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GENETIC DIVERSITY ASSESSMENT AND TRAIT ASSOCIATION IN INDIAN MUSTARD (*BRASSICA JUNCEA* L. CZERN& COSS) GENOTYPES FOR AGRO-MORPHOLOGICAL CHARACTERISTICS

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ABSTRACT

The present study was conducted at the Crop Research Centre, Sardar Vallabhbhai Patel University of Agriculture and Technology, Meerut, U.P., during the Rabi 2019-20 season to assess genetic variability, heritability, genetic advance, and trait associations in 45 Indian mustard (*Brassica juncea* L.) genotypes. A Randomized Complete Block Design with three replications was used to evaluate 14 quantitative traits. ANOVA revealed significant differences among genotypes, indicating substantial genetic variability. Traits such as plant height, number of branches, biological yield, and grain yield per plant exhibited moderate phenotypic and genotypic coefficients of variation (PCV and GCV). High heritability coupled with high genetic advance was observed for plant height, grain yield, length of the main shoot, number of secondary branches, and biological yield, suggesting the predominance of additive gene action. Genotypic correlations were generally higher than phenotypic correlations, with grain yield per plant showing significant positive associations with key yield-contributing traits. Path coefficient analysis identified biological yield, harvest index, plant height, siliqua length, and main shoot length as major direct contributors to grain yield, while biological yield and harvest index also had strong indirect effects. Genetic diversity analysis grouped the genotypes into seven clusters, with the highest inter-cluster distance observed between clusters I and VII, suggesting their potential for hybridization. Traits such as days to maturity, oil content, and grain yield contributed over 86% to total genetic divergence. The study highlights the potential for selecting superior genotypes and utilizing genetically diverse lines for hybrid development to enhance yield in Indian mustard.

***Keywords* :** Genetic variability, heritability, genetic advance, trait associations, *Brassica juncea*

Introduction

Indian mustard (*Brassica juncea* L. Czern& Coss.) is one of the most important oilseed crops cultivated in India, playing a vital role in the agricultural economy. It belongs to the *Brassicaceae* family and is widely grown due to its adaptability to diverse agro-climatic conditions, high oil content, and resistance to environmental stresses such as drought, salinity, and diseases. Indian mustard is a self-pollinated crop, though it exhibits an outcrossing rate of 20–30% The crop is predominantly cultivated for its oil, with the residual mustard cake commonly used as cattle feed. However, the presence of glucosinolates (18–120 µmoles/g in seed meal) limits its direct use as a protein source for human consumption. Rapeseed and mustard crops are the second most important oilseed group after groundnut, contributing approximately 25–30% of India's total oilseed production, Globally, rapeseed-mustard ranks as the third most significant oilseed crop after soybean and palm, with major producing countries including India, China, Canada, Germany, and Japan (Verma *et al*., 2016; Akansha *et al*., 2017). The leading mustard-producing states are Rajasthan (45%), Haryana (13%), Madhya Pradesh (13%), and Uttar Pradesh (11%), collectively accounting for 81.5% of the total cultivated area and 87.5% of the total production (Bahadur *et al*., 2021). The *Brassica* genus consists of three diploid species with distinct genomic compositions: *Brassica rapa* (AA, 2n = 20), *Brassica nigra* (BB, 2n = 16), and *Brassica oleracea* (CC, 2n = 18). Indian mustard (*B. juncea*) is an allotetraploid (AABB), resulting from natural hybridization between *B. rapa* and *B. nigra* (Verma *et al*., 2016). Mustard seeds contain approximately 30–46% oil and 17.8–22.0% protein, making them a valuable oilseed resource (Bahadur *et al.*, 2021). The economic importance of mustard in India is reflected in its contribution of 3% to the gross national product and 10% to total agricultural output (Statistical Yearbook of India, 2018). Despite its significant production, mustard yield is often constrained by environmental fluctuations and pest-disease incidences. The introduction of high-yielding and climate-resilient varieties is crucial to overcoming these challenges and improving mustard productivity.Genetic variability is the foundation of crop improvement, providing breeders with the necessary diversity to select for desirable agronomic traits (Ashana and Pandey, 1980; Ananda and Rawat, 1984). Understanding variability, heritability, and genetic advance helps determine the genetic potential of a crop and the effectiveness of selection in breeding programs. High heritability coupled with high genetic advance indicates additive gene action, which is crucial for effective selection (Verma *et al.*, 2016). Yield in mustard is a complex trait influenced by multiple quantitative factors. Correlation studies help in understanding the association between yield and its component traits, which aids in selection for breeding. However, correlation alone does not distinguish direct effects from indirect influences. To address this, path coefficient analysis is used to partition the correlation coefficients into direct and indirect effects, providing a more precise understanding of trait contributions to yield (Bahadur *et al.*, 2021). Additionally, genetic diversity analysis is essential for identifying diverse genotypes that can be used in hybridization programs to enhance genetic gains (Ashana and Pandey, 1980; Ananda and Rawat, 1984).The present study aims to Assess genetic variability, heritability, and genetic advance for yield and its contributing traits in Indian mustard genotypes, To evaluate the trait association, direct and indirect effects of yield components using correlation and path coefficient analysis and genetic diversity analysis to classify genotypes based on their divergence and potential for breeding programs. By understanding these genetic parameters, this research will contribute to the development of high-yielding, stress-tolerant mustard varieties, ultimately enhancing productivity and ensuring oilseed security in India.

Materials and Methods

Forty-five diverse genotypes (Table 1) of Indian mustard (*Brassica juncea* L. Czern& Coss.) were grown at Crop Research Centre, Sardar Vallabhbhai Patel University of Agriculture and Technology, Meerut (U.P.) during the *rabi* season of 2019-20 in randomized block design in three replications with row to row and plant to plant distance of 45 × 30 cm. Recommended cultural practices were used to raise a good crop. Five competitive plants were randomly selected from each entry in each replication and were tagged for recording detailed field observations for fourteen traits including days to 50% flowering, days to maturity, plant height (cm), number of primary branches per plant, number of secondary branches per plant, length of main shoot (cm), number of siliquae on main shoot, siliqua length (cm), number of seeds per siliqua, test weight (g), oil content (%), harvest index (%), biological yield per plant (g) and grain yield per plant (g). For statistical analysis, we used a randomized block design to determine the significance of variance among the genotypes. We applied statistical methods in line with the recommendations of Panse and Sukhatme (1969) to analyze the mean values of all quantitative traits, while coefficients of variation were calculated using the formula proposed by Burton (1952). Additionally, we estimated Broad Sense heritability and genetic advance as a percentage of the mean using the formulas introduced by Allard (1960) and Johnson *et al.* (1955), respectively. The analysis of Correlation was estimated the association between various character-pairs as suggested by Searle (1961). Path-coefficient was conducted following the procedure suggested by Wright (1921) and as elaborated by Dewey and Lu (1959). Mahalanobis (1936) D^2 statistics was used for assessing genetic divergence among all the genotypes. The clustering of D^2 values was done using Tocher's method as described by Rao (1952), while the intra and inter-cluster distances were calculated using the formula given by Singh and Choudhary (1985).

Table 1 : List of germplasm with their source

S. No.	Germplasm	Source/origin
1	UJM-1	Zonal Research Station, Ujhani, Badaun
2	UJM-2	Zonal Research Station, Ujhani, Badaun
5	UJM-3	Zonal Research Station Ujhani, Badaun
4	UJM-4	Zonal Research Station Ujhani, Badaun
5	UJM-5	Zonal Research Station, Ujhani, Badaun
6	UJM-6	Zonal Research Station, Ujhani, Badaun
7	UJM-7	Zonal Research Station, Ujhani, Badaun
8	UJM-8	Zonal Research Station, Ujhani, Badaun
9	UJM-9	Zonal Research Station, Ujhani, Badaun
10	UJM-10	Zonal Research Station, Ujhani, Badaun
11	UJM-11	Zonal Research Station, Ujhani, Badaun
12	UJM-12	Zonal Research Station, Ujhani, Badaun
13	UJM-13	Zonal Research Station, Ujhani, Badaun
14	UJM-14	Zonal Research Station, Ujhani, Badaun
15	UJM-15	Zonal Research Station, Ujhani, Badaun
16	UJM-16	Zonal Research Station, Ujhani, Badaun
17	UJM-17	Zonal Research Station, Ujhani, Badaun
18	UJM-18	Zonal Research Station, Ujhani, Badaun
19	UJM-19	Zonal Research Station, Ujhani, Badaun
20	UJM-20	Zonal Research Station, Ujhani, Badaun
21	UJM-21	Zonal Research Station, Ujhani, Badaun
22	UJM-22	Zonal Research Station, Ujhani, Badaun
23	UJM-23	Zonal Research Station, Ujhani, Badaun
24	UJM-24	Zonal Research Station, Ujhani, Badaun
25	UJM-25	Zonal Research Station, Ujhani, Badaun
26	UJM-26	Zonal Research Station, Ujhani, Badaun
27	UJM-27	Zonal Research Station, Ujhani, Badaun
28	UJM-28	Zonal Research Station, Ujhani, Badaun
29	UJM-29	Zonal Research Station, Ujhani, Badaun
30	Shivalik	DRMR, Bharatpur,
31	Pusa Bahar	DRMR, Bharatpur
32	Pusa Mustard-22	DRMR, Bharatpur
33	CS-54	DRMR, Bharatpur
34	GM-2	DRMR, Bharatpur
35	Saurabh	DRMR, Bharatpur
36	Aravali	DRMR, Bharatpur
37	RLM-619	DRMR, Bharatpur
38	Jawahar	DRMR, Bharatpur

	Mustard-1	
39	Jagannath	DRMR, Bharatpur
40	DRMR-IJ-31	DRMR, Bharatpur
41	BR-40	DRMR, Bharatpur
42	Geeta	DRMR, Bharatpur
43	Kranti	DRMR, Bharatpur
44	Gujarat Mustard-1	DRMR, Bharatpur
45	RH-819	DRMR, Bharatpur

Results and Discussion

Analysis of Variance and Mean Performance

The analysis of variance in Table 1 reveals a notable level of significance concerning mean squares attributed to various genotypes across all fourteen characteristics, which encompass days to 50% flowering, days to maturity, plant height (cm), number of primary branches per plant, number of secondary branches per plant, length of the main shoot (cm), number of siliquae on the main shoot, siliqua length (cm), number of seeds per siliqua, test weight (g), oil content (%), harvest index (%), biological yield per plant (g), and grain yield per plant (g). This implies the existence of substantial variability among the distinct genotypes. The observed range of variation spans from 0.363 (for siliqua length) to 3380.80 (for biological yield per plant). These findings align with previous studies conducted by Joya *et al.* (2016), Devi (2018), and Rout *et al.* (2019), all of which reported high levels of genetic variation. The mean performance of forty-five genotypes of Indian mustard for fourteen quantitative traits revealed significant variation (Table 2). Days to 50% flowering ranged from 48 days (Jagannath) to 64.67 days (UJM-12), with an overall mean of 55.59 days. Days to maturity varied between 141.33 days (BR-40) and 151.67 days (Geeta), with a mean of 146.46 days. Plant height showed substantial variation, from 192.22 cm (Shivalik) to 358.80 cm (GM-2), with a mean of 233.45 cm. The number of primary branches per plant ranged from 4.25 (UJM-1) to 6.89 (Pusa Mustard-22), averaging 5.57, while secondary branches ranged from 11.45 (UJM-15) to 20.33 (GM-2), with an overall mean of 15.73.

Table 2 : Analysis of variances (ANOVA) for fourteen characters of forty- five genotypes in Indian mustard (*Brassica juncea* L.)

Source of variation	DF	Days to 50% flowering	Days to maturity	Plant height (cm)	Number of primary branches per plant	Number of secondary branches per plant	Length of main shoot (cm)	Number of siliquae on main shoot
Replication	2	2.50	0.72	9.60	0.11	0.20	19.70	11.79
Treatment	44	54.58**	20.56**	5958.93**	1.33**	14.50**	451.27**	60.23**
Error	88	5.23	3.45	94.09	0.06	0.40	11.68	3.80

Source of variation	DF	Siliqua length (cm)	Number of seeds per siliqua	Test weight (g)	Oil content (%)	Harvest index (%)	Biological yield per plant (g)	Grain yield per plant (g)
Replication	2	0.060	0.336	0.049	0.196	0.33	60.55	0.51
Treatment	44	0.363**	1.196**	0.724**	0.956**	19.05**	3380.80**	274.45**
Error	88	0.032	0.166	0.031	0.106	2.51	103.92	5.10

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

Table 3 : Mean performance of 45 Indian mustard genotypes (*Brassica juncea* L.)

S. No.	Geno-types	Days to 50% flowering	Days to maturity	Plant height (cm)	Number of primary branche per plant	secondary branches per	Length of main shoot (cm)	Number of siliquae on main shoot	Siliqua length (cm)	Number of seeds per siliqua	Test weight (g)	Oil content (%)	Harvest index (%)	Biological yield per plant (g)	Grain yield per plant (g)
1	UJM-29	55.67	144.00	265.40	6.11	15.33	96.67	54.22	4.59	14.38	4.62	41.47	27.58	228.67	62.98
2	UJM-28	57.33	144.00	196.11	5.66	13.34	75.78	44.22	4.35	13.63	4.53	41.60	23.87	224.67	53.58
3	UJM-27	54.67	143.67	218.89	5.33	14.55	73.55	46.52	4.00	13.67	3.87	41.34	20.89	270.67	56.34
4	UJM-26	56.67	143.33	245.50	6.33	15.44	92.78	54.00	4.88	14.93	4.73	41.38	25.52	246.33	62.89
5	UJM-25	52.00	144.67	251.50	6.11	16.34	92.78	55.26	5.00	14.49	4.55	41.25	24.47	259.33	63.48
6	UJM-24	56.00	144.33	218.22	5.33	15.78	73.89	49.55	4.56	13.96	3.63	41.33	22.29	224.00	49.92
7	UJM-23	57.33	149.67	217.78	5.44	13.00	80.55	48.78	4.70	13.57	4.23	41.20	21.20	265.00	56.17
8	UJM-22	56.00	149.00	201.22	5.11	15.45	71.11	44.67	4.63	13.36	4.40	41.42	26.59	197.67	52.58
9	UJM-21	61.67	148.00	220.55	5.78	14.78	79.33	49.66	4.66	13.59	3.83	41.32	22.92	248.67	56.82
10	UJM-20	61.33	148.67	202.22	5.78	14.56	82.22	48.52	4.67	13.71	4.30	41.21	23.19	198.00	45.84
11	UJM-19	58.33	144.33	226.67	5.89	13.33	76.78	45.52	4.66	13.40	4.33	41.30	22.13	211.00	46.67
12	UJM-18	60.00	143.67	209.45	5.00	14.44	69.55	46.44	4.55	13.56	4.17	41.20	22.15	199.00	43.92

13	UJM-17	62.67	142.00	217.22	5.67	14.44	78.33	49.22	4.72	13.75	3.90	41.15	22.89	237.00	54.28
14	UJM-16	59.67	145.00	208.89	5.44	14.33	84.00	43.45	4.43	13.39	4.70	41.73	21.73	244.33	52.95
15	UJM-15	55.67	147.33	211.67	4.56	11.45	68.00	47.67	4.10	12.83	4.07	41.62	20.13	219.33	44.00
16	UJM-14	60.33	148.00	306.50	6.75	18.39	113.11	55.00	4.86	14.60	4.88	41.63	24.46	315.33	77.00
17	UJM-13	58.67	145.33	205.56	6.42	19.45	104.55	52.42	4.97	14.62	4.90	41.44	24.18	305.00	73.77
18	UJM-12	64.67	143.00	212.78	5.67	15.00	72.44	41.89	4.55	14.49	4.43	41.66	24.74	240.33	59.46
19	UJM-11	56.33	143.67	275.50	6.56	18.22	88.33	48.52	4.88	13.87	4.87	41.55	24.93	247.67	61.73
20	UJM-10	60.33	147.67	208.89	5.00	16.22	61.44	46.56	4.39	13.34	3.60	41.24	22.89	235.67	53.95
21	UJM-9	50.67	142.33	204.67	5.34	16.33	76.89	46.00	4.13	13.13	4.49	41.45	23.80	238.67	56.64
22	UJM-8	59.00	148.00	220.66	5.89	16.44	72.22	46.22	4.32	13.66	3.80	41.06	23.13	242.33	56.05
23	UJM-7	50.33	147.00	212.22	5.44	14.67	74.78	46.11	4.52	13.60	4.40	41.13	21.90	214.00	46.83
24	UJM-6	54.67	143.00	216.66	4.67	13.89	82.00	44.67	4.45	13.18	4.47	41.51	21.37	222.00	47.37
25	UJM-5	52.00	147.67	295.50	6.78	17.44	79.67	53.56	4.93	14.28	4.97	41.53	26.10	245.00	63.76
26	Shivalik	49.33	149.33	192.22	5.00	15.56	67.78	45.33	4.08	14.02	3.57	41.53	21.98	252.00	55.34
27	RH-819	50.67	148.00	211.67	4.55	15.11	78.55	43.78	4.60	14.09	4.37	41.37	22.32	263.33	58.57
28	UJM-3	60.00	150.33	207.78	5.00	13.00	65.56	49.55	4.32	13.69	4.20	41.49	23.41	203.67	47.69
29	UJM-1	62.00	149.33	220.00	4.44	11.56	77.50	60.45	4.27	13.58	4.63	41.27	25.89	228.33	58.96
30	UJM-2	57.67	147.33	200.00	6.55	13.33	78.56	40.22	4.28	13.42	3.99	40.28	16.52	299.00	49.33
31	Pusa Bahar	49.33	147.00	225.50	6.22	17.33	82.56	49.55	4.64	14.71	4.47	40.38	28.78	212.67	61.15
32	Pusa Mustard-22	56.67	149.00	352.50	6.89	20.33	115.52	57.52	5.13	15.23	5.30	40.27	32.02	256.67	81.89
33	CS-54	58.00	146.33	222.22	5.55	18.33	87.22	50.33	4.87	13.98	4.75	40.22	25.22	259.33	65.34
34	GM-2	54.33	147.67	358.80	6.56	19.89	108.50	56.00	5.11	15.08	5.73	40.51	25.68	313.67	80.43
35	Saurabh	49.33	142.67	287.50	5.33	17.55	79.11	52.00	4.66	14.35	3.57	40.23	23.93	263.33	62.97
36	Aravali	55.00	149.33	225.40	5.67	16.00	73.33	47.52	4.24	12.56	4.13	40.09	22.62	259.33	58.68
37	RLM-619	54.67	149.67	249.50	5.44	19.22	75.25	48.52	4.75	14.09	4.97	40.27	20.42	306.33	62.46
38	Jawahar Mustard-1	50.67	146.00	337.45	5.56	18.55	96.74	51.52	5.02	14.36	5.33	40.16	23.19	315.67	72.93
39	Jagannath	48.00	150.33	335.50	5.78	19.78	93.52	52.55	4.04	14.58	5.27	40.27	23.65	308.67	72.75
40	DRMR-IJ-31	48.33	147.67	200.00	5.00	13.78	73.89	47.22	4.25	14.16	4.37	40.16	26.46	214.67	56.65
41	BR-40	54.67	141.33	195.00	5.22	14.00	66.11	49.11	4.18	13.09	4.17	40.25	23.74	231.67	54.95
42	Geeta	54.00	151.67	219.00	5.11	14.00	83.89	52.56	3.75	12.87	4.20	40.30	24.13	243.33	58.64
43	Kranti	49.33	147.00	200.00	4.67	16.56	77.22	43.00	4.32	13.82	4.27	40.23	23.19	242.67	56.20
44	Gujarat Mustard-1	53.33	146.00	199.56	5.89	16.22	73.33	46.34	4.19	13.18	4.67	40.37	23.26	233.67	54.15
45	UJM-4	54.00	147.33	195.56	4.25	15.33	77.00	41.00	3.67	12.78	4.07	40.32	20.31	193.67	39.19
	Mean	55.59	146.46	233.45	5.57	15.73	81.15	48.73	4.51	13.84	4.42	40.99	23.59	246.25	57.94
	Max	48.00	141.33	192.22	4.25	11.45	61.44	40.22	3.67	12.56	3.57	40.09	16.52	193.67	39.19
	Min	64.67	151.67	358.80	6.89	20.33	115.52	60.45	5.13	15.23	5.73	41.73	32.02	315.67	81.89
	SE(d)	1.87	1.52	7.92	0.19	0.52	2.79	1.59	0.15	0.33	0.14	0.27	1.29	8.32	1.84
	C.D. at 5%	3.72	3.02	15.77	0.39	1.03	5.56	3.17	0.29	0.66	0.29	0.53	2.57	16.57	3.67
	C.V. (%)	4.12	1.27	4.16	4.25	4.03	4.21	4.00	4.00	2.94	3.97	0.79	6.71	4.14	3.90

The length of the main shoot varied from 61.44 cm (UJM-10) to 115.52 cm (Pusa Mustard-22), averaging 81.15 cm. The number of siliquae on the main shoot ranged from 40.22 to 60.45, with a mean of 48.73. Siliqua length varied between 3.67 cm (UJM-4) and 5.13 cm (Pusa Mustard-22), averaging 4.51 cm. The number of seeds per siliqua ranged from 12.56 (Aravali) to 15.23 (Pusa Mustard-22), with a mean of 13.84. Test weight ranged from 3.57 g (Saurabh) to 5.73 g (GM-2), averaging 4.42 g. biological yield per plant varied from 193.67 g to 315.67 g, with Jawahar Mustard-1 having the highest and UJM-4 the lowest biomass, with a mean of 246.25 g. The harvest index ranged from 16.52% (UJM-2) to 32.02% (Pusa Mustard-22), averaging 23.59%. Oil content varied from 40.09% (Aravali) to 41.73% (UJM-16), with an overall mean of 40.99%. Grain yield per plant ranged widely from 39.19 g (UJM-4) to 81.89 g (Pusa Mustard-22), averaging 57.94 g. These variations highlight the potential of different genotypes for trait-specific improvement in mustard breeding programs.

Variability analysis

The inherent variability in genotypic and phenotypic factors lacks a definitive threshold, making it difficult to classify them as either low or high. As a result, using absolute values for precise comparisons between two populations becomes impractical. To overcome this limitation, the genotypic and phenotypic coefficients of variation (GCV and PCV) offer a more effective means of comparing different metric traits within a population, as they remain independent of measurement units.In our study (as presented in Table-3), the findings reveal that GCV and PCV fall within the moderate range (10-20%) for several traits, including plant height (18.94 and 19.39), grain yield per plant (16.35 and 16.81), main shoot length (14.92 and 15.50), number of secondary branches per plant (13.78 and 14.35), biological yield per plant (13.42 and 14.05), number of primary branches per plant (11.68 and 12.43), harvest index (10.95 and 12.00), and test weight (10.89 and 11.59). In contrast, traits such as the number of siliquae on the main shoot (8.90 and 9.76), siliqua length (7.37 and 8.38), days to

50% flowering (7.30 and 8.38), number of seeds per siliqua (4.24 and 5.16), days to maturity (1.63 and 2.07), and oil content (1.30 and 1.52) exhibited lower values (<10%).The analysis of PCV and GCV demonstrated significant variability among the different genotypes across all fourteen studied traits. The minimal differences observed between PCV and GCV values suggest that environmental factors exerted a negligible influence on these traits, indicating that phenotype-based selection could be a reliable strategy. The moderate estimates of PCV and GCV for most traits further highlight the predominant role of genetic factors, with limited environmental impact. Consequently, these traits can be considered reliable for selection, and direct selection methods can be effectively utilized for their improvement. Similar findings have been previously reported by Rout *et al.* (2019), Tripathi *et al.* (2019), Gadi *et al.* (2020), and Singh *et al.* (2021).

Heartibility and Genetic Advanceanalysis

The heritability estimates were classified into three broad categories based on arbitrary thresholds: high heritability (>80%), moderate heritability (60-80%), and low heritability (<60%). Table 3 presents the broad-sense heritability (H²) estimates for the 14 traits examined. Traits such as plant height (95.41 cm), grain yield per plant (94.62 g), main shoot length (92.62 cm), number of secondary branches per plant (92.12), biological yield per plant (91.31 g), number of primary branches per plant (88.30 g), test weight (88.29), and number of siliquae on the main shoot (83.18) exhibited high to very high heritability. This indicates that genetic factors play a dominant role in the inheritance of these traits. Consequently, incorporating these traits into selection programs such as mass selection, progeny selection, or family selection can effectively exploit genetic diversity and facilitate the development of high-yielding genotypes.Traits such as siliqua length (77.27 cm), days to 50% flowering (75.87), oil content (72.87 g), harvest index (68.75%), number of seeds per siliqua (67.42), and days to maturity (62.35) showed moderate heritability. This suggests the presence of non-fixable genetic variance, likely due to dominance and epistatic interactions. High heritability values suggest that a substantial proportion of the observed trait variability is attributable to genetic factors, making these traits valuable for enhancing grain yield in breeding programs. However, heritability alone is not sufficient for effective genotype selection; additional insights into genetic advance are necessary. Genetic advance is categorized into three levels: high (>20%), moderate (10-20%), and low (<10%). Table 2 presents the expected genetic advance as a percentage of the mean for different traits

Table 4 : Estimates of range, GCV (%), PCV (%), Heritability h^2 % (BS), Genetic advance and genetic advance percentage of mean for fourteen characters in Indian mustard (*Brassica juncea* L.).

Characters	Range		Heritability h^2 (%) (BS)	GA	GA% mean	GCV (%)	PCV (%)
	Lowest	Highest					
Days to 50% flowering	48.00	64.67	75.87	7.28	13.09	7.30	8.38
Days to maturity	141.33	151.67	62.35	3.89	2.65	1.63	2.07
Plant height (cm)	192.22	358.80	95.41	88.97	38.11	18.94	19.39
Number of primary branches / plants	4.25	6.89	88.30	1.26	22.61	11.68	12.43
Number of secondary branches /plants	11.45	20.33	92.12	4.29	27.24	13.78	14.35
Length of main Shoot (cm)	61.44	115.52	92.62	24.00	29.57	14.92	15.50
Number of siliquae on main shoot	40.22	60.45	83.18	8.15	16.72	8.90	9.76
Siliqua length (cm)	3.67	5.13	77.27	0.60	13.34	7.37	8.38
Number of seeds per siliqua	12.56	15.23	67.42	0.99	7.16	4.24	5.16
Test weight(g)	3.57	5.73	88.29	0.93	21.08	10.89	11.59
Oil content %	40.09	41.73	72.87	0.94	2.28	1.30	1.52
Harvest index (%)	16.52	32.02	68.75	4.01	17.00	10.95	12.00
Biological yield per plant (g)	193.67	315.67	91.31	65.06	26.42	13.42	14.05
Grain yield per plant (g)	39.19	81.89	94.62	18.99	32.77	16.35	16.81

Traits such as plant height (38.11%), grain yield per plant (32.77%), main shoot length (29.57%), number of secondary branches per plant (27.24%), biological yield per plant (26.42%), number of primary branches per plant (22.61%), and test weight (21.08%) exhibited high genetic advance (>20%), indicating their suitability for selection in breeding programs. Moderate genetic advance was observed for traits like harvest index (17.00%), number of siliquae on the main shoot (16.72%), siliqua length (13.34%), and days to 50% flowering (13.09%). Conversely, traits such as the number of seeds per siliqua (7.16%), days to maturity (2.65%), and oil content (2.28%) exhibited low genetic advance. These findings align with previous reports by Chaurasiya *et al.* (2019), Awasthi *et al.* (2020), Yadav *et al.* (2021), and Singh *et al.* (2021).Traits such as plant height, grain yield per plant, main shoot length, number of secondary branches per plant, and biological yield per plant exhibited both high heritability and substantial genetic advance as a percentage of the mean. This suggests that their inheritance is primarily governed by additive genetic effects, making them promising targets for direct selection. These findings corroborate earlier research by Priyamedha *et al.* (2013), Singh *et al.* (2013), Chauhan *et al.* (2014), Bind *et al.* (2014), Meena *et al.* (2015), Sikarwar *et al.* (2017), and Maurya *et al.* (2018).In contrast, traits such as the number of primary branches per plant, test weight, number of siliquae on the main shoot, and siliqua length exhibited high heritability but moderate genetic advance. This indicates that dominance and epistatic effects contribute significantly to their inheritance, making selection for these traits less effective. Considering both heritability and genetic advance, selecting for traits such as plant height, grain yield per plant, main shoot length, number of secondary branches per plant, and biological yield per plant could be highly beneficial in developing high-yielding Indian mustard varieties.

Corelation analysis

Grain yield is a complex trait influenced by multiple quantitative characteristics, many of which exhibit strong associations with yield. Understanding these relationships is crucial for establishing effective selection criteria. In this study, correlation coefficients were estimated for fourteen traits at both the phenotypic and genotypic levels (Tables 4&5). The genotypic correlation coefficients were generally higher than the phenotypic correlations, suggesting a strong inherent association between these traits at the genetic level. This indicates that phenotypic selection based on these traits could be advantageous. Traits such as main shoot length, number of seeds per siliqua, plant height, number of secondary branches per plant, biological yield per plant, test weight, number of siliquae on the main shoot, number of primary branches per plant, siliqua length, and harvest index exhibited highly significant positive correlations with grain yield per plant at both the genotypic and phenotypic levels. This strong association may be due to gene linkage influencing these traits. Conversely, certain trait pairs exhibited highly significant negative correlations, including the number of secondary branches per plant and oil content; days to 50% flowering and the number of secondary branches per plant; days to maturity and oil content; oil content and biological yield per plant; oil content and grain yield per plant; plant height and oil content; and days to 50% flowering and plant height.

Table 5 : Correlations coefficients among fourteen characters in Indian mustard (*Brassica juncea L.*) at genotypic level.

Characters	Days to 50% Flowering	Days to Maturity	plant height (cm)	Number of Primary Branches / Plant	Number of Secondary Branches /Plant	Length of main Shoot (Cm)	Number of siliquae on Main Shoot	Siliqua length(cm)	Number of Seeds pe siliqua	Test weight (g)	Oil content %	Harvest Index (%)	Biological Yield per plant (g)	Grain Yield per plant (g)
Days to 50% Flowering	1	-0.088	-0.216*	0.143	-0.314**	-0.022	0.019	0.192*	-0.133	-0.135	0.490**	-0.107	-0.142	-0.171*
Days to Maturity			0.13	-0.103	0.096	0.054	0.179*	-0.163	-0.049	0.134	-0.289**	0.006	0.173*	0.131
plant height (cm)				0.586**	0.700**	0.759**	0.672**	0.555**	0.730**	0.685**	-0.252**	0.462**	0.609**	0.798**
Number of Primary Branches / Plant					0.582**	0.663**	0.441**	0.665**	0.634**	0.512**	-0.001	0.434**	0.459**	0.631**
Number of Secondary Branches / Plant						0.656**	0.362**	0.555**	0.675**	0.580**	-0.370**	0.433**	0.625**	0.788**
Length of main Shoot (Cm)							0.669**	0.606**	0.759**	0.736**	-0.103	0.520**	0.591**	0.819**
No of siliquae on Main Shoot								0.550**	0.561**	0.520**	-0.074	0.655**	0.342**	0.701**
siliqua length(cm)									0.863**	0.507**	0.137	0.494**	0.359**	0.599**
Number of Seeds per siliqua										0.625**	-0.038	0.652**	0.501**	0.813**
Test weight(g)											-0.161	0.500**	0.475**	0.702**
Oil content %												-0.086	-0.275**	-0.257**
Harvest Index (%)													-0.045	0.588**
Biological Yield per plant (g)														0.777**
Grain Yield per plant (g)														1

Table 6 : Correlations coefficient among fourteen characters in India mustard (*Brassica juncea L.*) at phenotypic level.

Characters	Days to 50% Flowering	Days to Maturity	plant height (cm)	Number of Primary Branches / Plant	Number of Secondary Branche /Plant	Length of main Shoot (Cm)	Number of siliquae on Main Shoot	siliqua length (cm)	Number of Seeds per siliqua	Test weight (g)	Oil content %	Harvest Index (%)	Biological Yield per plant (g)	Grain Yield per plant (g)
Days to 50% Flowering	1	-0.09	-0.167	0.092	-0.242**	-0.033	0.025	0.161	-0.113	-0.113	0.370**	-0.022	-0.131	-0.118
Days to Maturity			0.1	-0.045	0.051	0.03	0.136	-0.147	-0.007	0.081	-0.191*	0.063	0.105	0.122
plant height (cm)				0.503**	0.668**	0.697**	0.597**	0.510**	0.540**	0.647**	-0.202*	0.406**	0.554**	0.768**
Number of Primary Branches / Plant					0.474**	0.616**	0.337**	0.558**	0.509**	0.428**	0.013	0.313**	0.428**	0.572**
Number of Secondary Branches /Plant						0.567**	0.351**	0.419**	0.556**	0.528**	-0.320**	0.370**	0.565**	0.746**
Length of main Shoot (Cm)							0.517**	0.565**	0.553**	0.694**	-0.094	0.398**	0.545**	0.760**
No of siliquae on Main Shoot								0.319**	0.513**	0.374**	-0.063	0.528**	0.286**	0.631**
Siliqua length(cm)									0.430**	0.498**	0.115	0.329**	0.307**	0.502**
Number of Seeds per siliqua										0.388**	-0.003	0.476**	0.402**	0.669**

Test weight(g)											-0.124	0.380**	0.418**	0.633**
Oil content %												-0.045	-0.219*	-0.202*
Harvest Index (%)													-0.170*	0.582**
Biological Yield per plant (g)														0.696**
Grain Yield per plant (g)														1

The evaluation of genotypic and phenotypic correlations can help breeders design appropriate breeding strategies to maximize favorable correlations and mitigate undesirable ones by generating new variability for improved recombinants. As noted by Al-Jibouri *et al.* (1958), if negative associations between traits are due to pleiotropic effects, achieving desirable recombinants may be challenging. However, if linkage is the underlying cause, specialized breeding programs will be required to break these genetic linkages. According to Kaltsikes and Lee (1971), if morphological traits are highly correlated with yield, breeding programs incorporating yield per plant or plot as a selection criterion would be beneficial. Based on the current correlation analysis, key traits for improving Indian mustard include main shoot length, number of seeds per siliqua, plant height, number of secondary branches per plant, biological yield per plant, test weight, number of siliquae on the main shoot, number of primary branches per plant, siliqua length, and harvest index. These findings align with previous studies conducted by Rathod *et al.* (2013), Lohia *et al.* (2013), Ali *et al.* (2013), Shekhawat *et al.* (2014), Shweta and Om Prakash (2018), Meena *et al.* (2015), and Prasad and Patil (2018).While correlation coefficients provide insights into trait associations, they do not fully capture the relative contribution of each yield component to grain yield per plant. To gain a clearer understanding of these interrelationships, path analysis was conducted at the phenotypic level. This analysis quantified the direct and indirect effects of various yield components, helping to determine their relative significance. In this study, grain yield per plant was treated as the dependent variable, while the remaining traits served as independent variables. The results of the path coefficient analysis for *Brassica juncea* L. are presented in Tables 4 & 5, highlighting the direct and indirect contributions of each trait to yield improvement.

Path Coefficient Analysis

The phenotypic and genotypic path coefficient analysis indicated that biological yield per plant, harvest index, plant height, siliqua length, length of the main shoot, and oil content exhibited a strong positive direct contribution to grain yield per plant. (Table 6& 7). Additionally, days to maturity had an indirect positive effect on grain yield per plant through oil content. Plant height contributed indirectly to grain yield via the length of the main shoot, the number of seeds per siliqua, the number of secondary branches per plant, and test weight. The number of primary branches per plant influenced grain yield indirectly through days to maturity, while the number of secondary branches per plant had an indirect positive impact through biological yield per plant, harvest index, siliqua length, plant height, length of the main shoot, and days to 50% flowering. Several other indirect relationships were observed. Traits such as plant height, test weight, number of primary and secondary branches per plant, siliqua length, number of seeds per siliqua, and biological yield per plant positively influenced grain yield through the length of the main shoot. The number of siliquae on the main shoot had an indirect positive effect via the harvest index, biological yield per plant, siliqua length, plant height, and length of the main shoot. Similarly, the number of seeds per siliqua, number of primary branches per plant, length of the main shoot, plant height, test weight, and number of secondary branches per plant had an indirect positive impact through siliqua length.

Table 7 : Path coefficient characters on grain yield in Indian mustard (*Brassica juncea* L.) at the genotypic level

Characters	**Days to 50% Flowering**	**Days to Maturity**	**plant height (cm)**	**Number of Primary Branches / Plant**	**Number of Secondary Branches /Plant**	**Length of main Shoot (Cm)**	**Number of siliquae on Main Shoot**	**siliqua length (cm)**	**Number of Seeds per siliqua**	**Test weight (g)**	**Oil content %**	**Harvest Index (%)**	**Biological Yield per plant (g)**	**Grain Yield per plant (g)**
Days to 50% Flowering	**-0.0260**	0.0002	-0.026	-0.014	0.007	-0.003	-0.002	0.033	0.036	0.007	0.0213	-0.081	-0.125	-0.171*
Days to Maturity	0.0023	**-0.0023**	0.016	0.010	-0.002	0.006	-0.020	-0.028	0.014	-0.007	-0.0126	0.004	0.152	0.131
plant height (cm)	0.0056	-0.0003	**0.121**	-0.055	-0.016	0.087	-0.076	0.096	-0.199	-0.036	-0.0110	0.349	0.533	0.798**
Number of Primary Branches / Plant	-0.0037	0.0002	0.071	**-0.095**	-0.013	0.076	-0.050	0.115	-0.173	-0.027	-0.0001	0.328	0.402	0.631**
Number of Secondary Branches /Plant	0.0082	-0.0002	0.085	-0.055	**-0.023**	0.075	-0.041	0.096	-0.185	-0.031	-0.0161	0.327	0.547	0.788**

Length of main Shoot (Cm)	0.0006	-0.0001	0.092	-0.063	-0.015	**0.115**	-0.075	0.105	-0.208	-0.039	-0.0045	0.394	0.517	0.819**
No of siliquae on Main Shoot	-0.0005	-0.0004	0.081	-0.042	-0.008	0.077	**-0.112**	0.095	-0.153	-0.027	-0.0032	0.496	0.299	0.701**
Siliqua length(cm)	-0.0050	0.0004	0.067	-0.063	-0.013	0.069	-0.062	**0.173**	-0.236	-0.027	0.0060	0.374	0.314	0.599**
Number of Seeds per siliqua	0.0035	0.0001	0.088	-0.060	-0.015	0.087	-0.063	0.150	**-0.273**	-0.033	-0.0017	0.493	0.438	0.813**
Test weight(g)	0.0035	-0.0003	0.083	-0.049	-0.013	0.084	-0.058	0.088	-0.171	**-0.053**	-0.0070	0.378	0.416	0.702**
Oil content %	-0.0127	0.0007	-0.031	0.000	0.008	-0.012	0.008	0.024	0.010	0.009	**0.0435**	-0.065	-0.241	-0.257**
Harvest Index (%)	0.0028	0.0000	0.056	-0.041	-0.010	0.060	-0.074	0.086	-0.178	-0.026	-0.0038	**0.756**	-0.040	0.588**
Biological Yield per plant (g)	0.0037	-0.0004	0.074	-0.043	-0.014	0.068	-0.038	0.062	-0.137	-0.025	-0.0120	-0.034	**0.875**	0.777**

Resi = 0.00379 *, ** significant at 5% and 1% level, respectively

Table 8 : Path coefficient showing direct and indirect effects of component characters on grain yield at phenotypic level in Indian mustard (*Brassica juncea L.*)

Chara-cters	**Days to 50% Flowering**	**Days to Maturity**	**plant height (cm)**	**Number of Primary Branches / Plant**	**Number of Secondary Branches /Plant**	**Length of main Shoot (Cm)**	**Number of siliquae on Main Shoot**	**siliqua length (cm)**	**Number of Seeds per siliqua**	**Test weight (g)**	**Oil content %**	**Harvest Index (%)**	**Biological Yield per plant (g)**	**Grain Yield per plant (g)**
Days to 50% Flowering	**0.005**	0.001	-0.004	-0.003	-0.011	-0.002	0.001	0.0001	0.0027	0.0007	0.0067	-0.015	-0.101	-0.118
Days to Maturity	0.000	**-0.007**	0.002	0.001	0.002	0.002	0.003	-0.0001	0.0002	-0.0005	-0.0034	0.043	0.080	0.122
plant height (cm)	-0.001	-0.001	**0.023**	-0.016	0.030	0.041	0.013	0.0005	-0.0126	-0.0038	-0.0036	0.275	0.424	0.768**
Number of Primary Branches / Plant	0.001	0.000	0.011	**-0.031**	0.021	0.036	0.007	0.0005	-0.0119	-0.0025	0.0002	0.212	0.328	0.572**
Number of Secondary Branches /Plant	-0.001	0.000	0.015	-0.015	**0.045**	0.033	0.007	0.0004	-0.0130	-0.0031	-0.0058	0.250	0.433	0.746**
Length of main Shoot (Cm)	0.000	0.000	0.016	-0.019	0.025	**0.058**	0.011	0.0005	-0.0129	-0.0040	-0.0017	0.269	0.418	0.760**
No of siliquae on Main Shoot	0.000	-0.001	0.014	-0.010	0.016	0.030	**0.021**	0.0003	-0.0120	-0.0022	-0.0011	0.357	0.219	0.631**
Siliqua length(cm)	0.001	0.001	0.012	-0.017	0.019	0.033	0.007	**0.0009**	-0.0101	-0.0029	0.0021	0.223	0.235	0.502**
Number of Seeds per siliqua	-0.001	0.000	0.012	-0.016	0.025	0.032	0.011	0.0004	**-0.0234**	-0.0023	-0.0001	0.322	0.308	0.669**
Test weight(g)	-0.001	-0.001	0.015	-0.013	0.024	0.040	0.008	0.0005	-0.0091	**-0.0058**	-0.0022	0.257	0.320	0.633**
Oil content %	0.002	0.001	-0.005	0.000	-0.014	-0.005	-0.001	0.0001	0.0001	0.0007	**0.0180**	-0.030	-0.168	-0.202*
Harvest Index (%)	0.000	0.000	0.009	-0.010	0.017	0.023	0.011	0.0003	-0.0111	-0.0022	-0.0008	**0.676**	-0.130	0.582**
Biological Yield per plant (g)	-0.001	-0.001	0.013	-0.013	0.025	0.032	0.006	0.0003	-0.0094	-0.0024	-0.0040	-0.115	**0.766**	0.696**

Resi = 0.00632, *, ** significant at 5% and 1% level, respectively

Moreover, the number of seeds per siliqua contributed indirectly to grain yield via oil content and days to 50% flowering. Test weight also showed an indirect positive effect. Oil content influenced grain yield indirectly through days to 50% flowering and siliqua length. The harvest index indirectly contributed through the number of seeds per siliqua, length of the main shoot, test weight, siliqua length, plant height, number of primary branches per plant, and number of secondary branches per plant. Likewise, biological yield per plant had an indirect effect via secondary branches per plant, plant height, length of the main shoot, number of seeds per siliqua, test weight, number of primary branches per plant, siliqua length, number of siliquae on the main shoot, and days to maturity, all positively associated with grain yield.This study confirms that these traits directly influence grain yield per plant, aligning with the findings of Maurya *et al.* (2013), Shekhawat *et al.* (2014), Bind *et al.* (2014), Ray *et al.* (2014), Lodhi *et al.* (2014), Meena *et al.* (2015),Kumar *et al.* (2016), Tiwari *et al.* (2017), Tahira *et al.* (2017), Gupta *et al.* (2018), Devi (2018), Kumar *et al.* (2018), Raliya *et al.* (2018), Dawar *et al.* (2018), Kumar *et al.* (2019), and Saiyad *et al.* (2020).

Genetic diversity (D^2) analysis

In the present investigation, forty-five genotypes of Indian mustard were evaluated for Genetic diversity (D²) analysis was conducted using 14 quantitative traits. Based on D² values, the 45 Indian mustard genotypes included in the study were classified into seven clusters (Table 10 & figure 1). Among these clusters, Cluster II contained the highest number of genotypes (11), followed by Clusters III and IV with 8 genotypes each, while Clusters I, V, and VII each comprised 3 genotypes. The findings of this study suggest a correlation between genetic diversity and geographic distribution. The maximum intra-cluster distance was observed in Cluster I (2.855), whereas Cluster II exhibited the lowest intra-cluster distance (2.059). (Table 9) A greater intra-cluster distance indicates significant genetic diversity among genotypes within the same cluster. Conversely, crossing genotypes within a cluster that has a low intra-cluster distance is less likely to result in desirable segregates. Therefore, crossing genotypes from Cluster I (UJM15, UJM2, and UJM4), which are separated by larger inter-cluster distances, may be more beneficial compared to crosses within other clusters. Additionally, limited diversity within a cluster suggests that selecting parents from clusters with higher mean values for specific traits could be valuable in developing high-yielding mustard varieties.In this study, the maximum inter-cluster distance was recorded between Clusters I and VII (9.712), indicating a wide genetic divergence among genotypes within these clusters. This suggests that hybridization between genotypes from Cluster I (UJM15, UJM2, and UJM4) and Cluster VII (UJM-14, Pusa Mustard-22, and GM-2) could generate transgressive segregants, providing an opportunity to select highly diverse genotypes. These genotypes could be utilized in heterotic cross combinations to develop mustard hybrids. Additionally, the shortest inter-cluster distance (2.348) was observed between Clusters II and IV, indicating close genetic relationships among their genotypes, which limits their effectiveness in hybridization programs. The study also revealed significant genetic variation among clusters based on the mean values of 14 quantitative traits(Table 8)

Table 9 : Cluster mean values for fourteen characters of forty-five genotypes in Indian mustard (*Brassica juncea* L.).

Characters		**Days to 50 % Flowering**	**Days to Maturity**	**plant height (cm)**	**Number of Primary Branches / Plant**	**Number of Secondary Branches /Plant**	**Length of main Shoot (Cm)**	**Number of siliquae on Main Shoot**	**siliqua length (cm)**	**Number of Seeds per siliqua**	**Test weight(g)**	**Oil content %**	**Harvest Index (%)**	**Biological Yield per plant (g)**	**Grain Yield per plant(g)**
I	**Mean**	55.78	147.33	202.41	5.12	13.37	74.52	42.96	4.02	13.01	4.04	40.74	18.99	237.33	44.17
	± SE	1.84	0.25	8.32	1.25	1.94	5.70	4.09	0.31	0.36	0.05	0.76	2.14	54.93	5.07
II	**Mean**	57.58	143.33	211.32	5.38	14.49	75.39	46.05	4.42	13.57	4.24	41.32	22.69	231.21	52.37
	± SE	4.03	1.11	9.78	0.35	0.93	5.15	2.48	0.23	0.41	0.33	0.40	1.21	18.78	4.81
III	**Mean**	51.29	148.25	207.51	5.17	15.24	75.35	46.48	4.24	13.54	4.25	40.65	23.23	240.38	55.63
	± SE	2.48	1.80	11.35	0.47	1.03	4.70	2.91	0.26	0.60	0.32	0.59	1.50	18.66	3.93
IV	**Mean**	59.71	148.83	212.39	5.30	14.38	73.74	49.30	4.50	13.56	4.12	41.28	23.65	227.42	53.51
	± SE	2.14	0.92	8.31	0.50	1.72	7.48	4.84	0.19	0.14	0.35	0.14	1.75	25.27	4.60
V	**Mean**	51.11	148.67	307.48	5.59	19.18	88.50	50.86	4.60	14.35	5.19	40.23	22.42	310.22	69.38
	± SE	3.36	2.33	50.22	0.17	0.61	11.59	2.09	0.51	0.25	0.19	0.06	1.75	4.86	5.99
VI	**Mean**	54.22	144.96	252.69	6.16	17.27	89.30	52.21	4.82	14.40	4.60	41.05	25.63	251.93	64.23
	± SE	3.61	1.74	30.96	0.46	1.36	8.35	2.31	0.15	0.34	0.42	0.59	1.62	25.59	3.77
VII	**Mean**	57.11	148.22	339.27	6.73	19.54	112.38	56.17	5.03	14.97	5.30	40.80	27.39	295.22	79.77
	± SE	3.02	0.69	28.55	0.17	1.02	3.57	1.27	0.15	0.33	0.43	0.73	4.06	33.40	2.51

The highest mean value for days to 50% flowering was observed in Cluster IV (59.71 days), while the lowest was in Cluster V (51.11 days). Days to maturity showed the highest mean in Cluster IV (148.83) and the lowest in Cluster II (143.33). Cluster VII recorded the tallest plants (339.27 cm), whereas Cluster I had the shortest (202.41 cm). The number of primary branches per plant was highest in Cluster VII (6.73) and lowest in Cluster I (5.12). Similarly, Cluster VII had the highest number of secondary branches per plant (19.54), while Cluster I had the lowest (13.37).Cluster VII exhibited the longest main shoot (112.38 cm), while Cluster IV had the shortest (73.74 cm).

Table 10 : Average intra and Inter cluster distance (D^2 value) among seven clusters of forty-five genotypes in Indian mustard (*Brassica juncea* L.)

Clusters	I	II	III	IV	V	VI	VII
I	**2.855**						
II	3.117	**2.059**					
III	2.863	2.799	**2.290**				
IV	3.405	2.348	2.573	**2.155**			
V	6.784	5.999	4.922	5.832	**2.201**		
VI	6.077	3.892	4.074	4.031	3.806	**2.436**	
VII	9.712	8.011	7.778	7.653	4.416	4.483	**2.303**

Table 11 : Grouping of forty-five genotypes of Indian mustard (*Brassica juncea* L.) in seven clusters.

Clusters	No. of genotypes	Genotypes
I	3	UJM-15, UJM-2 and UJM-4
II	11	UJM-28, UJM- 27, UJM-24, UJM-19, UJM-18, UJM-17 UJM-16, UJM-12, UJM-9, UJM-6, BR-40
III	8	UJM-7, Shivalik, RH-819, Aravali, DRMR-IJ-31, Geeta, Kranti and Gujarat Mustard-1
IV	8	UJM-23, UJM-22, UJM-21, UJM-20, UJM-10, UJM-8, UJM-3 and UJM-1
V	3	RLM6-19, Jawahar mustard -1 and Jagannath
VI	9	UJM-29, UJM-26, UJM-25, UJM-13, UJM-11, UJM-5, Pusa Bahar, CS-54 and Saurabh
VII	3	UJM-14, Pusa Mustard -22 and GM-2.

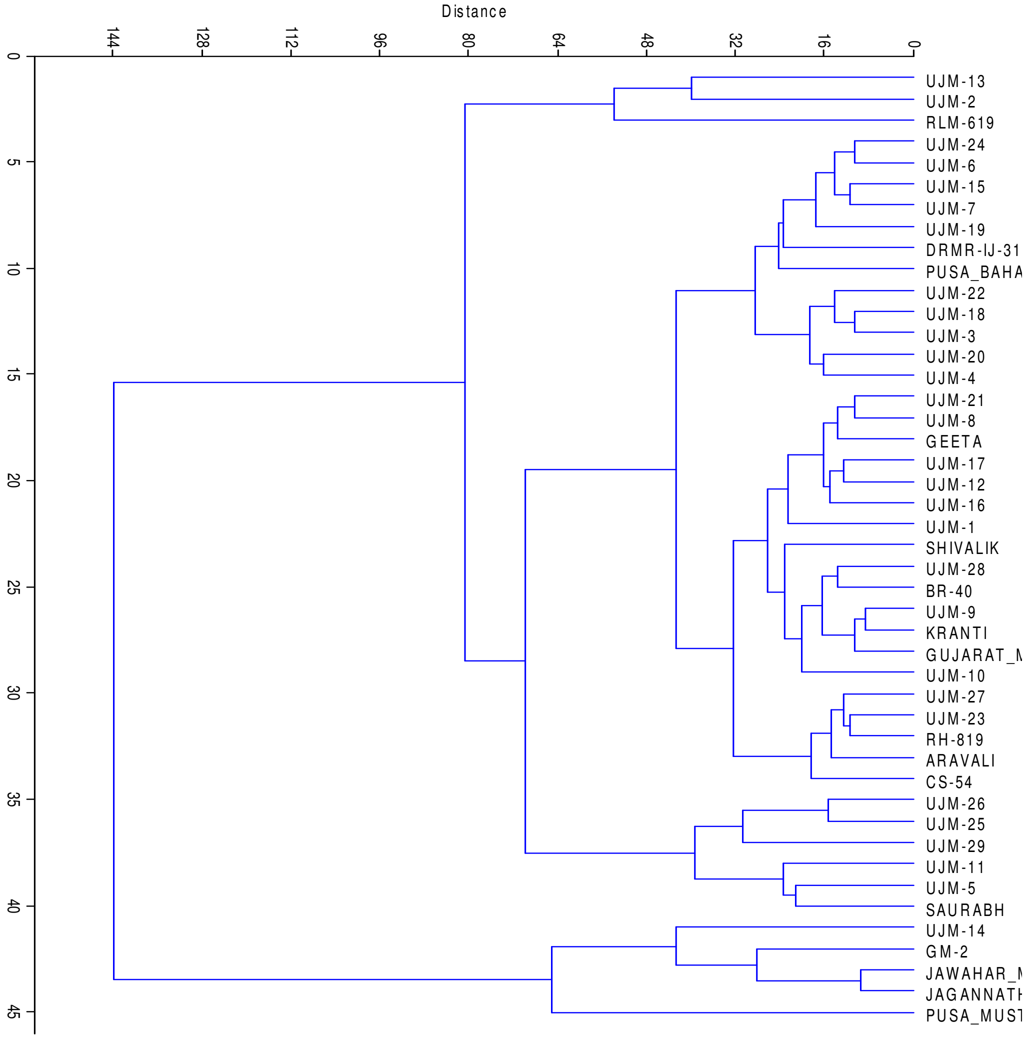

Fig. 1: Dendogram based on summarized data on differentiation among 45 genotypes of mustard according to Ward's method.

The highest number of siliquae on the main shoot was observed in Cluster VII (56.17), while Cluster I had the lowest (42.96). Siliqua length was greatest in Cluster VII (5.03 cm) and smallest in Cluster I (4.02 cm). The highest number of seeds per siliqua was found in Cluster VI (14.97), while the lowest was in Cluster I (13.01). The maximum test weight was recorded in Cluster VII (5.30 g) and the minimum in Cluster I (4.04 g). Oil content was highest in Cluster II (41.32%) and lowest in Cluster V (40.23%). The harvest index showed its highest value in Cluster VII (27.3) and its lowest in Cluster I (18.99). Biological yield per plant was highest in Cluster V (310.22 g) and lowest in Cluster IV (227.42 g), while grain yield per plant was highest in Cluster VII (79.77 g) and lowest in Cluster I (44.17 g).Similar results were reported by Kumar *et al.* (2013), Lodhi *et al.* (2013), Kumar *et al.* (2013a,b), SinFgh *et al.* (2014), Nagda *et al.* (2018), Gadi *et al.* (2019), and Singh *et al.* (2020).These findings indicate that genotypes with high mean values for specific traits were clustered together, suggesting their potential use in breeding programs. In heterosis breeding, genotypes from genetically diverse clusters serve as potential parents. When excellent genotypes from different clusters are crossed, they are likely to produce superior heterotic combinations. The selected genotypes, based on cluster analysis, are expected to contribute to germplasm improvement and serve as potential hybrids while also being evaluated for quality traits.The study also highlighted the key contributors to genetic divergence. Days to 50% flowering (9.73%), plant height (8.76%), siliqua length (7.09%), test weight (6.83%), harvest index (6.50%), number of primary branches per plant (6.93%), and number of secondary branches per plant (6.35%) played the most significant roles in genetic divergence. In contrast, traits such as the length of the main shoot (4.93%), the number of seeds per siliqua (4.82%), and the number of siliquae on the main shoot (2.95%) contributed minimally to genetic divergence. Similar observations were reported by Ahmad *et al.* (2009), Doddabhimappa *et al.* (2010), Kumar *et al.* (2013), Saleem *et al.* (2017), Singh *et al.* (2014), Rout *et al.* (2018), Gadi *et al.* (2019), and Singh *et al.* (2020).Key traits such as days to maturity, oil content, plant height, and days to 50% flowering were identified as major contributors to genetic diversity. These traits can be considered essential selection parameters for choosing diverse parents in hybridization programs aimed at yield improvement.

Table 12 : Contribution (%) of fourteen characters towards genetic divergence in Indian mustard (*Brassica juncea* L.)

S. No.	Characters	Contribution (%)
1.	days to Maturity	10.54
2.	oil content	10.14
3.	days to 50% flowering	9.73
4.	plant height	8.76
5.	grain yield per plant	8.09
6.	siliqua length	7.09
7.	number of primary branches per plant	6.93
8.	test weight	6.83
9.	harvest index	6.50
10.	number of secondary branches per plant	6.35
11.	biological yield per plant	6.35
12.	length of main shoot	4.93
13.	number of seeds per siliqua	4.82
14.	number of siliquae on main shoot	2.95

Conclusion

The present investigation on 45 Indian mustard (Brassica juncea) genotypes revealed significant genetic variability for all 14 quantitative traits, providing ample scope for selection and genetic improvement. Analysis of variance indicated substantial variation among genotypes, which shows their potential for breeding programs of Indian mustard. Moderate to high genotypic and phenotypic coefficients of variation (GCV and PCV) were observed for key traits such as plant height, grain yield per plant, length of the main shoot, and biological yield per plant, making them suitable for selection. High heritability estimates for traits like plant height, grain yield per plant, and number of secondary branches per plant suggest that these traits are predominantly controlled by genetic factors and can be effectively improved through selection. Furthermore, traits with high genetic advance, such as biological yield per plant and test weight, indicate the presence of additive genetic effects, making them ideal targets for breeding programs aimed at yield enhancement. Correlation and path analysis revealed that traits such as the length of the main shoot, number of seeds per siliqua, number of siliquae on the main shoot, test weight, and biological yield per plant had a strong positive association with grain yield per plant. These traits also exhibited a direct positive contribution towards yield, suggesting their importance in selection strategies. The presence of negative correlations between certain traits, such as oil content and plant height, indicates the need for strategic breeding approaches to balance desirable attributes. Genetic diversity analysis grouped the 45 genotypes into seven distinct clusters, with considerable intra- and inter-cluster variation. The wide genetic divergence observed among the genotypes suggests the potential for hybridization and recombination breeding to develop superior mustard varieties. Overall, the study shows the significance of genetic variation, heritability, and trait associations in mustard breeding. The findings provide valuable insights for selecting high-yielding genotypes and improving mustard productivity, thereby contributing to sustainable agriculture and food security.

Author Statement

I declare that this manuscript is original, has not been published before and is not currently being considered for publication elsewhere. I confirm that the manuscript has been read and approved by all named authors and that there are no other persons who satisfied the criteria for authorship but are not listed. I further confirm that the order of authors listed in the manuscript has been approved by all co-authors. I understand that the Corresponding Author is the sole contact for the Editorial process

Credit authorship contribution statement

Mahesh Upadhyay: Writing–original draft, Methodology, Investigation, Formal analysis. Mukesh Kumar: Writing – review & editing, Supervision, Resources, Funding acquisition, Conceptualization, Resources. Prafulla Kumar: Writing–review & editing,Methodology, Investigation, Formal analysis

Declaration of competing interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

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