.07
Gluten content	F ₁	1.27	1.07**	2.24**	0.85**	1.65**	0.37**	0.35**	0.03
	F ₂	2.56	1.64**	2.24**	1.54**	0.09	0.83**	0.48**	0.06

* & ** significant at 5% and 1% level, respectively

Table-2 Estimates of general combining ability effects for economic and biochemical traits in F₁ and F₂ generations

Genotypes → Traits↓		HD 2967	WH 1105	PBW343	Raj3077	RSP561	WH1080	DPW621-50	PBW 550	S.E. (Gi)	S.E. (Gi- Gi)
Days to 50% flowering	F ₁	0.25	0.05	-1.32**	-1.38**	2.25**	1.92**	0.92**	-2.68**	0.53	0.80
	F ₂	0.35	-0.48*	-0.68**	-1.45**	2.52**	1.71**	1.15**	-3.12**	0.51	0.76
Flag leaf area	F ₁	-1.13**	3.06**	0.18	-1.25**	-0.10**	-0.25	-0.96**	1.35**	0.35	0.53
	F ₂	-1.01**	1.85**	1.68**	0.85**	0.23**	-1.87**	-2.66**	0.92**	0.19	0.28
Days to maturity	F ₁	0.49**	0.02	-1.14**	-2.37**	1.79**	1.76**	0.56*	-1.11**	0.39	0.59
	F ₂	0.21	-0.22	-1.19**	-2.39**	2.07**	1.84**	0.81**	-1.12**	0.36	0.55
Plant height	F ₁	2.61**	-1.21**	-1.45**	-0.44	0.40	0.73	-0.30	-0.35	1.06	1.60
	F ₂	2.29**	0.08	-3.20**	0.89	-0.71	1.68**	0.22	-1.28*	1.25	1.89
No. of effective tillers/ plant	F ₁	0.15	-0.11	-0.26*	-0.17	0.27*	0.24	0.06	-0.15	0.29	0.44
	F ₂	0.17	0.01	-0.31**	0.17	0.04	-0.12	0.08	-0.04	0.26	0.39
Spike length	F ₁	0.41**	-0.21	-0.31**	-0.33**	0.29*	0.06	-0.05	0.14	0.26	0.40
	F ₂	-0.17	0.22	-0.73**	-0.41**	0.21	0.25	0.38**	0.25	0.32	0.48
No. of spikelet/ spike	F ₁	-0.21	0.36*	0.06	0.36*	-0.56**	-0.46*	0.35	0.11	0.42	0.64
	F ₂	0.19	0.89**	-0.41	0.25	-0.37	-0.97**	0.12	0.31	0.62	0.94
No. of grains /spike	F ₁	0.47	2.93**	-0.61	-3.96**	0.62	-1.36**	2.18**	-0.27	1.06	1.60
	F ₂	1.01*	3.42**	-1.93**	-1.57**	-2.50**	0.18	2.09**	-0.69	1.19	1.79
1000-grain weight	F ₁	1.50**	0.30*	1.12**	-0.84**	-0.30*	-0.58**	-0.78**	-0.42**	0.35	0.52
	F ₂	0.92**	0.34*	0.80**	-0.14	-1.39**	-0.55**	0.30	-0.28	0.38	0.58
Grain yield / plant	F ₁	-0.53**	-0.47**	0.08	0.15	0.83**	-0.45**	1.00**	-0.62**	0.26	0.39
	F ₂	-0.04	0.59**	-0.77**	-0.33*	0.25	0.41**	0.18	-0.31**	0.32	0.48
Biological yield/ plant	F ₁	-1.03**	-0.90**	-0.01	0.63**	2.70**	-1.15**	1.37**	-1.62**	0.44	0.66
	F ₂	-0.59*	2.52**	-1.98**	0.49	-0.47	-0.02	0.44	-0.39	0.65	0.98
Harvest index	F ₁	-0.47**	-0.28	-1.36**	-0.40*	0.60**	0.36*	0.34	1.21**	0.41	0.62
	F ₂	0.20	-0.28	-1.06**	-0.15	-0.03	0.03	1.19**	0.09	0.48	0.73
Total Protein content	F ₁	-0.09**	0.32**	0.34**	0.12**	0.11**	-0.14**	-0.28**	-0.37**	0.07	0.11
	F ₂	0.52**	0.56**	0.06	-0.25**	0.01	-0.14**	-0.25**	-0.49**	0.11	0.17
Gluten content	F ₁	-0.11**	0.25**	0.26**	0.08**	0.04	-0.18**	-0.25**	-0.09**	0.06	0.10
	F ₂	0.43**	0.46**	0.02	-0.25**	-0.05	-0.18**	-0.22**	-0.19**	0.10	0.15

* & ** significant at 5% and 1% level, respectively

Table-3 Estimates of specific combining ability effects for economic and biochemical traits in F₁ and F₂ generations.

Traits→	Days to 50% flowering		Flag leaf area		Days to maturity		Plant height		No. of effective tillers per plant			Spike length		No. of spikelet/ spike	
Crosses↓	F ₁	F ₂	F ₁	F ₂	F ₁	F ₁	F ₂	F ₁	F ₂	F ₂	F ₂	F ₁	F ₂	F ₁	F ₂
HD-2967 x WH-1105	-4.06**	-6.55**	-6.85**	1.06**	-356**	0.01	-0.12	-0.11	-0.75	0.67	0.01	-0.12	-0.11	-0.75	
HD-2967 x PBW-343	-5.69**	-4.68**	-5.96**	-7.25**	-3.06**	0.52	0.41	-0.31	0.56	-0.13	0.52	0.41	-0.31	0.56	
HD-2967 x Raj-3077	-2.96**	-4.25**	1.63**	4.28**	-3.83**	0.21	0.01	-0.81	3.03**	0.97**	0.21	0.01	-0.81	3.03**	
HD-2967 x RSP-561	-7.59**	-7.22**	4.21**	3.72**	-7.10**	0.35	0.38	-0.59	0.66	-0.06	0.35	0.38	-0.59	0.66	
HD-2967 x WH-1080	-7.26**	-8.42**	5.88**	-2.97**	-5.96**	0.99**	-0.54	1.01	-0.01	-0.35	0.99**	-0.54	1.01	-0.01	
HD-2967 x DPW-621-50	-7.93**	-5.18**	1.28**	0.44	-4.10**	0.50	0.06	2.00**	0.31	0.38	0.50	0.06	2.00**	0.31	
HD-2967 x PBW-550	-3.33**	-3.58**	0.55	-2.70**	-4.10**	-0.23	-0.91*	0.81	0.35	0.67	-0.23	-0.91*	0.81	0.35	
WH-1105 x PBW-343	-5.16**	-3.52**	10.23**	-0.28	-4.93**	1.34**	1.04*	1.21 *	1.28	-0.07	1.34**	1.04*	1.21*	1.28	
WH-1105 x Raj-3077	-4.76**	-4.42**	-2.31**	-5.87**	-2.36**	0.57	0.13	1.31 *	-1.07	-0.25	0.57	0.13	1.31*	-1.07	
WH-1105 x RSP-561	-8.39**	-9.05**	0.21	0.71**	-6.20**	-0.16	0.60	1.53 **	2.58**	0.80*	-0.16	0.60	1.53**	2.58**	
WH-1105 x WH-1080	-8.73**	-4.58**	2.90**	-0.57*	-5.83**	1.41**	-0.31	0.73	0.93	-0.59	1.41**	-0.31	0.73	0.93	
WH-1105 x DPW-621-50	-5.39**	-7.35**	4.72**	-0.36	-4.63**	-0.77*	-0.20	-1.28 *	0.69	-0.01	-0.77*	-0.20	-1.28*	0.69	
WH-1105 x PBW-550	0.87	-3.75**	-1.04 *	3.68**	-2.96**	0.46	2.72**	0.77	3.18**	0.80*	0.46	2.72**	0.77	3.18**	
PBW-343 x Raj-3077	-2.06**	-2.88**	-0.68	0.79**	-0.53	0.37	-0.09	0.71	0.56	-0.05	0.37	-0.09	0.71	0.56	
PBW-343 x RSP-561	-6.69**	-7.52**	-4.38**	3.11**	-4.36**	0.52	0.69	0.83	1.39	-0.13	0.52	0.69	0.83	1.39	
PBW-343 x WH-1080	-6.36**	-4.72**	-4.02**	-6.85**	-4.66**	0.56	-0.28	1.03	0.84	0.53	0.56	-0.28	1.03	0.84	
PBW-343 x DPW-621-50	-5.03**	-6.15**	-4.31**	5.48**	-3.80**	0.25	0.23	1.32 *	-0.73	1.08**	0.25	0.23	1.32*	-0.73	
PBW-343 x PBW-550	-2.09**	-2.55**	3.26**	0.48	-1.80**	-0.12	-0.10*	-0.53	-0.96	0.13	-0.12	-0.10*	-0.53	-0.96	
Raj 3077 x RSP-561	-4.29**	-3.42**	1.52**	2.85**	-3.13**	2.10**	0.18	2.53 **	-1.73*	0.02	2.10**	0.18	2.53**	-1.73*	
Raj 3077 x WH-1080	-4.63**	-4.95**	-4.13**	0.38	-3.43**	-1.16**	0.14	-0.37	1.92*	0.45	-1.16**	0.14	-0.37	1.92*	
Raj 3077 x DPW-621-50	-3.29**	-2.38**	4.45**	-0.01	-2.23**	1.40**	1.14*	0.42	0.70	0.03	1.40**	1.14*	0.42	0.70	
Raj 3077 x PBW-550	2.64**	1.21	-1.42**	0.39	-0.56	-0.80*	0.12	-0.03	0.51	0.80*	-0.80*	0.12	-0.03	0.51	
RSP-561 x WH-1080	-5.59**	-9.58**	-1.91**	3.52**	-7.60**	-0.41	1.18**	1.45 *	0.39	0.72*	-0.41	1.18**	1.45*	0.39	
RSP-561 x DPW-621-50	-5.59**	-5.02**	9.71**	3.76**	-7.40**	0.97**	0.99*	-0.76	1.07	-0.07	0.97**	0.99*	-0.76	1.07	
RSP-561 x PBW-550	-4.66**	-1.42*	11.78**	3.76**	-4.73**	1.24**	-0.46	-0.51	1.44	0.39	1.24**	-0.46	-0.51	1.44	
WH-1080 x DPW-621-50	-7.26**	-9.55**	7.36**	1.36**	-6.70**	-1.44**	-0.14	0.84	1.00	-0.34	-1.44**	-0.14	0.84	1.00	
WH-1080 x PBW-550	-4.33**	-4.62**	2.79**	2.85**	-5.36**	-0.38	-0.45	1.39 *	-0.46	0.20	-0.38	-0.45	1.39*	-0.46	
DPW-621-50 x PBW-550	-1.66*	-1.05**	0.31	1.39**	-3.50**	-0.13	-0.29	0.58	-0.23	-0.54	-0.13	-0.29	0.58	-0.23	
S.E. (Sij)	1.41	1.34	0.93	0.54	1.04	0.71	0.85	1.12	1.66	0.68	0.71	0.85	1.12	1.66	
S.E. (Sij-Sik)	2.08	1.99	1.37	0.73	1.53	1.04	1.25	1.66	2.46	1.01	1.04	1.25	1.66	2.46	

Table-3 Contd..

Traits→	No. of grains /spike		1000-grain weight		Grain yield / plant		Biological yield/ plant		Harvest index		Protein content		Gluten content	
Crosses↓	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-2967 x WH-1105	-2.63	-3.31*	-0.98*	2.16**	-0.77*	-2.23**	-3.60**	-8.80**	2.21**	1.43*	0.29**	-1.00**	0.29**	-0.86**
HD-2967 x PBW-343	-1.91	1.43	0.25	-0.81	-0.50	3.00**	-3.23**	6.56**	-0.16	-2.16**	-1.14**	-0.02	-0.99**	0.01
HD-2967 x Raj-3077	-3.53*	4.23*	0.90	-0.45	-1.70**	-3.86**	-3.91**	-9.23**	-1.80**	-1.14	-0.20*	0.32*	-0.16	0.31*
HD-2967 x RSP-561	-3.61 *	8.27**	-0.10	-3.03**	-2.09**	2.20**	-4.37**	9.37**	-2.45**	2.35**	-0.06	0.11	0.01	0.15
HD-2967 x WH-1080	2.57	-3.20*	2.42**	1.78**	2.37**	3.33**	9.48**	6.81**	-0.01	1.81**	0.11	1.18**	0.15	1.09**
HD-2967 x DPW-621-50	12.52**	8.01**	0.33	0.89	2.53**	2.13**	8.45**	3.44**	-0.23	-2.91**	0.68**	0.11	0.60**	0.09
HD-2967 x PBW-550	3.52*	-0.88	1.66**	0.03	-1.19**	-0.84*	-3.93**	-0.61	0.08	-2.83**	0.64**	1.33**	0.32**	0.93**
WH-1105 x PBW-343	4.75**	5.72**	0.73	-2.34**	0.54	0.51	0.35	4.38**	-1.02	2.39**	-0.39**	0.83**	-0.32**	0.76**
WH-1105 x Raj-3077	-0.19	-1.61	-3.56**	0.30	0.52	3.41**	-2.42**	10.94**	-3.11**	0.82	-0.22*	0.24	-0.17*	0.24
WH-1105 x RSP-561	8.83**	-10.95**	0.24	-1.53**	-1.70**	0.15	-2.95**	-0.85	-1.07	-1.26	-0.34**	-0.14	-0.24**	-0.07
WH-1105 x WH-1080	1.68	9.87**	0.09	0.92	-0.17	1.61**	3.23**	4.07**	-3.01**	-2.22**	-0.85**	-0.66**	0.81**	-0.53**
WH-1105 x DPW-621-50	-7.53**	7.65**	1.43**	0.02	-1.90**	1.98**	-3.87**	7.28**	-1.54**	0.12	0.57**	0.12	0.50**	0.10
WH-1105 x PBW-550	6.27**	11.24**	0.76	-2.20**	1.81**	0.25	8.63**	2.90**	0.48	1.56*	0.96**	-0.80**	0.61**	-0.96**
PBW-343 x Raj-3077	1.21	1.06	0.45	-1.59**	0.95**	2.48**	4.72**	3.92**	1.42*	-2.71**	0.44**	-1.27**	0.42**	-1.10**
PBW-343 x RSP-561	-2.13	7.57**	-0.20	-2.61**	0.95**	0.40	0.70	0.34	-0.21	-0.44	-0.10	-0.31*	-0.03	-0.22
PBW-343 x WH-1080	5.95**	3.68*	0.07	-0.51	-0.62	0.17	-0.50	0.42	-0.73	0.65	0.03	0.30*	0.08	0.32*
PBW-343 x DPW-621-50	2.40	-2.88	-4.24**	2.06**	-1.77**	-3.38**	-3.16**	-6.10**	-0.43	1.01	-0.50**	0.11	-0.44**	0.09
PBW-343 x PBW-550	-0.45	-6.57**	-0.40	-0.40	-0.13	-4.05**	0.55	-11.08**	-1.75**	-4.57**	0.08	0.57**	-0.17*	0.26*
Raj 3077 x RSP-561	6.23**	-2.04	0.24	0.45	2.24**	-2.04**	8.81**	-5.61**	0.97	-0.83	0.56**	0.01	0.54**	0.06
Raj 3077 x WH-1080	-2.89*	4.83**	1.26**	0.11	-1.91**	0.81	-4.77**	0.48	-0.15	1.26	-0.69**	0.63**	-0.56**	0.61**
Raj 3077 x DPW-621-50	3.66*	6.37**	2.55**	0.94	1.16**	-0.39	7.49**	6.13**	-3.68**	3.80**	0.15	-0.02	0.14	-0.02
Raj 3077 x PBW-550	-1.59	5.10**	-1.56**	1.70**	0.36	2.55**	-1.43*	8.19**	0.89	1.96*	0.47**	-0.40**	0.17*	-0.60**
RSP-561 x WH-1080	2.02	4.31**	-0.17	0.31	0.99**	0.33	0.78	4.62**	2.16**	-2.22**	0.60**	-1.07**	0.61**	-0.87**
RSP-561 x DPW-621-50	2.80	-1.67	1.31**	0.94	2.93**	-0.26	9.89**	-0.95	-0.68	-1.70*	-0.84**	-0.65**	-0.86**	-0.69**
RSP-561 x PBW-550	1.08	2.71	0.40	1.25*	-1.36**	1.97**	-0.23	-0.07	-0.82	0.11	0.53**	0.86**	0.10	0.40**
WH-1080 x DPW-621-50	0.36	1.34	1.05*	0.76	-1.12**	-1.23**	-3.76**	-4.09**	0.65	-0.68	-0.40**	-0.32*	-0.48**	-0.40**
WH-1080 x PBW-550	5.01**	5.50**	0.89	0.76	-0.18	0.92*	-2.99**	0.60	0.91	1.55*	1.21**	1.43**	1.17**	1.37**
DPW-621-50 x PBW-550	-0.24	0.26	-0.67	-1.09*	-1.80**	1.07*	-6.63**	5.86**	4.80**	4.26**	-0.98**	-0.77**	-0.26**	-0.08
S.E. (Sij)	2.82	3.15	0.92	1.02	0.69	0.84	1.17	1.72	1.09	1.30	0.19	0.29	0.17	0.26
S.E. (Sij-Sik)	4.17	4.67	1.36	1.50	1.02	1.24	1.73	2.55	1.62	1.90	0.28	0.43	0.25	0.38

* & ** significant at 5% and 1% level, respectively

Observations were recorded on ten randomly selected competitive plants of each parent and F₁'s and forty plants in F₂'s in every replication for following traits viz., flag leaf area (cm²), number of effective tillers per plant, spike length (cm), number of spikelets per spike, number of grains per spike, 1000-grain weight (g), grain yield per plant (g), biological yield per plants, harvest index, total protein content and gluten content. In case of maturity traits (days to 50 percent flowering & days to maturity), the data was recorded on the whole plot basis. The GCA and SCA variances and their effects were analysed as per Griffing's Method-2, Model-1. Diallel analysis was carried out according to Griffing [7] numerical approach as adopted by Singh and Choudhary, [13]. All statistical analyses were performed using the Windostat Version 9.2 software.

Results and Discussion

Mean squares due to GCA and SCA were significant for all the traits except number of effective tillers per plant for parent in both generations and plant height for parents vs. hybrids in F₁ generations and in F₂ generation 1000 seed weight, total protein content and gluten content were non-significant which revealed that existence of differences among the parents and hybrids [Table-1], revealed that additive as well as non-additive genes were important for majority of the traits. Importance of GCA variance for grain yield per plant was also observed by Akram, *et al* [14] and Baloch, *et al* [15] who suggested that additive genes were responsible for grain yield per plant, while Shabbir, *et al* [16] reported that non-additive genetic effects were high for grain yield, revealing the prevalence of SCA effects. Additive type gene action with high values of GCA for spike density was reported by Mahpara, *et al* [17], for spike length by Yucel, *et al* [18], for grains per spike by Shabbir, *et al* [16] and for 1000-grains by Dhadhal, *et al* [19]. The mean square for SCA were greater than the mean square of GCA for all the traits excepts for number of grains per spike, 1000-grain weight, grain yield per plant, protein content and gluten content in F₁ generation, and in F₂ generation for flag leaf area, plant height, spike length, number of spikelets per spike, 1000-grain weight and gluten content which indicated that non-additive type of gene effects were more pronounced than those of additive ones. Similar results were reported by Siddique, *et al* [20], Singh, *et al* [21], Padhar, *et al* [22] and Kaukab, *et al* [23]. The preponderance of non-additive genetic variance for all the traits indicated that superior cross combinations for different traits might be selected on the basis of SCA for further tangible advancement in bread wheat. General combining ability effects of bread wheat for all traits studied [Table-2] in both generations indicated that some varieties may contribute to high yield through individual yield components. For grain yield per plant, parents RSP561 and DPW621-50 in F₁ generation and in F₂ generation WH1105 and WH1080 were found to be good general combiners. In addition, parents PBW343, Raj3077 and PBW550 in F₁ generation and in F₂ generation parents WH1105, PBW343, Raj3077 and PBW550 for days to 50 percent flowering; WH1105 and PBW550 in F₁ generation and in F₂ generation WH1105, PBW343, Raj3077, PBW550 and RSP561 for flag leaf area; PBW343, Raj3077 and PBW550 in F₁ and F₂ generation for days to maturity; WH1105 and PBW343 in F₁ generation and in F₂ generation PBW343 for plant height; RSP561 in F₁ generation for number of effective tiller per plant; HD2967 and RSP561 in F₁ generation and in F₂ generation DPW621-50 for spike length; WH1105 and Raj3077 in F₁ generation and in F₂ generation WH1105 for number of spikelet per spike; WH1105 and DPW621-50 in F₁ generation and in F₂ generation HD2967, WH1105 and DPW621-50 for number of grains per spike; HD2967, WH1105 and PBW343 in both the generations for 1000-grain weight; DPW621-50 in F₁ generation and in F₂ generation WH1105 for biological yield per plant; RSP561, WH1080 and PBW550 in F₁ generation and in F₂ generation DPW621-50 for harvest index were found to be good combiners. For quality traits four parents viz., WH1105, PBW343, Raj3077 and RSP561 in F₁ generation, whereas in F₂ generation HD2967 and WH1105 for total protein content; for gluten content parents WH1105, PBW343, Raj3077 and RSP561 in F₁ generation and in F₂ generation HD2967 and WH1105 were found to be good combiners. Best parents possessing desirable GCA effects for different traits in both the generations are presented in [Table-2]. Therefore, these parents have good potential and may be used in synthesizing dynamic population for accumulating most of the desirable genes. Similar observations have been reported by Singh

[24], Joshi, *et al* [25], Desai, *et al* [26], Kumar, *et al* [27], Pancholi, *et al* [28] and Singh, *et al* [29]. In all such cases where GCA effect were more pronounced for particular trait indicated preponderance of additive gene action, so these genotypes could be involved in crosses to improve the specific trait in wheat improvement programmes. In self-pollinated crops, SCA effects are not of much importance as they are mostly related to dominance gene effects and cannot be fixed in the end product inbred lines. However, if a cross combination exhibits high SCA effects as well as per se performance and having at least one parent as good general combiner for a particular trait, it is expected that such a cross combination will generate desirable transgressive segregants in later generations [30,31]. Significant SCA effects of those combinations involving good × good combiners depicted the major role of additive type of gene effects, which is fixable. However, it can also be mentioned here that combinations of two good general combiners may not necessarily throw good segregants, but expectations are high. If the superior crosses involved both the parents having poor general combining ability for a specific trait, very little gain is expected because the high SCA effects are due to dominance and epistatic gene effects which may not be accumulated through simple breeding procedures. Those crosses involving good and poor general combiner indicate the additive × dominance interactions. This is one of the reasons why the discrepancies with regard to SCA effects in F₁ and F₂ generations are observed. In the present study, none of the cross showed consistently high SCA effects for all the traits in both the generations [Table-3]. An overall appraisal of SCA effects revealed that some crosses had significant SCA effects for few specific traits in both the generations with varied magnitudes. Keeping these facts in mind, superior crosses which had high SCA effects in both the generations were present in [Table-3]. In F₁ generation crosses viz., HD2967 × WH1080, HD2967 × DPW621-50, WH1105 × PBW550, PBW343 × Raj3077, PBW343 × RSP561, Raj3077 × RSP561, Raj3077 × DPW621-50, RSP561 × WH1080, RSP561 × DPW621-50 and in F₂ generation crosses viz., HD2967 × PBW343, HD2967 × RSP561, HD2967 × WH1105, HD2967 × DPW621-50, WH1105 × Raj3077, WH1105 × WH1080, WH1105 × DPW621-50, PBW343 × Raj3077, Raj3077 × PBW550, RSP561 × PBW550, WH1080 × DPW621-50 and DPW621-50 × PBW550 for grain yield per plant and yield contributing, traits were identify as superior specific crosses. 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 × good, good × poor or poor × poor combinations. Thus, it was evident that a good cross combination is not necessarily the result of good × good general combiners; rather it might occur from good × poor or poor × poor combiners as well. A number of studies also refer to such a situation [26,27,29, 32,33].

Conclusion

Analysis of variance revealed that both GCA and SCA variances were important for all traits in both generations except number of effective tillers per plant in F₂ generation for revealed the presence of non-additive gene action for all the traits in both the generations. Among the eight parents in half diallel cross, two parents in each generation showed significant GCA effects for grain yield per plant. In F₁ and F₂ generations nine and ten crosses respectively were found to be desirable crosses for grain yield per plant and biochemical traits in half diallel and can be used in the future breeding programmes. These cross combinations showing desirable SCA effects for grain yield per plant, yield contributing and biochemical traits and may produce transgressive segregants in succeeding generations, which can be selected and improved for increasing yield.

Application of research: Combining ability is useful for exploitation of wheat hybrid programs.

Research Category: Plant Breeding, Biometric

Abbreviations:

GCA: General Combining Ability

SCA: Specific Combining Ability

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