International Journal of Advanced Biochemistry Research

ISSN Print: 2617-4693
ISSN Online: 2617-4707
NAAS Rating: 5.29
IJABR 2025; 9(7): 545-553
www.biochemjournal.com
Received: 13-05-2025
Accepted: 16-06-2025

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Exploring combining ability for the selection of promising parents to harness heterosis for yield and associated traits in Indian mustard (*Brassica juncea* (L.) Czern & Coss)

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DOI: https://www.doi.org/10.33545/26174693.2025.v9.i7g.4789

Abstract

The present investigation aimed to explore the combining ability of mutant lines of Indian mustard (*Brassica juncea* (L.) Czern & Coss) to identify promising parents and hybrid combinations for enhancing seed yield and associated traits through heterosis breeding. Ten mutant lines were crossed with three testers (Giriraj, RH-749, and HUJM-10-6) using a line × tester design during Rabi 2019-20, producing 30 F_1 hybrids. These hybrids, along with 13 parents and one national check (Kranti), were evaluated during Rabi 2020-21 at Banaras Hindu University under a randomized block design with three replications. Data were recorded on 16 agro-morphological and physiological traits, and analyzed using standard statistical methods for variance partitioning and estimation of general (GCA) and specific combining ability (SCA).

The analysis revealed significant genetic variability among parents and hybrids for most traits. GCA effects were prominent for days to flowering and maturity, plant height, siliqua characteristics, and seed yield traits. Notably, TM-130, TM-117, and TM-263-3 were identified as superior general combiners for seed yield and biological yield, while RH-749 was the best tester. Hybrids such as RH-749 × TM-143, RH-749 × TM-217, RH-749 × TM-117, and HUJM-10-6 × TM-263-3 exhibited high SCA effects and outperformed the check variety in seed yield per hectare. The higher magnitude of SCA variance compared to GCA for most traits suggested the predominance of non-additive gene action, implying the potential of heterosis breeding. Crosses involving good × good and good × poor general combiners with high SCA effects are particularly valuable for developing superior transgressive segregants. The identified genotypes and hybrids hold significant promise for yield enhancement in mustard breeding programs and warrant further multilocation testing for stability and adaptability.

Keywords: *Brassica juncea*, combining ability, heterosis, seed yield, general combining ability

Introduction

Indian mustard (*Brassica juncea* (L.) Czern & Coss) is a predominant *rabi* season oilseed crop in India and occupies a premier position among oilseed species due to its high oil content (Singh *et al.*, 2020) [24]. Belonging to the genus *Brassica* and family *Brassicaceae* (Cruciferae), *B. juncea* is an economically significant crop extensively cultivated across Asia and Europe (Warwick *et al.*, 2006) [31]. Vavilov (1949) [30] identified Afghanistan and its adjoining regions as the primary centre of origin for *B. juncea*, with secondary centres of diversity reported in Asia Minor, central or western China, and eastern India. Historically, *B. juncea* is believed to have been introduced into India from China. Indian mustard thrives in a variety of environmental conditions, with annual rainfall ranging from 500 to 4,200 mm, temperatures between 6 and 27 °C, and soil pH levels from 4.3 to 8.3 (Karthik *et al.*, 2024) [8].

In India, the rapeseed-mustard group comprises both traditionally cultivated indigenous species and a few non-traditional ones. The indigenous species include brown sarson [*Brassica campestris* (syn. *B. rapa* L. var. *brown sarson*, 2n = 20, AA)], toria [*B. campestris* (syn. *B. rapa* L. var. *toria*, 2n = 20, AA)], Indian mustard [*B. juncea* (L.) Czern & Coss, 2n = 36, AABB], yellow sarson [*B. campestris* (syn. *B. rapa* L. var. *yellow sarson*, 2n = 20, AA)], black mustard [*B. nigra* (L.) Koch, 2n = 16, BB], and Taramira [*Eruca sativa/vesicaria* Mill., 2n = 22, EE], which have been cultivated since around 3500 BC (Chauhan *et al.*, 2011) [2].

Non-traditional species include white mustard [*Sinapis alba* L., 2n = 24, SS], gobhi sarson *[B. napus* L. ssp. *oleifera* DC var. *annua* L., 2n = 38, AACC], and Ethiopian mustard or karan rai [*B. carinata* A. Braun, 2n = 34, BBCC].

Nagaharu U (1935) proposed a genomic model elucidating the amphidiploid nature of certain *Brassica* species. According to this model, the diploid species include *B. nigra* (2n = 16, BB), *B. oleracea* (2n = 18, CC), and *B. rapa* (syn. *B. campestris*, 2n = 20, AA), while the amphidiploids are the result of natural hybridization events among them: *B. juncea* (AABB) arose from *B. rapa* × *B. nigra*, *B. carinata* (BBCC) from *B. nigra* × *B. oleracea*, and *B. napus* (AACC) from *B. rapa* × *B. oleracea*.

The primary goal of any crop improvement program is to increase the yield potential of the crop (Karthik *et al*., 2024) [8]. Despite its importance, the productivity of Indian mustard in India remains significantly lower than in countries like Germany, France, and the United Kingdom. Therefore, enhancing the seed yield is critical to achieving self-sufficiency in edible oil production (Yadav *et al*., 2020) [26]. Improvement in both seed yield and oil quality is necessary to meet the growing demand for edible oils, particularly in the context of a rapidly expanding population. One of the most effective approaches for yield enhancement is hybridization, which requires the strategic utilization of diverse and genetically rich germplasm.

A key concept in hybrid breeding is combining ability, which refers to the capacity of a genotype to transmit superior performance to its offspring. This concept is foundational in identifying elite parental lines for hybrid development and capitalizing on heterosis (hybrid vigor). Combining ability is typically assessed through biometrical approaches such as diallel, partial diallel, and line × tester (L×T) analyses, which help partition the genetic variance into additive and non-additive components. General combining ability (GCA) represents the average performance of a line across multiple hybrid combinations and is primarily attributed to additive gene effects. In contrast, specific combining ability (SCA) captures the deviations of specific crosses from the expected performance based on parental GCA values, reflecting non-additive gene action including dominance and epistasis. The concept of combining ability was formalized by Sprague and Tatum (1942) [27] during their work in maize, emphasizing its utility in plant breeding for selecting optimal parental combinations to achieve targeted genetic gains.

In nutshell, understanding the genetic basis of combining ability is indispensable for hybrid breeding programmes, particularly in crops like Indian mustard where improving seed yield and oil content is a national priority. Through a well-structured combining ability analysis, breeders can identify superior parent lines and promising hybrid combinations that contribute to sustainable genetic improvement and yield enhancement. Hence, the objective of this study was to identify mutant lines possessing desirable agronomic traits and strong combining ability, with the aim of exploiting heterosis to enhance yield potential and contribute to sustainable agricultural development.

Materials and Methods

Location and Agro-climatic and weather condition of experimental site

The present investigation was conducted at the Agricultural Research Farm, Institute of Agricultural Sciences, Banaras Hindu University (BHU), Varanasi, located along the banks of the Ganga River in Uttar Pradesh. The research farm is situated in the southeastern part of Varanasi at 25°15' N latitude and 82°59' E longitude, at an altitude of 75.5 meters above mean sea level. Varanasi has a moist subtropical climate, marked by considerable temperature fluctuations between the summer and winter seasons.

Experimental material

In this experiment, 10 mutant lines (TM-143, TM-258, TM-130, TM-108, TPM-1, TM-217, TM-108-1, TM-117, TM-52, and TM-263-3) of Indian mustard obtained from Bhabha Atomic Research Centre, Trombay were crossed with three testers *viz*., Giriraj, RH-749 and HUJM-10-6 (obtained from germplasm collection maintained in department of Genetics and Plant Breeding, Institute of Agricultural Sciences, BHU.) during *Rabi*-2019-20 to develop a total of 30 crosses. These 30 F_1 crosses along with 13 parents and national checks (Kranti) were evaluated in randomized block design with three replications during *Rabi* 2020-21. The experimental material consisting of a total of 44 entries (30 F_1 crosses, 13 parents and 1 checks) were sown in randomized block design with 3 replications during *rabi* 2020-21. Each genotype was sown in a two rows of 5-meter length. The spacing between rows and plants were 30 cm and 10 cm, respectively.

Trait assessment and data analysis

Data were recorded on 16 different traits namely plant height (PH), days to 50% flowering (DF), days to maturity (DM), number of primary branches (NPB), number of secondary branches (NSB), length of main raceme (LMR), number of siliquae on main raceme (NSMR), number of siliquae per plant (NSPP), siliqua length (SL), seeds per siliqua (SPS), seed yield per plant (SYPP), biological yield per plant (BYPP), harvest index (HI), test weight (TW), canopy temperature deficit (CTD), chlorophyll content (CC). Five competitive plants were tagged randomly from each genotype in each replication for recording field observations for all the traits except for days to 50% flowering and days to maturity, which were observed on plot basis during both the years. Harvest index was calculated by dividing seed yield per plant by biological yield per plant. The data were first subjected to the usual analysis followed for a randomized block design for individual environment as suggested by Panse and Sukhatme (1967). The analysis of variance for combining ability (*gca* and *sca*) and estimation of variance components for various characters were carried out using the procedure suggested by Kempthorne (1957) [11] for line × tester analysis.

Results and Discussion

Analysis of variance for combining ability

The details of the analysis of variance are presented in Table 1. The analysis, conducted on 30 hybrid combinations, partitioned the total variance into three components: line effect, tester effect, and line × tester interaction effect. The mean squares due to crosses were significant for all the traits studied, indicating substantial genetic variability. The line effects were significant for all traits except canopy temperature deficit, chlorophyll content, number of secondary branches, number of siliquae per plant, seeds per siliqua, biological yield, and harvest index. The tester effects showed significance for days to 50% flowering, canopy temperature deficit, seeds per siliqua, test weight, seed yield per plant, and seed yield per hectare. Additionally, the line × tester interaction effects were significant for all traits except the number of primary branches. Similarly, significant effect of line, tester and line × tester component for the various yield component traits were reported in Indian mustard (Patel *et al.*, 2013; Priyamedha *et al.*, 2016; Kumar *et al.*, 2017; Choudhary *et al.*, 2020; Kumar *et al.*, 2021) [18, 19, 13, 3, 12].

Estimation of general combing ability (*gca*) and specific combing ability (*sca*) effects

The combining ability plays an important role in the selection of suitable parents for hybridization. Parents having high mean performance may not necessarily transmit their superior performance to their offspring (Sprague and Tatum, 1942) [27]. Similarly, parents with good GCA effects may not always produce hybrids with good SCA effects (Griffing, 1956) [6]. GCA variance represents additive gene action, where simple selection is effective for the improvement of such traits, while SCA variance indicates the preponderance of non-additive gene action, where heterosis breeding may be more rewarding (Falconer and Mackay, 1996) [4]. For several traits, gca variance may be equal indicates that both additive and non-additive genes are equally important in that expression of that character (Fasahat *et al.*, 2016) [5].

Out of the thirteen parental lines evaluated, four—TPM-1, TM-143, HUJM-10-6, and TM-52—were identified as good general combiners for days to 50% flowering, days to maturity, and plant height (with the exception of HUJM-10-6 for plant height), corroborating the findings of Kaur *et al.* (2019) [9]. For chlorophyll content, TM-130, TM-108-1, TM-258, and RH-749 exhibited strong general combining ability. TM-130 and TPM-1 were effective general combiners for the number of primary branches per plant, while TM-263-3 and TPM-1 showed good GCA effects for the number of secondary branches per plant, consistent with earlier reports by Kumar *et al.* (2017) [13] and Singh *et al.* (2016) [25]. Five parents—TM-217, TM-258, TM-130, TM-117, and HUJM-10-6—demonstrated significant GCA effects for main raceme length. TM-130 was the sole parent with desirable GCA for the number of siliquae on the main raceme, whereas TPM-1 and TM-263-3 showed good combining ability for the total number of siliquae per plant. TM-143 was found to be a good general combiner for siliqua length, and Giriraj for the number of seeds per siliqua, aligning with the reports of Kumar *et al.* (2017) [13], Kumar *et al.* (2018) [14]. Among the lines, TM-143, TM-130, and TM-217, and among testers, HUJM-10-6, exhibited significantly positive GCA effects for test weight. Additionally, four lines—TM-130, TM-108-1, TM-263-3, and TM-117—and one tester, RH-749, were identified as superior general combiners for biological yield.

The list of lines and testers exhibiting significant general combining ability (GCA) effects for various traits, along with a summary of GCA estimates, is provided in Table 4. For traits such as plant height, days to 50% flowering, canopy temperature deficit, and days to maturity, significant negative GCA effects are considered desirable. Accordingly, lines and testers demonstrating positive and significant GCA effects for the remaining traits are regarded as good general combiners. In this context, TM-108 and TM-52 were identified as superior general combiners for harvest index. Furthermore, the parents TM-130, TM-117, TM-263-3, and RH-749 exhibited significant positive GCA effects for both seed yield per plant and seed yield per hectare. These genotypes represent valuable genetic resources for use in future breeding programs aimed at enhancing specific yield-related traits in Indian mustard. These observations are consistent with the results reported by Kumar *et al.* (2017) [13] and Tirkey *et al.* (2020) [29] and Choudhary *et al.* (2020) [3].

The list of crosses exhibiting significant specific combining ability (SCA) effects for various traits is presented in Table 5. The cross Giriraj × TM-143 demonstrated a significantly negative SCA effect for days to 50% flowering, indicating its potential for early maturity. Among the thirty crosses evaluated, none exhibited a significant negative SCA effect for days to maturity. However, the hybrid HUJM-10-6 × TM-258 showed a significantly negative SCA effect for plant height, which is desirable in terms of plant architecture and lodging resistance. These findings align with the results of Tirkey *et al.* (2020) [29] and Choudhary *et al.* (2020) [3].

Several hybrids—Giriraj × TM-52, RH-749 × TM-217, RH-749 × TM-143, RH-749 × TM-117, HUJM-10-6 × TPM-1, and HUJM-10-6 × TM-263-3—exhibited significant positive SCA effects for seed yield per plant, biological yield (excluding RH-749 × TM-217), and seed yield per hectare, in line with the findings of Saikia *et al.* (2019) [21] and Meena *et al.* (2017) [16]. Moreover, the crosses RH-749 × TM-130, RH-749 × TM-117, Giriraj × TM-143, Giriraj × TM-108, Giriraj × TM-52, and HUJM-10-6 × TM-263-3 showed significantly positive SCA effects for chlorophyll content. Only three hybrids—RH-749 × TM-117, Giriraj × TPM-1, and HUJM-10-6 × TM-258—displayed significant positive SCA effects for canopy temperature deficit, suggesting improved drought resilience. Significant positive SCA effects for the number of secondary branches per plant were recorded in HUJM-10-6 × TPM-1, HUJM-10-6 × TM-263-3, RH-749 × TM-143, RH-749 × TM-217, and Giriraj × TM-108. However, none of the crosses showed significant positive SCA effects for the number of primary branches per plant or number of seeds per siliqua, consistent with the findings of Meena *et al.* (2017) [16], Singh *et al.* (2019) [23], and Tirkey *et al.* (2020) [29].

Among all hybrids, only HUJM-10-6 × TM-108 exhibited significantly positive SCA effects for the number of siliquae per plant. The cross HUJM-10-6 × TM-258 showed positive and significant SCA effects for both thousand seed weight and harvest index, corroborating the observations of Singh *et al.* (2019) [23] and Choudhary *et al.* (2020) [3]. Furthermore, the crosses RH-749 × TM-143, RH-749 × TM-258, Giriraj × TM-52, and HUJM-10-6 × TM-108 demonstrated significant positive SCA effects for the length of the main raceme. Notably, no hybrid exhibited significant positive SCA effects for siliqua length. These specific cross combinations can be strategically employed in breeding programs to generate superior transgressive segregants. The parental lines involved in these hybrids may also be considered for introgression into the backgrounds of well-adapted cytoplasmic male sterile (CMS) or restorer lines for future hybrid development. These conclusions are in agreement with the reports of Kaur *et al.* (2019) [9] and Rashmi *et al.* (2018) [20].

Table 1: Analysis of variance for combining ability for different traits recorded in Indian mustard.

	DF	**Days to 50% flowering**	**Days maturity**	**Plant height (cm)**	**Canopy temperature deficit**	**Chlorophyll content**	**No. of primary branches**	**No. of secondary branches**	**No. of siliquae raceme**	**Length of main raceme (cm)**	**No. of siliquae per plant**	**Siliquae length (cm)**	**Seeds per siliquae**	**Test weight (gm)**	**Seed yield per plant (gm)**	**Biologic al yield per plant (gm)**	**Harvest index (%)**	**Seed Yield (Kg/ ha)**
Replicates	2	10.208	16.13*	710.53**	0.884**	0.91	1.30**	0.07	46.00**	0.16	14011.90**	0.008	0.161	0.016	4.378**	216.008**	12.656**	96081.650**
Crosses	29	88.71**	53.05**	810.62**	0.70**	33.22**	0.67**	9.58**	80.47**	191.48**	5392.25**	0.264**	2.918**	0.730**	11.104**	235.711**	23.978**	243708.300**
Line Effect	9	221.73**	142.28**	2014.27**	0.29	34.98	1.70**	14.31	177.17**	440.00**	9256.67	0.571**	1.554	1.036*	16.282*	368.597	31.211	357352.700*
Tester Effect	2	89.42*	18.92	113.67	4.03**	84.67	0.34	5.40	1.36	123.49	1253.20	0.265	5.069**	2.836**	34.062*	327.009	9.144	747581.200*
Line × Tester Eff.	18	22.11***	12.23**	286.24**	0.54***	26.63**	0.19	7.69**	40.92**	74.77**	3919.94**	0.110**	2.250**	0.343**	5.964**	159.125**	22.010**	130900.300**
Error	58	5.226	4.99	47.26	0.13	0.79	0.11	0.24	6.745	3.77	232.52	0.023	0.362	0.052	0.201	5.407	1.744	4416.616
Total	89	32.54	20.90	310.90	0.339	11.36	0.32	3.28	31.65	64.85	2223.43	0.101	1.19	0.272	3.848	85.183	9.234	84447.96

* and** Significant at 5% and 1% level of significance, respectively

Table 2: General combining ability effects for yield and associated traits in Indian mustard

Genotype	Days to 50% flowering	Days to maturity	Plant height (cm)	Canopy temperature deficit	Chlorophyll content	No. of primary branches	No. of secondary branches	No. of siliquae on main raceme	Length of main raceme (cm)
TM-143	-5.917**	-3.600**	-11.947*	-0.232	-1.635**	0.085	0.102	-5.742**	-5.060**
TM-258	1.917	3.400*	19.103**	-0.082	1.798**	-0.482*	-0.865**	1.742	6.840**
TM-130	1.917	2.733*	17.103**	0.135	2.498**	0.452*	0.235	5.958**	6.073**
TM-108	5.083**	4.233**	-3.913	0.002	0.965	-0.515*	-0.732*	1.258	1.94
TPM-1	-9.417**	-7.767**	-18.530**	-0.315*	-3.568**	0.668**	2.735**	-2.608	-5.560**
TM-217	2.917*	1.733	0.237	-0.015	-1.802**	-0.615**	-2.032**	1.225	8.773**
TM-108-1	3.083*	1.233	6.337	0.302*	1.932**	0.118	-0.332	2.725	1.14
TM-117	3.417**	2.067	13.937**	0.135	0.548	-0.015	-0.398	3.058	3.340*
TM-52	-5.417**	-4.767**	-24.797**	0.018	-1.268*	0.385	0.285	-8.808**	-13.92**
TM-263-3	2.417	0.733	2.47	0.052	0.532	-0.082	1.002**	1.192	-3.560**
Maximum	5.083	4.233	19.103	0.302	2.498	0.668	2.735	5.958	8.773
Minimum	-9.417	-7.767	-24.797	-0.315	-3.568	-0.615	-2.032	-8.808	-13.927
CD @ 5% GCA (Line)	2.445	2.527	9.002	0.2817	1.071	0.424	0.568	3.565	2.601
RH-749	1.167	0.483	1.85	-0.423***	1.683**	0.12	-0.115	-0.22	-0.537
Giriraj	0.817	0.433	-2.03	0.227**	-0.007	-0.035	0.470**	0.205	-1.707*
HUJM-10-6	-1.983**	-0.917	0.18	0.197*	-1.677**	-0.085	-0.355*	0.015	2.243**
Maximum	1.167	0.483	1.85	0.227	1.683	0.12	0.47	0.205	2.243
Minimum	-1.983	-0.917	-2.03	-0.423	-1.677	-0.085	-0.355	-0.22	1.707*
CD @ 5% GCA (Tester)	1.339	1.384	4.931	0.1543	0.586	0.232	0.311	1.953	1.425

* and** Significant at 5% and 1% level of significance, respectively

Genotype	Total siliquae per plant	Siliquae length (cm)	No. of seeds per siliquae	Test weight (gm)	Seed yield per plant (gm)	Biological yield per (gm)	Harvest index (%)	Yield (Kg/ ha)
TM-143	-3.188	0.463**	-0.58	0.320*	-0.14	-2.27	0.869	-20.691
TM-258	-38.48**	0.096	0.253	-0.113	0.51	1.997	0.45	75.605
TM-130	24.612	0.17	-0.213	0.487**	1.682**	9.797**	-1.797	249.185**
TM-108	-22.055	0.073	0.353	-0.18	-2.443**	-5.470**	-2.647**	-361.92**
TPM-1	51.145**	-0.147	0.253	-0.647**	-0.536	-3.770*	0.975	-79.457
TM-217	-30.788*	0.046	-0.247	0.287*	-0.613*	-5.903**	1.913	-90.815*
TM-108-1	-3.155	0.079	0.453	-0.280*	-0.023	3.830*	-2.349*	-3.407
TM-117	15.278	-0.459**	-0.213	-0.047	1.490**	5.563**	-0.111	220.790**
TM-52	-34.388*	-0.057	-0.58	-0.08	-1.433**	-10.003**	3.115**	-212.29**
TM-263-3	41.028**	-0.264*	0.52	0.253	1.505**	6.230**	-0.417	223.012**
Maximum	51.145	0.463	0.453	0.487	1.682	9.797	3.115	249.185
Minimum	-38.488	-0.459	-0.58	-0.647	-1.433	-10.003	-2.647	-361.926
CD @ 5% GCA (Line)	26.385	0.257	0.848	0.27	0.603	3.604	1.916	88.17
RH-749	6.983	0.104	0.21	0.147	1.213**	3.810**	0.527	179.704**
Giriraj	-5.772	-0.023	0.580*	-0.353**	-0.785**	-2.020*	-0.574	-116.29**
HUJM-10-6	-1.212	-0.08	-0.790**	0.207**	-0.428*	-1.79	0.047	-63.407*
Maximum	6.983	0.104	0.58	0.207	1.213	3.81	-0.574	179.704
Minimum	-5.772	-0.023	-0.79	-0.353	-0.785	-2.02	0.527	-116.296
CD @ 5% GCA (Tester)	14.452	0.141	0.465	0.148	0.33	1.974	1.05	48.293

* and** Significant at 5% and 1% level of significance, respectively

Table 3: Specific combining ability effects for yield and associated traits in Indian mustard

Sl. No	Hybrid	Days to 50% flowering	Days to maturity	Plant height (cm)	Canopy temperature deficit	Chlorophyll content	No of primary branches	No of secondary branches	No of siliquae on main raceme
1	RH-749 × TM-143	4.167	-0.15	6.017	-0.243	-4.000***	0.08	2.748***	2.887
2	RH-749 × TM-258	0.833	-0.15	12.217	-0.143	1.567	-0.053	0.615	3.353
3	RH-749 × TM-130	1.333	1.517	1.817	-0.01	1.917*	-0.087	-0.885	2.487
4	RH-749 × TM-108	-1.333	1.017	8.583	-0.027	0.55	-0.42	-1.618**	-5.713
5	RH-749 × TPM-1	-3.333	1.517	-1.15	-0.560*	1.033	0.047	-2.185***	0.753
6	RH-749 × TM-217	-1.667	-2.483	-11.017	-0.16	-0.233	0.28	1.582**	0.02
7	RH-749 × TM-108-1	-0.833	-1.983	-2.617	0.273	1.383	0.047	0.682	-0.98
8	RH-749 × TM-117	-1.667	-1.817	4.683	0.540*	2.917**	-0.02	1.648**	-0.113
9	RH-749 × TM-52	2.667	2.517	-13.783	0.057	-2.667**	0.18	-0.935	-2.647
10	RH-749 × TM-263-3	-0.167	0.017	-4.75	0.273	-2.467*	-0.053	-1.652**	-0.047
11	Giriraj × TM-143	-4.483*	-2.1	-5.453	0.007	3.690***	0.035	-0.337	-0.338
12	Giriraj × TM-258	2.183	1.9	5.397	-0.493*	-1.893*	-0.098	-0.87	1.378
13	Giriraj × TM-130	2.683	1.567	-3.003	0.14	-2.343*	-0.132	0.63	-1.038
14	Giriraj × TM-108	0.517	-0.933	-12.187	-0.127	2.640**	0.235	1.297*	-1.538
15	Giriraj × TPM-1	1.017	-1.933	1.23	0.540*	-1.327	-0.148	0.33	-3.272
16	Giriraj × TM-217	0.683	0.067	-2.837	-0.11	-0.043	-0.265	-1.103*	-2.505
17	Giriraj × TM-108-1	1.017	1.567	1.963	0.473	0.473	-0.098	-0.603	-0.205
18	Giriraj × TM-117	0.683	1.233	8.063	-0.11	-0.643	0.135	-0.137	5.262
19	Giriraj × TM-52	-3.983	-1.933	6.697	-0.293	3.123**	-0.165	0.93	1.628
20	Giriraj × TM 263-3	-0.317	0.567	0.13	-0.027	-3.677***	0.502	-0.137	0.628
21	HUJM-10-6 × TM-143	0.317	2.25	-0.563	0.237	0.31	-0.115	-2.412***	-2.548
22	HUJM-10-6 × TM-258	-3.017	-1.75	-17.613*	0.637*	0.327	0.152	0.255	-4.732
23	HUJM-10-6 × TM-130	-4.017	-3.083	1.187	-0.13	0.427	0.218	0.255	-1.448
24	HUJM-10-6 × TM-108	0.817	-0.083	3.603	0.153	-3.190**	0.185	0.322	7.252*
25	HUJM-10-6 × TPM-1	2.317	0.417	-0.08	0.02	0.293	0.102	1.855***	2.518
26	HUJM-10-6 × TM-217	0.983	2.417	13.853	0.27	0.277	-0.015	-0.478	2.485
27	HUJM-10-6 × TM-108-1	-0.183	0.417	0.653	-0.747**	-1.857*	0.052	-0.078	1.185
28	HUJM-10-6 × TM-117	0.983	0.583	-12.747	-0.43	-2.273*	-0.115	-1.512**	-5.148
29	HUJM-10-6 × TM-52	1.317	-0.583	7.087	0.237	-0.457	-0.015	0.005	1.018
30	HUJM-10-6 × TM-263-3	0.483	-0.583	4.62	-0.247	6.143***	-0.448	1.788***	-0.582
Minimum		-4.483	-3.083	-17.613	-0.747	-4	-0.42	-2.412	-5.713
Maximum		4.167	2.527	12.217	0.637	6.143	0.502	2.748	7.252
CD @ 5% SCA		4.2348	4.3762	15.5919	0.488	1.8543	0.7348	0.9841	6.1752

Sl. No	Genotype	Length of main raceme (cm)	No. of siliquae per plant	Average siliquae length (cm)	No. of seeds per siliquae	1000 seed weight (cm)	Seed yield per plant (gm)	Biologic yield per plant (gm)	Harvest index (%)	Seed Yield (Kg/ ha)
1	RH-749 × TM-143	6.270**	49.483*	0.283	0.89	0.12	1.774**	8.190*	-1.201	262.766**
2	RH-749 × TM-258	6.970**	4.883	0.04	0.357	-0.047	0.074	8.723**	-4.656**	10.914
3	RH-749 × TM-130	3.637	-23.517	0.026	0.523	0.053	-0.028	-4.477	1.786	-4.148
4	RH-749 × TM-108	-8.330**	-49.250*	0.033	-0.143	-0.18	-0.853	-8.210*	3.046	-126.37
5	RH-749 × TPM-1	-1.73	-52.950*	-0.277	0.557	-0.113	-1.320*	-5.51	0.28	-195.506*
6	RH-749 × TM-217	1.837	41.883	-0.25	-0.643	-0.047	1.827**	3.623	1.591	270.667**
7	RH-749 × TM-108-1	-0.23	15.55	0.207	0.357	0.02	0.697	3.79	-0.277	103.259
8	RH-749 × TM-117	1.57	23.917	-0.075	-0.677	0.387	1.454**	6.957*	-0.85	215.358**
9	RH-749 × TM-52	-4.863*	-1.817	0.063	0.59	0.02	-1.803**	-7.177*	0.88	-267.11**
10	RH-749 × TM-263-3	-5.130*	-8.183	-0.05	-1.810*	-0.213	-1.821**	-5.91	-0.599	-269.82**
11	Giriraj × TM-143	-2.66	-6.962	-0.08	-0.78	0.02	-0.438	-1.48	-0.184	-64.938
12	Giriraj × TM-258	-3.26	1.338	-0.023	0.487	-0.647**	-0.448	0.353	-2.014	-66.42
13	Giriraj × TM-130	-0.293	26.938	0.034	0.153	-0.347	-0.3	6.153	-3.042	-44.444
14	Giriraj × TM-108	0.44	20.305	0.01	0.887	0.12	0.855	3.92	-0.502	126.667
15	Giriraj × TPM-1	-0.26	1.205	-0.09	-0.513	0.187	-0.172	-3.88	2.016	-25.432
16	Giriraj × TM-217	-4.293	-39.562	0.267	0.287	-0.147	-1.635**	-6.347*	0.503	-242.22**
17	Giriraj × TM-108-1	0.14	-33.395	-0.047	-0.613	0.22	-0.715	-5.18	1.029	-105.926
18	Giriraj × TM-117	2.24	12.972	0.052	-0.247	-0.013	0.062	0.687	-0.219	9.136
19	Giriraj × TM-52	6.107**	25.338	0.04	-0.18	0.32	2.165***	6.553*	0.741	320.741**
20	Giriraj × TM-263-3	1.84	-8.178	-0.163	0.52	0.287	0.627	-0.78	1.673	92.84
21	HUJM-10-6 × TM-143	-3.61	-42.522	-0.203	-0.11	-0.14	-1.335*	-6.710*	1.385	-197.827*
22	HUJM-10-6 × TM-258	-3.71	-6.222	-0.017	-0.843	0.693**	0.375	-9.077**	6.670***	55.506
23	HUJM-10-6 × TM-130	-3.343	-3.422	-0.06	-0.677	0.293	0.328	-1.677	1.256	48.593
24	HUJM-10-6 × TM-108	7.890**	28.945	-0.043	-0.743	0.06	-0.002	4.29	-2.544	-0.296
25	HUJM-10-6 × TPM-1	1.99	51.745*	0.367	-0.043	-0.073	1.491**	9.390**	-2.296	220.938**
26	HUJM-10-6 × TM-217	2.457	-2.322	-0.017	0.357	0.193	-0.192	2.723	-2.094	-28.444
27	HUJM-10-6 × TM-108-1	0.09	17.845	-0.16	0.257	-0.24	0.018	1.39	-0.752	2.667
28	HUJM-10-6 × TM-117	-3.81	-36.888	0.023	0.923	-0.373	-1.515**	-7.643*	1.069	-224.49**
29	HUJM-10-6 × TM-52	-1.243	-23.522	-0.103	-0.41	-0.34	-0.362	0.623	-1.621	-53.63
30	HUJM-10-6 × TM-263-3	3.29	16.362	0.213	1.29	-0.073	1.195*	6.690*	-1.074	176.988*
Maximum		7.89	51.745	-0.277	1.29	0.693	2.165	9.39	6.67	320.741
Minimum		-8.33	-52.95	0.367	-1.81	-0.647	-1.821	-7.643	-4.656	-269.872
CD @ 5%		4.5048	45.701	0.4449	1.4696	0.4677	1.0446	6.2425	3.3192	152.7156

* and** Significant at 5% and 1% level of significance, respectively

In the present investigation, a higher magnitude of SCA variance was observed compared to GCA variance for the majority of the traits studied, indicating a predominance of non-additive gene action. Specifically, the condition $\sigma^2sca > \sigma^2gca$ was evident for all traits except days to 50% flowering, days to maturity, and number of primary branches per plant, where additive gene action was predominant ($\sigma^2gca > \sigma^2sca$). These findings are consistent with those reported by Meena *et al.* (2015) [17] and Synrem *et al.* (2015) [28], who also observed a preponderance of SCA variance in their studies. High SCA effects observed in crosses involving two good general combiners (good GCA × good GCA), such as RH-749 × TM-117 (Table 6), may be attributed to additive × additive gene interactions. In contrast, elevated SCA effects in crosses involving one good and one poor general combiner, such as RH-749 × TM-143, RH-749 × TM-217, and HUJM-10-6 × TM-263-3 (Table 6), could be the result of favorable additive effects from the good combiner and epistatic interactions contributed by the poor combiner parent. For traits predominantly governed by additive gene action, simple selection methods are expected to be effective. Furthermore, crosses involving good × good general combiners that display high SCA effects hold potential for the development of high-yielding genotypes and for recovering transgressive segregants in the F_2 generation, thereby offering opportunities for substantial genetic gain through selection.

Table 4: Lines and testers exhibiting good *gca* effects for yield associated traits of Indian mustard

Sr. No.	Characters	Lines
1	Days to 50% flowering	TM-143, TPM-1, TM-52
2	Days to maturity	TM-143, TPM-1, TM-52
3	Plant height (cm)	TM-143, TPM-1, TM-52
4	Canopy temperature deficit	TM-108-1
5	Chlorophyll Content	TM-258, TM-130, TM-108-1, TM-217
6	No. of primary branches	TM-130, TPM-1
7	No. of secondary branches	TPM-1, TM-263-3
8	No. of siliquae on main raceme	TM-130
9	Length of main raceme(cm)	TM-258, TM-130, TM-217, TM-117
10	No. of siliquae/plant	TPM-1, TM-263-3
11	Length of siliquae(cm)	TM-143
12	No. of seeds/ siliquae	--
13	Test weight (gm)	TM-143, TM-130, TM-217
14	Seed yield/ plant (gm)	TM-130, TM-117, TM-263-3
15	Biological yield (gm)	TM-130, TM-108-1, TM-117, TM-263-3
16	Harvest index (%)	TM-108, TM-52
17	Seed yield (kg/ hectare)	TM-130, TM-117, TM-263-3

Table 5: Cross combinations with good specific combining ability effects for yield associated traits in Indian mustard

SL. No.	Characters	Hybrid combinations
1	Days to 50% flowering	Giriraj × TM-143
2	Days to maturity	---
3	Plant height	HUJM-10-6 × TM-258
4	Canopy temperature deficit	RH-749 × TM-117, GIRIRAJ × TPM-1, HUJM-10-6 × TM-258
5	Chlorophyll Content	RH-749 × TM-130, RH-749 × TM-117, Giriraj × TM-143, Giriraj × TM-108, Giriraj × TM-52, HUJM-10-6 × TM-263-3
6	No. of primary branches	-----
7	No. of secondary branches	RH-749 × TM-143, RH-749 × TM-217, Giriraj × TM-108, HUJM-10-6 × TPM-1, HUJM-10-6 × TM-263-3
8	No. of siliquae on main raceme	HUJM-10-6 × TM-108
9	Length of main raceme	RH-749 × TM-143, RH-749 × TM-258. Giriraj × TM-52, HUJM-10-6 × TM-108
10	No. of siliquae/plant	HUJM-10-6 × TPM-1, RH-749 × TM-143
11	Length of siliquae	---
12	No. of seeds/ siliquae	----
13	Test weight	HUJM-10-6 × TM-258
14	Seed yield/ plant	RH-749 × TM-143, RH-749 × TM-217, RH-749 × TM-117, Giriraj× TM-52, HUJM-10-6 × TPM-1, HUJM-10-6 × TM-263-3
15	Biological yield	RH-749 × TM-258, RH-749 × TM-143, RH-749 × TM-117, Giriraj × TM-52, HUJM-10-6 × TPM-1, HUJM-10-6 × TM-263-3
16	Harvest index	HUJM-10-6 × TM-258
17	Seed yield (kg/ hectare)	RH-749 × TM-143, RH-749 × TM-217, RH-749 × TM-117, Giriraj × TM-52, HUJM-10-6 × TPM-1, HUJM-10-6 × TM-263-3

Table 6: Top five crosses exhibiting high *per se* performance, general combining ability and specific combining ability for seed yield per hectare (kg) in Indian mustard.

SL. No	Crosses	Per se performance	Specific combining ability effects of crosses	General combining ability effects of parents
1	RH-749 × TM-117	2222	215.358	Good × Good
2	RH-749 × TM-130	2030.74	-4.148	Good × Good
3	RH-749 × TM-143	2027.77	262.766	Good × Poor
4	RH-749 × TM-217	1965.55	270.667	Good × Poor
5	HUJM-10-6 × TM-263-3	1942.59	176.988	Poor × Good

Conclusion

The genotypes RH-749, TM-117, and TM-130 were identified as superior general combiners for seed yield, with TM-130, TM-117, TM-263-3, and RH-749 showing significantly positive GCA effects for seed yield per hectare. TM-143, TM-130, TM-217, and HUJM-10-6 were strong general combiners for thousand seed weight. Among hybrids, RH-749 × TM-143 excelled in siliquae number, main raceme length, biological yield, and seed yield per hectare, while HUJM-10-6 × TM-258 combined high thousand seed weight with reduced plant height. Hybrids like RH-749 × TM-117, RH-749 × TM-143, RH-749 × TM-217, and HUJM-10-6 × TM-263-3 outperformed the check variety 'Kranti', demonstrating strong potential for future breeding efforts. These findings underscore the utility of these hybrids and their respective parents for exploitation in heterosis breeding and the development of high-yielding mustard cultivars. To ensure broad adaptability and stable performance, these hybrids must be further evaluated through multilocation trials.

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