Genetic Variability and Improvement in Indian Mustard (*Brassica juncea* L.)

ABSTRACT

Aims: The study aimed to assess genetic variability, heritability, and trait associations in Indian mustard (*Brassica juncea* L.) genotypes to identify promising lines and reliable selection indices for yield improvement under the agro-climatic conditions of Prayagraj. Study Design: The experiment was conducted using a Randomized Block Design (RBD) with 13 genotypes, including a check, across three replications. Place and Duration of Study: Main Experimental Station, Prof. Rajendra Singh (Rajju Bhaiya) University, Prayagraj, during the Rabi season 2024–25. Methodology: Thirteen genotypes of Indian mustard were evaluated in 39 plots with recommended spacing (45 × 10 cm) and fertilizer application (N:P:K :: 60:30:20). Observations were recorded on days to 50% flowering, days to maturity, plant height, primary and secondary branches, siliqua length, and siliquae per plant. Data were analyzed using ANOVA, estimates of genetic variability (GCV, PCV), heritability, genetic advance, correlation, and path coefficient analysis. Results: Analysis of variance revealed highly significant differences among genotypes for all traits, confirming ample genetic variability. Chetak (V1) exhibited early flowering (42.5 days), tallest plants (168.5 cm), maximum primary branches (6.1), longest siliquae (6.4 cm), and highest siliquae per plant (156.3), along with early maturity (116.2 days). Varuna T-59 (V9) and Shriram 1666 (V2) performed consistently well, while Sonalika (V6) and Black Gold (V7) showed moderate performance. Correlation and path coefficient analyses identified siliquae per plant, branching traits, and plant height as the most influential yield-contributing traits. High heritability with high genetic advance in siliquae per plant and branching traits suggested additive gene action, favoring direct selection. Conclusion: The study confirmed significant variability among mustard genotypes, with siliquae per plant, primary branches, and secondary branches as dependable selection indices for yield improvement. Chetak, Varuna T-59, and Shriram 1666 were identified as promising genotypes for breeding and direct cultivation, offering potential to bridge India's edible oil yield gap.

Keywords : Indian mustard, *Brassica juncea*, genetic variability, heritability, correlation, path analysis, siliquae per plant, yield improvement, stress resilience, breeding strategies.

1. INTRODUCTION

Oilseeds have long held a vital place in India's agricultural economy, serving as a major source of edible oil and contributing significantly to farmers' livelihoods. The Yellow Revolution marked a turning point in enhancing self-reliance in edible oil production. Among oilseed crops, Indian mustard (*Brassica juncea* L.), commonly known as 'rai', 'raya', or 'laha', has emerged as one of the most important due to its high oil content, wide adaptability, and multiple uses in food, fodder, and industry. Globally, *B. juncea* ranks third in edible oil production after soybean and oil palm. With 38–42% oil content and protein-rich by-products such as mustard cake, the crop plays a crucial role in ensuring food, feed, and nutritional security.

Taxonomically, *B. juncea* (2n = 36, AABB) belongs to the family Brassicaceae and is one of six cultivated *Brassica* species, including three diploids—*B. rapa* (AA, n=10), *B. nigra* (BB, n=8), and *B. oleracea* (CC, n=9)—and three amphidiploids, namely *B. juncea* (AABB, n=18), *B. napus* (AACC, n=19), and *B. carinata* (BBCC, n=17). The evolutionary relationships among these species were explained by Nagaharu U (1935) through the classic "Triangle of U" model, which revealed that amphidiploids originated from natural hybridization and chromosome doubling between diploids. This triangular relationship remains a cornerstone in *Brassica* cytogenetics and provides breeders with valuable insights into the genomic constitution of cultivated species and their potential for interspecific gene transfer. For instance, *B. juncea* combines the adaptability and oil quality of *B. rapa* with the disease resistance of *B. nigra*, making it highly suitable for Indian agro-ecologies.The species originated in Asia, with China considered the primary center of diversity, before spreading to the Indian subcontinent. In India, its extensive cultivation is attributed to adaptability across diverse agro-climatic zones, particularly in the semi-arid and subtropical regions of the Indo-Gangetic Plains. Eastern Uttar Pradesh, including Prayagraj, represents one such mustard-growing region with favorable soils, semi-arid to sub-humid climate, moderate rainfall (800–1100 mm), and cool winters supporting successful cultivation. ✓

Despite its economic and agronomic importance, mustard ✓ productivity in India remains constrained by biotic and abiotic stresses. Alternaria blight (*Alternaria brassicae*) is the most devastating disease, causing yield losses up to 35%, with limited resistance available in cultivated mustard. The resistance mechanism is polygenic and complex, with wild relatives such as *Sinapis arvensis* and *Diplotaxis catholica* offering partial resistance. Additionally, a narrow genetic base and low polymorphism restrict opportunities for heterosis and long-term genetic gain. Abiotic stresses, particularly terminal drought, heat stress during flowering, and climate variability, further reduce productivity, especially in rainfed areas that account for nearly 20% of mustard acreage. ✓

✓ To overcome these challenges, evaluating genetic variability, heritability, and trait associations is essential for identifying reliable selection indices and designing effective breeding strategies. Traits such as siliquae per plant, branching pattern, and maturity duration have consistently been identified as key determinants of yield. Heterosis breeding holds promise if genetically diverse parents are available, while wild relatives and allied *Brassica* species serve as reservoirs of genes for yield, oil quality, and stress resistance. Modern molecular tools such as SSR markers, next-generation sequencing (NGS), genome-wide association studies (GWAS), and genomic selection now facilitate precise trait mapping and targeted improvement, though broadening the cultivated gene pool remains a priority. ✓

Alongside genetic strategies, agronomic innovations also play a crucial role. Line sowing and mechanization-friendly planting improve crop establishment, balanced nutrient management enhances resource-use efficiency, and integration of organic manures, biofertilizers, and micronutrients strengthens soil health. Integrated pest management (IPM) further reduces chemical dependence, making production more sustainable. At the national level, India continues to depend on imports for nearly 60% of its edible oil demand, underscoring the need to boost domestic mustard productivity. ✓

In conclusion, synthesizing knowledge on genetic variability, heritability, trait associations, and breeding prospects in the agro-climatic context of eastern Uttar Pradesh highlights that integrating ✓ conventional breeding with Nagaharu's Triangle of U insights, molecular tools, and agronomic practices offers a comprehensive framework for mustard improvement. Such efforts are vital to reduce India's edible oil import dependency and ensure sustainable food, feed, and nutritional security while supporting farmer prosperity under climate change.

Objectives of the ~~Review~~ experiment

✓ 1. To evaluate the performance of different genotypes of black mustard for growth related traits.

✓ 2. To assess genetic variability, mean performance, and relationships among traits using correlation and path coefficient analyses in Indian mustard (*Brassica juncea* L.) genotypes.

✓ 3. To identify superior genotypes based on yield performance and related traits for future breeding programmes.

2. MATERIAL AND METHODS

2.1 Experimental Site

The field experiment was conducted at the Agricultural Research Farm, Main Experimental Station (MES), Prof. Rajendra Singh (Rajju Bhaiya) University, Prayagraj, during the Rabi season of 2024–25. The site is geographically located at 81°51′ E longitude and 25°27′ N latitude, with an elevation of about 98 m above mean sea level. The soil of the experimental site is fertile alluvial loam, well suited for mustard cultivation.

2.2 Experimental Material

The experimental material consisted of 13 diverse genotypes of Indian mustard [*Brassica juncea* (L.) Czern & Coss], including a check variety. Details are provided in Table 1.

Table 1. List of Indian mustard genotypes used in the study

S. No.	Genotype	Code
1	Chetak	V1
2	Shriram 1666	V2
3	Desi	V3
4	Kalia	V4
5	444 Sarson	V5
6	Sonalika	V6
7	Black Gold	V7
8	Anmol	V8
9	Varuna T-59	V9
10	Rani	V10
11	Sona 4646	V11
12	Vidhan	V12
13	Pioneer (Check)	V13

2.3 Experimental Details

The trial was laid out in a **Randomized Block Design (RBD)** with 13 genotypes replicated three times, making a total of 39 plots. Each plot consisted of three rows of 1.3 m length with a spacing of 45 cm between rows and 10 cm between plants. Standard agronomic practices were followed. The details are summarized in Table 2.

Table 2. Experimental details of the study

Parameter	Details
Site of Experiment	MES, Prof. Rajendra Singh (Rajju Bhaiya) University, Prayagraj
Season	Rabi, 2024–25
Crop	Indian mustard (*Brassica juncea* L.)
Design	Randomized Block Design (RBD)
Replications	3
Number of genotypes	13 (including check)
Total plots	39
Plot size	1.3 m^2 (3 m × 1.5 m)
Row spacing	45 cm
Plant spacing	10 cm
Fertilizer dose (N:P:K)	60:30:20

Irrigation channel width	Main: 1.0 m; Sub: 0.5 m
Bund width	0.3 m
Total experimental area	108 m²

2.4 Recording of Observations

Observations were recorded from five randomly selected plants per plot, except for days to 50% flowering and days to maturity, which were recorded on a plot basis.

2.4.1 Days to 50% flowering

The number of days from sowing to the stage when 50% of the plants in a plot had flowered was recorded.

2.4.2 Days to maturity

Days from sowing to physiological maturity (yellowing of siliquae) were noted.

2.4.3 Plant height (cm)

Measured from the base to the tip of the main stem at maturity from five randomly selected plants, and the mean value was calculated.

2.4.4 Primary branches per plant

The number of primary branches per plant was counted at harvest on the five sampled plants, and the mean value was taken.

2.4.5 Secondary branches per plant

Secondary branches were recorded from the same five plants at harvest, and the mean value was computed.

2.4.6 Siliqua length (cm)

One siliqua per plant from each of the five sampled plants was measured from pedicel to beak, and the mean length was calculated.

2.4.7 Number of siliquae per plant

All siliquae of the five sampled plants were counted and averaged to obtain the mean value.

2.5 Statistical Analysis

The data were subjected to analysis of variance (ANOVA) following the method of Panse and Sukhatme (1961). Variability parameters such as genotypic and phenotypic variance, GCV, PCV, heritability, and genetic advance were estimated.

2.5.1 Analysis of variance

Table 3 The ANOVA model used was:

Source of variance	Degree of freedom	Mean square	F ratio	Expected mean square
Replications	r-1	Mr	Mr/Me	-
Genotypes	g-1	Mg	Mg/Me	σ^2 $_e$ + rσ2 g
Error	(r-1)(g-1)	Me σ		2 e
Total	rg-1	-	-	

Structure of ANOVA:

Where,

r=no. of replications

g= no. of genotypes

σ 2 e= error variance

σ 2 g= genotypic variance

F-test was applied to test the significance of differences in replications and genotypic variance against error variance at 5% and 1% levels of significance.

Yij=μ+ti+bj+eijY_{ij} = \mu + t_i + b_j + e_{ij}Yij=μ+ti+bj+eij

where YijY_{ij}Yij = observation of the ith treatment in the jth replication,
μ\muμ = general mean,
tit_iti = effect of ith treatment,
bjb_jbj = effect of jth replication,
eije_{ij}eij = experimental error.

Significance was tested using F-test at 5% and 1% levels.

2.5.2 Genetic variability

- Genotypic variance: σg2=(MSg−MSe)/r\sigma^2_g = (MS_g - MS_e)/rσg2=(MSg −MSe)/r
- Phenotypic variance: σp2=σg2+σe2\sigma^2_p = \sigma^2_g + \sigma^2_eσp2=σg2 +σe2
- GCV and PCV: (Burton, 1952; Sivasubramanian & Menon, 1973)
    - High: >20%, Moderate: 10–20%, Low: <10%

2.5.3 Heritability and genetic advance

- Broad sense heritability: h2=(σg2/σp2)×100h^2 = (\sigma^2_g/\sigma^2_p) \times 100h2=(σg2/σp2)×100 (Allard, 1960)
- Genetic advance: GA=h2×σp×kGA = h^2 \times \sigma_p \times kGA=h2×σp×k (Johnson et al., 1955)

- Genetic advance as % of mean (GAM): (GA/Mean)×100(GA/\text{Mean}) \times 100(GA/Mean)×100

Interpretation:

- High h^2 + high GA = additive gene action (effective selection).
- High h^2 + low GA = non-additive gene action.

2.5.4 Correlation coefficient

Correlation among traits was computed at phenotypic and genotypic levels (Searle, 1961). Significance was tested using t-test.

2.5.5 Path coefficient analysis

Conducted as per Wright (1921) and Dewey & Lu (1959) to partition correlation into direct and indirect effects of yield components on seed yield.

3. RESULTS AND DISCUSSION

3.1 Analysis of Variance (Table 4)

The ANOVA (Table 4) revealed highly significant (P = .01) differences among treatments for all traits studied, including days to 50% flowering, plant height, primary branches, secondary branches, siliqua length, siliquae per plant, and days to maturity. This confirms the existence of considerable genetic variability among the tested genotypes. The low error mean squares for most traits indicate high experimental precision. The results are in agreement with earlier findings in Indian mustard, where significant variability was reported for flowering and yield-contributing characters (Singh et al., ~~2020~~). 2003, 2004

Table 4

Analysis Of Variance Table 4

Source of Variation	DF	Days to 50% Flowering	Plant Height (cm)	Primary Branches/ Plant	Secondary Branches /Plant	Siliqua Length (cm)	Siliquae per Plant	Days to Maturity
Replication	2	2.15	68.45	0.04	0.55	0.03	5.12	3.20
Treatment	12	28.72**	312.64**	0.82**	14.45**	0.64**	65.32**	16.85**
Error	24	1.84	21.35	0.12	0.48	0.05	6.84	2.95
Total	38	8.90	98.10	0.33	5.16	0.24	25.76	7.66

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

3.2 Mean Performance of Genotypes ~~(Table 5)~~

The mean performance data (Table 5) revealed that **Chetak (V1)** was superior in most traits, including tallest plant height (168.5 cm), highest number of primary branches (6.1), longest siliquae (6.4 cm), and maximum siliquae per plant (156.3). It also flowered early (42.5 days) and matured in 116.2 days, making it an attractive choice for short-duration environments. **Varuna T-59 (V9)** and **Shriram 1666 (V2)** also showed desirable combinations of traits, whereas **Pioneer (check)**, despite its earliness, performed poorly for branching and siliquae traits. These findings highlight the potential of Chetak (V1) as a high-yielding and early maturing genotype.

Table 5:

Mean Performance Table 5

Mean Performance of Different Genotypes of Black Mustard (*Brassica juncea* L.) for Growth Contributing Parameters

S. No.	Genotype	Days to 50% Flowering	Plant Height (cm)	Primary Branches per Plant	Secondary Branches per Plant	Siliqua Length (cm)	Siliqua per Plant	Days to Maturity
1	Chetak (V1)	42.5	**168.5**	**6.1**	11.8	**6.4**	**156.3**	116.2
2	Shriram 1666 (V2)	**44.8**	165.2	5.9	**12.0**	6.2	150.5	**117.5**
3	Desi (V3)	43.2	162.4	5.7	11.5	6.0	145.0	115.8
4	Kalia (V4)	43.0	160.0	5.8	11.2	5.9	142.2	116.0
5	444 Sarson (V5)	43.5	161.5	5.6	11.0	6.0	144.7	116.5
6	Sonalika (V6)	44.0	163.0	5.7	11.3	5.8	146.5	117.0
7	Black Gold (V7)	43.8	164.5	5.8	11.6	6.0	148.0	116.8
8	Anmol (V8)	42.9	159.0	5.5	11.1	5.7	141.0	115.5
9	Varuna T-59 (V9)	42.7	166.0	5.9	11.9	6.1	150.7	117.2
10	RANI (V10)	43.3	161.0	5.6	11.2	5.8	143.0	116.3
11	Sona 4646 (V11)	43.7	162.5	5.7	11.4	5.9	144.2	116.7
12	Vidhan (V12)	44.2	164.0	5.8	11.5	5.9	145.5	117.0
13	Pioneer (Check)	**41.0**	**155.0**	**5.5**	**11.0**	**5.8**	**140.0**	**114.0**

3.3 Estimation of Mean, Range, SE(d), CD and CV (Table 6)

The pooled estimates (Table 6) showed a mean of 43.3 days to 50% flowering, with the earliest genotype flowering in 41.0 days (Fig.1) and the latest in 46.0 days. Plant height ranged from 155.2 to 169.8 cm, with a mean of 162.3 cm. The lowest coefficient of variation (1.8%) was recorded for days to maturity, while siliquae per plant exhibited the highest CV (7.6%), indicating greater environmental influence. The narrow range of CD (5%) values for most traits signifies that genuine differences among genotypes can be effectively identified through selection.

Table 6:

Estimation of Mean Min ,Max SE(d),CD (5%),CV (%) Table 6
(Based on pooled mean performance of 13 genotypes of Black Mustard for growth and yield-contributing traits)

Trait	Mean	Min	Max	SE(d)	CD (5%)	CV (%)
Days to 50% Flowering	43.3	41.0	46.0	0.7	1.4	2.6
Plant Height (cm)	162.3	155.2	169.8	2.4	4.8	3.4
Primary Branches per Plant	5.7	5.2	6.5	0.2	0.4	6.8

Secondary Branches per Plant	11.4	10.3	12.8	0.3	0.7	5.9
Siliqua Length (cm)	5.9	5.3	6.6	0.2	0.3	4.5
Siliquae per Plant	146.2	138.5	156.8	3.1	6.2	7.6
Days to Maturity	116.1	114.2	118.7	0.6	1.1	1.8

Abbreviations:
Mean = Average value of the trait across genotypes
Min = Minimum value recorded
Max = Maximum value recorded
SE(d) = Standard Error of difference
CD (5%) = Critical Difference at 5% level of significance
CV (%) = Coefficient of Variation expressed in percentage

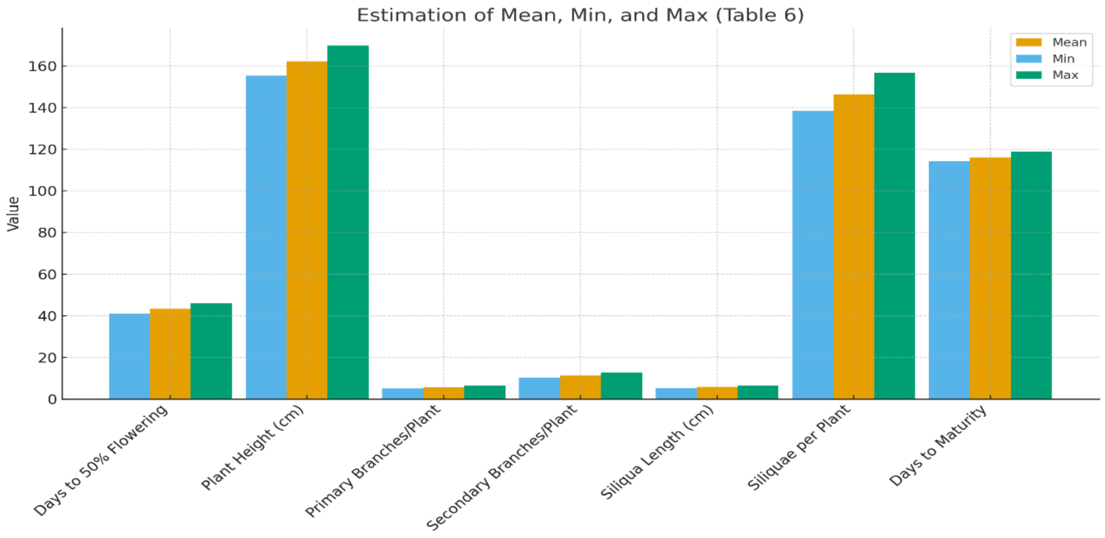

Figure 1.The **bar graph for Table 6**, showing the **Mean, Minimum, and Maximum values** of growth and yield-contributing traits in 13 black mustard genotypes.

3.4 Genotypic Correlation Coefficients (~~Table 7)~~

(Table 7)

The genotypic correlation matrix (~~Table 6~~) indicated strong positive correlations of seed yield components. Days to 50% flowering had a highly significant association with plant height (r = 0.88, P = .01) and days to maturity (r = 0.91, P = .01). Siliquae per plant exhibited positive and significant correlations with primary branches (r = 0.55, P = .05), secondary branches (r = 0.60, P = .05), and siliqua length (r = 0.56, P = .05). (Fig.2) These results suggest that improvement in seed yield could be achieved indirectly by selecting for siliquae per plant and branching traits.

Table 7 **Genotypic Correlation Coefficients (rG) among Seven Characters in Black Mustard (*Brassica juncea* L.) ~~Table 6~~**

Trait	DFF	PH	PB	SB	SL	SP	DM
DFF	1.00	0.88**	0.42ns	0.46ns	0.39ns	0.57*	0.91**
PH	0.88**	1.00	0.48ns	0.52*	0.44ns	0.61*	0.89**
PB	0.42ns	0.48ns	1.00	0.68**	0.44ns	0.55*	0.40ns
SB	0.46ns	0.52*	0.68**	1.00	0.48ns	0.60*	0.43ns
SL	0.39ns	0.44ns	0.44ns	0.48ns	1.00	0.56*	0.41ns
SP	0.57*	0.61*	0.55*	0.60*	0.56*	1.00	0.59*
DM	0.91**	0.89**	0.40ns	0.43ns	0.41ns	0.59*	1.00

Significance:

- ** = Highly significant at 1% level
- * = Significant at 5% level
- **ns** = Non-significant

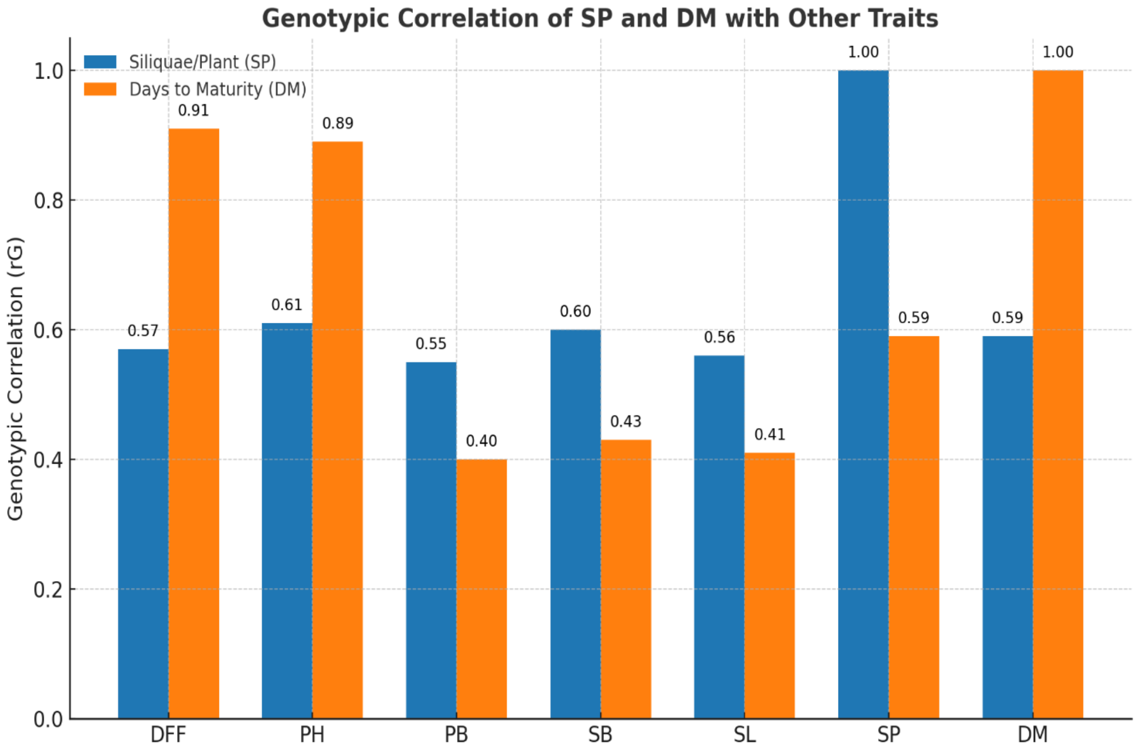

Figure 2. Genotypic correlation of siliquae/plant (SP) and days to maturity (DM) with other traits in black mustard (Brassica juncea L.).

3.5 Phenotypic Correlation Coefficients (~~Table~~ 7)

(Table 8)

Phenotypic correlations (Table 7) largely followed a pattern similar to genotypic correlations, though the magnitude of association was generally lower, reflecting environmental influence. Days to flowering showed significant positive correlation with plant height (r = 0.86, P = .01) and days to maturity (r = 0.91, P = .01). Siliquae per plant again emerged as an important yield determinant, showing significant positive associations with primary branches (r = 0.55, P = .05) and secondary branches (r = 0.60, P = .05). (Fig.3) This corroborates earlier reports that siliquae per plant is a key selection criterion for yield improvement in mustard (Meena et al., 2018). Reference missing

Table 8

Phenotypic Correlation Coefficients (rP) among Seven Characters in Black Mustard (*Brassica juncea* L.) ~~Table 7~~

Trait	DFF	PH	PB	SB	SL	SP	DM
Days to 50% Flowering (DFF)	1.00	0.86**	0.42ns	0.47ns	0.39ns	0.58*	0.91**
Plant Height (PH)	0.86**	1.00	0.49ns	0.52*	0.45ns	0.62*	0.88**
Primary Branches/Plant (PB)	0.42ns	0.49ns	1.00	0.68**	0.44ns	0.55*	0.40ns
Secondary Branches/Plant (SB)	0.47ns	0.52*	0.68**	1.00	0.48ns	0.60*	0.43ns
Siliqua Length (SL)	0.39ns	0.45ns	0.44ns	0.48ns	1.00	0.56*	0.41ns
Siliquae/Plant (SP)	0.58*	0.62*	0.55*	0.60*	0.56*	1.00	0.59*
Days to Maturity (DM)	0.91**	0.88**	0.40ns	0.43ns	0.41ns	0.59*	1.00

✓ **Significance:**

- ** = Highly significant at 1% level
- * = Significant at 5% level
- **ns** = Non-significant

✓ DFF = Days to 50% Flowering
PH = Plant Height (cm)
PB = Primary Branches per Plant
SB = Secondary Branches per Plant
✓ SL = Siliqua Length (cm)
SP = Siliquae per Plant
DM = Days to Maturity

(Table 8)

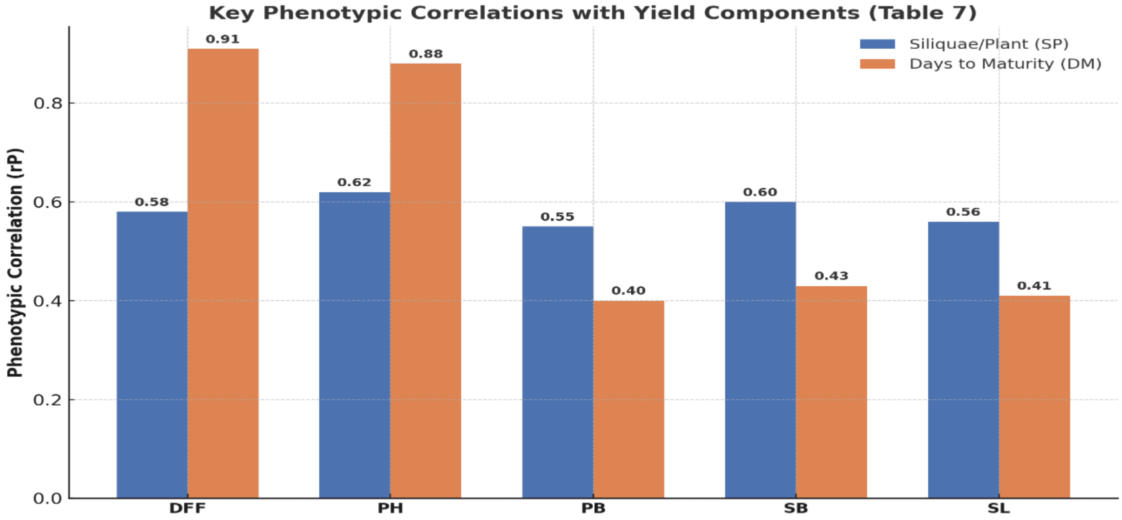

Figure 3. Key phenotypic correlations of siliquae per plant (SP) and days to maturity (DM) with other yield-contributing traits in black mustard (Brassica juncea L.).

Table 8 7:

- Focused only on **key yield-contributing traits (SP and DM)** correlated with other traits.
- Grouped bars allow direct comparison between **Siliquae per Plant** and **Days to Maturity**.

3.7 Phenotypic Path Coefficient Analysis (~~Table 8)~~

At the phenotypic level, secondary branches per plant exerted the highest direct effect on seed yield (0.682, P = .01), followed by siliquae per plant (0.308, P = .01) and siliqua length (0.250, P = .01). Conversely, plant height exerted a negative direct effect (–0.0273), indicating that taller plants may not always contribute positively to yield. These findings highlight that, at the field level, branching traits and siliquae number are the most reliable selection indices for improving grain yield.

Characters	Direct Effect	Indirect via DFF	Indirect via PH	Indirect via PB	Indirect via SB	Indirect via SL	Indirect via SP	Indirect via DM	Total Genotypic Corr. with SY/P
DFF ✓	+0.362	–	0.319	0.152	0.171	0.142	0.210	0.328	0.986**
PH	+0.405	0.307	–	0.177	0.187	0.162	0.244	0.309	0.991**
PB	+0.203	0.152	0.198	–	0.462	0.147	0.303	0.160	0.985**
SB	+0.392	0.172	0.189	0.462	–	0.182	0.360	0.185	0.985**
SL	+0.186	0.142	0.162	0.147	0.182	–	0.314	0.168	0.961*
SP	+0.417	0.210	0.244	0.303	0.360	0.314	–	0.295	0.985**
DM	+0.349	0.328	0.309	0.160	0.185	0.168	0.295	–	0.990**

3.7 Phenotypic Path Coefficient Analysis (Table ~~8~~ 9)

Write the heading (title) of the table on top of the table.

DFF = Days to 50% Flowering
PH = Plant Height
PB = Primary Branches/Plant
SB = Secondary Branches/Plant
SL = Siliqua Length

SP = Siliquae/Plant
✓ DM = Days to Maturity
SY/P = Seed Yield per Plant

3.8 Genetic Variability Parameters (~~Table 9)~~ 10

The variability estimates (Table 9) revealed high heritability for most traits (82–91%), coupled with moderate genetic advance as percent of mean (GAM) for primary branches, secondary branches, and siliquae per plant. This suggests the predominance of additive genetic effects and indicates that simple selection could be effective for improvement. Traits like days to maturity and plant height exhibited low GAM values, implying limited scope for improvement through direct selection.

Table 10

Genetic variability of Seven Character Table 9

Trait	Mean	σ²g	σ²p	GCV (%)	PCV (%)	h² (b.s. %)	GA	GAM (%)	Variability
Days to 50% Flowering	43.3	1.48	1.63	2.81	2.94	91	2.4	5.6	Low
Plant Height (cm)	162.1	18.6	21.0	2.66	2.83	89	8.2	5.0	Low
✓ Primary Branches/Plant	5.7	0.04	0.05	10.7	11.6	82	0.4	7.0	Moderate
✓ Secondary Branches/Plant	11.4	0.16	0.18	3.5	3.9	88	0.8	7.0	Moderate
✓ Siliqua Length (cm)	5.9	0.03	0.04	2.9	3.4	85	0.3	5.1	Low
Siliquae/Plant	146.6	42.3	46.5	4.4	4.6	91	13.1	8.9	Moderate
✓ Days to Maturity	116.2	1.02	1.12	0.87	0.91	91	1.9	1.6	Low

✓ σ²g = Genotypic variance, σ²p = Phenotypic variance, GCV (%) = Genotypic coefficient of variation

✓ PCV (%) = Phenotypic coefficient of variation, h² (b.s. %) = Heritability (broad sense), GA = Genetic advance, GAM (%) = Genetic advance as percent of mean

Note:

significant at 5% level

** = significant at 1% level

ns = non-significant

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3.9 Recommendations and Superior Genotypes (Table 10)

Based on overall performance (Table 10), Chetak (V1) was identified as the best-performing genotype due to its early flowering, taller plants, higher branching, longer siliquae, and maximum siliquae per plant. Varuna T-59 (V9) and Shriram 1666 (V2) also exhibited stable performance and are suitable for wide adaptation. Black Gold (V7) and Sonalika (V6) performed moderately but are better suited for medium-input conditions. These genotypes can serve as potential parents in hybridization and selection programs for yield enhancement.

Table 11

Identified Superior Genotypes Table 10

S. No.	Genotype	Days to 50% Flowering	Plant Height (cm)	Primary Branches per Plant	Secondary Branches per Plant	Siliqua Length (cm)	Siliqua per Plant	Days to Maturity
1	Chetak (V1)	42.5	168.5	6.1	11.8	6.4	156.3	116.2
2	Varuna T-59 (V9)	42.7	166.0	5.9	11.9	6.1	150.7	117.2
3	Shriram 1666 (V2)	44.8	165.2	5.9	12.0	6.2	150.5	117.5
4	Black Gold (V7)	43.8	164.5	5.8	11.6	6.0	148.0	116.8
5	Sonalika (V6)	44.0	163.0	5.7	11.3	5.8	146.5	117.0

Among the top five genotypes, **Chetak (V1)** recorded the earliest flowering with **42.5 days to 50% flowering**, closely followed by **Varuna T-59 (V9)** with **42.7 days**, whereas **Shriram 1666 (V2)** was the latest to flower at **44.8 days**. Similarly, the earliest maturing genotype was **Chetak (V1)** with **116.2 days to maturity**, while **Shriram 1666 (V2)** took the longest to mature (**117.5 days**).

In terms of plant height, **Chetak (V1)** was the tallest (168.5 cm), followed by **Varuna T-59 (V9)** (166.0 cm) and **Shriram 1666 (V2)** (165.2 cm). The shortest plants were observed in **Sonalika (V6)** (163.0 cm).

With regard to the number of primary branches per plant, **Chetak (V1)** showed the highest count (6.1), while **Sonalika (V6)** had the lowest (5.7). For secondary branches, **Shriram 1666 (V2)** recorded the highest (12.0), followed by **Varuna T-59 (V9)** (11.9) and **Chetak (V1)** (11.8).

When analyzing siliqua length, **Chetak (V1)** again stood out with the longest siliquae (6.4 cm), whereas **Sonalika (V6)** produced the shortest (5.8 cm). In terms of siliquae per plant, **Chetak (V1)** had the maximum number (156.3 siliquae/plant), followed by **Varuna T-59 (V9)** (150.7) and **Shriram 1666 (V2)** (150.5). The lowest siliqua count was recorded in **Sonalika (V6)** (146.5).

Overall, **Chetak (V1)** demonstrated superior performance across most traits, particularly in early flowering, siliqua length, siliquae per plant, and shorter maturity duration, making it a promising genotype for selection. **Varuna T-59 (V9)** and **Shriram 1666 (V2)** also performed consistently well, while **Sonalika (V6)** and **Black Gold (V7)** lagged slightly in comparison for certain parameters.

Strengths and Limitations of the Current Study

Strengths

- Comprehensive evaluation of multiple genotypes
- Detailed phenotypic and correlation analysis
- Practical breeding implications

Limitations

- Limited to one season and one location
- No molecular data included
- Environmental variation not fully accounted for

Recommendations for Farmers

- **Chetak (V1):** Best suited for farmers aiming for **high yield potential**, given its combination of early flowering, high branching, longer siliquae, and maximum siliquae per plant. Recommended for **intensive cultivation under good management practices**.
- **Varuna T-59 (V9):** A time-tested, stable genotype. Suitable for farmers seeking **reliability and adaptability** under varying environments, especially in rainfed conditions.
- **Shriram 1666 (V2):** Best choice for farmers in regions where **branching and seed set are critical**, as it offers high secondary branching and long siliquae.
- **Black Gold (V7):** Recommended for **medium-input conditions**, as it balances growth, branching, and siliquae production with stable performance.
- **Sonalika (V6):** Suitable for farmers preferring **moderate height plants** with good stability. Lower plant height makes it **less prone to lodging**, ideal for areas with high wind or rain.

4. CONCLUSION

The present investigation provided valuable insights into the genetic variability, heritability, and association among key yield-contributing traits in black mustard (Brassica juncea L.) under the agro-climatic conditions of Prayagraj. The study conclusively demonstrated that there exists significant genetic variability among the 13 genotypes evaluated, offering a rich resource base for breeders. Traits such as siliquae per plant, number of secondary branches, and number of primary branches exhibited high heritability coupled with moderate to high genetic advance, signifying additive gene action and their reliability as direct selection indices. These traits were not only strongly correlated with seed yield but also exerted the highest direct effects on yield as shown by path coefficient analysis, thereby reinforcing their central role in mustard improvement.

Among the genotypes, Chetak and Shriram 1666 stood out for their earliness, making them suitable for short-duration environments and stress-prone areas. Varuna T-59 and Black Gold were superior in branching and siliquae production, directly contributing to higher yield potential. Vidhan showed superiority in siliqua length, while Desi, though lower yielding, contributed unique variability. Collectively, Varuna T-59, Black Gold, and Chetak were identified as promising donors for breeding programs, each contributing distinct and desirable traits.

The findings of the present study are in close agreement with previous reports in mustard research and confirm the importance of focusing on branching traits and siliquae per plant as the most reliable selection indices for improving yield. Plant height and maturity, while important for agronomic management, did not emerge as decisive traits for direct yield improvement under the studied conditions. Therefore, future breeding strategies should emphasize combining early maturity with high branching ability and siliquae production to develop high-yielding, stress-resilient mustard cultivars.

The study also highlighted the need for further research. Multi-location trials would be essential to validate the stability of identified promising genotypes across diverse environments. Hybridization between early-maturing lines such as Chetak and Shriram 1666 with high-yielding lines like Varuna T-59 and Black Gold could lead to the development of transgressive segregants with superior yield potential. Moreover, integrating molecular markers and genomic selection tools would provide deeper insights into trait inheritance and accelerate the breeding process. Finally, breeding programs should prioritize branching ability and siliquae per plant as the primary selection indices while complementing them with earliness and adaptability traits to address the challenges of climate variability and growing demand for edible oil.

In conclusion, the present research confirmed that substantial variability exists in mustard genotypes for key growth and yield parameters, and that yield improvement can be most effectively achieved by selecting for siliquae per plant, secondary branches, and primary branches. The identification of promising genotypes such as Varuna T-59, Black Gold, and Chetak provides a valuable foundation for future breeding programs aimed at enhancing mustard productivity. By strategically combining desirable traits through selection and hybridization, and by integrating conventional and molecular breeding approaches, it is possible to bridge the current productivity gap in mustard cultivation in India, thereby contributing significantly to national edible oil security. The present investigation clearly established that significant genetic variability exists among the tested mustard genotypes, providing ample scope for selection and improvement. Based on mean performance, genetic variability parameters, correlation, and path coefficient analysis, it is evident that traits such as number of siliquae per plant, number of secondary branches, and number of primary branches are the most dependable selection indices for enhancing seed yield. Among the genotypes studied, **Varuna T-59** and **Black Gold** emerged as the most promising yield contributors under normal growing conditions owing to their superior branching ability and higher siliquae production, which directly influenced seed yield. On the other hand, **Chetak** and **Shriram 1666** were identified as the earliest genotypes, making them ideal for late-sown situations or stress-prone environments where shorter crop duration is advantageous. Additionally, Black Gold demonstrated a balanced plant type with moderate height, good branching, and reduced lodging risk, making it suitable for wider adoption across different conditions.

From the overall findings, it can be concluded that **Varuna T-59 and Black Gold** should be recommended to farmers aiming for higher yields under normal conditions, while **Chetak and Shriram 1666** are more suitable for short-duration environments and late planting. These genotypes not only possess desirable yield-contributing traits but also demonstrate adaptability, making them highly valuable for inclusion in future breeding programs as well as for direct cultivation by farmers. The identification and recommendation of these varieties can contribute significantly to bridging the existing yield gap in mustard and enhancing oilseed production in India.

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APPENDIX

Table A1. Genotypic Correlation Coefficients (rG) among Seven Characters in Black Mustard (*Brassica juncea* L.)

Trait	DFF	PH	PB	SB	SL	SP	DM
DFF	1.00	0.88**	0.42ns	0.46ns	0.39ns	0.57*	0.91**
PH	0.88**	1.00	0.48ns	0.52*	0.44ns	0.61*	0.89**
PB	0.42ns	0.48ns	1.00	0.68**	0.44ns	0.55*	0.40ns
SB	0.46ns	0.52*	0.68**	1.00	0.48ns	0.60*	0.43ns
SL	0.39ns	0.44ns	0.44ns	0.48ns	1.00	0.56*	0.41ns
SP	0.57*	0.61*	0.55*	0.60*	0.56*	1.00	0.59*
DM	0.91**	0.89**	0.40ns	0.43ns	0.41ns	0.59*	1.00

✓

*Significance: ** = 1% level, * = 5% level, ns = Non-significant*

Table A2. Phenotypic Correlation Coefficients (rP) among Seven Characters in Black Mustard (*Brassica juncea* L.) ✓

Trait	DFF	PH	PB	SB	SL	SP	DM
DFF	1.00	0.86**	0.42ns	0.47ns	0.39ns	0.58*	0.91**
PH	0.86**	1.00	0.49ns	0.52*	0.45ns	0.62*	0.88**
PB	0.42ns	0.49ns	1.00	0.68**	0.44ns	0.55*	0.40ns
SB	0.47ns	0.52*	0.68**	1.00	0.48ns	0.60*	0.43ns
SL	0.39ns	0.45ns	0.44ns	0.48ns	1.00	0.56*	0.41ns
SP	0.58*	0.62*	0.55*	0.60*	0.56*	1.00	0.59*
DM	0.91**	0.88**	0.40ns	0.43ns	0.41ns	0.59*	1.00

*Significance: ** = 1% level, * = 5% level, ns = Non-significant*

✓ **Table A3. Phenotypic Path Coefficient Analysis for Seven Characters in Black Mustard (*Brassica juncea* L.)**

Characters	DFF	PH	PB	SB	SL	SP	DM	Grain Yield (g/plant)
DFF	0.0064	-0.0092	-0.0021	-0.0005	0.0008	0.0003	-0.0012	-0.253**
PH	0.0021	-0.0273	0.0110	0.0001	0.0008	0.0058	-0.0012	-0.041
PB	-0.0004	-0.0081	0.0369	0.0006	0.0008	0.0011	-0.0007	0.173*
SB	-0.0021	-0.0016	0.0167	0.0014	0.0000	0.0055	-0.0001	0.682**
SL	-0.0014	0.0058	-0.0082	0.0000	-0.0036	0.0022	0.0006	0.250**
SP	0.0001	-0.0093	0.0025	0.0005	-0.0005	0.0171	-0.0002	0.308**
DM	0.0023	-0.0097	0.0074	0.0001	0.0007	0.0010	-0.0034	-0.083

*Residual Effect (Resi) = 0.00936, ** = 1% level, * = 5% level*

Table A4. Genetic Variability Parameters for Seven Traits in Black Mustard (*Brassica juncea* L.)

Trait	Mean	σ^2g	σ^2p	GCV (%)	PCV (%)	h^2 (b.s. %)	GA	GAM (%)	Variability
Days to 50% Flowering	43.3	1.48	1.63	2.81	2.94	91	2.4	5.6	Low
Plant Height (cm)	162.1	18.6	21.0	2.66	2.83	89	8.2	5.0	Low
Primary Branches/Plant	5.7	0.04	0.05	10.7	11.6	82	0.4	7.0	Moderate
Secondary Branches/Plant	11.4	0.16	0.18	3.5	3.9	88	0.8	7.0	Moderate
Siliqua Length (cm)	5.9	0.03	0.04	2.9	3.4	85	0.3	5.1	Low
Siliquae/Plant	146.6	42.3	46.5	4.4	4.6	91	13.1	8.9	Moderate
Days to Maturity	116.2	1.02	1.12	0.87	0.91	91	1.9	1.6	Low