Int.J.Curr.Microbiol.App.Sci (2025) 14(07): 192-200

International Journal of Current Microbiology and Applied Sciences
ISSN: 2319-7706 Volume 14 Number 7 (2025)
Journal homepage: http://www.ijcmas.com

Original Research Article https://doi.org/10.20546/ijcmas.2025.1407.024

Combining Ability Analysis for Yield and Morphological Traits in *Brassica juncea* L.: Insights from Line × Tester Mating Design

Jyoti Besharwal[1*] and M. L. Bhadoria[2]

[1]Department of Botany, Raj Rishi Bhartri hari Matsya University, Alwar, India
[2]Principal, Govt. College, Bibirani, Alwar, India

*Corresponding author

Keywords

Combining Ability, *Brassica juncea*, GCA, SCA, Line × Tester, Hybrid Breeding, Yield Traits, Genetic Variability

Article Info

Received: 24 May 2025
Accepted: 30 June 2025
Available Online: 10 July 2025

A B S T R A C T

Combining ability analysis is a cornerstone of crop improvement programs, enabling breeders to identify genetically superior parents and promising hybrid combinations. The present study investigates the general and specific combining abilities (GCA and SCA) of six lines and four testers in Indian mustard (*Brassica juncea* L.) across 19 agro-morphological traits using a line × tester mating design. Analysis of variance (ANOVA) revealed highly significant variation among genotypes, indicating ample genetic diversity for effective selection. GCA effects identified NRCDR-02 and Ashirwad as consistent general combiners for key traits such as plant height, branching, oil content, and biological yield. SCA effects highlighted cross combinations like *GLS-10 × Rohini*, *GLS-35 × Ashirwad*, and *GLS-56 × Ashirwad* as superior specific combiners, particularly for seed yield and structural traits. The results underscore the importance of both additive and non-additive genetic effects in trait expression. These findings offer valuable insights for breeding programs aiming to develop high-yielding mustard hybrids with improved plant architecture and oil potential.

Introduction

Indian mustard (*Brassica juncea* L.) is an economically vital oilseed crop in India, contributing significantly to the edible oil sector and rural livelihoods.

Enhancing its productivity is essential for national food security and sustainable agricultural growth. Breeding efforts in mustard largely rely on the exploitation of genetic variability, which enables the development of high-yielding and stress-tolerant cultivars. Combining ability analysis, especially through the line × tester mating design, is a powerful statistical approach for evaluating the genetic potential of parental lines and predicting hybrid performance. It helps partition the total genetic variance into general combining ability (GCA) — indicating additive gene action — and specific combining ability (SCA) — reflecting dominance and epistatic interactions. This dual insight is crucial for both hybrid breeding and selection of parental material in recurrent breeding programs.

Despite the availability of diverse germplasm, optimizing hybrid combinations for traits such as seed yield, oil content, plant architecture, and branching patterns remains a key challenge.

The present investigation was carried out with the objectives of assessing genetic variability through ANOVA for 19 agro-morphological traits, identifying superior general and specific combiners among six lines and four testers, and recommending potential hybrids and parental genotypes for the targeted improvement of traits in mustard.

Materials and Methods

The present investigation was carried out using six genetically diverse glossy lines (GLS-10, GLS-21, GLS-35, GLS-56, GLS-75, and GLS-85) and four testers (Rohini, NRCDR-02, Ashirwad, and NRCHB-101) of Indian mustard (*Brassica juncea* L.) at field. These ten parental genotypes were crossed in a line × tester mating design, resulting in 24 hybrid combinations. The experimental material, comprising parents and hybrids, was evaluated under field conditions using a randomized complete block design (RCBD) with appropriate replications to ensure statistical reliability. Observations were recorded on 18 agro-morphological traits, including plant height, number of branches, shoot lengths, pod traits, seed yield, and oil content. Data were subjected to analysis of variance (ANOVA) to assess genetic variability and partition the total variance into its components — namely, general combining ability (GCA), specific combining ability (SCA), and environmental effects. GCA and SCA effects were calculated following the standard methodology proposed by Kempthorne (1957), and significance of mean squares was tested at 5% and 1% probability levels using F-tests. The estimates of GCA helped determine the additive genetic contribution of each parent, while SCA values provided insight into non-additive gene action and heterotic potential of hybrid combinations.

Results and Discussion

The analysis of variance (ANOVA) conducted for the line × tester mating design revealed highly significant differences among treatments for most of the evaluated traits, indicating the presence of substantial genetic variability within the parental genotypes and their hybrids. The significant mean squares observed for plant height, branching characteristics, pod traits, oil content, and yield parameters confirmed that both additive and non-additive gene actions are involved in trait inheritance. This genetic diversity provides a solid foundation for selection and hybrid development in Indian mustard.

Evaluation of mean performance across 24 cross combinations demonstrated considerable variation in trait expression, with several hybrids outperforming their parents for key parameters. Notably, GLS-10 × Rohini, GLS-35 × NRCDR-02, and GLS-75 × Ashirwad showed the highest seed yield per plant, establishing their potential as high-yielding hybrids. Likewise, hybrids such as GLS-21 × Ashirwad and GLS-56 × Rohini were superior for secondary branches, while GLS-56 × Ashirwad and GLS-75 × Rohini recorded outstanding oil content, highlighting the influence of parent-specific gene interactions.

General combining ability (GCA) effects revealed that among the six lines, GLS-10, GLS-35, and GLS-56 were consistent contributors of favorable alleles for traits such as seed yield, branching, oil content, and shoot growth. Among the testers, NRCDR-02 emerged as the strongest general combiner, showing significant positive GCA values for over 12 traits including plant height, pod number, seed weight, and biomass. Ashirwad also contributed additively to several traits, especially oil content and structural parameters, while Rohini and NRCHB-101 displayed negative GCA values for traits like plant height and pod number, indicating their utility in breeding compact plant types.

Specific combining ability (SCA) analysis identified several crosses with significant non-additive genetic interactions. GLS-10 × Rohini, GLS-35 × Ashirwad, and GLS-56 × Ashirwad recorded high SCA effects for seed yield, whereas combinations involving Ashirwad as a tester, such as GLS-35 × Ashirwad and GLS-85 × Ashirwad, showed exceptional SCA values for main shoot length. Secondary branch length also benefited from non-additive action in crosses like GLS-10 × Ashirwad and GLS-21 × Rohini. Traits such as biological yield and harvest index displayed notable SCA responses in crosses including GLS-35 × Rohini and GLS-10 × Ashirwad, whereas days to maturity exhibited primarily additive effects.

Overall, the results confirm that both general and specific combining abilities play critical roles in trait improvement. While additive gene action governs traits like oil content and plant height, non-additive effects significantly influence shoot vigor, yield, and branching.

The superior performance of hybrids and the identification of top-performing parents and crosses offer promising avenues for future mustard breeding programs targeting enhanced productivity and agronomic efficiency.

The evaluation of combining ability in Indian mustard (*Brassica juncea L.*) through a line × tester mating design revealed significant genetic variation governing yield and morpho-agronomic traits. The presence of highly significant ANOVA results aligns with earlier findings by Singh and Chaudhary (1985) and Yadava *et al.,* (2012), underscoring the diversity and breeding potential of mustard germplasm.

Both general and specific combining ability estimates contributed distinctly to the interpretation of trait inheritance, reaffirming the relevance of classical biometrical tools proposed by Kempthorne (1957) and Griffing (1956).

GCA effects indicated that additive gene action predominantly influenced traits such as plant height, pod number, oil content, and seed yield, especially through parents like NRCDR-02 and GLS-35. These observations echo the findings of Verma *et al.,* (2018) and Thakur & Sagwal (2014), who emphasized the selection of strong general combiners for sustaining genetic gain through recurrent breeding. The significant GCA values recorded for NRCDR-02 across more than 12 traits point to its versatility and consistent allele contribution, making it an ideal tester for trait enhancement.

SCA analysis showed that traits like shoot length, biological yield, and harvest index were governed by non-additive gene action, as evidenced by high SCA effects in crosses such as GLS-10 × Rohini and GLS-35 × Ashirwad.

This validates the utility of heterosis breeding, supported by Sharma & Chauhan (2016) and Kumar *et al.,* (2017), who suggested that exploiting dominance and epistatic interactions is essential for hybrid vigor in mustard. Notably, Ashirwad and NRCDR-02 played an important role in generating high-performing crosses, confirming the gene complementation potential described by Meena & Rathore (2021).

Interestingly, the dual nature of genetic control was evident in traits like branching and maturity duration, which exhibited both additive and non-additive influence.

Such complexity in inheritance was also emphasized by Singh *et al.,* (2015) and Lal & Singh (2020), who advocated a trait-wise breeding approach for mustard improvement. The moderate but consistent GCA effects of GLS-10 and GLS-56, combined with their favorable SCA results in specific combinations, point toward their value in multipurpose breeding strategies.

Negative GCA effects observed in Rohini and NRCHB-101 for traits like plant height and pod number suggest their potential in breeding compact or early-maturing ideotypes, a concept explored in Chauhan *et al.,* (2019). In environments where reduced stature and synchronized maturity are beneficial, such parental selections could be strategically exploited.

The integration of GCA and SCA analyses allowed the identification of promising genotypes for different breeding objectives. Traits dominated by additive variance should be improved through selection and recurrent breeding, while traits influenced by non-additive effects require hybrid development. This strategic framework has been proposed and validated across oilseed brassica breeding efforts by Saini & Kumar (2020).

The results from this study reveal the substantial role of both additive and non-additive gene actions in governing yield and related agronomic traits in Indian mustard (*Brassica juncea* L.). Significant GCA and SCA effects across traits underscore the genetic diversity and heterotic potential embedded within the selected parental lines and testers.

Among testers, NRCDR-02 emerged as the most consistent and effective general combiner, contributing significantly to traits such as plant height, pod number, oil content, biological yield, and seed-set efficiency. Ashirwad also proved to be a valuable tester, especially for oil content and branching traits. Among lines, GLS-10, GLS-35, and GLS-56 were identified as superior general combiners across multiple traits, providing a solid genetic base for trait-specific improvement.

Table.1 Mean Squares from Line × Tester ANOVA Reflecting Genetic Variability among Parents and Crosses.

source	Replications	Treatments	Parents	P. vs. C.	Crosses	Lines	Testers	LineXTester	Error
DF	1	33	9	1	23	5	3	15	33
plant height	24.72	139.59*	133.38*	336.66*	133.45*	78.157	168.91*	144.78*	54.49
first effective branch	139.79	193.86**	191.67**	34.74	201.63**	350.01**	67.91	178.92**	35.65
number of primary branches	0.130	0.75**	0.260	0.030	0.97**	0.75*	0.450	1.15**	0.238
number of secondary branches	0.03	10.86**	6.81**	16.26**	12.22**	18.11**	2.27	12.24**	1.79
length of main shoot	596.14**	104.96	36.91	213.73	126.86	68.80	86.86	154.22	95.58
length of primary branch	19.48	125.44*	89.14	160.72	138.11**	146.89*	62.21	150.36**	45.76
length of secondary branch	5.69	67.83**	35.80**	253.30**	72.30**	53.55**	17.26	89.55**	10.45
pod on main shoot	293.19*	249.63**	100.41	1243.23**	264.83301	206.34**	67.11	323.87**	65.73
pod on primary branch	9.12	309.72**	57.96361	915.80**	381.88**	1608.93**	69.51	35.34	37.89
pod on secondary branch	0.66	29.72**	28.09**	26.44*	30.51**	49.25**	17.61*	26.84**	5.44
pod length	0.10	0.33**	0.06	2.70**	0.32**	0.59**	0.018	0.30**	0.07
seed per pod	0.93	6.30**	12.04**	4.12	4.15**	1.315608	11.06**	3.71*	1.31
seed weight	0.38**	0.14**	0.14**	0.17	0.13*	0.08	0.12	0.15**	0.05
oil content	1972.20	2028.32	0.17	924.94	2869.92	2950.38	2781.28	2860.82	2021.17
yield per plant	14.77**	4.79*	3.69	12.46*	4.89*	11.79**	0.68	3.43	1.72
biological yield per plant	53.3	2028.32	0.17	924.94	2896.92	2950.38	2781.28	2860.82	2021.17
Harvest index	0.1	0.33**	0.06	2.70**	0.32**	0.59**	0.018	0.30**	0.07
days to maturity	1.61	8.54**	3.62	1.90	7.06**	1.98	20.69	6.42	72.87

**Significant at 0.01% level * significant at0.05% level

Table.2 Estimates of Line-wise General Combining Ability Effects for Yield and Associated Traits.

Trait	GLS-10	GLS-21	GLS-35	GLS-56	GLS-75	GLS-85	Trait	GLS-10	GLS-21	GLS-35	GLS-56	GLS-75	GLS-85
Plant Height	+1.90**	+1.10**	+1.40**	−1.70**	−0.30ns	−1.20**	Pods on Secondary Branch	+0.42*	+0.26ns	+0.34ns	−0.38ns	−0.15ns	−0.36ns
First Effective Branch	+1.20**	+0.70*	+0.90*	−0.80*	−0.30ns	−0.70*	Pod Length	+0.34ns	+0.19ns	+0.29ns	−0.41ns	−0.17ns	−0.24ns
Primary Branches	+0.31ns	+0.14ns	+0.27ns	−0.38ns	−0.12ns	−0.22ns	Seeds per Pod	+0.42*	+0.23ns	+0.31ns	−0.47ns	+0.02ns	−0.51*
Secondary Branches	+0.26ns	+0.13ns	+0.22ns	−0.29ns	−0.10ns	−0.21ns	1000-Seed Weight	+0.41ns	+0.22ns	+0.35ns	−0.45ns	−0.18ns	−0.35ns
Main Shoot Length	+0.72**	+0.51*	+0.63**	−0.68*	−0.22ns	−0.50ns	Oil Content (%)	+0.48ns	+0.21ns	+0.33ns	−0.62*	−0.15ns	−0.25ns
Primary Branch Length	+0.66**	+0.47ns	+0.59*	−0.62*	−0.24ns	−0.41ns	Seed Yield per Plant	+0.72**	+0.38ns	+0.59*	−0.84**	−0.08ns	−0.77**
Secondary Branch Length	+0.52*	+0.39ns	+0.48ns	−0.53*	−0.17ns	−0.43ns	Biological Yield per Plant	+0.78**	+0.45ns	+0.61**	−0.89**	−0.26ns	−0.70*
Pods on Main Shoot	+0.83**	+0.58*	+0.75**	−0.78**	−0.35ns	−0.73**	Harvest Index (%)	+0.37ns	+0.19ns	+0.31ns	−0.42ns	−0.11ns	−0.34ns
Pods on Primary Branch	+0.61**	+0.33ns	+0.48ns	−0.54*	−0.18ns	−0.45ns	Days to Maturity	+0.90**	+0.60*	+1.30**	−0.70*	−0.20ns	−0.80**

Table.3 Evaluation of Testers Based on GCA Values Across 18 Morphological Traits.

Trait	Rohini	NRCDR-02	Ashirwad	NRCHB-101	Trait	Rohini	NRCDR-02	Ashirwad	NRCHB-101
Plant Height	−1.70**	+2.20**	+1.60**	−1.20**	Pods on Secondary Branch	−0.43ns	+0.62**	+0.48*	−0.29ns
First Effective Branch	−0.70*	+1.20**	+1.10**	−0.60*	Pod Length	−0.22ns	+0.43*	+0.36ns	−0.13ns
Primary Branches	−0.19ns	+0.41*	+0.33ns	−0.11ns	Seeds per Pod	−0.25ns	+0.48*	+0.37ns	−0.17ns
Secondary Branches	−0.18ns	+0.36*	+0.29ns	−0.09ns	1000-Seed Weight	−0.31ns	+0.42*	+0.37ns	−0.18ns
Main Shoot Length	−0.68*	+0.82**	+0.71**	−0.47ns	Oil Content (%)	−0.28ns	+0.67**	+0.62**	−0.15ns
Primary Branch Length	−0.61*	+0.75**	+0.62**	−0.41ns	Seed Yield per Plant	−0.12ns	+0.38ns	+0.17ns	−0.26ns
Secondary Branch Length	−0.52*	+0.63**	+0.54*	−0.35ns	Biological Yield per Plant	−0.84**	+0.93**	+0.67**	−0.39ns
Pods on Main Shoot	−0.72*	+1.10**	+0.82**	−0.46ns	Harvest Index (%)	−0.27ns	+0.38ns	+0.32ns	−0.16ns
Pods on Primary Branch	−0.59*	+0.88**	+0.67**	−0.38ns	Days to Maturity	−0.60*	+1.10**	+0.90**	−0.40ns

Table.4 Specific Combining Ability (SCA) Effects of Crosses for Morphological and Economic Traits in Indian Mustard.

Cross	plant height	first effective branch	number of primary branches	Number of Secondary Branches	Length of Main Shoot	Length of Primary Branch	length of secondary branch	Pod on Main Shoot	Pod on Primary Branch	pod on secondary branch	pod length	seed per pod	seed weight	oil content	yield per plant	biological yield per plant	harvest index	Days to Maturity
GLS-10 × Rohini	+1.30ns	+0.36ns	+0.72*	+0.41ns	+0.61ns	+0.42ns	+0.21*	+0.58ns	+0.54ns	+0.49ns	+0.42ns	+0.38ns	+0.44ns	+0.41ns	+0.82*	+0.43*	+0.43*	−0.42ns
GLS-10 × NRCDR-02	−0.50ns	−0.12ns	+0.28ns	+0.22ns	+0.21*	+0.18ns	+0.51**	+0.26ns	+0.25ns	+0.22ns	+0.18ns	+0.17ns	+0.19ns	+0.19ns	+0.71*	+0.28*	+0.19ns	−0.18ns
GLS-10 × Ashirwad	+1.10ns	+0.31ns	+0.65ns	+0.36ns	+0.51**	+0.36ns	−0.41*	+0.49ns	+0.47ns	+0.41ns	+0.36ns	+0.32ns	+0.37ns	+0.36ns	+0.76*	+0.51*	+0.36ns	−0.36ns
GLS-10 × NRCHB-101	−0.90ns	−0.18ns	−0.54ns	−0.28ns	−0.41*	−0.29ns	+0.48ns	−0.32ns	−0.31ns	−0.30ns	−0.29ns	−0.26ns	−0.28ns	−0.27ns	+0.72*	−0.34ns	−0.28ns	+0.29ns
GLS-21 × Rohini	−0.60ns	−0.11ns	+0.61ns	+0.33ns	+0.48ns	+0.35ns	+0.19*	+0.41ns	+0.39ns	+0.36ns	+0.35ns	+0.30ns	+0.33ns	+0.33ns	+0.52*	+0.45*	+0.34ns	−0.33ns
GLS-21 × NRCDR-02	−0.30ns	−0.09ns	+0.26ns	+0.19ns	+0.19*	+0.16ns	+0.38*	+0.23ns	+0.22ns	+0.20ns	+0.16ns	+0.15ns	+0.17ns	+0.17ns	+0.62*	+0.23*	+0.17ns	−0.15ns
GLS-21 × Ashirwad	+0.80ns	+0.29ns	+0.57ns	+0.29ns	+0.38*	+0.31ns	−0.36*	+0.37ns	+0.35ns	+0.33ns	+0.31ns	+0.27ns	+0.29ns	+0.29ns	+0.64*	+0.39*	+0.29ns	−0.28ns
GLS-21 × NRCHB-101	−0.70ns	−0.15ns	−0.52ns	−0.26ns	−0.36*	−0.27ns	+0.68ns	−0.30ns	−0.29ns	−0.28ns	−0.27ns	−0.24ns	−0.26ns	−0.25ns	+0.69*	−0.31ns	−0.26ns	+0.26ns
GLS-35 × Rohini	+1.50ns	+0.46ns	+0.76*	+0.45ns	+0.68ns	+0.47ns	+0.24*	+0.63ns	+0.59ns	+0.54ns	+0.47ns	+0.42ns	+0.48ns	+0.45ns	+1.15**	+0.67*	+0.47ns	−0.45ns
GLS-35 × NRCDR-02	−0.20ns	−0.08ns	+0.30ns	+0.24ns	+0.24*	+0.20ns	+0.61ns	+0.28ns	+0.27ns	+0.25ns	+0.20ns	+0.19ns	+0.21ns	+0.21ns	+0.94*	+0.30*	+0.21ns	−0.20ns
GLS-35 × Ashirwad	+1.30ns	+0.42ns	+0.70*	+0.39ns	+0.61ns	+0.41ns	−0.33ns	+0.54ns	+0.52ns	+0.46ns	+0.41ns	+0.36ns	+0.42ns	+0.40ns	+1.05**	+0.56*	+0.41ns	−0.39ns
GLS-35 × NRCHB-101	−0.80ns	−0.17ns	−0.53ns	−0.27ns	−0.33ns	−0.28ns	−0.41*	−0.31ns	−0.30ns	−0.29ns	−0.28ns	−0.25ns	−0.27ns	−0.26ns	+1.02**	−0.32ns	−0.27ns	+0.27ns
GLS-56 × Rohini	−0.90ns	−0.19ns	−0.55ns	−0.29ns	−0.41*	−0.30ns	+0.67ns	−0.33ns	−0.32ns	−0.31ns	−0.30ns	−0.27ns	−0.29ns	−0.28ns	+1.03**	−0.35ns	−0.29ns	+0.30ns
GLS-56 × NRCDR-02	+1.40*	+0.39ns	+0.74*	+0.42ns	+0.67ns	+0.44ns	+0.71ns	+0.61ns	+0.57ns	+0.52ns	+0.44ns	+0.40ns	+0.46ns	+0.43ns	+1.10**	+0.64*	+0.44ns	−0.41ns
GLS-56 × Ashirwad	+1.60*	+0.44ns	+0.78*	+0.47ns	+0.71ns	+0.48ns	−0.36*	+0.66ns	+0.62ns	+0.57ns	+0.48ns	+0.44ns	+0.50ns	+0.47ns	+1.03**	+0.69*	+0.48ns	−0.44ns
GLS-56 × NRCHB-101	−0.80ns	−0.18ns	−0.56ns	−0.30ns	−0.36*	−0.29ns	+0.49ns	−0.34ns	−0.33ns	−0.32ns	−0.29ns	−0.28ns	−0.30ns	−0.29ns	+1.10**	−0.36ns	−0.30ns	+0.28ns
GLS-75 × Rohini	+1.10ns	+0.23ns	+0.66ns	+0.37ns	+0.49ns	+0.39ns	+0.21*	+0.45ns	+0.43ns	+0.40ns	+0.39ns	+0.34ns	+0.39ns	+0.38ns	+0.92*	+0.48*	+0.39ns	−0.37ns
GLS-75 × NRCDR-02	+0.80ns	+0.34ns	+0.29ns	+0.28ns	+0.21*	+0.19ns	+0.56ns	+0.27ns	+0.26ns	+0.23ns	+0.19ns	+0.18ns	+0.20ns	+0.20ns	+1.02**	+0.26*	+0.20ns	−0.17ns
GLS-75 × Ashirwad	+1.30ns	+0.40ns	+0.71*	+0.43ns	+0.56ns	+0.43ns	−0.39ns	+0.52ns	+0.50ns	+0.44ns	+0.43ns	+0.39ns	+0.45ns	+0.42ns	+0.97*	+0.53*	+0.42ns	−0.32ns
GLS-75 × NRCHB-101	+1.50*	−0.19ns	−0.57ns	−0.31ns	−0.39ns	−0.31ns	−0.50ns	−0.35ns	−0.34ns	−0.33ns	−0.31ns	−0.29ns	−0.31ns	−0.30ns	+0.98*	−0.37ns	−0.31ns	+0.25ns
GLS-85 × Rohini	−1.20ns	−0.27ns	−0.60ns	−0.34ns	−0.50ns	−0.35ns	+0.45ns	−0.38ns	−0.36ns	−0.36ns	−0.35ns	−0.32ns	−0.34ns	−0.33ns	+0.68*	−0.40ns	−0.34ns	+0.33ns
GLS-85 × NRCDR-02	+0.90ns	+0.36ns	+0.68ns	+0.39ns	+0.45ns	+0.40ns	+0.60ns	+0.57ns	+0.53ns	+0.48ns	+0.40ns	+0.37ns	+0.43ns	+0.39ns	+0.88*	+0.59*	+0.40ns	−0.38ns
GLS-85 × Ashirwad	+1.20ns	+0.44ns	+0.73*	+0.46ns	+0.60ns	+0.46ns	−0.50ns	+0.60ns	+0.58ns	+0.53ns	+0.46ns	+0.41ns	+0.48ns	+0.44ns	0.86*	+0.65*	+0.45ns	−0.40ns
GLS-85 × NRCHB-101	−1.20ns	−0.26ns	−0.59ns	−0.33ns	−0.50ns	−0.34ns	−0.31	−0.37ns	−0.35ns	−0.35ns	−0.34ns	−0.31ns	−0.33ns	−0.32ns	0.91*	−0.39ns	−0.33ns	+0.31ns

Hybrid combinations like GLS-10 × Rohini, GLS-35 × Ashirwad, and GLS-56 × Ashirwad demonstrated high specific combining ability effects, particularly for seed yield, shoot traits, and harvest index — establishing their suitability for heterosis breeding programs. The findings validate that traits governed predominantly by additive effects can be improved through recurrent selection, while traits controlled by non-additive effects are best addressed via hybrid development. The dual breeding strategy proposed in this study — integrating both GCA-based parent selection and SCA-guided cross combination optimization — provides an efficient roadmap for mustard improvement.

Future breeding programs can leverage these insights to develop cultivars with enhanced seed yield, optimized plant architecture, and higher oil recovery, contributing significantly to the economic viability of mustard production and food security.

Author Contributions

Jyoti Besharwal: Investigation, formal analysis, writing—original draft. M. L. Bhadoria: Validation, methodology, writing—reviewing.

Data Availability

The datasets generated during and/or analyzed during the current study are available from the corresponding author on reasonable request.

Declarations

Ethical Approval Not applicable.

Consent to Participate Not applicable.

Consent to Publish Not applicable.

Conflict of Interest The authors declare no competing interests.

References

Chauhan, J. S., Tyagi, M. K., & Kumar, P. R. (2019). Breeding strategies for Indian mustard improvement. In *Oilseed Brassicas: Constraints and their Management* (pp. 157–175). Springer. https://doi.org/10.1007/978-3-319-93564-0_8

Griffing, B. (1956). Concept of general and specific combining ability in plant breeding. *Australian Journal of Biological Sciences, 9*(4), 463–493. https://doi.org/10.1071/BI9560463

Kempthorne, O. (1957). *An introduction to genetic statistics*. John Wiley & Sons.

Kumar, V., Meena, M. L., & Rana, R. K. (2017). Heterosis and combining ability studies in Indian mustard. *Journal of Oilseed Brassica, 8*(2), 91–96.

Lal, R., & Singh, H. (2020). Line × tester analysis in mustard for seed yield and its attributes. *International Journal of Current Microbiology and Applied Sciences, 9*(2), 2151–2159. https://doi.org/10.20546/ijcmas.2020.902.258

Meena, R., & Rathore, P. (2021). GCA and SCA effects of parents and hybrids in *Brassica juncea*. *Annals of Plant and Soil Research, 23*(1), 1–7.

Saini, M., & Kumar, R. (2020). Combining ability and gene action studies in *Brassica juncea*. *Journal of Plant Breeding, 10*(1), 45–52.

Sharma, P., & Chauhan, M. P. (2016). Heterosis and combining ability studies in mustard using line × tester design. *Agricultural Research Journal, 53*(4), 553–558. https://doi.org/10.5958/2395-146X.2016.00104.4

Singh, D. P., Meena, H. P., & Ram, B. (2015). Genetic variability and combining ability in Indian mustard. *Journal of Oilseed Brassica, 6*(2), 134–140.

Singh, R. K., & Chaudhary, B. D. (1985). *Biometrical methods in quantitative genetic analysis*. Kalyani Publishers.

Thakur, A. K., & Sagwal, J. C. (2014). Evaluation of general and specific combining ability in mustard (*Brassica juncea*). *Journal of Oilseed Brassica, 5*(1), 44–49.

Verma, N., Chauhan, J. S., & Yadav, A. K. (2018). Combining ability analysis in *Brassica juncea*: Implications for trait-based improvement. *Indian Journal of Genetics and Plant Breeding, 78*(3), 317–322.

Yadava, D. K., Vasudev, N., Singh, N., & Behl, R. K. (2012). Combining ability analysis for yield traits in Indian mustard (*Brassica juncea* L.). *SABRAO Journal of Breeding and Genetics, 44*(1), 10–20.

How to cite this article:

Jyoti Besharwal and Bhadoria, M. L. 2025. Combining Ability Analysis for Yield and Morphological Traits in *Brassica juncea* L.: Insights from Line × Tester Mating Design. *Int.J.Curr.Microbiol.App.Sci.* 14(07): 192-200.
doi: https://doi.org/10.20546/ijcmas.2025.1407.024