

Estimation of General and Specific Combining Abilities in Six-Row Barley (*Hordeum vulgare* L.) Using “Line × Tester” Analysis Across Different Environmental Conditions

Anil Kulheri^{1*}, Shyam Singh Rajput¹, Sumer Singh Punia¹ and Kiran Jakhar²

¹ Department of Genetics and Plant Breeding, Sri Karan Narendra Agriculture University, Jobner, Rajasthan

² Department of Biochemistry, Central University of Rajasthan, Bandar Sindri, Ajmer, Rajasthan, India

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*Corresponding author:

E-mail: jat04051997@gmail.com

Abstract

In order to identify appropriate parents and desirable cross combinations in six-row barley under three different environmental conditions, the current study used line × tester analysis with fifteen lines and three testers to evaluate the combining ability for grain yield and its contributing traits. Pooled analysis of variance for combining ability revealed significant mean squares for lines, testers, and line × tester interactions for all traits. The line × environment interactions were significant for all traits except plant height, 1000-grain weight, harvest index, and starch content. Tester × environment interactions were significant for most traits, except days to 75% heading, days to maturity, harvest index, protein content, and starch content. The line × tester × environment interactions were significant for all traits except the harvest index. Parental lines BG 105, BH 959, DWRUB 64, PL 751, and RD 2552, along with the tester RD 2508, were identified as good general combiners for grain yield and its contributing traits across environments. Out of forty-five crosses, six in early sowing (E_1), six in normal sowing (E_2), and eleven in late sowing (E_3) exhibited significantly positive SCA effects for grain yield per plant, with crosses BH 959 × RD 3005 and RD 2907 × RD 3005 performing well across all three environments, while DWRUB 64 × RD 2508 and RD 2660 × F_1 showed strong performance in early (E_1) and normal (E_2), RD 2035 × RD 2508 in early (E_1) and late (E_3), and RD 2552 × RD 2508 in normal (E_2) and late (E_3) sowing condition, indicating these as promising specific cross combinations for grain yield and its contributing traits.

Keywords: Barley, GCA, line × tester analysis, SCA

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1. Introduction

Barley (*Hordeum vulgare* L.) is an important self-pollinated, cleistogamous winter cereal cultivated across temperate and tropical regions for food, feed, forage, and malting purposes. It was domesticated approximately 10,000 years ago from its wild progenitor, *Hordeum vulgare* ssp. *spontaneum*, in the Fertile Crescent of the Middle East (Potla *et al.*, 2013). The genus *Hordeum* belongs to the Triticeae tribe of the Poaceae family and comprises diverse genetic resources, including wild relatives and landraces

that harbour valuable alleles for improving abiotic stress tolerance, disease resistance, adaptation, and grain quality (Patial *et al.*, 2026). Exploiting this genetic diversity is particularly important for developing barley cultivars with stable performance under changing and contrasting environmental conditions.

Barley ranks among the major cereal crops globally and is widely utilized for food, animal feed, forage, and malting (Ashok *et al.*, 2023; Shabrangy *et al.*, 2021). In addition to its agronomic importance, barley possesses considerable



nutritional value because of its dietary fibre, -glucan, vitamins, minerals, and other bioactive compounds (Patial *et al.*, 2025). However, improving productivity and quality simultaneously remains a major challenge because these traits are quantitatively inherited and strongly influenced by both genetic background and environmental conditions. Therefore, identifying genetically superior parents and understanding the inheritance of complex traits are essential for designing effective barley breeding strategies.

Combining ability analysis provides an important framework for assessing the breeding value of parental genotypes and their cross combinations. Sprague and Tatum (1942) classified combining ability into general combining ability (GCA) and specific combining ability (SCA). GCA primarily reflects the contribution of additive genetic effects and helps identify parents that consistently transmit favourable alleles across different crosses, whereas SCA is largely associated with non-additive genetic effects, including dominance and epistatic interactions, and identifies particular cross combinations that perform better or differently than expected from parental GCA (Begna 2021). Consequently, simultaneous assessment of GCA and SCA can provide valuable information for determining the relative importance of additive and non-additive gene action and for selecting suitable parents and cross combinations for barley improvement.

The line $\times$ tester mating design is a practical and efficient approach for estimating GCA and SCA effects in breeding populations, particularly when a relatively large number of parental combinations need to be evaluated. Previous studies have demonstrated the usefulness of line $\times$ tester analysis for identifying superior combiners and elucidating the genetic control of yield and yield-associated traits in barley and other cereals (Kumari *et al.* 2018; Rashid *et al.*, 2007). Nevertheless, an important research gap remains in the systematic evaluation of GCA and SCA in six-row barley across contrasting environmental conditions. Combining ability estimates obtained from a single environment may not adequately represent the breeding value of parents because environmental variation can alter trait expression, parental ranking, and the magnitude and direction of combining ability effects. Moreover, limited information is available on the consistency of desirable combining ability effects across

environments in six-row barley, particularly for identifying parents that can contribute to stable performance under environmental variability. Thus, evaluating the same line $\times$ tester progenies across multiple environments is necessary to distinguish genetically consistent combiners from combinations whose performance is strongly environment-dependent.

The present study was therefore undertaken with the hypothesis that both additive and non-additive genetic effects contribute significantly to the expression of agronomic and yield-related traits in six-row barley, and that the magnitude and expression of GCA and SCA effects vary across environmental conditions. It was further hypothesized that some parental lines and specific cross combinations would exhibit consistently desirable combining ability across environments and could consequently serve as valuable genetic resources for developing high-yielding and stable six-row barley cultivars. Therefore, the present study was undertaken to estimate the general combining ability (GCA) effects of selected lines and testers and the specific combining ability (SCA) effects of their line $\times$ tester crosses for important agronomic and yield-related traits in six-row barley across different environmental conditions. The study further aimed to determine the relative contribution of additive and non-additive genetic effects to trait expression, assess the influence of environmental conditions on the magnitude and consistency of GCA and SCA effects, and identify superior parental lines and cross combinations with desirable and stable combining ability across environments. It was hypothesized that both additive and non-additive gene actions contribute significantly to the inheritance of the studied traits, with their relative importance varying across environments, and that certain parents and cross combinations would exhibit consistently favourable combining ability. Identification of such stable and superior combiners would provide useful genetic resources for selecting appropriate parents, designing effective crossing programmes, and developing high-yielding and environmentally adaptable six-row barley cultivars.

2. Materials and Methods

The experiment was conducted at the instructional farm of SKN College of Agriculture, Jobner, Jaipur (Rajasthan), during the *Rabi* seasons of 2021–22 and 2022–23. In



the *Rabi* season of 2021–22, a hybridization program was carried out using the Line $\times$ Tester mating design. Fifteen genetically diverse six-row barley genotypes were used as lines, and three genotypes RD 2508, RD 3005, and their F_1 hybrid (RD 2508 $\times$ RD 3005) were used as testers in a crossing block. A total of 45 crosses were developed, including thirty single crosses and fifteen three-way crosses. The experimental material, comprising 63 genotypes i.e. three testers, fifteen lines, and forty-five F_1 hybrids (thirty single crosses and fifteen three-way crosses) was evaluated during the *Rabi* season of 2022–23 using a randomized block design with three replications, under three distinct environments: early (E1), normal (E2), and late (E3) sowing conditions. Two rows, each 2.5 meters long, were planted with a 30-cm gap between each genotype. In each environment, a consistent 10-cm plant-to-plant spacing was maintained. Plant protection measures and standard methods of agriculture were followed to maintain a healthy crop population throughout field. Observations were made for fourteen traits: days to 75% heading, effective tillers per plant, days to maturity, 1000-grain weight (g), plant height (cm), grains per spike, spike length (cm), grain yield per plant (g), biological yield per plant (g), harvest index (%), proline content ($\mu\text{g}/100$ mg fresh weight), protein content (%), starch content (%), and chlorophyll content (SPAD). Observations for all fourteen traits were recorded from ten randomly selected plants in every plot of F_1 crosses and parent populations across all replications and environments, except for days to 75% heading, days to maturity, and 1000-grain weight, which were recorded on a plot basis. Harvest index (%) was estimated following Singh and Stoskopf (1971), protein content (%) using the method of Yin *et al.* (2002), starch content (%) as described by Hodge *et al.* (1962), proline content ($\mu\text{g}/100$ mg FW) following Bates *et al.* (1973), and chlorophyll content (SPAD) using a Minolta SPAD-502 chlorophyll meter.

The combining ability effects for the Line $\times$ Tester mating design were evaluated according to Kempthorne (1957), both individually and across environments, using the method proposed by Singh and Choudhary (1985). The observations for every trait were subjected to analysis of variance within each environment and across all environments, following the methodology outlined by Panse and Sukhatme (1985).

Table 1: Parental genotypes (lines and testers) and their pedigree

S. No.	Parental Genotypes	Parentage
		Lines
1.	BG 105	C 141 / MONTLESSO
2.	BH 959	BH 393/ BH 331
3.	DWRUB 64	DL 472 / PL 705
3.	DWRB 137	DWRB 28/ DWRUB 64
5.	HUB 113	KARAN 280/ C138
6.	JB 110	LAKHAN/ PL 512
7.	K 551	P 464/ JYOTI
8.	NDB 1445	NDB 940/ Ratna
9.	PL 751	K 226/ PL 226
10.	VLB 118	14 th EMBSN 9313
11.	RD 2035	RD 103/ PL 101
12.	RD 2052	API CM 67/ SO 727// PL 101
13.	RD 2552	RD 2035/ DL 472
14.	RD 2660	RD 2052/ RD 2566
15.	RD 2907	RD 103/ RD 2518// RD 2592
		Testers
1.	RD 2508	RD 2035 / P 490
2.	RD 3005	DWR 16/ RD 2503// RD 2667
3.	$F_1 (T_1 \times T_2)$	RD 2508 $\times$ RD 3005

Results and Discussion

In the current study, pooled analysis of variance across the three environments indicated significant $G \times E$ interactions for most of the traits. Combining ability analysis was therefore carried out independently for every environment. Analysis of variance for combining ability as shown in table 1 revealed that mean sum of square due to lines, tester, and lines $\times$ tester were significant for all the trait in individuals as well as across the environment, except due to tester for days to maturity in E_3 and due to line $\times$ tester for harvest index in E_1 . Significant mean squares for each trait as a result of lines and testers showed that lines and testers played a significant role in the general combining (GCA) effects. Similar to lines $\times$ testers, significant mean squares showed a significant contribution of crosses for specific combining (SCA) effects. Similar observations were also reported by Amiruzzaman *et al.* (2008), Potla *et al.* (2013), Singh *et al.* (2017), Swati *et al.* (2018), Kumari *et al.* (2020), Kamboj *et al.* (2021), Joshi *et al.* (2024) and Kalyar *et al.* (2024).



Table 2: Analysis of variance showing mean squares of parents and F₁'s in individual environment for different traits

S. No.	Traits	Env.	Rep. [2]	Genotype [62]	Tester [2]	Lines [14]	L X T [28]	Error [124]
1	Days to 75% heading	E ₁	0.19	49.68**	77.39**	85.17**	14.24**	2.07
		E ₂	2.31	39.04**	72.47**	75.13**	10.05**	2.61
		E ₃	1.54	20.70**	51.12**	25.63**	7.45**	2.75
2	Days to maturity	E ₁	5.59	35.65**	42.96**	47.96**	8.18**	4.28
		E ₂	5.99	28.89**	28.16**	43.06**	8.23**	3.87
		E ₃	5.42	23.85**	8.14	34.60**	15.61**	3.17
3	Plant height (cm)	E ₁	14.35	61.19**	59.19**	91.90**	25.90**	7.65
		E ₂	14.21	56.92**	44.91**	100.33**	23.67**	8.21
		E ₃	14.28	66.05**	63.38**	67.83**	38.74**	7.14
4	Effective tillers per plant	E ₁	0.23	8.95**	17.85**	15.15**	1.61**	0.18
		E ₂	0.52	10.50**	17.96**	17.37**	1.62**	0.22
		E ₃	0.10	8.79**	42.81**	15.59**	2.63**	0.14
5	Grains per spike	E ₁	20.01*	94.12**	348.18**	45.43**	21.62**	6.56
		E ₂	10.99	90.39**	248.46**	45.15**	18.28**	6.95
		E ₃	9.90	105.83**	558.93**	122.45**	46.71**	6.44
6	Spike length (cm)	E ₁	0.14	3.51**	17.18**	4.19**	0.70**	0.14
		E ₂	0.30	3.79**	16.69**	3.46**	0.81**	0.13
		E ₃	0.22	3.14**	21.97**	5.50**	0.85**	0.12
7	1000-grain weight (g)	E ₁	3.66	31.19**	30.54**	35.62**	8.98**	1.65
		E ₂	3.88	37.32**	75.38**	39.97**	13.07**	1.68
		E ₃	2.08	28.49**	83.12**	50.70**	7.22**	1.44
8	Grain yield per plant (g)	E ₁	2.43	22.58**	47.85**	34.46**	4.62**	1.10
		E ₂	2.88	27.24**	59.18**	41.26**	5.60**	0.99
		E ₃	1.42	24.91**	123.85**	43.61**	8.11**	0.68
9	Biological yield per plant (g)	E ₁	0.53	54.01**	151.76**	72.73**	20.61**	3.00
		E ₂	2.57	67.46**	156.32**	81.07**	23.96**	3.18
		E ₃	4.99	71.05**	366.31**	96.91**	30.84**	2.15
10	Harvest index (%)	E ₁	18.70	58.28**	142.62**	63.52**	10.68	10.02
		E ₂	9.66	55.30**	100.42**	80.15**	14.77**	7.40
		E ₃	9.86	63.22**	260.13**	115.83**	20.80*	11.44
11	Protein content (%)	E ₁	0.08	0.67**	0.89**	0.96**	0.41**	0.04
		E ₂	0.01	0.69**	0.88**	0.96**	0.46**	0.06
		E ₃	0.14	0.76**	1.14**	0.90**	0.66**	0.05
12	Starch content (%)	E ₁	0.57	2.57**	13.29**	4.96**	0.99**	0.42
		E ₂	1.31	2.64**	13.07**	4.99**	1.20**	0.43
		E ₃	0.80	3.25**	17.64**	4.88**	1.93**	0.42



13.	Proline content ($\mu\text{g}/100\text{ mg}$ fresh weight)	E_1	1.79	178.69**	510.39**	454.99**	6.77**	1.16
		E_2	2.00	178.92**	526.13**	460.96**	6.93**	1.23
		E_3	1.38	185.47**	564.86**	446.17**	11.80**	1.42
14	Chlorophyll content (SPAD)	E_1	1.71	15.81**	49.82**	25.17**	6.42**	1.65
		E_2	3.79	18.32**	24.43**	32.85**	7.22**	1.56
		E_3	4.12	20.41**	77.19**	29.86**	6.06**	1.37

*, ** Significant at 5% and 1%, respectively, [] Degree of freedom

On a pooled basis (Table 3) mean square due to lines, tester and lines $\times$ tester were also found to be significant for all the traits. Significant mean squares due to lines and testers for all the traits showed that lines and testers played an essential role in the general combining (GCA) effects over the environment. Similarly, crosses were found to contribute significantly to specific combining ability (SCA) impacts across the environment, according to considerable mean sum of squares due to lines $\times$ tests. The interaction of lines with environments was significant for all the traits except plant height, 1000-grain weight, harvest index and starch content. Furthermore, the interaction of testers with environments was reported significant for most traits excluding days to 75% heading, days to maturity, harvest index, protein content and the starch content. Interaction of lines $\times$ testers $\times$ environments was significant for all traits except harvest index. The significant interaction of lines, tester and lines $\times$ tester with environments indicated that the estimates of general combining ability (GCA) and specific combining ability (SCA) effects were influenced by environments for most of the traits studied. Verma *et al.* (2007) and Ram and Shekawat (2017b) also reported similar findings.

The present study revealed that both magnitude and the direction of general combining ability (GCA) effect of the parents varied across various environments for grain yield per plant and the other contributing traits. Some parents (lines and tester) consistently show desirable general combining ability (GCA) estimates for multiple traits across all environments, although the magnitudes varied. Estimation of GCA effects explained that parents having consistent desirable GCA estimates for most of the traits in all the three environments were RD 2508 for days to 75% heading, effective tillers per plant, grain yield per plant, grains per spike, spike length, starch content, 1000-grain weight, biological yield per plant, protein content, proline content and chlorophyll content; BG 105 for plant

height, effective tillers per plant, grains per spike, spike length, 1000-grain weight, grain yield per plant, harvest index, proline content and chlorophyll content; BH 959 for effective tillers per plant, 1000-grain weight, grain yield per plant, proline content and chlorophyll content; DWRUB 64 for the days to 75% heading, grains per spike, days to maturity, effective tillers per plant, spike length, 1000-grain weight, grain yield per plant, biological yield per plant, harvest index, starch content and proline content; DWRB 137 for plant height and harvest index; PL 751 for grain yield per plant, biological yield per plant and starch; RD 2035 for days to 75% heading, grains per spike, effective tillers per plant, spike length, starch content, 1000-grain weight, and proline content; RD 2052 for days to 75% heading and days to maturity; RD 2552 for plant height, effective tillers per plant, grain yield per plant, harvest index, biological yield per plant, protein content and proline content. Parents with superior *per se* performance also tended to exhibit favorable GCA effects, although this correspondence was not consistent across all traits and environments. Since GCA effects are attributed to additive and additive $\times$ additive gene interactions, the parents listed in Table 4 for GCA effects demonstrate strong potential for their individual traits. These parents can be effectively utilized in a multiple-crossing program to develop a dynamic population that accumulates the majority of appropriate genes (Griffing, 1956).

The parents that shown desirable GCA effects for grain yield per plant also displayed desirable GCA effects for one or more yield-attributing traits, as shown in Table 4. The parental lines BG 105, BH 959, DWRUB 64, PL 751, RD 2552 and tester RD 2508 in E_1 and E_2 and parental lines BG 105, BH 959, DWRUB 64, PL 751, RD 2035, RD 2552 and tester RD 2508 in E_3 appeared as superior general combiners for the grain yield per plant and some other related traits. A comprehensive assessment across all environments revealed that parental lines BG 105,





Table 3: Pooled analysis of variance showing mean squares of parents and F₁'s for different characters

S. No.	1	2	3	4	5						
Source	Env.	Rep./Env.	Genotype	Tester	Line	L x T	G x E	T x E	L x E	L x T x E	Pooled Error
Degree of freedom	2	6	62	2	14	28	124	4	28	56	372
Days to 75% heading	10325.19**	1.35	8769**	198.61**	144.73**	20.48**	10.86**	1.18	20.60**	5.63**	2.48
Days to maturity	6104.13**	5.67	69.33**	70.34**	98.34**	19.48**	9.53**	4.45	13.64**	6.27**	3.77
Plant height (cm)	15520.61**	14.28	161.12**	89.85**	246.45**	64.52**	11.52**	38.81**	6.8	11.89**	7.67
Effective tillers per plant	245.94**	0.28	26.61**	73.98**	46.09**	5.21**	0.81**	2.32**	1.01**	0.33**	0.18
Grains per spike	11603.02**	13.63	258.82**	1109.40**	170.37**	60.26**	15.76**	23.08**	21.33**	13.17**	6.65
Spike length (cm)	99.16**	0.22	9.77**	54.32**	12.58**	1.99**	0.34**	0.76**	0.28**	0.19*	0.13
1000-grain weight (g)	3390.20**	3.2	91.08**	180.67**	121.61**	24.16**	2.96**	4.18*	2.34	2.56**	1.59
Grain yield per plant (g)	1636.57**	2.24*	70.20**	219.37**	115.62**	15.29**	2.27**	5.75**	1.86**	1.52**	0.92
Biological yield per plant(g)	4150.93**	2.7	176.23**	639.18**	223.53**	67.61**	8.14**	17.61**	13.60**	3.90*	2.78
Harvest index (%)	1995.33**	12.74	157.14**	461.11**	236.62**	28.83**	9.83	21.03	11.44	8.71	9.62
Protein content (%)	22.53**	0.08	1.98**	2.86**	2.65**	1.36**	0.07**	0.02	0.09*	0.08**	0.05
Starch content (%)	166.29**	0.89	7.65**	43.48**	14.41**	2.68**	0.4	0.26	0.21	0.72**	0.43
Proline content (µg/100mg)	6491.10**	1.72	535.96**	1594.24**	1354.52**	21.52**	3.56**	3.57*	3.80**	2.00**	1.27
Chlorophyll content (SPAD)	2892.80**	3.21	44.59**	136.13**	66.81**	14.71**	4.98**	7.65**	10.54**	2.49**	1.53

*, ** Significant against pool error at 5% and 1%, respectively

Table 4: Promising general combiners for different traits in different environments

Traits	Early sowing (E ₁)		Normal sowing (E ₂)		Late sowing (E ₃)	
	Lines	Testers	Lines	Testers	Lines	Testers
Days to 75% heading	BH 959, DWRUB 64, DWRB 137, RD 2035, RD 2052	RD 2508	BG 105, BH 959, DWRUB 64, DWRB 137, RD 2035, RD 2052	RD 2508	BG 105, DWRUB 64, RD 2035, RD 2052, RD 2907	RD 2508
Days to maturity	BH 959, DWRUB 64, DWRB 137, HUB 113, RD 2052	RD 2508	DWRUB 64, DWRB 137, RD 2052	RD 2508	BG 105, DWRUB 64, RD 2035, RD 2052, RD 2660	-
Plant height (cm)	BG 105, DWRB 137, RD 2552	-	BG 105, DWRB 137, RD 2552	-	BG 105, BH 959, DWRB 137, RD 2552, RD 2907	F ₁
Effective tiller per plant	BG 105, BH 959, DWRUB 64, PL 751, RD 2035, RD 2552	RD 2508	BG 105, BH 959, DWRUB 64, PL 751, RD 2035, RD 2552	RD 2508	BG 105, BH 959, DWRUB 64, RD 2035, RD 2552	RD 2508
Grain per spike	BG 105, DWRUB 64, RD 2035, RD 2660	RD 2508, F ₁	BG 105, DWRUB 64, RD 2035	RD 2508	BG 105, DWRUB 64, PL 751, RD 2035, RD 2552	RD 2508
Spike length (cm)	BG 105, DWRUB 64, K 551, RD 2035	RD 2508, F ₁	BG 105, DWRUB 64, K 551, RD 2035	RD 2508, F ₁	BG 105, DWRUB 64, K 551, RD 2035, RD 2052, RD 2552	RD 2508
1000- grain weight (g)	BG 105, BH 959, DWRUB 64, RD 2035, RD 2552	RD 2508	BG 105, BH 959, DWRUB 64, RD 2035, RD 2552	RD 2508	BG 105, BH 959, DWRUB 64, RD 2035	RD 2508
Grain yield per plant (g)	BG 105, BH 959, DWRUB 64, PL 751, RD 2552	RD 2508	BG 105, BH 959, DWRUB 64, PL 751, RD 2552	RD 2508	BG 105, BH 959, DWRUB 64, PL 751, RD 2035	RD 2508
Biological yield per plant (g)	BG 105, BH 959, DWRUB 64, PL 751, RD 2552	RD 2508	BH 959, DWRUB 64, PL 751, RD 2552	RD 2508	BG 105, DWRUB 64, PL 751, RD 2035, RD 2552	RD 2508
Harvest index (%)	BG 105, DWRUB 64, DWRB 137, PL 751, RD 2552	F ₁	BG 105, DWRUB 64, DWRB 137, PL 751, RD 2552	F ₁	BG 105, BH 959, DWRUB 64, DWRB 137, RD 2552	RD 2508
Protein content (%)	BH 959, DWRB 137, VLB 118, RD 2552, RD 2660	RD 2508	BH 959, DWRB 137, VLB 118, RD 2552, RD 2660	RD 2508	JB 110, VLB 118, RD 2552, RD 2660	RD 2508
Starch content (%)	DWRUB 64, PL 751, RD 2035	RD 2508	DWRUB 64, PL 751, RD 2035	RD 2508	DWRUB 64, PL 751, RD 2035	RD 2508
Proline content (µg/100mg fresh weight)	BG 105, BH 959, DWRUB 64, RD 2035, RD 2552	RD 2508	BG 105, BH 959, DWRUB 64, RD 2035, RD 2552	RD 2508	BG 105, BH 959, DWRUB 64, RD 2035, RD 2552	RD 2508
Chlorophyll content (SPAD)	BG 105, BH 959, DWRUB 64, DWRB 137, HUB 113, K 551	RD 2508	BG 105, BH 959, HUB 113, JB 110, RD 2660	RD 2508	BG 105, BH 959, DWRUB 64, DWRB 137, RD 2035	RD 2508



Table 5: Cross combinations showing significant and desirable SCA effects, along with the GCA status of the parents for grain yield per plant, as well as significant and desirable SCA effects for other yield-contributing traits across different environments

Env.	Crosses	SCA effect	GCA status	Days to heading	Days to maturity	Plant height (cm)	Effective tillers per plant	Grains per spike	Spike length (cm)	1000 grain weight (g)	Biological yield per plant (g)	Harvest index (%)	Protein content (%)	Starch content (%)	Proline content (µg/100 mg fresh weight)	Chlorophyll content (SPAD)
E ₁	JB 110 x RD 3005	1.93**	P x P	+	-	-	+	-	-	+	+	-	-	-	-	-
	BH 959 x RD 3005	1.84*	G x P	-	-	-	+	-	-	+	-	-	+	-	-	-
	DWRUB 64 x RD 2508	1.79*	G x G	-	-	-	-	-	-	-	-	-	-	-	-	-
	RD 2660 x F ₁	1.66*	P x P	-	-	-	-	-	-	+	+	-	-	-	-	-
	RD 2035 x RD 2508	1.49*	G x G	-	-	-	-	-	-	+	+	-	-	-	-	-
E ₂	RD 2907 x RD 3005	1.47*	P x P	+	-	-	+	-	-	-	-	-	+	-	-	-
	RD 2660 x F ₁	1.99**	P x P	-	-	-	-	-	-	+	+	-	-	-	-	-
	DWRUB 64 x RD 2508	1.84**	G x G	-	-	-	+	-	-	-	-	-	-	-	-	+
	BH 959 x RD 3005	1.64*	G x P	-	-	-	+	-	-	+	-	-	+	-	-	-
	RD 2907 x RD 3005	1.64*	P x P	-	-	-	+	-	-	+	-	-	+	-	-	+
E ₃	RD 2552 x RD 2508	1.50*	G x G	-	-	+	+	-	+	-	+	-	-	-	-	-
	BG 105 x RD 2508	1.36*	G x G	-	-	-	+	-	-	+	+	-	-	-	-	-
	RD 2052 x RD 2508	3.09**	P x G	-	-	+	+	+	+	+	+	+	+	+	-	-
	RD 2035 x RD 2508	1.95**	G x G	-	-	-	+	+	+	+	+	+	-	+	-	-
	DWRB 137 x F ₁	1.63**	G x P	-	-	-	+	-	-	+	+	-	-	-	-	-
	RD 2907 x RD 3005	1.55**	P x P	-	-	-	+	-	-	-	-	-	+	-	-	-
	BH 959 x F ₁	1.49**	G x P	-	-	-	+	-	-	-	+	-	-	-	-	+
	BH 959 x RD 3005	1.43*	G x P	-	-	-	+	-	-	-	+	-	+	-	-	-
	HUB 113 x RD 3005	1.39*	P x P	-	-	-	-	-	-	-	-	-	+	-	-	-
	DWRUB 64 x F ₁	1.34*	G x P	-	-	-	-	+	-	-	+	-	+	+	-	-
E ₄	PL 751 x RD 2508	1.32*	G x G	-	-	-	+	-	-	-	-	-	+	-	+	-
	RD 2552 x RD 2508	1.29*	G x G	-	-	-	+	-	+	-	-	-	+	-	-	-
	BG 105 x F ₁	1.17*	G x P	-	+	-	-	-	+	-	-	-	-	-	-	-

+ = Significant and desirable SCA effect, - = Non significant and undesirable SCA effect

G = Desirable significant GCA effect, A = Desirable non-significant GCA effect, P = undesirable significant or non significant GCA effect



BH 959, DWRUB 64, PL 751 and RD 2552 in all three environments emerged as superior general combiners for the grain yield with simultaneous consideration of others traits. Among three testers, tester RD 2508 in all three environments emerged as good general combiners for the grain yield per plant and other related traits. In barley, several studies have reported parents with good general combining ability, including those by Sharma *et al.* (2002), Sharma *et al.* (2003), Verma *et al.* (2007), Amiruzzaman *et al.* (2008), Potla *et al.* (2013), Madic *et al.* (2014), Kumar *et al.* (2015), Patial *et al.* (2016), Sultan *et al.* (2016), Ram and Shekhawat (2017a), Singh *et al.* (2017), Rathore and Chauhan (2017), Lal *et al.* (2018), Madakemohekar *et al.* (2018), Swati *et al.* (2018), Panwar and Sharma (2019), Kumari *et al.* (2020), Kamboj *et al.* (2021) and Joshi *et al.* (2024).

In the current study, most of crosses showed changes in both the direction and the magnitude of SCA effects across variable environments, likely due to a significant SCA $\times$ Environment interaction. Estimates of the SCA effect revealed that, out of the forty five crosses, six cross in E_1 (JB 110 $\times$ RD 3005, BH 959 $\times$ RD 3005, DWRUB 64 $\times$ RD 2508, RD 2660 $\times$ F_1 , RD 2035 $\times$ RD 2508, and RD 2907 $\times$ RD 3005), six crosses in E_2 (RD 2660 $\times$ F_1 , DWRUB 64 $\times$ RD 2508, BH 959 $\times$ RD 3005, RD 2907 $\times$ RD 3005, RD 2552 $\times$ RD 2508, and BG 105 $\times$ RD 2508), and eleven crosses in E_3 (RD 2052 $\times$ RD 2508, RD 2035 $\times$ RD 2508, DWRB 137 $\times$ F_1 , RD 2907 $\times$ RD 3005, BH 959 $\times$ F_1 , BH 959 $\times$ RD 3005, HUB 113 $\times$ RD 3005, DWRUB 64 $\times$ F_1 , PL 751 $\times$ RD 2508, RD 2552 $\times$ RD 2508, and BG 105 $\times$ F_1) were found to be good specific combiners for grain yield per plant. Hence, the analysis of SCA effects in individual environment showed that the crosses with high SCA effect in a particular environment may be utilized for specific breeding conditions *viz.*, crosses with significant SCA effects in E_1 for early sown condition, in E_2 for normal sowing condition and in E_3 for late sowing (heat stress) condition.

In the current investigation, none of the crosses showed significant SCA effects for all the traits across all environments; instead, their effects varied across different traits in the three environments studied. Overall assessment of SCA effects showed that, among the 45 crosses, two crosses BH 959 $\times$ RD 3005 and RD 2907 $\times$ RD 3005 consistently showed high SCA effects for grain

yield per plant across all three environments. Additionally, the crosses DWRUB 64 $\times$ RD 2508 and RD 2660 $\times$ F_1 in E_1 and E_2 , RD 2035 $\times$ RD 2508 in E_1 and E_3 , and RD 2552 $\times$ RD 2508 in E_2 and E_3 showed significant SCA effects. The remaining crosses showed substantial SCA effects in only one of the environments studied (Table 4). In the present research, crosses also exhibited significant and desirable SCA effects for one or more traits. The crosses BH 959 $\times$ RD 3005 for effective tiller per plant, 1000- grain weight and the protein content and RD 2907 $\times$ RD 3005 for effective tiller per plant and protein content exhibited desirable SCA estimates constantly among all the environments.

Interestingly, the SCA effects of crosses and the GCA effects of their parents (Table 4) indicate that the good specific cross combinations resulted from good $\times$ good, good $\times$ poor, or poor $\times$ poor combinations. Thus, this study demonstrated that good cross combination does not necessarily require both parents to be good general combiners (good $\times$ good); it can also result from combinations involving at least one poor general combiner (good $\times$ poor or poor $\times$ poor). Therefore, cross combinations with good $\times$ good general combiner parents hold greater significance in self-pollinated crops like barley, where genes controlling these effects can potentially be fixed in final product of barley hybrid breeding programme. Similar findings were also supported by studies conducted by Sharma *et al.* (2002), Amiruzzaman *et al.* (2008), Madic *et al.* (2014), Kumar *et al.* (2015), Ram and Shekhawat (2017a), Rathore and Chauhan (2017), Swati *et al.* (2018), Panwar and Sharma (2019).

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Author's Contribution

All authors contributed to the manuscript.

Conflict of interest

No

Ethical Compliance Statement

NA



Declaration on the use of Generative AI or AI-assisted technologies in manuscript preparation

No

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