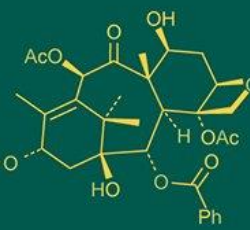
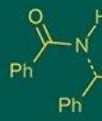
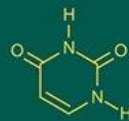
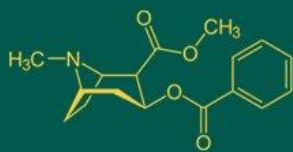


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Assessment of genetic variability and selection parameters in Indian mustard (*Brassica juncea* L. Czern. & Coss.)

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Abstract

The present study was undertaken to assess the extent of genetic variability, heritability, and genetic advance for yield and related traits in Indian mustard (*Brassica juncea* L. Czern & Coss.). The experimental material consisted of ten genotypes—Varuna, Rohini, Azad Mahak, NRC-DR-2, Maya, PR-21, KMR(L)17-5, Mathura Rai, Narendra Rai-4, and NDR-8501—evaluated along with their F₁ and F₂ generations derived from a diallel mating design (excluding reciprocals). The experiment, comprising 100 treatments (10 parents, 45 F₁s, and 45 F₂s), was conducted in a Randomized Block Design with three replications during the Rabi season of 2024-2025 at C.S. Azad University of Agriculture and Technology, Kanpur. Highly significant variability was observed among genotypes for all agronomic and biochemical traits. High heritability coupled with high genetic advance for number of siliques per plant, biological yield, and seed yield per plant indicated the predominance of additive gene action and the effectiveness of direct selection for these traits. Narrow differences between genotypic and phenotypic coefficients of variation suggested minimal environmental influence. Conversely, quality traits with lower heritability and genetic advance may require hybridization or recurrent selection.

Keywords: Mustard, genetic diversity, variability

Introduction

Indian mustard (*Brassica juncea* L. Czern. & Coss.), commonly known in India as Rai, Raya, or Laha, represents one of the nation's most significant oilseed crops. Within the broader rapeseed-mustard complex, it occupies a dominant position, contributing substantially to India's edible oil supply. Approximately 90% of the total area under rapeseed-mustard cultivation is dedicated to this species, underscoring its pivotal role in the country's oilseed economy (Sharma *et al.*, 2021) [16]. A member of the family Brassicaceae, Indian mustard is primarily a Rabi-season crop, well adapted to the semi-arid and subtropical climates of northern and central India. It is prized for its high oil content (37-49%) and protein-rich seed cake (23-25%), which serves as a valuable source of livestock feed (Kumar *et al.*, 2018) [9]. Beyond its culinary use, mustard oil is also important in traditional medicine, cosmetics, soap manufacturing, lubrication, and biofuel production (Singh *et al.*, 2017) [17]. Although predominantly self-pollinated, Indian mustard exhibits a variable degree of natural cross-pollination, ranging from 7.5% to 30%, depending on floral morphology and pollinator activity (Abraham, 1994) [1]. This partial outcrossing offers useful opportunities for hybridization and genetic improvement. Despite its economic significance, however, the crop's yield potential is often constrained by limited genetic diversity and environmental variability. Consequently, exploring and utilizing the existing genetic variation within mustard germplasm is critical for developing superior, high-yielding cultivars.

Genetic variability serves as the foundation of any effective crop improvement program. It enables breeders to identify and combine favorable traits associated with yield, adaptability, and stability (Burton & De Vane, 1953; Panse & Sukhatme, 1967) [3, 11]. The extent of such variability is commonly quantified through the genotypic and phenotypic coefficients of variation (GCV and PCV).

A close correspondence between GCV and PCV suggests limited environmental influence on a trait, while a wider disparity indicates stronger environmental effects (Burton & De Vane, 1953) [3].

Heritability, another critical parameter, measures the proportion of phenotypic variance that is heritable across generations. High heritability coupled with high genetic advance reflects predominant additive gene action, suggesting that direct selection could be effective (Johnson *et al.*, 1955; Panse & Sukhatme, 1967) [8, 11]. Conversely, low heritability and low genetic advance point to non-additive gene effects, where hybridization and population improvement methods may yield better outcomes.

Assessing genetic variability and heritability among Indian mustard genotypes is therefore essential for identifying promising parental lines to be used in breeding programs targeting yield and adaptability enhancement. Evaluation of GCV, PCV, heritability, and genetic advance offers valuable insights into the genetic architecture of yield and its related traits. Such knowledge assists breeders in formulating efficient selection strategies and accelerates the development of improved cultivars. Ultimately, broadening the genetic base of Indian mustard remains vital for achieving sustainable yield gains and ensuring crop resilience under changing climatic conditions.

Materials and Methods

The basic material for the present investigation comprised ten varieties/strains of Indian mustard, namely Varuna, Rohini, Azad Mahak, NRC-DR-2, Maya, PR-21, KMR(L)17-5, Mathura Rai, Narendra Rai-4, and NDR-8501, which were obtained from the germplasm maintained at the Oilseed Section, Department of Genetics and Plant Breeding, C.S. Azad University of Agriculture and Technology, Kanpur.

All ten genotypes were crossed in a diallel mating design (excluding reciprocals) in all possible combinations to produce sufficient F₁ seeds of 45 cross combinations during 2022-2023. The mature seeds were harvested separately and stored individually. Half of the F₁ seed of each cross obtained during 2022-2023 was used to raise the crop for obtaining the source seed of the F₂ generation, and the parental lines were selfed during 2023-2024 to obtain sufficient seed. The mature seeds were harvested separately and stored properly.

In the final trial, 100 treatments (10 parents + 45 F₁s + 45 F₂s) were evaluated in a Randomized Block Design (RBD) with three replications during the *Rabi* season of 2024-2025 at the Oilseed Research Farm, C.S. Azad University of Agriculture and Technology, Kanpur-208002 (U.P.). Each parent and F₁ was planted in a single row, while each F₂ was planted in two rows of 5 m length with a row-to-row spacing of 45 cm. A plant-to-plant distance of 15 cm was maintained by thinning. All recommended agronomic practices were followed to raise a healthy crop.

Data were recorded on the following traits—days to 50% flowering, days to maturity, plant height (cm), main axis height (cm), leaf area index (cm²/m²), chlorophyll content, number of primary branches per plant, number of secondary branches per plant, number of siliquae per plant, number of seeds per silique, biological yield per plant (g), 1000-seed weight (g), harvest index (%), oil content (%), seed yield per plant (g), protein content (%), tryptophan content (%), and methionine content (%).

The statistical analysis and variance due to different sources was worked out according to Panse and Sukhatme (1967) [11]. Phenotypic and Genotypic coefficient of variation were calculated according to method given by Singh *et al.*, (1985) [18]. GCV and PCV were sub-grouped as low (20%) as suggested by Burton and De Vane (1953) [3]. Broad sense heritability (H²) and genetic advance as percent of mean (GAM) were estimated as suggested by Allard (1999) [2]. Heritability was sub-grouped as low (60%) in accordance with Robinson *et al.*, (1949) [8], whereas, GAM was categorized as low (0-10%), moderate (10-20%) and high (>20%).

Results and Discussion

The analysis of variance for twenty agronomic and biochemical traits in the parents, F₁, and F₂ generations of Indian mustard (*Brassica juncea* L. Czern. & Coss.) revealed highly significant differences among genotypes for all studied characters, indicating substantial genetic variability within the material. The significant mean squares for treatments, parents, F₁, and F₂ generations confirmed the influence of both additive and non-additive gene effects governing trait inheritance. Such wide genetic variation provides valuable opportunities for selecting superior genotypes for yield and related traits. Similar results were reported by Choudhary *et al.* (2025) [4], Gupta *et al.* (2025) [7], and Sharma *et al.* (2025) [15], who also observed highly significant differences among mustard genotypes for yield and its component traits, reflecting a broad genetic base in *B. juncea*.

The mean performance of the parents, F₁, and F₂ populations showed considerable variation across nearly all traits. Characters such as the number of siliquae per plant, number of secondary branches per plant, biological yield per plant, and seed yield per plant displayed wide ranges, highlighting the presence of strong variability and the potential for effective selection. The mean seed yield per plant was 15.31 g in parents, 15.32 g in F₁, and 13.68 g in F₂, while the number of siliquae per plant ranged from 274.51 in parents to 282.33 in F₁ and 257.56 in F₂. This pattern demonstrated inheritance of desirable yield attributes and segregation within the F₂ population. Comparable findings were reported by Patel *et al.* (2021) [12] and Duluri Sowmya *et al.* (2024) [6], who also recorded large variability among mustard genotypes for yield-related traits and emphasized its effective utilization in selection programmes.

The genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) values exhibited noticeable variation across the traits studied. In all three generations, PCV values were slightly higher than their corresponding GCV values, suggesting a moderate environmental influence on trait expression. However, the small differences between GCV and PCV for key yield traits such as number of siliquae per plant, biological yield, and seed yield per plant indicated that these traits are predominantly governed by genetic factors and can be improved through direct selection. High GCV and PCV values for number of secondary branches, leaf area index, biological yield, and seed yield reflected substantial inherent genetic variability, a prerequisite for effective breeding progress. Similar conclusions were drawn by Perween *et al.* (2024) [13] and Verma *et al.* (2023) [19], who noted that traits with high GCV and PCV in mustard populations reliably indicate strong genetic potential.

Heritability estimates were high for most characters across all three generations. Traits such as days to 50% flowering, days to maturity, plant height, number of siliquae per plant, 1000-seed weight, biological yield per plant, oil content, and seed yield per plant recorded heritability values above 80%, suggesting that much of the observed variation is heritable. High heritability implies that these traits are mainly controlled by additive gene action and can be effectively improved through phenotypic selection. Similar high heritability for seed yield and its component traits has been reported by Choudhary *et al.* (2025) ^[4], Sharma *et al.* (2025) ^[15], and Gupta *et al.* (2025) ^[7], supporting the reliability of selection for these attributes in mustard breeding.

The estimates of genetic advance (GA) and genetic advance as percent of mean (GAM) provided additional insight into the expected genetic improvement under selection. High GA and GAM were recorded for number of secondary branches per plant, leaf area index, number of siliquae per plant, biological yield per plant, and seed yield per plant, indicating the predominance of additive gene action and strong potential for genetic improvement through selection. Moderate genetic advance was observed for traits such as days to flowering, raceme length, and 1000-seed weight,

suggesting that recurrent selection over successive generations could enhance these traits. Conversely, low genetic advance for oil and protein content indicated that these characters are largely influenced by non-additive gene effects and may require hybridization or multi-environment testing for improvement. Similar observations were made by Patel *et al.* (2021) ^[12], Duluri Sowmya *et al.* (2024) ^[6], and Devi *et al.* (2024) ^[5], who reported that yield and its component traits with high heritability and genetic advance are primarily controlled by additive genes, whereas quality traits show stronger environmental influence.

High GAM values were observed for number of secondary branches per plant (42.84% in parents), leaf area index (43.58% in parents and 60.17% in F₁ and F₂), number of siliquae per plant (32.51% in parents and 28.51% in F₂), biological yield (31.22% in parents and 27.87% in F₂), and seed yield per plant (35.86% in parents and 27.23% in F₂). These results reaffirmed that these characters are under additive genetic control. Comparable results were reported by Verma *et al.* (2023) ^[19] and Mehta (2025) ^[10], who concluded that high GAM associated with high heritability reflects additive gene action and suggests that simple selection would be effective in mustard improvement.

Table 1.1: Combined analysis of variance of parents for 20 characters in 10 x 10 diallel cross of Indian mustard (*Brassica juncea* L.) for various agronomic and biochemical traits:

Sourced of variation	df	Days of 50(%) flowering	Days to maturity	Plant height (cm)	Length of main raceme (cm)	Leaf area index	Chlorophyll content (mg/g)	Number of primary branches/Plant	Number of secondary branches/Plant	Number of siliquae/Plant	Number of seeds/Plant
Replication	2	0.533	1.033	20.62	1.873	0.001956	19.219	1.2443	1.417	81.5	0.0601
Treatment	9	6.459**	122**	1035.62**	131.862**	0.297684**	36.311**	3.7371**	22.1902**	6108**	7.1918**
Error	18	0.681	0.922	16.66	6.872	0.000744	12.143	0.8751	1.2103	124.7	0.3555

Sourced of variation	df	Biological yield/Plant	1000-seed weight (g)	Harvest index (%)	Oil content (%)	Protein (%)	Tryptophan content (%)	Methionine content (%)	Erucic acid	Linoleic acid content (%)	Seed yield/Plant
Replication	2	0.397	0.00177	0.345	0.1516	1.0536	0.000043	0.00025	7.14	0.2485	0.3159
Treatment	9	221.544**	0.44971**	8.5209**	18.9197**	9.3605**	0.1110**	0.158**	796.8**	6.6622**	23.4193**
Error	18	4.527	0.00984	1.9806	0.2067	2.517	0.000151	0.000217	8.23	1.1198	0.5579

Table 1.2: Combined analysis of variance of F₁ for 20 characters in 10 x 10 diallel cross of Indian mustard (*Brassica juncea* L.) for various agronomic and biochemical traits:

Sourced of variation	df	Days of 50(%) flowering	Days to maturity	Plant height (cm)	Length of main raceme (cm)	Leaf area index	Chlorophyll content (mg/g)	Number of primary branches/Plant	Number of secondary branches/Plant	Number of siliquae/Plant	Number of seeds/Plant
Replication	2	1.70	3.39	195.84	7.51	0.00	14.17	0.01	0.43	248.94	0.20
Treatment	9	85.23**	83.58**	522.27**	84.14**	0.56**	34.99**	2.17**	13.95**	2938.18**	6.03**
Error	18	0.47	0.76	125.50	17.57	0.00	6.58	0.13	0.38	266.62	0.69

Sourced of variation	df	Biological yield/Plant	1000-seed weight (g)	Harvest index (%)	Oil content (%)	Protein (%)	Tryptophan content (%)	Methionine content (%)	Erucic acid	Linoleic acid content (%)	Seed yield/Plant
Replication	2	18.70	0.05	2.96	8.07	2.15	0.00	0.00	2.36	0.12	0.53
Treatment	9	172.56**	0.42**	57.63**	15.02**	9.12**	0.11**	0.15**	4.34**	265.49**	13.64**
Error	18	10.71	0.05	4.51	5.84	2.18	0.01	0.01	1.16	4.86	0.60

Table 1.3: Combined analysis of variance of F₂ for 20 characters in 10 x 10 diallel cross of Indian mustard (*Brassica juncea* L.) for various agronomic and biochemical traits:

Sourced of variation	df	Days of 50(%) flowering	Days to maturity	Plant height (cm)	Length of main raceme (cm)	Leaf area index	Chlorophyll content (mg/g)	Number of primary branches/Plant	Number of secondary branches/Plant	Number of siliquae/Plant	Number of seeds/Plant
Replication	2	5469.100	0.120	40.070	5.259	0.000	1.534	0.058	0.243	95.500	0.717
Treatment	9	76.800**	340.390**	969.600**	106.301**	0.558**	44.853**	2.644**	14.894**	4572.200**	8.491**
Error	18	19.900	0.350	117.770	13.329	0.001	7.377	0.135	0.637	210.100	0.692

Sourced of variation	df	Biological yield/Plant	1000-seed weight (g)	Harvest index (%)	Oil content (%)	Protein (%)	Tryptophan content (%)	Methionine content (%)	Erucic acid	Linoleic acid content (%)	Seed yield/Plant
Replication	2	5.600	0.027	3.076	14.701	0.827	0.003	0.003	0.336	3.400	0.267
Treatment	9	183.254**	0.637**	65.984**	14.531**	7.911**	0.106**	0.153**	4.430**	347.460**	12.135**
Error	18	8.762	0.045	4.637	5.105	2.198	0.007	0.010	1.161	3.650	0.652

s*, ** significant at 5% and 1% level, respectively

Table 1.4: Combined analysis of variance of parents, F₁ and F₂ for 20 characters in 10 x 10 diallel cross of Indian mustard (*Brassica juncea* L.) for various agronomic and biochemical traits:

Sourced of variation	df	Days of 50(%) flowering	Days to maturity	Plant height (cm)	Length of main raceme (cm)	Leaf area index	Chlorophyll content (mg/g)	Number of primary branches/Plant	Number of secondary branches/Plant	Number of siliquae/Plant	Number of seeds/Plant
Replication	2	2409.94	2409.94	2409.94	2409.94	2409.94	2409.94	2409.94	2409.94	2409.94	2409.94
Treatment	54	134.75	134.75	134.75	134.75	134.75	134.75	134.75	134.75	134.75	134.75
PAR	9	116.46	116.46	116.46	116.46	116.46	116.46	116.46	116.46	116.46	116.46
F ₁	44	85.22	85.22	85.22	85.22	85.22	85.22	85.22	85.22	85.22	85.22
F ₂	44	76.80	340.39	969.60	106.30	0.56	44.85	2.64	14.89	4572.19	8.49
PVF ₁	1	676.51	676.51	676.51	676.51	676.51	676.51	676.51	676.51	676.51	676.51
F ₁ VF ₂	1	612.79	612.79	612.79	612.79	0.00	325.01	325.01	325.01	325.01	325.01
Error	243	39.11	39.11	39.11	39.11	39.11	39.11	39.11	39.11	39.11	39.11
Total	299	72.24	87.92	334.48	43.32	0.17	19.00	0.97	5.34	1580.12	2.80

Sourced of variation	df	Biological yield/Plant	1000-seed weight (g)	Harvest index (%)	Oil content (%)	Protein (%)	Tryptophan content (%)	Methionine content (%)	Erucic acid	Linoleic acid content (%)	Seed yield/Plant
Replication	2	2409.94	2409.94	2409.94	2409.94	2409.94	2409.94	2409.94	2409.94	2409.94	2409.94
Treatment	54	134.75	134.75	134.75	134.75	134.75	134.75	134.75	134.75	134.75	134.75
PAR	9	116.46	116.46	116.46	116.46	116.46	116.46	116.46	116.46	116.46	116.46
F ₁	44	85.22	85.22	85.22	85.22	85.22	85.22	85.22	85.22	85.22	85.22
F ₂	44	183.25	0.64	65.98	14.53	7.91	0.11	0.15	347.46	4.43	12.14
PVF ₁	1	676.51	676.51	676.51	676.51	676.51	676.51	676.51	676.51	676.51	676.51
F ₁ VF ₂	1	325.01	325.01	325.01	325.01	325.01	325.01	325.01	325.01	325.01	325.01
Error	243	39.11	39.11	39.11	39.11	39.11	39.11	39.11	39.11	39.11	39.11
Total	299	66.95	0.21	21.92	10.74	4.43	0.04	0.06	130.17	91.47	5.58

Table 1.5: Genetic variability, Mean, range and coefficient of variation for 20 characters derived from 10 parental diallel cross in Indian mustard (*Brassica juncea* L.) in parents:

Genotypes	Mean	Min	Max	var (g)	var (p)	Heritability (%)	GA	GA% mean	GCV (%)	PCV (%)
Days of 50(%) flowering	54.13	46.00	63.00	38.59	39.27	0.9826	12.68	23.43	11.47	11.576
Days to maturity	120.67	108	129	40.35	41.2815	0.9777	12.94	10.72	5.26	5.32
Plant height (cm)	175.98	139.6	198.7	339.65	356.31	0.95	37.07	21.06	10.47	10.73
Length of main raceme (cm)	68.05	55.39	79.26	41.66	48.53	0.85	12.32	18.1	9.49	10.24
Leaf area index	1.48	1.03	1.93	0.099	0.099	0.99	0.646	43.58	21.23	21.3
Chlorophyll content (mg/g)	44.41	33.8	52.9	8.05	20.19	0.39	3.69	8.31	6.39	10.12
Number of primary branches/Plant	6.22	3.8	8.4	0.95	1.82	0.52	1.45	23.35	15.69	21.73
No. of secondary branches/Plant	11.74	5.4	15.6	6.99	8.20	0.85	5.03	42.84	22.53	24.4
Number of siliquae/Plant	274.51	195.1	339	1994.43	2119.14	0.94	89.25	32.51	16.27	16.77
Number of seeds/Plant	14.13	11.78	17	2.278	2.63	0.86	2.89	20.47	10.68	11.48
Biological yield/Plant	54.44	41.2	68.9	72.33	76.86	0.94	17	31.22	15.62	16.1
1000-seed weight (g)	3.86	3.1	4.4	0.14	0.15	0.93	0.764	19.78	9.92	10.24
Harvest index (%)	28.07	22.98	31.39	2.18	4.16	0.52	2.2	7.84	5.26	7.27
Oil content (%)	44.33	41	49.81	6.23	6.44	0.96	5.06	11.42	5.63	5.73
Protein (%)	23.13	19.32	26.54	2.28	4.79	0.47	2.15	9.28	6.53	9.47
Tryptophan content (%)	1.85	1.52	2.22	0.037	0.0372	0.99	0.39	21.35	10.39	10.42
Methionine content (%)	2.31	1.93	2.62	0.05	0.05	0.99	0.47	20.44	9.94	9.96
Erucic acid	45.65	14.52	64.58	262.85	271.08	0.96	32.89	72.05	35.52	36.07
Linoleic acid content (%)	17.37	15.2	21.5	1.84	2.96	0.62	2.21	12.72	7.82	9.92
Seed yield/Plant	15.31	10.6	20.3	7.62	8.17	0.93	5.49	35.86	18.03	18.68

Table 1.6: Genetic variability, Mean, range and coefficient of variation for 2 characters derived from 10 parental diallel cross in Indian mustard (*Brassica juncea* L.) in F₁:

Genotypes	Mean	Min	Max	var (g)	var (p)	Heritability (%)	GA	GA% mean	GCV (%)	PCV (%)
Days of 50(%) flowering	54.10	43.00	67.00	28.25	28.72	98.37	10.86	20.07	9.82	9.91
Days to maturity	120.35	106.00	130.00	27.61	28.36	97.33	10.68	8.87	4.37	4.43
Plant height (cm)	184.28	147.83	217.63	132.26	257.75	51.31	16.97	9.21	6.24	8.71
Length of main raceme (cm)	70.12	55.06	81.71	22.19	39.76	55.82	7.25	10.34	6.72	8.99
Leaf area index	1.47	0.51	2.61	0.19	0.19	99.68	0.89	60.17	29.26	29.31
Chlorophyll content (mg/g)	44.47	34.10	53.71	9.47	16.05	58.99	4.87	10.95	6.92	9.01
Number of primary branches/Plant	6.51	4.72	8.87	0.68	0.81	83.45	1.55	23.83	12.67	13.86
No. of secondary branches/Plant	12.41	7.62	20.29	4.52	4.90	92.34	4.21	33.94	17.14	17.84
Number of siliquae/Plant	282.33	204.09	368.48	890.52	1157.14	76.96	53.93	19.10	10.57	12.05
Number of seeds/Plant	14.38	11.17	18.07	1.78	2.47	71.93	2.33	16.20	9.27	10.93
Biological yield/Plant	55.32	37.24	72.93	53.95	64.66	83.43	13.82	24.98	13.28	14.54
1000-seed weight (g)	3.94	3.00	4.69	0.12	0.17	71.54	0.61	15.52	8.91	10.53
Harvest index (%)	28.08	16.84	44.36	17.71	22.22	79.69	7.74	27.56	14.99	16.79
Oil content (%)	39.59	33.88	46.84	3.06	8.90	34.41	2.11	5.34	4.42	7.53
Protein (%)	24.42	20.64	30.48	2.32	4.49	51.54	2.25	9.21	6.23	8.68
Tryptophan content (%)	1.82	1.35	2.38	0.03	0.04	81.55	0.34	18.45	9.92	10.98
Methionine content (%)	2.30	1.80	2.88	0.05	0.06	82.07	0.41	17.74	9.51	10.49
Erucic acid	18.55	15.51	22.45	1.06	2.22	47.73	1.47	7.90	5.55	8.03
Linoleic acid content (%)	38.40	14.19	59.37	86.88	91.74	94.70	18.69	48.66	24.27	24.94
Seed yield/Plant	15.32	10.59	20.40	4.35	4.94	87.92	4.03	26.28	13.61	14.51

Table 1.7: Genetic variability, Mean, range and coefficient of variation for 20 characters derived from 10 parental diallel cross in Indian mustard (*Brassica juncea* L.) in F₂:

Genotypes	Mean	Min	Max	var (g)	var (p)	Heritability (%)	GA	GA% mean	GCV (%)	PCV (%)
Days of 50(%) flowering	51.09	33.54	74.00	18.97	38.86	48.81	6.27	12.27	8.52	12.20
Days to maturity	129.70	106.00	149.00	113.35	113.70	99.69	21.90	16.88	8.21	8.22
Plant height (cm)	178.86	126.50	232.43	283.94	401.72	70.68	29.18	16.32	9.42	11.21
Length of main raceme (cm)	67.40	52.21	85.79	30.99	44.32	69.93	9.59	14.23	8.26	9.88
Leaf area index	1.47	0.51	2.61	0.19	0.19	99.68	0.89	60.17	29.26	29.31
Chlorophyll content (mg/g)	42.37	32.29	57.19	12.49	19.87	62.87	5.77	13.63	8.34	10.52
Number of primary branches/Plant	6.29	4.37	8.55	0.84	0.97	86.08	1.75	27.78	14.54	15.67
No. of secondary branches/Plant	12.17	7.27	19.35	4.75	5.39	88.19	4.22	34.64	17.91	19.07
Number of siliquae/Plant	257.56	183.44	345.80	1454.02	1664.16	87.37	73.42	28.51	14.81	15.84
Number of seeds/Plant	14.41	9.73	19.24	2.60	3.29	78.97	2.95	20.48	11.19	12.59
Biological yield/Plant	52.55	35.39	72.14	58.16	66.93	86.91	14.65	27.87	14.51	15.57
1000-seed weight (g)	3.68	2.64	4.74	0.20	0.24	81.39	0.83	22.41	12.06	13.36
Harvest index (%)	26.50	14.58	44.59	20.45	25.09	81.51	8.41	31.74	17.07	18.90
Oil content (%)	38.91	33.54	47.08	3.14	8.25	38.10	2.25	5.79	4.56	7.38
Protein (%)	24.55	19.99	29.10	1.90	4.10	46.43	1.94	7.89	5.62	8.25
Tryptophan content (%)	1.82	1.35	2.38	0.03	0.04	81.55	0.34	18.45	9.92	10.98
Methionine content (%)	2.30	1.79	2.88	0.05	0.06	82.07	0.41	17.74	9.51	10.49
Erucic acid	19.13	15.76	22.53	1.09	2.25	48.42	1.50	7.82	5.46	7.84
Linoleic acid content (%)	36.45	13.54	58.96	114.60	118.25	96.92	21.71	59.56	29.37	29.83
Seed yield/Plant	13.68	9.23	19.22	3.83	4.48	85.44	3.73	27.23	14.30	15.47

Conclusion

The present investigation revealed highly significant genetic variability among parents, F₁, and F₂ generations for all agronomic and biochemical traits in Indian mustard. The higher estimates of heritability and genetic advance for key yield components such as number of siliquae per plant, biological yield, and seed yield per plant indicate that these traits are predominantly governed by additive gene action and can be effectively improved through direct selection. The narrow differences between genotypic and phenotypic coefficients of variation further suggest that environmental effects were minimal for these traits. Overall, the results confirm that simple selection based on these characters can lead to substantial improvement in seed yield, while quality traits with lower genetic advance may require hybridization or recurrent selection. These findings provide a strong genetic basis for developing high-yielding mustard cultivars suited to diverse growing conditions.

References

1. Abraham V. Pollination mechanism and floral biology of *Brassica* species. Indian J Genet Plant Breed. 1994;54(2):187-192.
2. Allard RW. Principles of plant breeding. New York: John Wiley and Sons; 1999.
3. Burton GW, De Vane EH. Estimating heritability in tall fescue from replicated clonal material. Agron J. 1953;45:478-481.
4. Choudhary R, Singh J, Barela A, Patel T, Yadav PK. Assessment of genetic variability and heritability in Indian mustard (*Brassica juncea* L.) genotypes. J Adv Biol Biotechnol. 2025;28(7):436-443.
5. Devi SA, Barua PK, Phukan A. Assessment of genetic variability for seed yield and related traits in some mutant and non-mutant lines of Indian mustard (*Brassica juncea* L.). J Exp Agric Int. 2024;46(4):48-55.

6. Duluri Sowmya IR, Ginoya AV. Genetic variability, correlation, path coefficient and cluster analysis in Indian mustard (*Brassica juncea* L.). Electron J Plant Breed. 2024;15(1):201-208.
7. Gupta KK, Singh MK, Singh SM, Raghuvanshi AK. Genetic variability, heritability, correlation and path analysis of quantitative traits in Indian mustard (*Brassica juncea* L.). J Exp Agric Int. 2025;47(6):27-33.
8. Johnson HW, Robinson HF, Comstock RE. Estimates of genetic and environmental variability in soybeans. Agron J. 1955;47:314-318.
9. Kumar A, Singh D, Sharma P. Genetic variability studies in Indian mustard (*Brassica juncea* L.). J Oilseeds Res. 2018;35(2):107-112.
10. Mehta H. Genetic variability of quantitative traits in Indian mustard (*Brassica juncea* L.). Int J Eng Appl Biol. 2025;10(5):23-31.
11. Panse VG, Sukhatme PV. Statistical methods for agricultural workers. New Delhi: ICAR; 1967.
12. Patel PB, Patel PJ, Patel JR, Patel PC. Elucidation of genetic variability and interrelationship studies for seed yield and quality traits in Indian mustard [*Brassica juncea* (L.) Czern. & Coss.]. Electron J Plant Breed. 2021;12(2):589-596.
13. Perween S, Kumar A, Chakraborty M, Ahmad E, Mahto CS, Barnwal MK. Assessment of genetic variability and diversity in Indian mustard (*Brassica juncea* L.) under timely and late sown conditions. J Adv Biol Biotechnol. 2024;27(10):331-341.
14. Saroj R, Singh AK, Singh S, Kumar R. Unraveling the relationship between seed yield and its components in Indian mustard (*Brassica juncea* L.). Front Plant Sci. 2021;12:125-128.
15. Sharma A, Tripathi MK, Dangi D, Mishra R. Genetic analysis for yield improvement in *Brassica* species: insights from variability and trait relationships. J Sci Res Rep. 2025;31(8):749-766.
16. Sharma HK, Kumar A, Singh VV, Meena HS, Sharma P, Rai PK. Variability and genetic diversity study based on agro-morphological traits in a diverse set of Indian mustard [*Brassica juncea* (L.) Czern. & Coss.] germplasm. J Environ Biol. 2021;42(6):1495-1504.
17. Singh P, Verma OP, Tiwari RK. Genetic variability and heritability in mustard. Environ Ecol. 2017;35(3A):1692-1696.
18. Singh RK, Chaudhry BD. Biometrical methods in quantitative genetic analysis. New Delhi: Kalyani Publishers; 1985.
19. Verma D, Pandey AP, Gaur RS, Bhagat A. Variability, heritability and genetic advance studies of mustard [*Brassica juncea* (L.)] genotypes at Satna District of Madhya Pradesh. Int J Plant Res. 2023;12(4):142-150.