ANSF®
APPLIED AND NATURAL SCIENCE FOUNDATION
Boundless Science

Journal of Applied and Natural Science
17(1), 277 - 284 (2025)
ISSN : 0974-9411 (Print), 2231-5209 (Online)
journals.ansfoundation.org

Research Article

Identification of most prominent parents and cross combinations in indian mustard for seed yield and quality traits

Durga Prasad*
Department of Genetics and Plant Breeding, School of Agriculture, Lovely Professional University, Phagwara- 144411 (Punjab), India
Rajendra Kumar Yadav
Department of Genetics and Plant Breeding, Chandra Shekhar Azad University of Agriculture &Technology, Kanpur-208 002 (Uttar Pradesh) India
Shiv Prakash Shrivastav
Department of Genetics and Plant Breeding, School of Agriculture, Lovely Professional University, Phagwara- 144411 (Punjab), India
Mohammad Amir
Department of Genetics and Plant Breeding, School of Agriculture, Lovely Professional University, Phagwara- 144411 (Punjab), India
Deshraj Gurjar
Department of Genetics and Plant Breeding, School of Agriculture, Lovely Professional University, Phagwara- 144411 (Punjab), India
Kanhaiya lal
Department of Genetics and Plant Breeding, Chandra Shekhar Azad University of Agriculture &Technology, Kanpur-208 002 (Uttar Pradesh) India

*Corresponding author. Email: dpchaudhary.agri03@gmail.com

Article Info
https://doi.org/10.31018/jans.v17i1.5669
Received: April 21, 2024
Revised: February 22, 2025
Accepted: February 28, 2025

How to Cite

Prasad, D. *et al.* (2025). Identification of most prominent parents and cross combinations in indian mustard for seed yield and quality traits. *Journal of Applied and Natural Science*, 17(1), 277 - 284. https://doi.org/10.31018/jans.v17i1.5669

Abstract

Indian mustard is an important oilseed crop with significant economic and nutritional value. Understanding the genetic mechanisms governing key traits like seed yield is crucial for developing high-yielding varieties. This study aimed to evaluate the general combining ability (GCA) of parental lines and the specific combining ability (SCA) of their cross combinations to improve yield potential. A diallel model (excluding reciprocals) was used, involving 45 hybrids (F1's) produced by crossing 10 diverse genotypes: Aashirwad, Basanti, NDR501-26, Rohini, KMR17-5-21, KMR17-5-22, KMR17-5-23, N8501, PR20, and PR21. These hybrids were developed during the Rabi season of 2018-19 and evaluated in the 2019-2020 Rabi season using a Randomized Complete Block Design (RCBD) with three replications at the Student Instructional Farm of CSAUA&T, Kanpur. The study assessed GCA and SCA effects, focusing on additive and non-additive gene actions in trait inheritance. The results showed that SCA variance exceeded GCA variance across all traits, with a predictability ratio and GCA/SCA ratio of less than one, indicating a dominance of non-additive gene action. While GCA variance was high for most traits except primary branches and 1000-seed weight, SCA effects were more significant for traits like maturity days, siliquae per plant, 1000-seed weight, oil yield, and seed yield. Parents like NDR 501-26 and Rohini demonstrated strong GCA effects, making them suitable for breeding. Specific crosses, such as KMR 17-5-22 × KMR 17-5-21 and NDR 501-26 × Rohini, showed desirable SCA effects, suggesting potential for early-maturing and high-yielding hybrids. These findings highlight the potential of heterosis breeding and the use of non-additive gene action for improving Indian mustard yield, offering insights to meet agricultural demands.

Keywords: Diallel, Genetic variance, GCA, SCA and *Brassica juncea* L.

INTRODUCTION

In India, the primary oilseed crops include soybean, peanut, mustard, sesame, sunflower, castor seed, safflower, linseed, and niger seed. According to the Ministry of Agriculture & Farmers Welfare (2022-23), soybean leads in oilseed production, contributing 35% of the total output, followed by rapeseed-mustard at 32% and groundnut at 25%, with the remaining oilseed crops collectively contributing only 8%. In terms of acreage, soybeans dominate 44% of the total area dedicated to oilseed crops, rapeseed-mustard accounts for 24%, and groundnut covers 20%. On average, *kharif* crops contribute 67% to the total oilseed production, while the remaining 33% is produced during the rabi season. Cytologically, *Brassica juncea* L. (Indian mustard) is an amphidiploid (2n=4x=36), resulting from the hybridization of B. campestris L. (2n=2x=20) and B. nigra L. (2n=2x=16), followed by chromosome doubling (Tomar and Singh, 2015). The third advance estimate from the Ministry of Agriculture and Farmers Welfare (DAC and FW 2022-23) predicts a record total oilseed production of 40.9 million metric tonnes (MT) for the nation, including record outputs of soybean, mustard, and peanut. Soybean production is expected to reach 14.9 MT, and both rapeseed-mustard and peanut are projected to produce 12.4 MT each, representing increases of 1.9 MT and 0.5 MT, respectively, over the previous year.

Globally, India leads in the area covered with oilseeds, although the yield of most Indian oilseed crops is below the global average. Despite this, the demand for edible oils in India is expected to rise significantly due to population growth, projected to reach 28.40 MT by 2030 and 41.6 MT by 2050 (Kumar, 2017). To further increase yields, it is essential to develop improved high-yielding cultivars. Effective hybridization programs rely on identifying superior parents and understanding their combining behavior to produce desirable segregants, as hybridization is a fundamental mechanism for overcoming yield barriers (Sheera *et al*., 2024). Therefore, the first step in creating superior, high-yielding varieties is to identify these superior parents (Prasad, 2014; Sheera *et al*., 2022).

The present study aimed to evaluate genetic variance components, including general combining ability (GCA) and specific combining ability (SCA) variances and their effects in Indian mustard. Combining ability analysis highlighted the significant impact of GCA on seed yield and quality traits, indicating the predominance of additive gene action. Conversely, SCA effects on seed yield and quality traits underscored the importance of non-additive gene action.

MATERIALS AND METHODS

Ten diverse genotypes were used to generate forty-five single cross hybrids using a half-diallel crossing scheme at the Student Instructional Farm of CSA-UA&T, Kanpur, during the *Rabi* season 2018-19. The details of diverse genotypes used in the experiment are listed in Table 1, along with their sources and characteristics. Forty-five F1 single cross progenies, their parents and one check cultivar were planted during the *Rabi* season 2019-20 using a randomized complete block design in three replications with each row being 3 meters long and 45 cm apart, and a plant-to-plant distance of 20 cm was maintained during thinning. Each plot had two rows. The border row was placed at both ends of each replication/block to reduce the border effect. Agronomic practices, including fertilizer application, weeding, and pest control, were carried out following the standard recommendations.

Data were collected from five randomly selected plants in each treatment (parents and F□ hybrids) for morpho-physiological and biochemical traits. The recorded traits included plant height (cm), leaf area index, number of primary and secondary branches, main raceme length (cm), number of siliques per plant, seed yield per plant (g), 1000-seed weight (g), harvest index (%), oil content (%), protein content (%), erucic acid (%), and total glucosinolate content (µmol/g). The determination of fatty acid composition, including erucic acid (%) and total glucosinolate content (µmol/g), was performed using

Table 1. Parental genotypes, their sources, and characteristic features

S.N.	Genotype	Source	Characteristics of Genotype
1	Aashirwad	CSAUT, Kanpur	Maturity (125-130 days), oil content (37-41%), medium seed size
2	NDR 501-26	ANDAUT, Ayodhya	Days to maturity (128-131), oil content (40-41%)
3	Rohini	CSAUT, Kanpur	Medium plant height, medium maturity, shattering resistant, medium seed size
4	Basanti	CSAUT, Kanpur	Days to maturity (130-135 days), oil content (40-42%)
5	KMR 17-5-23	CSAUT, Kanpur	Bold seed size, tall plant height
6	KMR 17-5-22	CSAUT, Kanpur	Bold seed size, black seed
7	KMR 17-5-21	CSAUT, Kanpur	Medium maturity, bold seed
8	Narendra Rai 8501 (N 8501)	ANDUT, Ayodhya	Medium maturity, brown seed color
9	PR 21	GBPUT, Pantnagar	Medium maturity, oil content (40-42%), tall plant height, medium seed size
10	PR-20	GBPUT, Pantnagar	Medium maturity, tall plant height

CSAUAT- Chandra Shekhar Azad University of Agriculture and technology, Kanpur; ANDUAT- Acharya Narendra Deva University Of Agriculture And Technology; GBPUAT- Govind Ballabh Pant University of Agriculture and Technology

Gas-Liquid Chromatography (GLC) as per the methodology described by Ostrikov et al. (2020). Additionally, plot-based data were recorded for days to 50% flowering and days to maturity. Genetic variance components were estimated following the procedures outlined by Hayman (1954), while combining ability analysis was performed using Griffing's (1956) Model I, Method II. Statistical calculations were carried out using INDOSTAT software and Microsoft Excel.

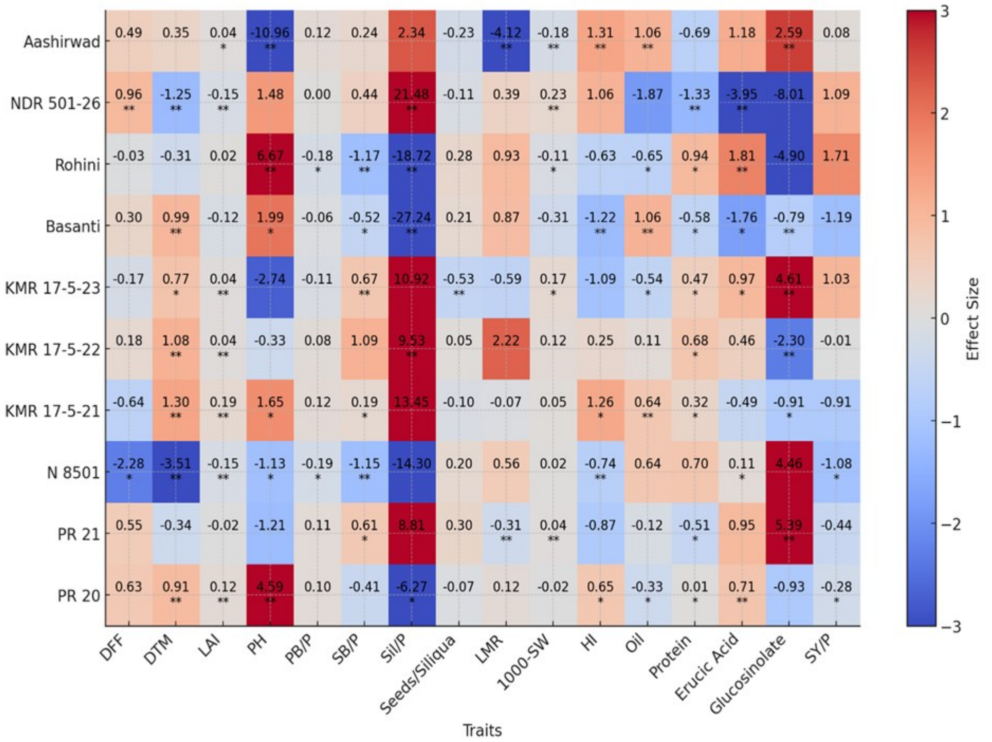
RESULTS AND DISCUSSION

The analysis of variance for combining ability (Table 2) revealed significant genetic variation for most of the traits studied, with both GCA and SCA highly significant ($P < 0.01$). This indicates the involvement of both additive and non-additive genetic effects. Significant GCA effects for traits like plant height and siliquae suggest potential for improvement through selection, while significant SCA effects for seed yield point to the benefits of hybrid breeding. However, the number of primary branches per plant and number of seeds per siliqua displayed an exception in this pattern, as GCA did not reach significance, reflecting the predominance of non-additive gene action. The low error variances ensure reliable estimates, highlighting the need for targeted breeding strategies based on the genetic nature of each trait. Similarly, previous studies by Singh *et al.* (2019) and Rout *et al.* (2025) also observed significant mean squares for GCA and SCA across various morphological and seed yield traits in brown mustard.

The estimates of genetic variance components, including general combining ability (GCA) and specific combining ability (SCA) variances, as well as additive and dominance variances, predictability ratio, and GCA/SCA ratio, are presented in Table 1. Across all traits, SCA variance consistently exceeded GCA variance, while the predictability ratio and GCA/SCA ratio were less than 1. These findings indicate a predominance of non-additive gene action in the inheritance of the studied traits in Indian mustard, aligning with the observations of Patel *et al.* (2015) and Chand *et al.* (2022).

The general combining ability variance was notably high for nearly all traits except primary branches and 1000-seed weight, suggesting that both additive and non-additive genes significantly influence the inheritance of these traits (Table 3 and Figure 1). Specific combining ability contributed more significantly to traits such as maturity days, number of siliquae per plant, 1000-seed weight, oil yield, and seed yield, as evidenced by the higher mean sum of squares. Negative *gca* effects are considered desirable for traits like days to 50% flowering, days to maturity, erucic acid, and glucosinolate levels. Conversely, for the remaining traits, parents showing positive *gca* effects were regarded as good combiners (Patel *et al*., 2013; Barfa *et al*., 2017).

The consistent performance of good combiners reflects



	DFF	DTM	LAI	PH	PB/P	SB/P	Sil/P	Seeds/Siliqua	LMR	1000-SW	HI	Oil	Protein	Erucic Acid	Glucosinolate	SY/P
Aashirwad	0.49	0.35	0.04 *	-10.96 **	0.12	0.24	2.34	-0.23	-4.12 **	-0.18 **	1.31 **	1.06 **	-0.69	1.18	2.59 **	0.08
NDR 501-26	0.96 **	-1.25 **	-0.15 **	1.48	0.00	0.44	21.48 **	-0.11	0.39	0.23 **	1.06	-1.87	-1.33 **	-3.95 **	-8.01	1.09
Rohini	-0.03	-0.31	0.02	6.67 **	-0.18 *	-1.17 **	-18.72 **	0.28	0.93	-0.11 *	-0.63	-0.65 *	0.94 *	1.81 **	-4.90	1.71
Basanti	0.30	0.99 **	-0.12	1.99 *	-0.06	-0.52 *	-27.24 **	0.21	0.87	-0.31	-1.22 **	1.06 **	-0.58 *	-1.76 *	-0.79 **	-1.19
KMR 17-5-23	-0.17	0.77 *	0.04 **	-2.74	-0.11	0.67 **	10.92	-0.53 **	-0.59	0.17 *	-1.09	-0.54 *	0.47 *	0.97 *	4.61 **	1.03
KMR 17-5-22	0.18	1.08 **	0.04 **	-0.33	0.08	1.09	9.53 **	0.05	2.22	0.12	0.25	0.11	0.68 *	0.46	-2.30 **	-0.01
KMR 17-5-21	-0.64	1.30 **	0.19 **	1.65 *	0.12	0.19 *	13.45	-0.10	-0.07	0.05	1.26 *	0.64 **	0.32 *	-0.49	-0.91 *	-0.91
N 8501	-2.28 *	-3.51 **	-0.15 **	-1.13 *	-0.19 *	-1.15 **	-14.30	0.20	0.56	0.02	-0.74 **	0.64	0.70	0.11 *	4.46	-1.08 *
PR 21	0.55	-0.34	-0.02	-1.21	0.11	0.61 *	8.81	0.30	-0.31 **	0.04 **	-0.87	-0.12	-0.51 *	0.95	5.39 **	-0.44
PR 20	0.63	0.91 **	0.12 **	4.59 **	0.10	-0.41	-6.27 *	-0.07	0.12	-0.02	0.65 *	-0.33 *	0.01 *	0.71 **	-0.93	-0.28 *

Fig. 1. *GCA estimates for different genotypes and traits, with significance levels (* at 5% and ** at 1% probability). Traits include DFF - Days to 50% flowering, DTM - Days to maturity, LAI - Leaf area index, PH - Plant height, PB/P - Primary branches per plant, SB/P - Secondary branches per plant, Sil/P - Siliqua per plant, Seeds per siliqua, LMR - Length of main raceme, 1000-SW - Seed weight, HI - Harvest index, and SY/P - Seed yield per plant*

Table 2. Analysis of variance for sixteen characters for combining ability in 10 × 10 diallel model in Indian mustard

Characters	**GCA**	**SCA**	**Error**
	9	45	108
Days to 50% flowering	10.22 **	4.26 **	1.54
Days to maturity	25.96 **	10.03 **	1.44
Leaf Area Index	0.15 **	0.12 **	0.003
Plant Height	272.90 **	127.10 **	10.39
No. of Primary branches per plant	0.196	0.282 **	0.1
No. of secondary branches per plant	7.25 **	7.60 **	0.84
No. of siliquae per plant	3029.18 **	1610.64 **	97.1
No. of seeds per siliqua	0.82	2.17 **	0.422
Leaf of main raceme (cm)	32.67 **	28.37 **	8.51
1000-seed weight (m)	0.32 **	0.46 **	0.03
Harvest Index (%)	12.40 **	5.69**	0.61
Oil Content (%)	9.88 **	6.77 ***	0.97
Protein content (%)	6.68 **	6.82 **	0.54
Erucic Acid (%)	34.95 **	19.73 **	0.31
Total Glucosinolate (µmol/g)	229.72**	318.09**	2.82
Seed Yield per Plant (g)	11.80 **	11.62 **	0.92

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

stability across generations, possibly due to diversity in parents with significant desirable and high *gca* effects (Table 3). Parent NDR 501-26 showed desirable and substantial *gca* effects for days to 50% flowering. Similarly, other parents demonstrated commendable and statistically significant *gca* effects for distinct traits: N 8508 for days to maturity, Aashirwad and Basanti for oil content, Rohini for protein percent, Aashirwad and KMR 17-5-23 for erucic acid content, NDR 501-26 for total glucosinolate content, and Rohini and NDR 501-26 emerged as good combiners for seed yield. Parents with *good gca* can potentially transmit additive genes in the desired way to their hybrids. Therefore, Rohini and NDR 501-26 parents can be considered a good source of favourable genes for increasing seed yield and other yield attributes. Thus, using these parental lines in hybridization programs would be worthwhile. Previous studies by Nassimi *et al.* (2006), Aher *et al.* (2009), Akabari *et al.* (2017), and Srivastava *et al.* (2022) exposed comparable findings.

Assessments of SCA effects (Table 5) revealed significant desirable SCA effects for crosses such as KMR 17-5-22 × KMR 17-5-21, Basanti × KMR 17-5-23, and NDR 501-26 × Rohini, which can be used to isolate early maturing crosses in later generations. For erucic acid, negative and desirable SCA effects were recorded for crosses such as N 8501 × PR 21, KMR 17-5-23 × KMR 17-5-22, and NDR 501-26 × PR 21. Substantial and desirable SCA effects were recorded for NDR 501-26 × Rohini, KMR 17-5-23 × PR 20, and Aashirwad × KMR 17-5-22 for glucosinolate content. The top cross combinations for oil content were Aashirwad × PR 21, Aashirwad × KMR 17-5-23, and N 8501 × PR 20. Significant and positive SCA effects were observed for protein content in Aashirwad × PR 21, NDR 501-26 × Basanti, and NDR 501-26 × KMR 17-5-21. The SCA effect of the best crosses for the key traits is visually represented in Fig. 2. The crosses exhibiting significant SCA effects are anticipated to produce transgressive segregants in subsequent segregating generations. Therefore, these crosses hold the potential for enhancing yield and specific yield-contributing traits through selective breeding. Significant positive SCA effects on seed yield and its important yield component traits have also been reported by Vaghela *et al*. (2014), Kumar *et al*. (2015), Kaur *et al*. (2019), Tel *et al*. (2014).

The cross combinations KMR 17-5-23 × N 8501, Rohini × KMR 17-5-21, and KMR 17-5-23 × PR 20 exhibited a positive and significant SCA effect on seed yield. This indicates that most characters closely associate their performance and parental *gca* effects. However, crosses displaying significant and desirable SCA effects for different traits involved parents with diverse combinations of gca effects. These combinations consisted of pairs of general combiner parents categorized as high × high (H × H), high × average (H × A), high × low (H × L), average × average (A × A), average × low (A × L), and low × low (L × L) (Shrivastav et al. 2022). High *gca* effects observed in cross combinations, whether involving both parents or just one, suggest the influence of additive gene action in trait expression. These cross-combinations are likely to produce transgressive segre-

Table 3. Estimate of components of genetic variance and related parameter of half diallel crosses in Indian mustard

Source of variation	Days to 50% flowering	Days to maturity	Leaf Area Index	Plant Height (cm)	No. of Primary branches per plant	No. of secondary branches per plant	No. of siliquae per plant	No. of seeds per siliqua	Length of main raceme (cm)	1000-seed weight (g)	Harvest Index (%)	Oil Content (%)	Protein content (%)	Erucic Acid (%)	Total Glucosinolate (µmol/g)	Seed Yield per Plant (g)
σ^2GCA	0.72	2.04	0.01	21.88	0.01	0.53	244.34	0.03	2.01	0.02	0.98	0.74	0.51	2.89	18.91	0.91
σ^2SCA	2.72	8.59	0.12	116.75	0.18	6.77	1513.50	1.75	19.86	0.43	5.07	5.80	6.28	19.42	315.27	10.70
σ^2A	1.45	4.09	0.03	43.75	0.02	1.07	488.68	0.07	4.03	0.05	1.96	1.49	1.03	5.77	37.82	1.81
σ^2D	2.72	8.59	0.12	116.72	0.18	6.77	1513.53	1.75	19.86	0.43	5.07	5.80	6.28	19.42	315.27	10.70
GPR	0.35	0.32	0.18	0.27	0.08	0.14	0.24	0.04	0.17	0.10	0.28	0.20	0.14	0.23	0.11	0.15
GCA/SCA Ratio	0.27	0.24	0.11	0.19	0.04	0.08	0.16	0.02	0.10	0.06	0.19	0.13	0.08	0.15	0.06	0.09

σ^2GCA=gca variance, σ^2SCA= SCA variance, $\sigma^2 A$ =additive genetic variance, $\sigma^2 D$ =Dominance genetic variance, GPR=General predictability ratio

Table 4. General combining ability effects for 10 parents in for sixteen traits in Indian mustard

Source of variation	Days to 50% flowering	Days to maturity	Leaf Area Index	Plant Height (cm)	No. of Primary branches per plant	No. of secondary branches per plant	No. of siliquae per plant	No. of seeds per siliqua	Length of main raceme (cm)	1000-seed weight (g)	Harvest Index (%)	Oil Content (%)	Protein content (%)	Erucic Acid (%)	Total Glucosinolate (µmol/g)	Seed Yield per Plant (g)
Aashirwad	0.49	0.35	0.04*	-10.96**	0.12	0.24	2.34	-0.23	-4.12**	-0.18**	1.31**	1.06**	-0.69**	1.18**	2.59**	0.08
NDR 501-26	0.96**	-1.25**	-0.15**	1.48	0.00	0.44	21.48**	-0.11	0.39	0.23**	1.06**	-1.87**	-1.33**	-3.95**	-8.01**	1.09**
Rohini	-0.03	-0.31	0.02	6.67**	-0.18*	-1.17**	-18.72**	0.28	0.93	-0.11	-0.63*	-0.65*	0.94**	1.81**	-4.9**	1.71**
Basanti	0.30	0.99**	-0.12**	1.99*	-0.06	-0.52*	-27.24**	0.21	0.87	-0.31**	-1.22**	1.06**	-0.58*	-1.76**	-0.79	-1.19**
KMR 17-5-23	-0.17	0.77*	0.04**	-2.74**	-0.11	0.67**	10.92**	-0.53**	-0.59	0.17**	-1.09**	-0.54*	0.47*	0.97**	4.61**	1.03**
KMR 17-5-22	0.18	1.08**	0.04**	-0.33	0.08	1.09**	9.53**	0.05	2.22**	0.12	0.25	0.11	0.68**	0.46*	-2.30**	-0.01
KMR 17-5-21	-0.64	1.30**	0.19**	1.65	0.12	0.19	13.45**	-0.10	-0.07	0.05	1.26**	0.64*	0.32	-0.49*	-0.06	-0.91**
N 8501	-2.28*	-3.51**	-0.15**	-1.13	-0.19*	-1.15**	-14.3**	0.20	0.56	0.02	-0.74**	0.64*	0.70**	0.11	4.46**	-1.08**
PR 21	0.55	-0.34	-0.02	-1.21	0.11	0.61*	8.81*	0.30	-0.31	0.04	-0.87**	-0.12	-0.51	0.95**	5.39**	-0.44
PR 20	0.63	0.91**	0.12**	4.59**	0.10	-0.41	-6.27*	-0.07	0.12	-0.02	0.65*	-0.33	0.01	0.71**	-0.93	-0.28
SE(gi)+	0.76**	0.74**	0.03**	1.99**	0.20**	0.57**	6.10*	0.40**	1.80**	0.11**	0.49**	0.61**	0.45**	0.35**	1.04**	0.59**
SE (gi-gj)+	1.14**	1.11**	0.05**	2.97**	0.30**	0.84**	2.34	-0.23	2.69**	0.16**	0.73**	0.91**	0.68**	0.52**	1.55**	0.89**

σ^2GCA=gca variance, σ^2SCA= SCA variance, $\sigma^2 A$ =additive genetic variance, $\sigma^2 D$ =Dominance genetic variance, GPR=General predictability ratio

Table 5. Estimates of SCA effects of top three cross combinations for sixteen characters in Indian mustard

Characters	Top three cross-combinations	SCA effects	Characters	Top three cross-combinations	SCA effects
Days to 50% flowering	KMR 17-5-21 × PR 20 PR 21 ×PR 20 KMR 17-5-23 × PR 21	-3.601 * -2.795 * -2.323 *	Length of Main Raceme (LMR)	KMR 17-5-21 × PR 20 Rohini × KMR 17-5-21 KMR 17-5-22 × KMR 17-5 -21	9.017 * 8.443 * 7.881 *
Days to maturity	KMR 17-5-22 ×KMR 17-5-21 Basanti × KMR 17-5 -23 NDR 501-26 × Rohini	-7.960 ** -6.348 ** -5.348 **	1000-seed weight (g)	NDR 501-26 × PR 21 Aashirwad × KMR 17-5-22 KMR 17-5-23×PR 20	1.089 ** 1.084 ** 1.011 **
Plant Height (c)	Aashirwad × NDR 501-26 Aashirwad × KMR 17-5-21 NDR 501-26 × Basanti	28.428 ** 15.595 ** 14.470 **	Harvest Index (%)	NDR 501-26 × KMR 17-5-21 Aashirwad × PR 20 Aashirwad × Rohini	4.346 ** 4.309 ** 3.657 **
Leaf Area Index	KMR 17-5-22 × KMR 17-5-21 NDR 501-26 × PR 21 Rohini × PR 21	0.966 ** 0.638 ** 0.636 **	Oil Content (%)	Aashirwad × PR 21 Aashirwad × KMR 17-5-23 N 8501 × PR 20	5.208 ** 4.630 ** 4.369 **
No. of Primary branches per plant	NDR 501-26 × PR 21 Rohini × PR 21 Aashirwad × KMR 17-5 -23	1.453 ** 1.041 * 0.883 *	Protein content %	Aashirwad × PR 21 NDR 501-26 × Basanti NDR 501-26 × KMR 17-5-21	3.926 ** 3.870 ** -3.371 **
No. of secondary branches per plant	KMR 17-5-23 × PR 20 Aashirwad × KMR 17-5-22 Aashirwad × Basanti	5.651 ** 5.217 ** 5.077 **	Erucic acid content (%)	N 8501 × PR 21 KMR 17-5-23 × KMR 17-5 -22 NDR 501-26 × PR 21	-6.426 ** -6.295 ** -6.523 **
Number of siliquae per plant	Aashirwad × KMR 17-5-22 Aashirwad × KMR 17-5 -23 KMR 17-5-23 × PR 20	76.316 ** 76.260 ** 67.538 **	Total Glucosinolate content (µmol/g)	NDR 501-26 × Rohini KMR 17-5-23 × PR 20 Aashirwad × KMR 17-5-22	-29.966 ** -25.12** -24.572 **
Number of seeds per siliqua	Rohini × KMR 17-5-21 Rohini x Basanti NDR 501-26 × Basanti	3.144 ** 2.830 * 2.083 *	Seed Yield per Plant (g)	KMR 17-5-23 × N 8501 Rohini × KMR 17-5-21 KMR 17-5-23 × PR 20	8.169 ** 7.495 ** 5.937 **

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

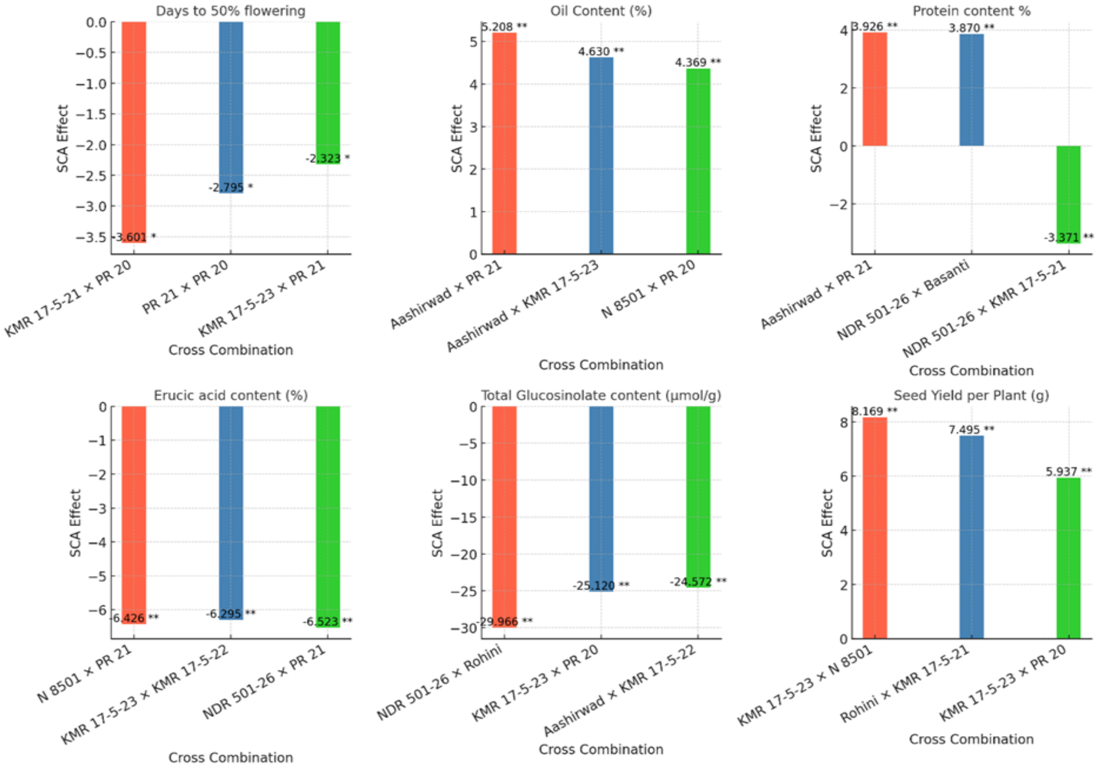


Fig. 2. *Visual representation of SCA effects of the best cross combinations for key traits*

gants in subsequent generations. Conversely, L × L cross combinations demonstrate non-additive gene action, which can not be fixed in a natural population and can only be manipulated through heterosis breeding to enhance specific traits (Singh et al. 2009; Vaghela et al. 2011; Parmar et al. 2011; Chaurasia et al. 2014).

Conclusion

The findings of the present experiment underscore the importance of considering both gca and sca effects when selecting parents for hybrid breeding. Parents with good general combining ability (gca) can be utilized to develop superior varieties through selection in segregating populations. The cross combinations KMR 17-5-23 × N 8501 and Rohini × KMR 17-5-21 were identified as the best for seed yield. For quality traits, the cross N 8501 × PR 21 was most effective for reducing erucic acid, and NDR 501-26 × Rohini was most effective for reducing glucosinolate content. Additionally, hybrids exhibiting significant *sca* for a broad range of desirable traits should be further tested to improve seed yield and quality traits for commercial utilization through heterosis.

ACKNOWLEDGEMENTS

We are extremely grateful to the chairman of the Department of Genetics and Plant Breeding, CSAUT, Kanpur, India, for his valuable advice and logistical support necessary to conduct the research work. We extend our profound gratitude to the oil section department at C.S.A. University Kanpur for providing the facilities and assistance needed to complete this study.

Conflict of interest

The authors declare that they have no conflict of interest.

REFERENCES

1. Aher, C. D., Shelke, L. T., Chinchane, V. N., Borgaonkar, S. B., Akbar, M., Tahira, Babar, M. A., & Hussain, M. (2009). Combining ability studies in rapeseed (Brassica napus). *International Journal of Agriculture and Biology, 10*(2), 205-208.
2. Akabari, V. R., Sasidharan, N., & Kapadiya, V. (2017). Combining ability and gene action study for grain yield and its attributing traits in Indian mustard. *Electronic Journal of Plant Breeding, 8*(1), 226-235. https://doi.org/10.5958/0975-928X.2017.00032.1
3. Barfa, D., Tripathi, M. K., Kandalkar, V. S., Gupta, J. C., & Kumar, G. (2017). Heterosis and combining ability analysis for seed yield in Indian mustard [Brassica Juncea (L.) Czern & Coss.]. *Ecology, Environment and Conservation, 23*, 75-83.
4. Chand, S. P., Debnath, S., Rahimi, M., Ashraf, M., Bhatt, P., & Rahin, S. A. (2022). Contextualization of trait nexus and gene action for quantitative and qualitative characteristics in Indian mustard. *Journal of Food Quality, 22*, 1-24. https://doi.org/10.1155/2022/4387318
5. Chaurasia, R. K., & Bhajan, R. (2015). Heterosis and combining ability studies in Indian mustard (Brassica juncea L.). *Trends in Bioscience, 7*(22), 3687-3690.
6. Griffing, B. (1956). Concept of general and specific combining ability in relation to diallel crossing systems. *Australian Journal of Biological Sciences, 9*(4), 463-493.
7. Hayman, B. I. (1954). The theory and analysis of diallel crosses. *Genetics, 39*(6), 789.
8. Kaur, S., Kumar, R., Kaur, R., Singh, I., Singh, H., & Kumar, V. (2019). Heterosis and combining ability analysis in Indian mustard (Brassica juncea L.). *Journal of Oilseed Brassica, 10*(1), 38–46.
9. Kumar, R., Prasad, Y., & Kumar, K. (2015). Combining ability for some developmental traits in Indian mustard (Brassica juncea L.). *Frontiers in Crop Improvement Journal, 3*(1), 43–45.
10. Kumar, A. (2017). *Proceedings of 3rd National Brassica Conference held at IARI New Delhi; 16-18*.
11. DAC & FW. (2022-23). *Estimates of production of food grains*. Directorate of Economics and Statistics. Ministry of Agriculture and Farmers Welfare, Government of India.
12. Nassimi, A. W., Raziuddin, R., Sardar Ali, S. A., Ghulam Hassan, G. H., & Naushad Ali, N. A. (2006). Combining ability analysis for maturity and other traits in rapeseed (Brassica napus L.). *Journal of Agronomy, 5*(3), 523-526.
13. Ostrikov, A. N., Kleymenova, N. L., Bolgova, I. N., & Kopylov, M. V. (2020). Gas chromatographic analysis of the fatty acid composition of mustard oil obtained by cold pressing. *Emirates Journal of Food and Agriculture, 32*(5), 391.
14. Patel, A. M., Arha, M. D., & Khule, A. A. (2013). Combining ability analysis for seed yield and its attributes in Indian mustard [Brassica juncea (L.) Czern and Coss]. *Asian Journal of Bio Science, 8*(1), 11-14.
15. Patel, R., Solanki, S. D., Gami, R. A., Prajapati, K. P., Patel, P. T., & Bhadauria, H. S. (2015). Genetic study for seed yield and seed quality traits in Indian mustard [Brassica juncea L. Czern & Coss.]. *Electronic Journal of Plant Breeding, 6*(3), 672-679.
16. Parmar, A. S., Jaimini, S. N., & Ram, B. (2016). Combining ability analysis for seed yield and its components over environments in Indian mustard (Brassica juncea L.). *Journal of Oilseed Brassica, 2*(2), 61-66.
17. Prasad, B. (2014). Heterotic vigor studies in forage sorghum hybrid by multiple criteria. *Journal of Hill Agriculture, 5*, 182.
18. Rout, S., Roy, S. K., Mandal, R., et al. (2025). Genetic analysis and heterosis breeding of seed yield and yield attributing traits in Indian mustard (Brassica juncea (L.) Czern & Coss.). *Scientific Reports, 15*, 2911. https://doi.org/10.1038/s41598-025-86621-8
19. Singh, M., Ranjeet, & Srivastava, S. B. L. (2009). Heterosis and combining ability estimates in Indian mustard (Brassica juncea L. Czern & Coss). *Journal of Oilseed Research, 26*, 61-63.
20. Sheera, A., Dey, T., Pandey, M. K., Singh, T., Bhagat, T., & Shruthi, K. (2022). Genetic divergence in micronutrient-

rich wheat tool to identify diverse parents. *International Journal of Environment and Climate Change, 1*, 150-156. https://doi.org/10.9734/ijecc/2022/v12i1030779

21. Sheera, A., Dey, T., Pandey, M. K., Singh, T., Sandhu, R., Dhillon, L., Chikkeri, S. S., Kumawat, S., & Kumar, R. (2024). Deciphering combining behavior and magnitude of heterosis in bread wheat cross combinations under subtropical region. *Electronic Journal of Plant Breeding, 15* (2). https://doi.org/10.37992/2024.1502.039
22. Shrivastav, S. P., Verma, O. P., Jakhar, D. S., Singh, V., & Lal, K. (2022). Component of genetic variance, combining ability and heterotic response in rice (Oryza sativa L.) for high yield with quality and sodicity tolerance. *Indian Journal of Genetics & Plant Breeding, 82*(04). https://doi.org/10.18805/IJARe.A-5976
23. Singh, M., Singh, R., Yadav, K., & Chaurasiya, J. P. (2022). Genetic analysis for seed yield and its contributing traits in Indian mustard (Brassica juncea L. Czern & Coss). *Journal of Oilseeds Research, 37*, 66–67. https://doi.org/10.56739/jor.v37ispecialissue.139500
24. Srivastava, M. K. (2022). Gene action analysis for yield and its component traits in Indian mustard (Brassica juncea L. Czern & Coss). *International Journal for Research in Applied Science and Engineering Technology, 10*(4), 3667-3669.
25. Tele, R. B., Patil, S. R., Lole, M. D., Khillari, A. V., Solanke, P. D., & Bansod, S. C. (2014). Genetic analysis in Indian mustard (Brassica juncea L.) through diallel mating. *Journal of Oilseed Brassica, 5*(1), 55–60.
26. Tomar, A., Singh, M., & Singh, S. K. (2015). Genetic analysis of yield and its components based on heterotic response and combining ability parameters in Indian mustard (Brassica juncea L. Czern & Coss). *Progressive Agriculture, 15*(1), 85-91.
27. Vaghela, P. O., Thakkar, D. A., Bhadauria, H. S., Sutariya, D. A., Parmar, S. K., & Prajapati, D. V. (2016). Heterosis and combining ability for yield and its component traits in Indian mustard [Brassica juncea (L.)]. *Journal of Oilseed Brassica, 1*, 39-43.
28. Vaghela, P. O., Bhadauria, H. S., & Thakor, D. M. (2014). Combining ability for seed yield and quality components in Indian mustard. *International Journal of Multidisciplinary Research and Development, 1*(2), 45–47.