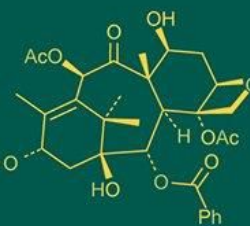
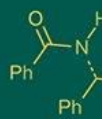


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Evaluation of genetic variability, heritability and genetic advance for yield traits in Indian mustard (*Brassica juncea* L.)

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Abstract

Brassica juncea (L.) (Indian mustard) is the most widely cultivated oilseed species among the Brassica crops. Evaluating genetic divergence within germplasm is essential for identifying diverse parental combinations for hybridization, particularly to exploit transgressive segregation for developing high-yielding, quality, stress-resistant, and widely adaptable varieties. In the present study, 45 diverse genotypes of Indian mustard were evaluated in a Randomized Block Design (RBD) with three replications at the Agricultural Research Farm, Department of Genetics and Plant Breeding, School of Agriculture, Lovely Professional University, Phagwara, Punjab, India, during the rabi season of 2024-2025. Data were recorded on 12 yield and yield-attributing traits, and statistical analyses were performed to estimate mean performance, genetic variability, heritability, and variance components. The analysis of variance revealed highly significant differences among genotypes for all the traits, indicating the presence of substantial genetic variability. High genotypic and phenotypic coefficients of variation were observed for number of siliques per plant and seed yield per plant, suggesting greater scope for selection. Furthermore, high heritability coupled with high genetic advance as percent of mean was recorded for number of siliques per plant, seed yield per plant, and number of primary branches per plant, indicating the predominance of additive gene action. These results highlight that direct selection for these traits would be effective in improving seed yield in Indian mustard and provide a strong basis for future breeding programmes.

Keywords: Indian mustard, genetic variability, phenotypic coefficient of variation, genotypic coefficient of variation, heritability, genetic advance

Introduction

Brassica juncea (L.), commonly known as Indian mustard, is the most predominant species among cultivated oilseed Brassica species and is a naturally occurring amphidiploid ($2n = 36$, AABB genome) derived from interspecific hybridization between *B. rapa* (AA) and *B. nigra* (BB) (Nagaharu, 1935; Yang *et al.*, 2016) [19, 39]. The genome size of Indian mustard is approximately 920 Mb, and the crop is primarily self-pollinated with a certain degree of cross-pollination, contributing genetic plasticity under diverse environments (Yang *et al.*, 2016; Rakow, 2004) [39, 27]. It is one of the most important oilseed crops in India, contributing significantly to nutritional, industrial, and economic sectors (Shekhawat *et al.*, 2012; Chauhan *et al.*, 2011) [32, 4]. India is one of the leading producers of rapeseed-mustard globally. During 2023-2024, rapeseed and mustard production reached approximately 5.98 million tonnes, with Rajasthan contributing nearly 45.4% (2.71 million tonnes), followed by Uttar Pradesh and Madhya Pradesh. The national average productivity was about 1, 443 kg per hectare. Major mustard-growing states include Rajasthan, Uttar Pradesh, Madhya Pradesh, Haryana, Bihar, Assam, Gujarat, Punjab, and West Bengal (Economic Survey of India, 2023-24) [9]. Rapeseed mustard oil serves as a primary cooking medium in many parts of India. Apart from edible oil extraction, seeds are utilized in condiments, pickles, salad dressings, and traditional preparations. The residual oil cake is an important source of cattle feed and organic manure, thereby enhancing its economic value (Shekhawat *et al.*, 2012) [32]. Indian mustard is predominantly cultivated during the Rabi season under both irrigated and rainfed conditions.

Seed yield is a complex quantitative trait governed by multiple component characters and significantly influenced by environmental factors. Therefore, understanding the association among yield and its contributing traits is essential for formulating effective selection criteria (Johnson *et al.*, 1955; Falconer and Mackay, 1996) [12, 10]. Since phenotypic expression is influenced by both genetic and environmental components, identifying heritable traits with stable performance improves breeding efficiency. Recent studies confirm abundant genetic variability in Indian mustard populations, indicating substantial scope for trait improvement. For instance, diversity assessments reported moderate to high genotypic and phenotypic coefficients of variation for key yield components such as seed yield per plant and secondary branches, along with high heritability and genetic advance, emphasizing the value of these traits in selection strategies.

Genetic diversity is the foundation of crop improvement programs. The magnitude of genetic variation available in germplasm determines the effectiveness of selection and hybrid breeding strategies (Falconer and Mackay, 1996; Chand *et al.*, 2023) [10, 8]. Genetic variability is a

fundamental requirement in crop improvement, as it creates a broad base for selecting superior genotypes. Understanding how seed yield is associated with other traits is essential for making effective selection decisions in breeding programs. Since seed yield is controlled by multiple genes, improving it can also influence several other characteristics, making it important to consider these relationships during selection. (Pal *et al.*, 2019) [20]. In hybrid breeding, selection of parents with diverse genetic backgrounds is critical for achieving heterosis and broad variability. Therefore, the present study was to assess the extent of genetic variability and diversity among Indian mustard genotypes for yield and its contributing traits.

Materials and Methods

Experimental materials and site description

A Total 45 mustard genotypes were employed in the study (Table 1). Details are presented in the Table 1. The present experiment was undertaken during rabi season 2023-2024 at Punjab (31°14'30"N, 75°42'09.3"E) in Experimental farm Genetics and Plant Breeding, School of Agriculture, Lovely Professional University.

Table 1: List of genotypes used

S.N.	Genotypes	S.N.	Genotypes	S.N.	Genotypes	S.N.	Genotypes	Sr.no.	Genotypes
1.	Lakshmi	10.	Pusa-26	19.	Aravali	28.	Durgamani	37.	Pusa Vijay
2.	Giriraj	11.	PM-30	20.	Ashirwad	29.	Pusa Tarak	38.	PM 29
3.	DRMR-1665	12.	RH-761	21.	DRMR IJ-31	30.	NRCHB-101	39.	PM 30
4.	NRCHB-101	13.	Geeta	22.	Krishna	31.	PM 27	40.	MS90-6
5.	Pusa Bold	14.	Gujarat mustard-1	23.	CS-52	32.	PM 28	41.	PM 24
6.	Pusa Jaykisan	15.	Navgold	24.	Jawahar mustard-1	33.	Bankura black	42.	Sarama
7.	Pusa Tarak	16.	Basanti	25.	Jawahar mustard 2	34.	Kranti	43.	Sanjukta Asech
8.	Pusa Mahak	17.	Bhagirathi	26.	Gujarat mustard-2	35.	Shivani	44.	Bhagirathi
9.	PM-28	18.	Jagannath	27.	Maya	36.	Pusa Karishma	45.	Seeta

Experimental design

The field design was in a randomized block design (RBD) with three replications. Each genotype was sown in five rows of 3 m row length with spacing of 30 cm between rows and 10 cm between plants. Recommended agronomic practices, including the application of fertilizers, manual weeding and need-based plant protection measures, were followed on regular intervals during the experiment.

Data collection

Twelve quantitative traits were recorded in the study. Five healthy plants from each genotype were randomly selected for data recording in each replication except DFF and DM, which were assessed on a population basis. Twelve traits included are (i) Date of 50% flowering (DFF), (ii) Date of maturity (DM), (iii) Plant height (PH), (iv) Number of primary branches (NPB), (v) Number of secondary branches (NSB), (vi) Length of main raceme (LMR), (vii) Number of siliques per plant (NSP), (viii) Number of seeds per silique (NSS), (ix) Test weight (TW): 1000 seed weight, (x) Biological yield per plant (BYP), (xi) Harvest index (HI), (xii) Seed yield per plant (SY)

Statistical analysis

The mean data of 45 genotypes of different replications for 12 characters were subjected to standard procedure of analysis of variance (ANOVA) suggested by (Panse and

Sukhatme, 1961) [22]. Component of Variance was calculated by the formula suggested by Burton and Devane (1953) [3], Cockerham (1963) [6]. The coefficient of variation (genotypic (GCV), phenotypic (PCV), and environmental (ECV) $\sigma_e^2 = Mse$; $\sigma_g^2 = \frac{MSG - MSe}{r}$; $\sigma_p^2 = \sigma_g^2 + \sigma_e^2$, where, MSe , MSG , and r are the mean squares of error, mean squares of genotypes, and the number of blocks, respectively. $(GCV) = \frac{\sqrt{\sigma_g^2}}{\bar{X}} \times 100$; $(PCV) = \frac{\sqrt{\sigma_p^2}}{\bar{X}} \times 100$; $(ECV) = \frac{\sqrt{\sigma_e^2}}{\bar{X}} \times 100$, where $\bar{X}$ are the grand mean for each measured trait according to Sivasubramanian and Menon (1973) [34], the GCV and PCV values fall into three categories: low (0-10%), moderate (10-20%), and high (>20%). Heritability in broad sense is the ratio of genotypic variance to the total variance and is also calculated as $H^2(Broadsense) = \frac{\sigma_g^2}{\sigma_p^2} \times 100$, and it's percentage was categorized as low (0-30%), moderate (31-60%) and high (> 60%) by Robinson *et al.*, (1949) [28]. It is also characterized as the portion of total variability or phenotypic variability which is heritable and is due to genotype. It was calculated by the formula given by Lush (1949) [17], Burton and Devane (1953) [3]. Genetic advance is the improvement in mean genotypic value of selected plants over the parental population and it was computed by the formula given by Lush (1949) [17] and Johnson *et al.* (1955) [12]. Genetic advances as a percentage of the mean (GAM) were also

calculated by the formula suggested by Comstock and Robinson (1952) [7], $GAM = \frac{GA}{x} \times 100$. The dataset was initially organized in MS Excel and subsequently analyzed in R using the RStudio platform, with genetic parameters across years estimated via the variability package. A clustered column chart was prepared using MS Excel.

Results

Analysis of Variance (ANOVA)

The analysis of variance (ANOVA) for twelve traits revealed highly significant differences among the genotypes (Table 2), indicating the presence of substantial genetic variability.

Table 2: Analysis of Variance (ANOVA)

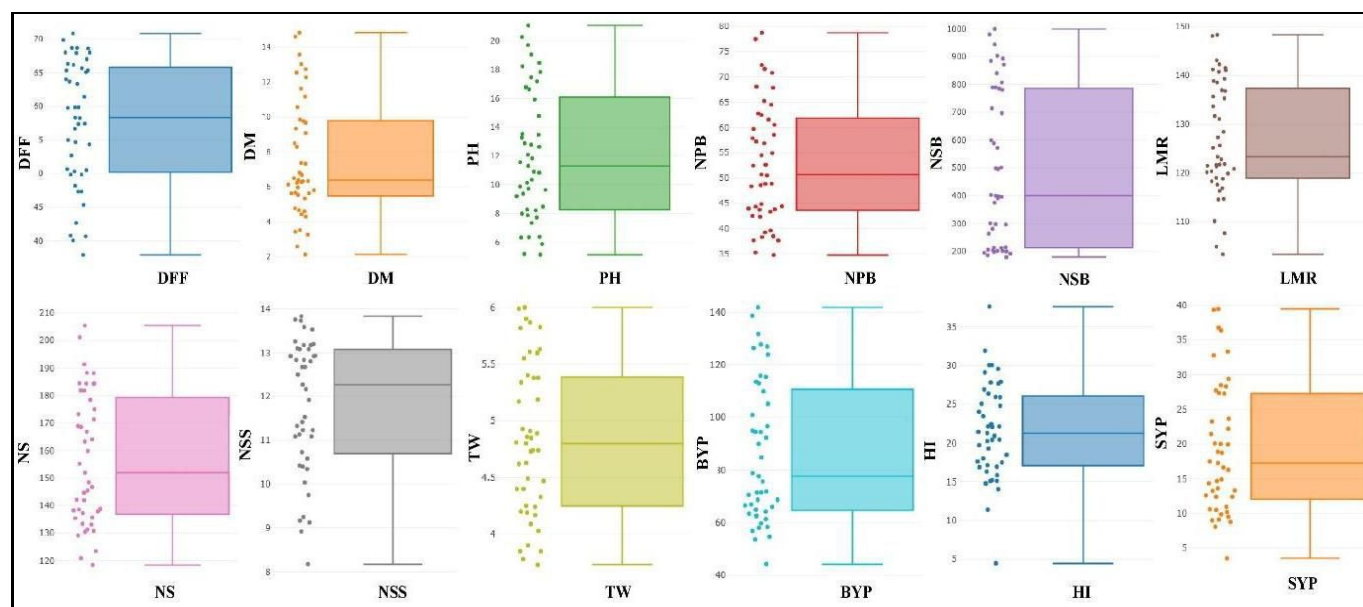
SV	DFF	DM	PH	NPB	NSB	LMR	NSP	NSS	TW	BYP	HI	SY
Replications (df = 2)	210.82	1018.74	1591.57	3.87	9.31	184.26	14624	9.87	1.47	481.57	27.9	21.69
Treatments (df = 44)	265.48**	404.27**	1696.38**	33.52**	60.50**	427.14**	231432.00**	6.94**	1.36**	2144.47**	114.79**	261.42**
Error (df = 88)	0.37	0.86	2.27	0.02	0.04	0.36	102.00	0.01	0.002	1.70	0.07	0.16

(*, ** indicate significance at 5%, 1% levels of probability; SV: Source of variation; df: Degree of freedom; DFF: Date of 50% flowering; DM: Date of maturity; PH: Plant height, NPB: Number of primary branches per plant; NSB: Number of secondary branches per plant, LMR: Length of main raceme; NSP: Number of siliques per plant; NSS: Number of seeds per silique; TW: Test weight; BYP: Biological yield per plant; HI: Harvest index; SY: Seed yield per plant)

Mean performance

The general mean, range, and mean performance of each of the forty-five genotypes for 12 traits are presented in Table 3. DFF ranged from 37.92 to 70.83 days (earliest: Jagannath; latest: CS-52), and DM from 103.33 to 148.33 days (earliest: Navgold; latest: Pusa Jaykisan). PH varied from 118.43 cm (Pusa Tarak) to 205.43 cm (PM-27). NPB ranged from 2.13 (Seeta) to 14.83 (PM-28), and NSB from 5.13 (Seeta) to 21.07 (Pusa Mahak). LMR varied between 34.75 cm (Pusa Tarak) and 78.75 cm (Lakshmi). NSP showed a wide range from 178.77 (Navgold) to 999.68 (DRMR IJ-31), while NSS ranged from 8.17 (PM-28) to 13.83 (Shivani). SY ranged from 3.53 g (Jagannath) to

39.51 g (PM-28). Test weight varied from 3.73 g (Jawahar Mustard-1) to 6.00 g (Ashirwad). Biological yield ranged from 44.30 g (Gujarat Mustard-1) to 141.70 g (PM-27), and harvest index from 4.48% (Jagannath) to 37.58% (PM-28). The box plot illustrates the mean performance of different quantitative traits among the studied genotypes (Fig 1). In each plot, the central line represents the median, the box indicates the interquartile range, and the whiskers show the minimum and maximum values. The overlaid scatter dot plot represents individual observations for each genotype, providing a clearer visualization of data distribution, variability, and the presence of outliers within each trait.



(DFF: Date of 50% flowering; DM: Date of maturity; PH: Plant height, NPB: Number of primary branches per plant; NSB: Number of secondary branches per plant, LMR: Length of main raceme; NSP: Number of siliques per plant; NSS: Number of seeds per silique; TW: Test weight; BYP: Biological yield per plant; HI: Harvest index; SY: Seed yield per plant)

Fig 1: Box plot with scatter dot plot showing mean values of 45 genotypes across 12 traits in Indian mustard.

Table 3: Mean performance of Indian mustard genotypes in the study

Genotypes	DFF	DM	PH	NPB	NSB	LMR	NSP	NSS	TW	BYP	HI	SY
Lakshmi	59.75	131.67	184.33	12.54	17.83	78.75	944.50	12.67	4.74	123.86	26.91	33.33
Giriraj	61.42	135.67	168.67	9.34	15.93	62.75	871.67	13.25	4.89	96.69	22.16	21.43
DRMR-1665	40.08	118.33	130.80	6.39	8.27	44.83	399.75	11.08	5.38	70.56	11.38	8.03
NRCHB-101	65.08	121.67	164.10	14.60	18.47	54.50	714.00	12.83	4.09	92.25	30.06	27.73
Pusa Bold	47.33	120.33	123.43	3.43	6.33	35.25	211.17	12.83	5.38	58.10	15.09	8.77
Pusa Jaykisan	67.00	148.33	181.93	8.30	17.47	64.50	839.83	12.92	4.86	109.90	24.81	27.27
Pusa Tarak	56.67	125.63	144.67	6.13	10.83	37.63	203.42	13.75	5.90	62.56	17.47	10.93
Pusa Mahak	65.33	142.33	178.46	13.57	21.07	62.42	599.17	12.50	4.47	94.40	21.26	20.07
PM-28	45.33	114.67	148.40	6.28	13.27	44.33	498.67	8.17	3.85	71.44	27.90	19.93
Pusa-26	58.33	107.67	137.27	5.81	10.13	39.25	263.45	12.92	4.19	64.89	25.06	16.26
PM-30	68.00	117.67	171.33	5.63	11.83	42.50	191.68	13.17	5.19	90.00	16.30	14.67
RH-761	49.83	135.33	130.47	4.78	6.37	43.33	495.95	8.92	5.61	66.09	15.84	10.47
Geeta	68.00	133.67	188.27	9.85	13.53	68.08	893.35	11.92	3.78	127.70	21.43	27.37
Gujarat mustard-1	59.83	127.33	129.17	6.69	9.63	38.50	297.25	9.75	5.17	44.30	20.25	8.97
Navgold	50.50	103.33	145.56	4.30	6.35	50.67	178.77	10.42	4.81	68.69	17.99	12.36
Basanti	63.33	136.99	191.33	9.07	19.70	67.83	789.50	13.20	4.80	131.67	27.67	36.43
Bhagirathi	68.58	138.92	163.28	11.17	20.27	72.33	587.93	13.53	4.91	84.89	16.92	14.36
Jagannath	37.92	121.50	133.13	5.67	9.37	42.33	212.38	11.13	5.82	78.86	4.48	3.53
Aravali	68.67	123.33	168.91	10.57	11.56	61.58	501.10	12.80	4.40	94.49	23.45	22.16
Ashirwad	49.83	121.33	131.29	4.43	7.33	43.75	200.69	13.73	6.00	64.17	25.93	16.64
DRMR IJ-31	69.83	141.58	184.28	7.36	12.63	65.25	999.68	12.93	4.17	126.42	25.95	32.81
Krishna	50.67	120.83	151.92	6.23	7.87	44.42	390.10	11.53	5.63	66.92	18.48	12.37
CS-52	70.83	141.25	184.43	9.67	14.77	60.50	789.43	11.23	4.25	112.88	20.94	23.64
Jawahar mustard-1	48.17	125.17	138.87	5.53	9.20	54.92	280.68	10.40	3.73	56.90	22.09	12.57
Jawahar mustard 2	59.83	119.00	142.23	4.67	9.73	37.67	184.87	12.27	4.33	61.43	22.14	13.60
Gujarat mustard-2	67.92	121.83	173.24	6.33	9.87	57.83	201.10	13.10	4.85	94.95	14.04	13.33
Maya	40.75	141.08	135.65	4.60	8.20	50.50	571.60	10.73	5.83	77.61	17.12	13.29
Durgamani	66.17	139.33	181.85	12.27	18.23	70.83	807.03	11.23	3.90	113.49	20.46	23.22
Pusa Tarak	57.42	114.58	118.43	5.97	8.47	34.75	196.95	10.03	5.60	54.79	19.27	10.56
NRCHB-101	58.25	110.17	141.98	3.52	5.87	48.58	199.33	10.34	4.74	53.69	17.62	9.46
PM 27	57.33	138.58	205.43	13.03	16.79	71.57	902.77	13.58	4.63	141.70	27.78	39.37
PM 28	68.67	143.08	155.17	14.83	17.18	77.50	784.52	13.17	4.62	105.14	37.58	39.51
Bankura black	42.67	121.75	135.44	6.50	11.30	38.33	295.58	11.08	5.87	66.52	30.05	19.99
Kranti	63.67	120.17	175.08	12.73	16.63	56.87	696.68	12.67	4.20	115.45	31.91	36.84
Shivani	40.67	128.42	120.89	2.59	5.18	39.63	300.42	13.83	5.55	63.36	29.56	18.73
Pusa Karishma	65.33	140.75	188.11	9.77	13.47	57.20	780.37	12.17	4.73	126.94	22.46	28.51
Pusa Vijay	54.67	122.83	159.91	5.33	12.78	48.87	194.08	12.92	5.40	68.70	14.76	10.14
PM 29	65.67	148.08	166.83	11.63	19.06	58.53	884.83	11.33	4.49	100.92	29.12	29.39
PM 30	50.33	119.92	146.80	6.33	12.88	52.43	402.60	9.17	4.03	71.88	24.00	17.25
MS90-6	55.00	116.33	138.20	6.81	12.08	43.83	205.87	13.08	4.24	71.51	26.40	18.88
PM 24	64.00	118.83	184.33	7.33	10.91	48.33	395.11	13.08	4.93	115.83	15.11	17.50
Sarama	47.33	131.08	133.43	3.27	7.98	48.83	374.93	9.25	5.99	59.81	15.18	9.08
Sanjukta Asech	66.33	136.83	201.21	8.50	10.35	59.73	979.69	11.42	3.85	138.55	20.43	28.31
Bhagirathi	54.33	116.92	137.91	5.63	7.73	43.97	396.53	9.12	5.34	58.39	16.89	9.86
Seeta	52.67	104.92	138.58	2.13	5.13	52.63	214.12	10.58	4.40	75.65	19.72	14.92
Min.	37.92	103.33	118.43	2.13	5.13	34.75	178.77	8.17	3.73	44.30	4.48	3.53
Max.	70.83	148.33	205.43	14.83	21.07	78.75	999.68	13.83	6.00	141.70	37.58	39.51
CD (5%)	0.99	1.50	2.45	0.23	0.34	0.97	16.42	0.17	0.07	2.12	0.44	0.64
CD (1%)	1.32	1.99	3.24	0.31	0.45	1.29	21.75	0.23	0.10	2.81	0.58	0.85
CV (%)	1.06	0.73	0.96	1.89	1.75	1.13	2.04	0.91	0.92	1.51	1.25	2.06
SE (±)	0.35	0.53	0.87	0.08	0.12	0.35	5.84	0.06	0.03	0.75	0.16	0.23

(Min: Minimum; Max: Maximum; CD (5% and 1%): Critical difference at 5% and 1% respectively; CV (%): Coefficient of variation; SE (±): Standard error; DFF: Date of 50% flowering; DM: Date of maturity; PH: Plant height, NPB: Number of primary branches per plant; NSB: Number of secondary branches per plant, LMR: Length of main raceme; NSP: Number of siliquae per plant; NSS: Number of seeds per siliqua; TW: Test weight; BYP: Biological yield per plant; HI: Harvest index; SY: Seed yield per plant)

Estimation of genetic parameters

The estimation of genetic parameters revealed the presence of considerable variability among the genotypes for the traits studied. The magnitude of genotypic and phenotypic coefficients of variation, along with heritability and genetic

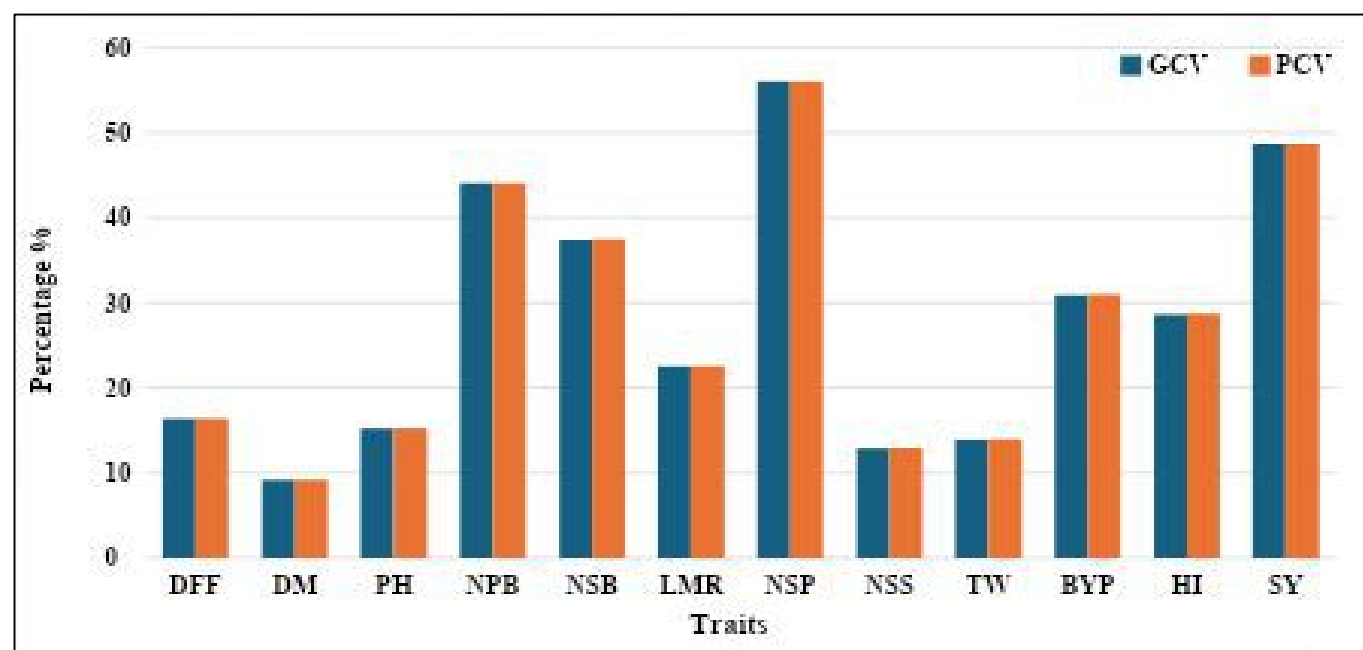
advance, provided insights into the nature and extent of genetic control governing these traits. These results indicate the potential effectiveness of selection for improvement of yield and its contributing characters. The results are presented as follows:

Table 4: Estimates of genetic parameters of 12 traits in mustard germplasm

S.N.	Traits	GCV	PCV	H ² (%)	GA (% mean)	σ^2_e	σ^2_g	σ^2_p
1.	DFF	16.34	16.37	99.58	33.58	0.37	88.37	88.74
2.	DM	9.14	9.17	99.37	18.77	0.86	134.47	135.33
3.	PH	15.16	15.19	99.60	31.16	2.27	564.70	566.97
4.	NPB	44.08	44.12	99.82	90.73	0.02	11.17	11.19
5.	NSB	37.42	37.46	99.78	77.00	0.04	20.15	20.20
6.	LMR	22.56	22.59	99.75	46.43	0.36	142.26	142.62
7.	NSP	55.98	56.01	99.87	115.24	102.38	77109.98	77212.36
8.	NSS	12.86	12.89	99.50	26.42	0.01	2.31	2.32
9.	TW	13.91	13.94	99.56	28.59	0.00	0.45	0.45
10.	BYP	30.88	30.91	99.76	63.53	1.70	714.25	715.96
11.	HI	28.64	28.67	99.81	58.95	0.07	38.24	38.31
12.	SY	48.61	48.66	99.82	100.05	0.16	87.09	87.24

(S.N.: Serial number; GCV: Genotypic Coefficient of Variation; PCV: Phenotypic Coefficient of Variation; H² %: Heritability in broad sense; GA % mean: Genetic Advance as percent of mean; σ^2_e : Environmental Variance; σ^2_g : Genotypic Variance; σ^2_p : Phenotypic Variance; DFF: Date of 50% flowering; DM: Date of maturity; PH: Plant height; NPB: Number of primary branches per plant; NSB: Number of secondary branches per plant; LMR: Length of main raceme; NSP: Number of siliques per plant; NSS: Number of seeds per silique; TW: Test weight; BYP: Biological yield per plant; HI: Harvest index; SY: Seed yield per plant)

Estimation of genotypic and phenotypic coefficient of variations



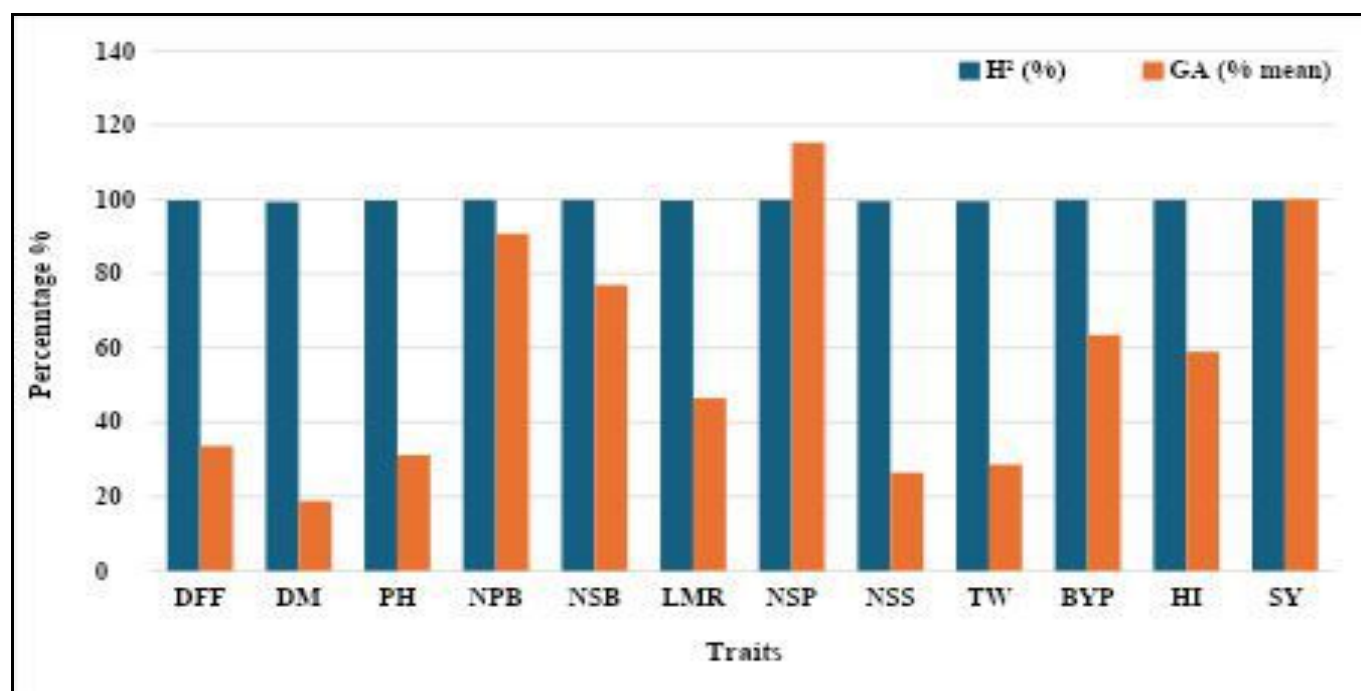
(GCV: Genotypic Coefficient of Variation; PCV: Phenotypic Coefficient of Variation; DFF: Date of 50% flowering; DM: Date of maturity; PH: Plant height; NPB: Number of primary branches per plant; NSB: Number of secondary branches per plant; LMR: Length of main raceme; NSP: Number of siliques per plant; NSS: Number of seeds per silique; TW: Test weight; BYP: Biological yield per plant; HI: Harvest index; SY: Seed yield per plant)

Fig 2: Graphical representation of estimation of genotypic coefficient of variation and phenotypic coefficient of variation in Indian mustard

The estimates of GCV, PCV for twelve traits are presented in Table 4, Fig 2. PCV values were slightly higher than GCV for all traits, indicating minimal environmental influence. High GCV and PCV were observed for number of siliques per plant (55.98 and 56.01), seed yield per plant (48.61 and 48.66), primary branches (44.08 and 44.12), and secondary branches (37.42 and 37.46) respectively, suggesting high variability and good scope for selection. Moderate values were recorded for biological yield (30.88, 30.91), harvest index (28.64, 28.67), and length of main raceme (22.56, 22.59), while lower values were observed for days to maturity (9.14, 9.17) and seeds per silique (12.86, 12.89) respectively.

Estimation of Environmental Variance (σ^2_e), Genotypic Variance (σ^2_g), Phenotypic Variance (σ^2_p)

The estimates of environmental variance (σ^2_e), genotypic variance (σ^2_g), and phenotypic variance (σ^2_p) for all twelve traits are presented in Table 4. For all traits, the phenotypic variance was slightly higher than the corresponding genotypic variance, indicating a minor influence of environmental factors on trait expression. High genotypic and phenotypic variances were observed for NSP (77109.98 and 77212.36), PH (564.70 and 566.97), and BYP (714.25 and 715.96). Moderate variance was recorded for traits like LMR, DM, and SY, while relatively low variance was observed for NSS, TW, NPB, and NSB.

Estimation of heritability (H^2) and Genetic advance (GA % mean)

(H^2 : broad sense heritability; GA % mean: Genetic advance in per cent of mean; DFF: Date of 50% flowering; DM: Date of maturity; PH: Plant height; NPB: Number of primary branches per plant; NSB: Number of secondary branches per plant; LMR: Length of main raceme; NSP: Number of siliquae per plant; NSS: Number of seeds per siliqua; TW: Test weight; BYP: Biological yield per plant; HI: Harvest index; SY: Seed yield per plant)

Fig 3: Graphical representation of H^2 (broad sense) and GA % mean (genetic advance in per cent of mean) in Indian mustard.

The estimates of heritability broad sense (H^2) and genetic advance as percent of mean (GA%) for all traits are presented in Table 4. High heritability values were observed for all traits, ranging from 99.37% (DM) to 99.87% (NSP), indicating that the traits are largely governed by genetic factors with minimal environmental influence. High genetic advance as percent of mean was recorded for NSP (115.24%), SY (100.05%), NPB (90.73%), and NSB (77.00%), suggesting the predominance of additive gene action and effectiveness of selection for these traits. Moderate GA% was observed for BYP (63.53%), HI (58.95%), and LMR (46.43%), indicating scope for improvement through selection. Relatively lower GA% was recorded for DM (18.77%), NSS (26.42%), TW (28.59%), PH (31.16%), and DFF (33.58%), suggesting comparatively lesser expected gain from selection despite high heritability.

Discussion

The ANOVA showed highly significant differences among genotypes for all traits, indicating substantial genetic variability and good scope for selection. Variation in DFF and DM suggests potential for early maturity, while plant height variability aids selection for lodging resistance (Kumar and Misra, 2007; Prajapati *et al.*, 2025) [15, 24]. Significant differences in yield traits (NPB, NSB, LMR, NSP, NSS, TW, BYP, HI, SY) highlight their importance in improving productivity (Sharma *et al.*, 2025; Aslam and Qayyum, 2025; Sowmya *et al.*, 2024) [30, 2, 35]. The coefficient of variation (CV) values were low (0.91-2.06), indicating high experimental precision and reliability. Traits with low CV were more stable for selection, while slightly higher CV suggested some environmental influence. PCV values were slightly higher than GCV for all traits, indicating that environmental influence was minimal and the

observed variation was largely governed by genetic factors. This result aligns with Pant and Singh (2001) [23], Rai *et al.* (2005) [26], Sharma *et al.* (2014) [29], Akabari and Niranjana (2015) [11] and Yadav *et al.* (2022) [38]. High GCV and PCV for NSP, SY, NPB, and NSB suggest the presence of substantial variability and indicate that these traits are governed largely by additive gene action, making them suitable for effective selection. These characters have been reported as main yield contributing traits (Kardam and Singh 2005) [13]. Similar findings pertaining to presence of high genetic variability were reported for different traits including seed yield/plant (Singh, 2004) [33]. Moderate values observed for BYP, HI, and LMR indicate reasonable scope for improvement through selection. In contrast, lower GCV and PCV for DM and NSS suggest limited variability, indicating comparatively less scope for selection as same as the findings by (Jahan *et al.*, 2025) [11]. Overall, the results highlight that traits with higher variability can be effectively utilized in breeding programmes for yield improvement. Phenotypic variance was slightly higher than genotypic variance for all traits, indicating low environmental influence (Choudhary *et al.*, 2025) [5]. Small differences between σ^2_p and σ^2_g suggest that most variation is genetically controlled but with slight environmental effect. High variances were observed for NSP, BYP, PH, and LMR, indicating substantial genetic variability. Moderate variance was recorded for DFF, DM, and SY, while lower variance was observed for NSS and TW. Environmental variance was generally low, especially for TW and branch traits, indicating minimal environmental effects. Even where environmental variance was relatively higher, genetic variance remained predominant. The present findings corroborate the earlier report Sharma *et al.*, (2014) [29], Tiwari *et al.*, (2017) [36] and Pal *et al.*, (2019) [20].

High heritability for different traits such as days to flowering, plant height, and number of siliquae per plant has also been reported earlier by Singh (2004) ^[33] and Kumar and Misra (2007) ^[15], while high heritability for other traits was reported by Khulbe *et al.* (2000) ^[14], Mahla *et al.* (2003) ^[18], Priyamedha *et al.* (2013) ^[25], Pandey and Pandey (2014) ^[21], Vanukuri and Pandey (2022) ^[37], and Kumar *et al.* (2019) ^[16]. High genetic advance as percent of mean (>50%) observed for traits like NSP, SY, NPB, and NSB indicates the predominance of additive gene action and good scope for improvement through direct selection. Moderate values (20-50%) for traits such as BYP, HI, LMR, PH, DFF, NSS, and TW suggest the involvement of both additive and non-additive gene effects, while lower values (<20%) as observed in DM indicate limited scope for selection. Similar findings were also reported by Sharma *et al.* (2025) ^[31].

Conclusion

The present study revealed significant genetic variability among Indian mustard genotypes for yield and yield-related traits, indicating ample scope for selection and crop improvement. High genotypic and phenotypic coefficients of variation, along with very high heritability estimates, suggest that most of the traits are predominantly controlled by genetic factors with minimal environmental influence. The high genetic advance as percentage of mean observed for key traits such as number of siliquae per plant, seed yield per plant, and branch numbers indicates the predominance of additive gene action and highlights their potential for effective improvement through direct selection. Overall, these findings emphasize that selection based on these traits would be reliable and beneficial for developing high-yielding and superior mustard genotypes.

Conflict of Interest:

The authors declare that there is no conflict of interest regarding the publication of this paper.

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