



Components of Genetic Variance and Combining Ability Analysis in Wheat (*Triticum aestivum* L.)

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ABSTRACT

Background: Wheat is a major cereal crop, ranking first in global production. The Line $\times$ Tester analysis identifies the best-performing combinations based on the general combining ability of parents and specific combining ability of hybrids. This information helps in selecting suitable parents for developing high-yielding hybrids.

Methods: The experiment involved forty-five genotypes, including thirteen parental lines (ten lines and three testers), thirty F_1 s and two checks, to estimate variance components and combining ability using a Line $\times$ Tester mating design in wheat (*Triticum aestivum*). It was conducted in a randomized block design (RBD) during the Rabi seasons of 2021-2022 and 2022-2023 at the Agriculture Research Farm, Department of plant breeding and genetics, Lovely Professional University, Phagwara (Punjab).

Result: The results showed significant genetic variability among lines, testers and hybrids. The variance due to specific combining ability (σ^2_s) was higher than that due to general combining ability (σ^2_g). Dominance genetic variance (σ^2_D) was greater than additive genetic variance (σ^2_A) and the degree of dominance was greater than one (>1) for most traits, except for plant height and flag leaf area in F_1 s. The predictability ratio was less than one (<1) for all traits, indicating the presence of non-additive gene action with some influence of additive gene. General combining ability (GCA) analysis identified lines such as PBW677, 10th HPYT438 and 10th HPYT422, along with tester HD3226, as good combiners with strong potential for developing improved wheat lines through hybridization. Specific combining ability (SCA) analysis showed PBW677 $\times$ PBW725, 10th HPYT422 $\times$ HD3226, PBW677 $\times$ DBW222 and 10th HPYT402 $\times$ DBW222 as the best specific combiners, suggesting their potential for yield enhancement in breeding programs. These findings are an important step in advancing wheat breeding programs and ensuring sustainable food production.

Key words: Combining ability, Components of genetic variance, Gca, Sca, Wheat (*Triticum aestivum*).

INTRODUCTION

Bread wheat (*Triticum aestivum* L.) is a hexaploid crop with six sets of chromosomes ($2n = 6 \times = 42$). It belongs to the Poaceae family and has been originated in the Middle East. It is one of the three main cereal crops, with about 600 million tonnes harvested annually (Shewry 2009). Wheat is consumed in various forms like bread, chapatti, porridge, flour and suji and is rich in essential nutrients like niacin and thiamine.

Globally, wheat production reached 773.4 million metric tons in 2021-2022 (United States Department of Agriculture, 2022). In India, it is mainly grown in northern states such as Punjab, Haryana, Uttar Pradesh and Rajasthan, with a total cultivation area of 34.95 million hectares and a production of 109.24 million metric tons in 2021-2022 (Ministry of Agriculture and Farmers' Welfare, 2021). Uttar Pradesh is the largest wheat producer, followed by Punjab, Madhya Pradesh, Haryana and Rajasthan. Punjab ranks third in wheat production, with a yield of 111.3 million tonnes (Directorate of Economics and Statistics, 2021).

Despite its importance, wheat faces challenges like low productivity, diseases and environmental stress. To address these, breeding programs and mating designs like half diallel, full diallel and Line $\times$ Tester analysis aim to develop new varieties using both indigenous and exotic germplasm. These programs rely on analyzing gene action and combining ability.

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Combining ability, or the ability of parents to transmit desirable genes to their progeny, is crucial for hybridization success. Estimating combining ability helps select suitable parents and understand gene actions (Begna (2021). The Line $\times$ Tester analysis, which involves crossing testers with lines to identify the best-performing combinations, is a key method for studying general and specific combining ability in wheat hybrids.

MATERIALS AND METHODS

The study was conducted during the Rabi seasons of 2021-2022 and 2022-2023 at the Agriculture Research Farm, Department of Genetics and Plant Breeding, Lovely

Professional University, Phagwara (Punjab). The experiment included 45 treatments, consisting of 30 F₁s, 13 parental lines (10 lines and 3 testers) and 2 check varieties (HD2967 and PBW343), arranged in a randomized complete block design with three replications. Single-row plots of 2 m length were used for each genotype, with intra-row and inter-row spacing of 22.5 cm.

Observations were recorded on yield and yield-related traits. In each plot, five randomly sampled plants were tagged for data collection, except for days to 50% flowering, which were recorded on a plot basis. The traits studied included days to 50% flowering, plant height, spike-bearing tillers per plant, spike length, flag leaf area, number of spikelets per spike, number of grains per spike, biological yield per plant, harvest index, 1000-grain weight and grain yield per plant.

The data were analyzed using various statistical and genetic methods, including analysis of variance for randomized block design (Panse and Sukhatme, 1967), Line $\times$ Tester analysis for combining ability (Kempthorne, 1957), heritability (Kempthorne and Curnow, 1961) and estimation of general and specific combining ability variances and their effects (Kempthorne, 1957). Methodologies for estimation of heterosis were provided by Fonseca and Patterson (1968) and Meredith and Bridge (1972).

RESULTS AND DISCUSSION

Analysis of variance (ANOVA) was performed for all eleven characters, as shown in Table 1. The Line $\times$ Tester interaction indicated that differences among treatments, parents, lines, parents vs. crosses, crosses and line vs. testers were highly significant for all characters in F₁s. A similar finding was reported by El-Gammaal et al. (2018), except for thousand grain weight, where no significance was observed for the parent vs. crosses. Variance due to testers was highly significant for all characters except for harvest index in F₁s. Variance due to line vs. tester was highly significant for all characters except for 1000-grain weight in F₁s. Line effects were not significant for any trait, while tester effects were highly significant for plant height, flag leaf area and 1000-grain weight. Analysis of variance for most parents and crosses revealed significant genotypic effects for all characters under study. This confirms the presence of sufficient genetic variability among lines, testers and hybrids, supporting further general combining ability analysis. Similar findings were reported by Fellahi et al. (2013) and Roy et al. (2021).

Component of variance

The estimates of Component of variance presented in Table 2. SCA variance was higher than GCA variance for all eleven traits, indicating the presence of non-additive gene action controlling these traits. A similar finding was reported by Akram et al. (2011); Srivastava et al. (2012) and Istiqlil et al. (2015). Dominance genetic variance (σ^2_D) was greater

Table 1: Analysis of variance for 11 characters in line $\times$ tester mating design in wheat including parents and F₁s generation.

Character	Sources of variation										
	Replications		Treatments		Parents		Lines		Testers		Error
	2	42	12	9	12	9	9	1	2	18	
df	2	42	12	9	12	9	1	1	2	18	84
Days to 50% flowering	1.36	68.59**	32.81**	8.09**	32.81**	8.09**	142.28**	1949.70**	18.53**	17.17**	1.56
Plant height (cm)	4.77**	159.29**	58.21**	65.92**	58.21**	65.92**	3.79**	902.93**	175.47**	126.14**	0.42
spike bearing tillers plant ⁻¹	0.00	74.53**	38.04**	48.00**	38.04**	48.00**	17.67**	286.84**	82.31**	91.82**	0.16
spike length (cm)	0.01	3.83**	6.64**	8.47**	6.64**	8.47**	1.19**	0.91**	2.77**	2.30**	0.10
Flag leaf area (cm ²)	0.17	56.41**	64.49**	47.43**	64.49**	47.43**	297.99**	54.39**	53.14**	37.61**	0.49
Number of spikelet spike ⁻¹	0.16	5.01**	5.66**	6.64**	5.66**	6.64**	4.96**	33.05**	3.77**	3.56**	0.10
Number of grains spike ⁻¹	4.11*	202.33**	140.62**	183.67**	140.62**	183.67**	17.82**	1308.50**	189.71**	186.37**	1.17
Biological yield plant ⁻¹ (g)	0.67	1466.85**	443.82**	386.81**	443.82**	386.81**	1216.04**	15728.65**	1398.38**	1538.53**	8.04
Harvest index (%)	3.75	200.49**	237.67**	271.10**	237.67**	271.10**	408.21**	269.44**	182.73**	194.33**	6.39
1000 grain weight (g)	2.05	147.83**	75.11**	87.56**	75.11**	87.56**	7.17	1088.77**	145.48**	124.48**	2.71
Grain yield plant ⁻¹ (g)	2.26	484.81**	290.90**	373.69**	290.90**	373.69**	38.15**	563.28**	562.34**	623.18**	4.25

*, ** Significant at 5 and 1 per cent probability levels, respectively.

than additive genetic variance (σ^2A) and the average degree of dominance was greater than one (>1) for nine traits, including days to 50% flowering, spike-bearing tillers per plant, spike length, number of spikelets per spike, number of grains per spike, biological yield per plant, harvest index, 1000-grain weight and grain yield per plant, suggesting over-dominance for these traits. In contrast, for plant height and flag leaf area, additive genetic variance (σ^2A) was higher than dominance genetic variance (σ^2D), with average degrees of dominance less than one (<1), indicating partial dominance. A similar result for plant height was reported by Ullah et al. (2009). The predictability ratio was less than one for all characters in F_1 s, indicating the presence of non-additive gene action for most traits, with some additive gene action for others. Similar results were found by Joshi et al. (2004); Seelam et al. (2006); Dhadhal et al. (2008) and Riaz et al. (2021).

Heritability in the narrow sense was high for five traits, days to 50% flowering, plant height, spike length, flag leaf area and 1000-grain weight suggesting that selection would be highly effective for these traits. A similar result was reported by Saeed et al. (2017).

Combining ability

General combining ability

The general combining ability of all thirteen genotypes (ten lines and three testers) is presented in Table 3. The significant and positive gca effects for seed yield per plant were exhibited by three lines and one tester which in order of merit were PBW677, 10thHPYT438 and 10th HPYT422, among lines and HD3226 among the testers. On the basis of gca effects and mean performance, parent PBW677 (12.38) was found good combiner for grain yield per plant along with days to 50% flowering, spike bearing tillers plant⁻¹, spike length, flag leaf area, biological yield plant⁻¹ and harvest index. Parent 10th HPYT438 (6.93) for grain yield

per plant with days to 50% flowering, plant height, number of spikelet spike⁻¹, number of grains spike⁻¹, biological yield plant⁻¹ and 1000 grain weight. Parent 10th HPYT422 for grain yield per plant with spike bearing tillers plant⁻¹, spike length and biological yield plant⁻¹, while, among testers, HD3226 (4.72) was found good general combiner for grain yield per plant in addition to flag leaf area, number of spikelet spike⁻¹, number of grains spike⁻¹, harvest index and 1000 grain weight.

The presence of significant general combining ability (GCA) values suggests the importance of additive or additive $\times$ additive gene effects, as previously reported by Griffing (1956). These parents demonstrate strong potential for the development of improved wheat lines through hybridization programs. Similar finding has been reported by Sharma et al. (2019).

Specific combining ability

Table 4 presents the specific combining ability (SCA) of thirty crosses. Fourteen crosses showed significant positive SCA effects for grain yield and other yield components. The top ten promising crosses were: PBW677 $\times$ PBW725, 10th HPYT422 $\times$ HD3226, PBW677 $\times$ DBW222, 10th HPYT402 $\times$ DBW222, 10th HPYT423 $\times$ HD3226, HD2967 $\times$ DBW222, 8th HPYT489 $\times$ HD3226, 10th HPYT438 $\times$ DBW222, 9thHPYT425 $\times$ PBW725 and 10th HPYT403 $\times$ HD3226. Notably, PBW677 $\times$ PBW725 (29.49) showed the best SCA effects for grain yield, plant height, spike-bearing tillers, biological yield and harvest index in F_1 s. Other promising crosses include 10th HPYT422 $\times$ HD3226 (18.60) for most traits except days to 50% flowering and flag leaf area, PBW677 $\times$ DBW222 (16.01) for plant height and 10th HPYT402 $\times$ DBW222 (15.75) for all traits except plant height, spike length and flag leaf area in F_1 s.

According to Kenga et al. (2004), cross combinations with high means, favorable SCA estimates and at least

Table 2: Components of variance, degree of dominance, additive and dominance components and heritability in narrow sense for 11 characters in wheat (F_1 s).

Character	GCA variance (σ^2g)	SCA variance (σ^2s)	Average degree of dominance $\sqrt{\sigma^2s/2\sigma^2g}$	Predictability ratio ($2\sigma^2g/2\sigma^2g + \sigma^2s$)	σ^2A	σ^2D	Heritability (ns)
Days to 50% flowering	1.28*	5.26**	1.43	0.33	2.57	5.26	30.98
Plant height (cm)	28.25**	41.94**	0.86	0.57	56.50	41.94	57.33
Spike bearing tillers plant ⁻¹	4.23	30.55**	1.90	0.22	8.47	30.55	21.67
Spike length (cm)	0.25*	0.73**	1.22	0.40	0.49	0.73	39.09
Flag leaf area (cm ²)	7.96**	12.35**	0.88	0.56	15.93	12.35	55.96
Number of spikelet spike ⁻¹	0.18	1.16**	1.80	0.24	0.36	1.16	23.23
Number of grains spike ⁻¹	6.41	61.95**	2.20	0.17	12.83	61.95	17.11
Biological yield plant ⁻¹ (g)	39.11	510.37**	2.55	0.13	78.23	510.37	13.24
Harvest index (%)	11.25	62.95**	1.67	0.26	22.51	62.95	25.79
1000 grain weight (g)	18.37*	40.81**	1.05	0.47	36.74	40.81	46.96
Grain yield plant ⁻¹ (g)	28.24	206.82	1.91	0.21	56.47	206.82	21.37

*, ** significant at 5 and 1 per cent probability levels, respectively.

Table 3: Estimates of GCA effects of parents (females and males) for 11 characters in wheat.

Lines	Days to 50% flowering	Plant height (cm)		Spike bearing tillers plant ⁻¹		Spike length (cm)		Flag leaf area (cm ²)		Number of spikelet spike ⁻¹		Number of grains spike ⁻¹		Biological yield plant ⁻¹ (g)		Harvest index (%)		1000 grain weight (g)		Grain yield plant ⁻¹ (g)			
		Mean	GCA	Mean	GCA	Mean	GCA	Mean	GCA	Mean	GCA	Mean	GCA	Mean	GCA	Mean	GCA	Mean	GCA	Mean	GCA		
9 th HPT425	100.33	-1.31**	71.93	1.84**	10.07	-2.02**	12.17	0.03	29.43	2.39**	19.13	0.14	73.40	2.43**	111.53	1.34	26.46	-1.05	40.12	2.48**	29.60	-1.36*	
PBW677	100.00	-2.76**	78.39	2.39**	17.53	5.25**	14.27	0.51**	34.70	2.30**	21.60	-0.22*	78.00	0.12	108.80	9.07**	45.33	4.27**	40.44	0.30	55.40	12.38**	
HD2967	98.67	0.91*	74.02	-5.27**	19.00	0.32*	10.13	-1.05**	32.37	-2.39**	16.40	-1.26**	57.33	-4.35**	114.40	0.30	46.09	-3.74**	49.15	-1.85**	53.65	-6.51**	
8 th HPT489	99.67	0.91*	86.52	0.79**	16.73	-0.75**	15.13	-0.38**	34.70	-1.13**	20.73	1.09**	79.20	8.65**	95.67	-11.84**	42.91	3.31**	30.55	-2.33**	40.39	0.20	
10 th HPT402	97.00	0.80*	74.00	5.17**	12.67	-1.48**	11.23	0.74**	27.19	1.99**	17.73	-0.38**	58.93	-5.75**	109.93	-15.10**	27.30	4.15**	40.26	5.67**	30.07	0.30	
10 th HPT403	97.33	1.58**	82.97	-3.35**	7.00	-2.06**	15.17	-0.09	41.71	0.72*	19.00	0.00	62.73	-1.72**	109.13	-16.90**	16.39	2.22**	40.59	1.19*	17.79	-3.39**	
10 th HPT421	100.00	1.24**	75.38	-2.46**	19.20	-1.04**	13.93	-0.13	33.37	0.26	20.00	-0.35**	66.27	-4.46**	139.53	-8.17**	27.78	-5.65**	30.41	-4.75**	38.69	10.36**	
10 th HPT422	102.33	0.36	82.33	0.84**	16.40	3.85**	14.20	0.74**	35.00	-2.52**	20.20	-0.44**	61.40	-2.99**	111.60	16.01**	33.84	0.35	37.03	-1.34**	37.42	5.65**	
10 th HPT423	97.67	-0.53	75.56	1.68**	16.87	-1.68**	13.07	-0.33**	37.24	0.63*	19.53	0.49**	61.87	-0.32	115.13	9.85**	36.89	-5.31**	40.28	-1.01	42.21	-3.83**	
10 th HPT438	98.33	-1.20**	77.45	-1.62**	13.67	-0.37*	12.33	-0.03	34.09	-2.26**	18.80	0.94**	63.80	8.39**	102.13	15.45**	36.89	1.46	40.28	1.64**	35.35	6.93**	
Mean	99.13		77.86		14.91		13.16		33.98		19.31		66.29		111.79		33.99		38.91		38.06		
C.D at 5%		0.79		0.38		0.28		0.23		0.49		0.17		0.48		1.82		1.56		0.96		1.46	
SE(gi) lines		0.39		0.19		0.14		0.11		0.25		0.09		0.24		0.91		0.78		0.48		0.55	
SE(gi - gi)		0.56		0.27		0.20		0.16		0.35		0.12		0.34		1.28		1.10		0.68		0.78	
Testers																							
DBW222	97.67	0.76**	72.91	-3.36	16.60	-0.69**	14.27	-0.10	30.62	-3.48**	17.67	-0.30**	65.93	-0.12	108.67	-2.33**	40.63	-3.03**	40.34	-2.28**	44.10	-4.90**	
PBW725	105.00	-1.24**	81.13	6.72	15.40	2.14**	13.37	0.53**	25.11	1.32**	19.07	0.00	65.33	-0.66**	98.73	2.00**	42.24	-0.43	40.31	-3.05**	40.73	0.18	
HD3226	108.33	1.55	77.30	-3.36	17.53	-1.46**	13.10	-0.43**	26.53	2.16**	18.67	0.30**	62.80	0.79**	88.20	0.33	41.51	3.47**	33.04	5.33**	36.39	4.72**	
Mean	103.67		77.11		16.51		13.58		27.42		18.47		64.69		98.53		41.46		37.90		40.41		
C.D at 5%		0.43		0.21		0.15		0.12		0.27		0.09		0.26		0.99		0.86		0.52		0.80	
SE (gi) tester		0.22		0.10		0.08		0.06		0.14		0.05		0.13		0.50		0.43		0.26		0.30	
SE(gi - gi)		0.31		0.15		0.11		0.09		0.19		0.07		0.19		0.70		0.61		0.37		0.43	

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

Table 4: Estimates of SCA effects of parents (females and males) for 11 characters in wheat.

Lines	Days to 50% flowering		Plant height (cm)		Spike bearing tillers plant ⁻¹		Spike length (cm)		Flag leaf area (cm ²)		Number of spikelet spike ⁻¹		Number of grains spike ⁻¹		Biological yield plant ⁻¹ (g)		Harvest index (%)		1000 grain weight (g)		Grain yield plant ⁻¹ (g)	
	Mean	SCA	Mean	SCA	Mean	SCA	Mean	SCA	Mean	SCA	Mean	SCA	Mean	SCA	Mean	SCA	Mean	SCA	Mean	SCA	Mean	SCA
9 th HPYT425 × DBW222	109.33	1.24	60.66	-9.75**	14.33	-1.49**	13.97	0.60**	33.50	0.71	20.40	0.34*	73.60	-1.56**	131.87	0.09	25.71	-2.62	32.05	-0.49	33.87	-3.02**
9 th HPYT425 × PBW725	104.33	-1.76*	83.05	2.57**	22.67	4.01**	14.07	0.07	34.10	-3.49**	19.40	-0.96**	70.67	-3.96**	150.20	14.09**	32.59	1.67	30.61	-1.16	48.79	6.82**
9 th HPYT425 × HD3226	108.33	0.51	77.58	7.17**	12.53	-2.52**	12.37	-0.67**	41.20	2.77**	21.27	0.61**	81.60	5.52**	120.27	-14.17**	35.77	0.95	41.81	1.66*	42.71	-3.80**
PBW677 × DBW222	107.67	1.02	65.52	-5.44**	15.87	-7.22**	13.77	-0.09	32.65	-0.06	19.33	-0.37*	71.60	-1.25**	136.40	-3.11	25.49	-8.15**	30.52	0.15	34.62	16.01**
PBW677 × PBW725	101.67	-2.98**	87.75	6.72**	40.33	14.41**	13.53	-0.95**	36.50	-1.00*	20.27	0.27	71.00	-1.31**	166.87	23.02**	46.33	10.08**	27.02	-2.58**	85.19	29.49**
PBW677 × HD3226	108.33	1.96**	69.68	-1.28**	15.13	-7.19**	14.57	1.04**	39.40	1.06*	20.40	0.10	76.33	2.57**	122.27	-19.91**	38.22	-1.93	40.41	2.43**	46.77	-13.48**
HD2967 × DBW222	108.67	-1.64*	65.87	2.58**	22.73	4.58**	10.87	-1.42**	27.74	-0.28	16.40	-2.26**	55.33	-13.05**	109.60	-21.14**	38.83	13.20**	33.55	5.33**	42.18	10.45**
HD2967 × PBW725	109.00	0.69	67.61	-5.76**	21.47	0.48	14.07	1.15**	35.90	3.09**	21.13	2.18**	80.73	12.89**	160.73	25.66**	22.20	-6.03**	20.62	-6.83**	35.63	-1.18
HD2967 × HD3226	111.00	0.96	66.47	3.18**	12.33	-5.06**	12.23	0.27	30.85	-2.81**	19.33	0.08	69.47	0.17	128.87	-4.53**	24.97	-7.16**	37.32	1.50	32.09	-9.27**
8 th HPYT489 × DBW222	110.33	0.02	77.38	8.03**	15.60	-1.49**	14.03	1.07**	28.38	-0.90*	22.07	1.06**	85.33	3.95**	129.00	10.40**	31.34	-1.35	30.07	2.33**	40.19	1.74
8 th HPYT489 × PBW725	106.00	-2.31**	79.05	-0.38	19.67	-0.26	13.07	-0.53**	35.88	1.81**	20.33	-0.98**	75.87	-4.98**	101.27	-21.67**	33.26	-2.02	22.67	-4.30**	33.69	-9.85**
8 th HPYT489 × HD3226	112.33	2.29**	61.70	-7.65**	18.07	1.74**	12.10	-0.54**	34.00	-0.91*	21.53	-0.08	83.33	1.03*	132.53	11.27**	42.55	3.37*	37.32	1.97*	56.18	8.11**
10 th HPYT402 × DBW222	109.00	-1.20	77.03	3.30**	17.67	1.31**	13.13	-0.95**	31.56	-0.84	20.20	0.66**	75.73	8.75**	141.87	26.53**	38.26	4.73**	40.53	4.79**	54.29	15.75**
10 th HPYT402 × PBW725	109.00	0.80	88.27	4.46**	14.53	-4.66**	16.13	1.43**	36.26	-0.93*	20.13	0.29	70.73	4.29**	111.13	-8.54**	42.86	6.74**	46.35	11.38**	47.54	3.92**
10 th HPYT402 × HD3226	110.33	0.40	65.98	-7.76**	18.93	3.34**	13.27	-0.48*	39.80	1.77**	19.20	-0.94**	54.87	-13.03**	100.00	-18.00**	28.55	-11.48**	27.19	-16.17**	28.50	-19.67**
10 th HPYT403 × DBW222	113.00	2.02**	74.07	8.85**	12.67	-3.11**	14.30	1.05**	34.45	3.32**	19.93	0.01	70.33	-0.68	108.33	-5.20**	24.67	-6.92**	29.94	-1.33	26.69	-8.17**
10 th HPYT403 × PBW725	108.67	-0.31	65.08	-10.21**	18.47	-0.14	13.47	-0.41*	35.86	-0.06	20.53	0.31*	74.00	3.53**	130.53	12.66**	32.47	-1.72	30.87	0.37	42.14	2.20*
10 th HPYT403 × HD3226	109.00	-1.71*	66.57	1.36**	18.27	3.26**	12.28	-0.64**	33.50	-3.26**	20.20	-0.32*	69.07	-2.86**	108.73	-7.46**	46.73	8.64**	39.83	0.96	50.45	5.96**

Table 4: Countinue....

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10 th HPYT 421 × DBW222	114.67	4.02**	65.60	-0.50	17.07	0.27	13.37	0.15	26.37	-4.30**	20.20	0.63**	74.93	6.66**	123.87	1.60	22.24	-1.49	21.48	-3.85**	27.56	-0.32
10 th HPYT 421 × PBW725	109.00	0.36	73.91	-2.26**	18.07	-1.57**	13.70	-0.14	34.26	-1.20**	20.00	0.13	69.20	1.46**	111.47	-15.14**	34.49	8.17**	30.62	6.07**	38.28	5.31**
10 th HPYT 421 × HD3226	106.00	-4.38**	68.87	2.77**	17.33	1.30**	12.87	-0.02	41.80	5.50**	19.40	-0.77**	61.07	-8.12**	138.47	13.54**	23.55	-6.68**	30.70	-2.23**	32.52	-4.99**
10 th HPYT 422 × DBW222	109.00	-0.76	67.12	-2.28**	25.93	4.24**	14.03	-0.05	25.08	-2.81**	18.80	-0.68**	62.40	-7.34**	110.93	-35.51**	30.82	1.09	21.03	-7.70**	34.06	-9.84**
10 th HPYT 422 × PBW725	109.00	1.24	79.55	0.08	19.53	-4.99**	14.17	-0.54**	38.40	5.72**	19.33	-0.44**	65.07	-4.14**	170.67	19.89**	23.63	-8.69**	31.52	3.56**	40.22	-8.76**
10 th HPYT 422 × HD3226	109.00	-0.49	71.61	2.20**	21.67	0.74**	14.33	0.59**	30.61	-2.91**	21.20	1.12**	82.13	11.48**	164.73	15.63**	43.83	7.60**	40.47	4.13**	72.13	18.60**
10 th HPYT 423 × DBW222	107.33	-1.53*	65.05	-5.19**	15.33	-0.82**	12.87	-0.15	33.30	2.27**	20.73	0.32*	76.27	3.86**	143.87	3.58*	25.06	1.00	31.04	1.98*	36.13	1.72
10 th HPYT 423 × PBW725	108.67	1.80*	85.66	5.34**	15.47	-3.52**	13.37	-0.27	31.13	-4.70**	21.13	0.42**	69.80	-2.07**	132.40	-12.22**	18.14	-8.52**	22.18	-6.11**	24.01	-15.49**
10 th HPYT 423 × HD3226	108.33	-0.27	70.09	-0.15	19.73	4.34**	13.10	0.42*	39.10	2.43**	20.27	-0.74**	71.53	-1.79**	151.60	8.65**	38.09	7.53**	40.81	4.14**	57.81	13.77**
10 th HPYT 438 × DBW222	105.00	-3.20**	67.35	0.40	21.20	3.73**	13.10	-0.21	31.01	2.87**	21.13	0.28	81.80	0.68	168.67	22.78**	31.34	0.51	30.50	-1.21	52.88	7.70**
10 th HPYT 438 × PBW725	108.67	2.47**	76.46	-0.56	16.53	-3.77**	14.13	0.19	33.70	0.76	19.93	-1.22**	74.87	-5.71**	112.47	-37.76**	33.76	0.33	30.53	-0.40	37.80	-12.46**
10 th HPYT 438 × HD3226	108.67	0.73	67.11	0.16	16.73	0.03	13.00	0.02	30.14	-3.64**	22.40	0.94**	87.07	5.03**	163.53	14.98**	36.49	-0.84	40.93	1.61	59.56	4.76**
Mean	108.64		71.92		18.53		13.44		33.88		20.22		72.86		132.77		32.41		32.35		43.15	
C.D at 5%		1.37	0.65			0.49		0.39		0.86		0.30		0.84		3.14		2.71		1.66		1.90
SE (Sij)		0.68	0.33			0.24		0.20		0.43		0.15		0.42		1.57		1.35		0.83		0.95
SE (Sij - Skl)		0.96	0.46			0.34		0.28		0.60		0.21		0.59		2.22		1.91		1.17		1.35

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

one parent with high GCA can enhance favorable alleles for improving target traits. In this study, the fourteen F_1 s crosses mentioned above showed the similar results and hence can be considered for breeding programs aimed at yield enhancement. Similar results were reported by Kumar *et al.* (2005); Jogendra and Raje (2007); Kumar *et al.* (2008); Jaiswal *et al.* (2010); Hakeem *et al.* (2020) and Riaz *et al.* (2021).

CONCLUSION

The results indicated sufficient genetic variability among lines, testers and hybrids. Combining ability analysis revealed that the variance due to specific combining ability (σ^2_s) was higher than that due to general combining ability (σ^2_g). Dominance genetic variance (σ^2_D) was greater than additive genetic variance (σ^2_A) and the degree of dominance was greater than one (>1) for all traits except plant height and flag leaf area in F_1 s. The predictability ratio was less than one (<1) for all traits studied in F_1 s, suggesting the presence of non-additive gene action, with some influence of additive gene action.

The analysis of general combining ability (GCA) effects identified lines such as PBW677, 10th HPYT438 and 10th HPYT422, along with tester HD3226, as good combiners for grain yield per plant and other important traits. These lines are valuable candidates for hybridization programs aimed at developing high-yielding wheat varieties or generating transgressive segregants for pure line development. Their selection as parents can contribute to the enhancement of key traits and overall wheat genotype improvement.

The specific combining ability (SCA) analysis revealed PBW677 $\times$ PBW725, 10th HPYT422 $\times$ HD3226, PBW677 $\times$ DBW222 and 10th HPYT402 $\times$ DBW222 as the best specific combiners for grain yield per plant and other attributing traits. These crosses could be considered for breeding programs focused on yield enhancement.

Conflict of interest

All authors declared that there is no conflict of interest.

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