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Genetic Basis of Morpho-Physiological Traits in F₁ Hybrids of Bread Wheat [*Triticum aestivum* (L.) em. Thell]: A Combining Ability Approach

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ABSTRACT

Keywords

Bread Wheat, Combining Ability, Diallel, GCA, SCA

Article Info

Received: 18 August 2025 Accepted: 30 September 2025 Available Online: 10 October 2025 In order to estimate the combining ability of bread wheat, 45 crosses were made using a 10 × 10 diallel design excluding reciprocals. A total of 57 genotypes (10 parents, 45 crosses, and 2 checks) were evaluated in a randomized block design with three replications across three different environments (E₁, E₂, and E₃) at separate locations during the Rabi season of 2020-21. ANOVA estimations for combining ability revealed significant mean squares for both general combining ability (GCA) and specific combining ability (SCA) for nearly all traits in all three environments, indicating the presence of both additive and non-additive genetic variance in the inheritance of most characters. Based on pooled GCA effects, five of the ten parents: Raj4037, Raj4079, HD3086, Raj4238, and WR544 were identified as good general combiners for the majority of the traits. Across all three environments, nine of the 45 crosses exhibited notable favorable SCA effects. The crosses HD3086 × WR544, Raj4238 × Raj4079, HD3086 × Raj4079, and Raj4238 × Raj4079 showed significant positive SCA effects for grain yield per plant as well as other yield-contributing traits.

Introduction

Wheat (*Triticum aestivum* L. em. Thell) is one of the most widely cultivated cereal crops globally and serves

as a fundamental component of food and nutritional security (Shewry and Hey, 2015). In India, this crop is grown across diverse agro-climatic regions, occupying approximately 31.76 million hectares, with an average

productivity of 3464 kg/ha and a total production of 109.52 million tonnes (ICAR-IIW&BR, 2022; Kumari *et al.*, 2022; Kumari *et al.*, 2025a, 2025b).

Enhancing yield potential in wheat is particularly complex due to the quantitative and polygenic nature of yield and its contributing traits (Curtis and Halford, 2014). Regional disparities in productivity further underscore the untapped potential for genetic improvement through focused breeding efforts. In this context, strategic plant breeding is essential to enhance yield stability and performance.

A key step in this process is the identification of genetically diverse and agronomically superior parental lines that can be used to develop high-yielding hybrids. Hybridization remains a foundational technique in plant breeding, and its success largely depends on the selection of appropriate parental combinations with complementary genetic effects (Thakur *et al.*, 2024).

The selection of suitable parental lines is a fundamental consideration in the development of superior cultivars (Bertan *et al.*, 2007). In systematic breeding programmes, high estimates of specific combining ability (SCA) are essential for identifying parents that possess favourable traits along with strong general combining ability (GCA) for grain yield and its related components (Desale *et al.*, 2014).

Such estimates facilitate the formulation of effective breeding strategies aimed at accelerating genetic gains. Beyond identifying promising crosses, combining ability analysis provides valuable insights into the nature and magnitude of gene action involved in trait inheritance and is instrumental in evaluating genetic divergence among genotypes (Begna, 2021). Therefore, the identification of potential parental combinations based on combining ability is critical for guiding cross-selection and defining appropriate breeding approaches (Salgotra et al., 2009).

In the present study, a diallel mating design was employed in bread wheat to estimate combining ability and thereby elucidate the scope and nature of gene actions governing grain yield and associated traits. The identification and selection of superior parental lines and cross combinations are recommended for incorporation into future breeding programmes, as they hold significant potential for enhancing yield-related components in wheat improvement efforts.

Materials and Methods

The experimental material comprised ten parental genotypes, their 45 F₁ hybrids, and two check varieties: Sonalika and HD2967. The 45 F₁ crosses were developed through half-diallel mating among the ten parents, excluding reciprocals.

During the Rabi season of 2020-21, all 57 genotypes (10 parents, 45 hybrids, and 2 checks) were evaluated using a randomised complete block design with three replications across three distinct environments: the Botany Farm, Department of Genetics and Plant Breeding, Rajasthan College of Agriculture, Udaipur (E₁); the Instructional Farm, CTAE, Udaipur (E₂); and Krishi Vigyan Kendra, Badgaon, Udaipur (E₃).

Each genotype was sown in a single row plot of three metres in length, maintaining a spacing of 22.5 cm between plants and 10 cm between rows. The experiment was conducted under irrigated conditions, following recommended agronomic and plant protection practices to ensure a successful crop.

From each genotype in every replication, ten competitive plants were randomly selected for data collection on fifteen traits, namely: days to 50% flowering, days to 75% maturity, plant height (cm), number of effective tillers per plant, spike length (cm), number of spikelets per plant, length of awns (cm), number of grains per spike, flag leaf area (cm square), 1000-grain weight (g), biological yield per plant (g), grain yield per plant (g), harvest index (%), total protein content in grain (%), and total chlorophyll content (mg/g). These traits were recorded under each of the three environments. To analyse combining ability across environments, the method suggested by Singh (1973 and 1979), an extension of Griffing's method II, model I (1956), was employed to estimate general and specific combining ability variances and their interactions with environments.

Results and Discussion

The analysis of variance for combining ability revealed that all traits across the three environments exhibited significant mean squares due to general combining ability (GCA), except for plant height in E_3 and flag leaf area in E_2 . In contrast, mean squares due to specific combining ability (SCA) were significant for all traits in all three environments (Table 1).

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Table.1 Analysis of variance (ANOVA) for combining ability across 15 characters in bread wheat (Triticum aestivum L. em. Thell.).

Characters	Environment ⁱ		Source		Variance	Model Iiv
		GCA ⁱⁱ	SCAiii	Error	GCA ^v	SCA ^v
		[9]	[45]	[108]		
Days to 50% flowering	1	9.28** ^{vi}	13.50**	1.94	1.83	173.34
	2	12.52**	13.83**	1.97	2.64	177.91
	3	23.46**	14.08**	2.22	5.31	177.89
Days to 75% maturity	1	47.90**	14.19**	1.97	11.48	183.25
	2	45.99**	11.94**	2.85	10.79	136.43
	3	15.85**	10.28**	3.49	3.09	101.82
Plant height (cm)	1	77.80**	36.17**	4.76	18.26	471.21
	2	32.96**	26.03**	5.70	6.82	305.08
	3	10.34	22.09**	7.17	0.79	223.71
Number of effective tillers per plant	1	7.54**	8.55**	1.00	1.63	113.24
	2	9.47**	11.31**	1.81	1.92	142.48
	3	1.16**	1.07**	0.14	0.26	14.01
Spike length (cm)	1	3.94**	0.49**	0.14	0.95	5.29
	2	3.16**	0.54**	0.11	0.76	6.49
	3	1.98**	0.38**	0.13	0.46	3.76
Number of spikelets per plant	1	55.95*	137.47**	23.09	8.22	1715.63
	2	43.64*	158.25**	17.68	6.49	2108.49
	3	68.74**	98.69**	19.92	12.21	1181.68
Length of awns (cm)	1	1.12**	1.16**	0.10	0.25	15.86
	2	0.26*	0.89**	0.12	0.03	11.59
	3	1.16**	1.07**	0.14	0.26	14.01
Number of grains per spike	1	35.79**	17.66**	2.29	8.37	230.58
	2	29.97**	20.80**	2.88	6.77	268.82

Total chlorophyll content (mg/g)		3	26.19**	16.29**	2.92	5.82	200.67
1000-Grain weight (g)	Flag leaf area (cm²)	1	6.90**	7.73**	1.36	1.39	95.58
1 6.98** 4.59** 0.99 1.50 53.92		2	2.51	6.26**	1.35	0.29	73.60
2 5.11** 4.10** 0.99 1.03 46.70		3	5.75**	8.15**	1.12	1.16	105.44
Biological yield per plant (g)	1000-Grain weight (g)	1	6.98**	4.59**	0.99	1.50	53.92
Biological yield per plant (g)		2	5.11**	4.10**	0.99	1.03	46.70
2 23.31** 38.65** 1.24 5.52 561.21		3	2.70*	3.38**	1.13	0.39	33.74
3	Biological yield per plant (g)	1	32.81**	31.94**	1.19	7.91	461.26
Grain yield per plant (g) 1 5.58** 4.41** 0.27 1.33 62.15 2 8.69** 5.74** 0.24 2.11 82.51 3 8.79** 5.06** 0.33 2.11 70.93 Harvest index (%) 1 19.60** 37.15** 2.21 4.35 524.11 2 39.91** 55.21** 3.07 9.21 782.11 3 38.13** 43.98** 3.98 8.54 600.05 Total protein content in grains (%) 1 0.17* 0.30** 0.07 0.02 3.41 2 0.26** 0.41** 0.06 0.05 5.26 3 0.15* 0.31** 0.07 0.02 3.60 Total chlorophyll content (mg/g) 1 0.05** 0.11** 0.00 0.01 1.70 2 0.05** 0.15** 0.00 0.01 2.29		2	23.31**	38.65**	1.24	5.52	561.21
2 8.69** 5.74** 0.24 2.11 82.51 3 8.79** 5.06** 0.33 2.11 70.93 Harvest index (%)		3	17.58**	36.86**	1.45	4.03	531.26
3 8.79** 5.06** 0.33 2.11 70.93 Harvest index (%)	Grain yield per plant (g)	1	5.58**	4.41**	0.27	1.33	62.15
Harvest index (%)		2	8.69**	5.74**	0.24	2.11	82.51
2 39.91** 55.21** 3.07 9.21 782.11 3 38.13** 43.98** 3.98 8.54 600.05		3	8.79**	5.06**	0.33	2.11	70.93
Total protein content in grains (%) 1 0.17* 0.30** 0.07 0.02 3.41	Harvest index (%)	1	19.60**	37.15**	2.21	4.35	524.11
Total protein content in grains (%) 1 0.17* 0.30** 0.07 0.02 3.41 2 0.26** 0.41** 0.06 0.05 5.26 3 0.15* 0.31** 0.07 0.02 3.60 Total chlorophyll content (mg/g) 1 0.05** 0.11** 0.00 0.01 1.70 2 0.05** 0.15** 0.00 0.01 2.29		2	39.91**	55.21**	3.07	9.21	782.11
2 0.26** 0.41** 0.06 0.05 5.26 3 0.15* 0.31** 0.07 0.02 3.60 Total chlorophyll content (mg/g) 1 0.05** 0.11** 0.00 0.01 1.70 2 0.05** 0.15** 0.00 0.01 2.29		3	38.13**	43.98**	3.98	8.54	600.05
3 0.15* 0.31** 0.07 0.02 3.60 Total chlorophyll content (mg/g) 1 0.05** 0.11** 0.00 0.01 1.70 2 0.05** 0.15** 0.00 0.01 2.29	Total protein content in grains (%)	1	0.17*	0.30**	0.07	0.02	3.41
Total chlorophyll content (mg/g) 1 0.05** 0.11** 0.00 0.01 1.70 2 0.05** 0.15** 0.00 0.01 2.29		2	0.26**	0.41**	0.06	0.05	5.26
2 0.05** 0.15** 0.00 0.01 2.29		3	0.15*	0.31**	0.07	0.02	3.60
	Total chlorophyll content (mg/g)	1	0.05**	0.11**	0.00	0.01	1.70
3 0.05** 0.13** 0.00 0.01 1.95		2	0.05**	0.15**	0.00	0.01	2.29
		3	0.05**	0.13**	0.00	0.01	1.95

ⁱEnv. – Environment (E₁, E₂, E₃)

iiGCA – General Combining Ability

iiiSCA – Specific Combining Ability
ivModel I – Based on Griffing's Method II, Model I (fixed effects)
vGCA Variance / SCA Variance – Variance components estimated from mean squares
vi*, ** Significant at 5 and 1 percent, respectively (Model I)

Table.2 Pooled analysis of variance for combining ability across 11 characters in bread wheat (*Triticum aestivum* L. em. Thell.).

Characters		Source							Variance	e Model Ivi	
	Env.i	GCA ⁱⁱ	SCAiii	GCA x E ^{iv}	SCA x E ^{iv}	Pool Error		GCA	SCA	GCA x E	SCA x E
	[2]	[9]	[45]	[18]	[90]	[324]	[2]				
Days to 50% flowering	34.53**vii	32.38**	35.66**	6.44**	2.87*	2.04	0.60	1.18	7.58	504.28	6.59
Plant height (cm)	53.58**	86.70**	65.31**	17.20**	9.49**	5.87	4.61	1.73	20.21	891.51	16.99
Spike length (cm)	2.12**	8.43**	1.11**	0.32**	0.15	0.13	1.91	0.07	2.08	14.74	0.29
No. of spikelets per plant	171.73**	125.98**	335.59**	21.18	29.41*	20.23	1.94	5.51	26.44	4730.37	1.42
Length of awns (cm)	6.56**	2.06**	2.64**	0.24*	0.24**	0.12	2.15	0.23	0.49	37.75	0.18
No. of grains per spike	111.66**	84.24**	48.26**	3.85	3.25	2.70	1.93	3.96	20.39	683.38	1.73
Flag leaf area (cm²)	46.51**	11.58**	18.55**	1.79	1.80*	1.28	1.32	1.64	2.58	259.02	0.77
1000- Grain weight (g)	24.01**	11.99**	9.36**	1.39	1.35*	1.04	0.67	0.84	2.74	124.86	0.53
Biological yield per plant (g)	33.32**	71.38**	103.41**	1.16	2.02**	1.29	1.18	1.16	17.52	1531.75	-0.19
Grain yield per plant (g)	32.46**	22.10**	14.07**	0.48*	0.57**	0.28	2.92	1.17	5.46	206.78	0.30
Total protein content (%)	0.79**	0.41**	0.76**	0.08	0.13**	0.07	0.34	0.03	0.09	10.47	0.03

ⁱEnv. – Environment (E₁, E₂, E₃)

iiGCA – General Combining Ability

iiiSCA – Specific Combining Ability

 $^{^{}iv}GCA \times E / SCA \times E - Interaction of GCA and SCA with environments$

^vBartlett Test – Used to assess homogeneity of error variances across environments for each trait

viModel I – Based on Griffing's Method II, Model I (fixed effects)

vii*, ** Significant at 5 and 1 percent, respectively (Model I)

Table.3 General combining ability (GCA) performance of 10 parents for 15 characters in bread wheat (*Triticum aestivum* L. em. Thell.).

Characters	HD3086	Raj4238	Raj3077	Raj4037	MP1203	HI1544	Raj4079	MP3288	WR544	DBW187
Days to 50% flowering	G	G	G	A	P	A	A	P	P	A
Days to 75% maturity	G	P	P	P	P	P	P	A	G	A
Plant height (cm)	P	G	P	G	G	A	A	A	P	P
Number of effective tillers per plant	P	G	G	P	A	A	G	A	A	P
Spike length (cm)	A	P	G	G	G	P	A	P	A	P
Number of spikelets per plant	G	P	A	G	P	A	A	A	A	A
Length of awns (cm)	P	A	P	G	P	A	G	G	A	A
Number of grains per spike	G	G	P	P	P	G	P	G	G	P
Flag leaf area (cm²)	P	A	P	A	A	P	G	G	G	G
1000-grain weight (g)	A	A	P	A	G	A	P	P	A	G
Biological yield per plant (g)	P	P	G	G	P	G	G	P	G	P
Grain yield per plant (g)	G	G	A	P	P	G	G	G	P	G
Harvest index (%)	G	G	P	P	A	A	A	P	G	P
Total protein content in grains (%)	A	A	P	G	A	A	G	G	A	A
Total chlorophyll content (mg/g)	P	P	G	G	P	G	G	P	G	P

G = good combiner, A= average combiner, P= poor combiner

Table.4 Total number of crosses exhibiting significant specific combining ability (SCA) effects on a pooled basis for 11 characters in bread wheat (*Triticum aestivum* L. em. Thell.).

Characters	SCA effects (Number of crosses)
Days to 50% flowering	12
Plant height (cm)	13
Spike length (cm)	06
No. of spikelets per plant	18
Length of awns (cm)	18
No. of grains per spike	15
Flag leaf area (cm²)	13
1000-Grain weight (g)	14
Biological yield per plant (g)	21
Grain yield per plant (g)	17
Total protein content (%)	10

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Table.5 General and specific combining ability (GCA and SCA) effects for grain yield per plant in individual environments and across environments in bread wheat (Triticum aestivum L. em. Thell.).

Genotype	GCA and SCA Effects for Grain yield per plant					
	$\mathbf{E_1}$	$\mathbf{E_2}$	$\mathbf{E_3}$	Pool		
HD3086	0.11	0.47**	0.48**	0.36**		
Raj4238	0.70**	1.01**	0.81**	0.84**		
Raj3077	0.28	-0.15	-0.31*	-0.06		
Raj4037	-0.41**	-0.82**	-0.95**	-0.73*		
MP1203	-0.46**	-0.43**	-0.39*	-0.43*		
HI1544	0.37*	0.36**	0.69**	0.48**		
Raj4079	0.13	0.40**	0.50**	0.34**		
MP3288	-0.89**	-0.82**	-0.76**	-0.82*		
WR544	1.14**	1.30**	1.24**	1.23**		
DBW187	-0.99**	-1.32**	-1.31**	-1.20*		
Raj4238 × HD3086	-1.89**	-0.88	-0.14	-0.97**		
Raj3077 × HD3086	-1.52**	-1.27**	-0.44	-1.08**		
Raj4037 × HD3086	-3.34**	-3.01**	-3.09**	-3.15**		
MP1203 × HD3086	-0.51	-0.43	-0.44	-0.46		
HI1544 × HD3086	0.03	-3.03**	-1.10*	-1.37**		
Raj4079 × HD3086	2.98**	2.97**	2.37**	2.77**		
MP3288 × HD3086	-1.65**	-2.30**	-2.76**	-2.24**		
WR544 × HD3086	2.53**	3.16**	2.06**	2.58**		
DBW187 × HD3086	-2.20**	-2.89**	-2.73**	-2.61**		
Raj3077 × Raj4238	3.01**	2.82**	3.20**	3.01**		
Raj4037 × Raj4238	-0.46	1.70**	0.95	0.73*		
MP1203 × Raj4238	-0.88	0.91*	0.85	0.29		
HI1544 × Raj4238	-2.27**	-3.47**	-3.98**	-3.24**		
Raj4079 × Raj4238	2.44**	2.02**	2.32**	2.26**		
MP3288 × Raj4238	0.07	-0.26	-0.54	-0.24		
WR544 × Raj 238	1.32**	2.12**	1.90**	1.78**		
DBW187 × Raj4238	2.50**	2.02**	1.86**	2.13**		
Raj4037 × Raj3077	-1.51**	-0.67	-0.53	-0.90**		
MP1203 × Raj3077	1.18*	1.04*	0.95	1.06**		
HI1544 × Raj3077	0.05	-0.74	-0.85	-0.51		
Raj4079 × Raj3077	-3.36**	-3.94**	-3.76**	-3.69**		

MP3288 × Raj3077	-3.01**	-2.94**	-2.21**	-2.72**
	-0.08	-0.11	-1.36*	-0.52
WR544 × Raj3077				0.37
DBW187 × Raj3077	-0.01	0.58	0.53	0.0.
MP1203 × Raj4037	-2.43**	-2.10**	-2.27**	-2.27**
HI1544 × Raj4037	-0.34	-0.37	-0.72	-0.48
Raj4079 × Raj4037	2.93**	1.55**	2.02**	2.17**
MP3288 × Raj4037	-0.86	-1.19**	-1.62**	-1.22**
WR544 × Raj4037	2.19**	1.16*	0.75	1.37**
DBW187 × Raj4037	0.45	-0.17	-0.30	-0.00
HI1544 × MP1203	0.84	0.87	0.26	0.66*
Raj4079 × MP1203	-2.04**	-3.45**	-3.44**	-2.97**
MP3288 × MP1203	-0.09	-0.55	-0.48	-0.38
WR544 × MP1203	-0.53	-1.93**	-1.36*	-1.27**
DBW187 × MP1203	4.74**	4.51**	5.07**	4.77**
Raj4079 × HI1544	0.79	3.51**	3.12**	2.47**
MP3288 × HI1544	1.87**	-0.65	1.08*	0.77**
WR544 × HI1544	1.28**	1.40**	0.70	1.13**
DBW187 × HI1544	-1.71**	-1.96**	-2.27**	-1.98**
MP3288 × Raj4079	1.03*	2.22**	1.21*	1.49**
WR544 × Raj4079	-1.62**	-2.67**	-1.91**	-2.07**
DBW187 × Raj4079	-1.63**	-1.78**	-1.88**	-1.76**
WR544 × MP3288	2.38**	1.95**	0.81	1.71**
DBW187 × MP3288	-1.47**	-1.49**	-1.33*	-1.43**
DBW187 × WR544	-0.73	-1.49**	-1.64**	-1.29**

^{*, **} Significant at 5 and 1 percent, respectively (Model I).

Table.6 Crosses and their respective parents identified based on per se performance and combining ability (GCA/SCA) effects.

Genotypes	Per se performance of grain yield (g)	GCA/SCA effects
HD3086 × WR544	17.02	2.58**
Raj4238 × WR544	16.70	1.78**
Raj4238 × Raj3077	16.65	3.01**
HD3086 × Raj4079	16.33	2.77**
Raj4238 × Raj4079	16.30	2.26**
HD3086	16.83	0.36**
HI1544	15.09	0.48**

^{*, **} Significant at 5 and 1 percent, respectively (Model I).

Pooled analysis for combining ability was performed for days to 50% flowering, plant height, spike length, number of spikelets per plant, length of awns, number of grains per spike, flag leaf area, 1000-grain weight, biological yield per plant, grain yield per plant, and total protein content in grains, as Bartlett's test indicated homogeneity of error variances for these traits. Significant mean squares for both GCA and SCA across all these traits suggest substantial genetic variation among the parents and crosses. Interaction of GCA with environments (GCA × E) was significant for days to 50% flowering, plant height, spike length, length of awns, flag leaf area, and grain yield per plant. While the interaction of SCA with environments (SCA × E) was significant for days to 50% flowering, plant height, number of spikelets per plant, length of awns, flag leaf area, 1000-grain weight, biological yield per plant, grain yield per plant, and total protein content in grains (Table 2).

Based on pooled GCA effect estimates, five parents, namely Raj4037, Raj4079, HD3086, Raj4238, and WR544, were identified as good general combiners for most traits. Specifically, HD3086, Raj4238, and Raj4079 were good general combiners for grain yield per plant; HD3086 and Raj4238 for the number of grains per spike; HD3086, Raj4238, and WR544 for harvest index; and Raj4037, Raj4079, and WR544 for biological yield per plant and total chlorophyll content (Table 3).

Crosses involving these high GCA parents are expected to produce promising segregants with superior per se performance for these traits and can be effectively used in developing high-yielding cultivars through pedigree selection in desirable segregating generations. These results align with the findings of Khan *et al.*, (2007), Aida *et al.*, (2012), Kalhoro *et al.*, (2015), Ashraf *et al.*, (2015), Ismail (2015), Kandil *et al.*, (2016), Murugan and Kannan (2017), Kumar *et al.*, (2019), and Malav *et al.*, (2020).

Reviewing SCA effects for grain yield per plant on a pooled basis, the number of crosses showing significant SCA effects across yield and yield-contributing traits ranged from 6 (spike length) to 21 (biological yield per plant) (Table 4). Among the 45 crosses, nine demonstrated significantly favourable SCA across all three environments and under pooled analysis. Crosses such as HD3086 × WR544, Raj4238 × WR544, Raj4238 × Raj3077, HD3086 × Raj4079, and Raj4238 × Raj4079 showed significant positive SCA effects for grain yield per plant and for other related traits including days to

50% flowering, days to 75% maturity, spike length, number of spikelets per plant, length of awns, number of effective tillers per plant, 1000-grain weight, biological yield per plant, harvest index, total protein content in grains, and total chlorophyll content. These results suggest the predominance of non-additive gene action in the expression of these traits (Table 5). Similar findings were also reported by Aida *et al.*, (2012), Raj and Kandalkar (2013), Desale and Mehta (2013), Ismail (2015), Rahul (2017), Kumar *et al.*, (2019), Malav *et al.*, (2020), and Askander *et al.*, (2021).

Among the evaluated genotypes, five cross combinations, HD3086 × WR544, Raj4238 × WR544, Raj4238 × Raj3077, HD3086 × Raj4079, and Raj4238 × Raj4079 exhibited high per se grain yield (16.30-17.02 g) coupled with significant positive SCA effects. Parental lines HD3086 and HI1544 also showed significant positive GCA effects, indicating their potential for developing high-yielding hybrids (Table 6).

The evaluation of GCA in parents, SCA in crosses, and the breeding values of both provides an effective approach to assess the nature and magnitude of gene actions controlling the inheritance of various quantitative characters.

Parental lines with strong GCA effects and superior per se performance offer a practical route for the exploitation of hybrid vigour when using conventional breeding approaches.

In summary, five out of the ten parental lines: Raj4037, Raj4079, HD3086, Raj4238, and WR544, were identified as efficient general combiners for most of the traits studied. Of the 45 hybrid combinations, nine showed consistently significant and favorable SCA effects across all three environments. The crosses HD3086 × WR544, Raj4238 × WR544, Raj4238 × Raj3077, HD3086 × Raj4079, and Raj4238 × Raj4079 demonstrated significant positive effects on grain yield per plant along with other yield-related traits.

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Author Contributions

Manisha Kumari: Conceived the original idea and designed the model and Analysed, Investigated and wrote the manuscript. Hemlata Sharma: Validation, Formal Analysis, Project Administration, Supervision. Amit Dadheech: Writing - Review & Editing. Abhay Dashora: Review and Editing. R. B. Dubey: Created supplementary visual material. M. K. Kaushik: Rechecked all major findings to validate their accuracy. S. S. Lakhawat: Review, Contributed to data representation in the final manuscript.

Declarations

Ethical Approval Not applicable.

Consent to Participate Not applicable.

Consent to Publish Not applicable.

Conflict of Interest The authors declare no competing interests.

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