



Plant Archives

Journal homepage: <http://www.plantarchives.org>

DOI Url : <https://doi.org/10.51470/PLANTARCHIVES.2026.v26.supplement-2.045>

GENETIC DIVERSITY, VARIABILITY AND TRAIT ASSOCIATION ANALYSIS IN INDIAN MUSTARD (*Brassica juncea* L.) GENOTYPES UNDER RABI CONDITIONS

Mahmood Alam, S.N. Mishra*, Sandeep Maurya and Shubham Kumar Patel

Department of Genetics and Plant Breeding, Faculty of Agriculture, PRSU, Prayagraj, India

*Corresponding author E-mail: sonmishra2@gmail.com

(Date of Receiving : 05-03-2026; Date of Revision : 18-04-2026; Date of Acceptance : 11-05-2026)

ABSTRACT

The present study was conducted to evaluate genetic variability, heritability, and trait associations among Indian mustard (*Brassica juncea* L.) genotypes under the agro-climatic conditions of Prayagraj during the Rabi season 2025–26. The experiment was laid out in a Randomized Block Design with 20 genotypes and three replications. Observations were recorded on thirteen quantitative traits including plant height at different growth stages, days to 50% flowering, biological yield, seed yield, number of branches, and siliqua-related traits. Analysis of variance revealed significant differences among genotypes for all characters, indicating the presence of substantial genetic variability. The mean performance showed wide variation, particularly for total siliqua per plant (172.27–353.33), seed yield per plot (825.33–1275.67 g), and number of branches (15.93–28.07). High phenotypic coefficient of variation (PCV) compared to genotypic coefficient of variation (GCV) for most traits suggested environmental influence. High heritability was observed for days to 50% flowering (84.54%) along with moderate genetic advance, indicating its reliability for selection. Correlation analysis revealed that biological yield, total siliqua per plant, and number of branches exhibited strong positive association with seed yield. Path coefficient analysis further confirmed that these traits had a direct positive effect on yield. Cluster analysis grouped genotypes into three clusters, with maximum genotypes in cluster I, indicating genetic diversity among lines. Overall, traits such as total siliqua per plant, number of branches, and biological yield were identified as important selection criteria for yield improvement. The study highlights the potential of these traits and genotypes for future breeding programs aimed at enhancing mustard productivity.

Keywords : *Brassica juncea*, genetic variability, genetic diversity, path coefficient analysis, correlation analysis.

Introduction

Mustard is a classic *rabi* crop, planted in October–November and ready to harvest by March–April. It does best in medium to deep, well-drained soils. Indian mustard (*Brassica juncea* L.), a key oilseed, belongs to the Brassicaceae family and Brassica genus. Black mustard seeds go mainly for oil, white mustard serves as fodder or green manure, and black seeds spice up dishes. Mix ground seeds with water, vinegar, or other liquids, and you get that familiar yellow prepared mustard. Press the seeds for mustard oil, or eat the leaves as a veggie. Traditionally, mustard tackles all sorts of ailments like sore throats, chest congestion, fevers, flu, muscle aches, and joint or back pain.

Rapeseed seed meal packs a nutritional punch: 35–40% protein, 14–15% carbs, 10–12% fiber, 4–6% ash, 1–1.5% minerals and vitamins, plus smaller amounts of glucosinolates (2–3%), tannins (1.6–3.1%), sinapinic acid (1–1.5%), and phytic acid (3–6%) (Prasad, 2015). The seeds themselves hold 37–49% oil. The leftover oil cake makes great cattle feed and fertilizer, delivering about 4.9% nitrogen, 2.5% phosphorus, and 1.5% potassium. From flavoring food to medicine and preservation, every part of the mustard plant supports daily life.

India ranks as a major global player in mustard, ranking second worldwide in seed production (behind Canada). Canada dominates thanks to vast canola

fields suited to its cool climate. In India, mustard shines in the north and central regions due to its toughness across climates, cementing its role in the oilseed economy.

Mustard, or *Brassica juncea* L., ranks among the top oilseed crops grown in varied climates, especially across South Asia like India and Bangladesh. In the Indian subcontinent, Indian mustard stands out as the most popular variety. Farmers mainly plant it in the *rabi* (winter) season, where it boosts the economy through oil extraction, green manure, and livestock fodder. In India, it thrives everywhere from the hilly northeast and northwest to the south under irrigated or rainfed setups, with early or late sowing, even in salty soils or mixed crops. Globally, it's prized as an oilseed, veggie, and spice crop (Saleem *et al.*, 2017; Kumar *et al.*, 2018).

Rapeseed-mustard crops from the Brassicaceae family are key for edible oils and veggies. They include six main cultivated species: diploids like *B. campestris/rapa* (2n=20, AA), *B. nigra* (2n=16, BB), and *B. oleracea* (2n=18, CC); plus tetraploids such as *B. juncea* (2n=36, AABB), *B. napus* (2n=38, AACC), and *B. carinata* (2n=34, BBCC). These tetraploids arose naturally from crosses between the diploids (Prakash *et al.*, 2011; Rakow, 2004). Mustard likely originated in Central Asia, especially northwest India, with secondary hotspots in central and western China, eastern India, Burma, and areas from Iran to the Near East.

Uttar Pradesh is one of India's top three mustard-producing states, leading in both cultivated land and output. Lately, the state has dedicated over 17 lakh hectares to mustard, helping push India to the world's second-largest producer. While Rajasthan tops the list and Madhya Pradesh comes second, Uttar Pradesh has ramped up its game with better seed varieties and farming techniques. This makes it a vital hub in the northern plains, supporting the country's edible oil needs and the incomes of countless farmers.

In Prayagraj district, Uttar Pradesh, mustard is steadily catching on as a key winter crop alongside wheat. Research from (Singh *et al.*, 2022) in Jasra and Soraon blocks shows average yields of 14.04 quintals per hectare, with a solid benefit-cost ratio of 1.77 great news for small farmers. Kumar and Verma (2023) found that sowing around mid-October with the Ratna variety really boosts growth and yields in the local climate. Still, India's mustard production falls short of our edible oil demands, so we need tougher, higher-yielding varieties that handle pests, weather extremes, and climate shifts while making the most of land, time,

and inputs. That said, farmers face hurdles like steep input costs, fertilizer shortages, and not enough workers. Tackling these with training on smart pesticide use, ways to cut costs, and recycling organic waste could really lift productivity in the area.

Botanical Classification

Mustard belongs to the *Cruciferae* (or *Brassicaceae*) family, which includes roughly 150 species. The three primary types used as condiments are:

- **Yellow/White Mustard (*Sinapis alba*):** Indigenous to southern Europe, now widely cultivated globally; known for its mild flavor.
- **Brown/Indian Mustard (*Brassica juncea*):** Originally introduced from China to northern India; it is the primary source of pungency in cultivated mustards and is widely used for oil production.
- **Black Mustard (*Brassica nigra*):** Likely endemic to the Mediterranean; historically considered the "true" mustard, though less popular in some regions due to harvesting difficulties.

Research Objective

The present investigation was conducted to analyze the association among yield and its component traits in Indian mustard. The study also aimed to evaluate the correlation and path coefficient analysis in order to understand the direct and indirect effects of different characters on seed yield. In addition, the experiment was undertaken to estimate the nature and magnitude of variability present among the Indian mustard genotypes for various growth, yield, and yield contributing traits.

Material and Methods

Experimental Site

We carried out the field experiment at the Agricultural Research Farm, Main Experimental Station (MES), Prof. Rajendra Singh (Rajju Bhaiya) University in Prayagraj, during the Rabi season of 2025–26. The location sits at 81°51' E longitude and 25°27' N latitude, about 98 meters above sea level. The soil there is fertile alluvial loam, perfect for growing mustard.

Experimental Material

The study used 20 diverse genotypes of Indian mustard (*Brassica juncea* L. Czern & Coss), including one check variety. Full details are in Table 1.

Table 1: List of Indian mustard genotypes used in the present study along with their sources.

Variety Notation	Experimental material	Source (Material received)
V ₁	Bhagirathi	PORS, Berhampur (W.B)
V ₂	Maya	CSA. (Kanpur)
V ₃	RH-819	C.C.S.H.A.U, (Hisar, Haryana)
V ₄	RH-749	C.C.S.H.A.U, (Hisar, Haryana)
V ₅	ND-2005-1	ANDUAT, (Ajodhya)
V ₆	PM-29	ICAR-IARI, (New Delhi)
V ₇	PM-28	ICAR-IARI, (New Delhi)
V ₈	C-724	DRMR, (Bharatpur)
V ₉	CS-58	CSSRI, (Karnal, Haryana)
V ₁₀	Krishna	GBPAUT
V ₁₁	PusaTarak	ICAR-IARI, (New Delhi)
V ₁₂	Arawali	DRMR, (Bharatpur)
V ₁₃	Sona-4646	CSA. (Kanpur)
V ₁₄	Local-1	Prayagraj
V ₁₅	Anmol	(DRMR), Bharatpur
V ₁₆	Local-2	Prayagraj
V ₁₇	Local-3	Prayagraj
V ₁₈	Sarson-444	Prayagraj
V ₁₉	Blackgold	Prayagraj
V ₂₀	Local-4(Check Variety)	Prayagraj

Methodology of studied parameters

The present study was conducted to evaluate various quantitative traits. Observations were recorded on five randomly selected plants from each plot, and the average values were used for statistical analysis. The methodology adopted for each parameter is described below:

- Plant height at 30 DAS (cm):** Plant height was measured at 30 DAS from the base of the plant to the tip of the main shoot in five randomly selected plants using a measuring scale, and the mean value was expressed in centimeters.
- Plant height at 60 DAS (cm):** The height of the same five randomly selected plants was recorded at 60 DAS and averaged.

- Plant height at 90 DAS (cm):** Final plant height was measured at 90 DAS in the selected plants and mean values were calculated.
- Days to 50% flowering:** The number of days from sowing to the stage when 50% of the plants in each plot had at least one open flower was recorded on a plot basis.
- Number of branches per plant:** The total number of primary branches was counted in five randomly selected plants at maturity and averaged.
- Number of siliqua on main branch:** The number of siliqua present on the main branch of each of the five selected plants was counted and the mean value was calculated.
- Total number of siliqua per plant:** Total siliqua per plant were counted in the selected plants at maturity and averaged.
- Test weight (g):** Test weight was determined by weighing 1000 seeds from each plot and expressed in grams.
- Biological yield per plant (g):** Total above-ground biomass of five randomly selected plants was recorded after harvest, and the mean value was expressed in grams.
- Seed yield per plant (g):** Seeds obtained from each of the five selected plants were weighed separately and the average was calculated.
- Seed yield per plot (g):** Total seed yield harvested from each plot was recorded and expressed in grams.
- Harvest index (%):** Harvest index was calculated using the formula:

$$\text{Harvest Index (\%)} = (\text{Seed Yield per plant} / \text{Biological Yield per plant}) \times 100$$

Statistical analysis

- Analysis of variance (ANOVA)
- Frequency distribution for all traits
- Range and variance
- Genetic variability
- Heritability and genetic advance
- Correlation and path coefficient analysis

Table 2: Mean performance table of mustard

Genotypes	Plant height 30 DAS	Plant height 60 DAS	Plant height 90 DAS	Days to 50% Flowering	Biological yield (kg)	Seed yield per plot (Kg)	Number of branches	Number of siliqua on main branches	Total siliqua per plant	Harvest index (%)	Seed yield q/hac	Test weight (g)	Seed yield per plant (g)
V ₁	13.1	104.1	208.47	58.00	4.86	1.27	16.93	49.00	209.40	26.55	27.05	5.20	13.40
V ₂	15.9	101.7	208.93	58.67	2.95	0.827	19.67	38.73	230.33	27.98	16.51	5.05	14.20
V ₃	13.9	100.3	207.73	60.00	4.10	1.027	17.80	48.53	254.40	25.17	20.53	5.45	18.93
V ₄	15.6	105.7	214.33	55.33	5.98	1.277	26.80	26.33	353.33	21.68	24.39	4.69	15.20
V ₅	11.7	104.8	205.53	56.67	3.51	1.027	16.47	33.60	232.73	29.90	20.52	5.01	17.60
V ₆	16.5	101.5	202.47	55.67	3.89	1.123	18.47	41.47	246.73	28.90	22.42	5.91	16.07
V ₇	12.7	105.1	207.27	61.00	4.58	1.203	17.33	40.00	211.27	26.27	24.09	5.38	15.73

V ₈	11.8	108.5	198.20	60.67	4.19	1.273	17.40	40.93	235.67	30.35	25.43	4.12	17.73
V ₉	12.1	100.1	201.47	62.33	4.48	0.93	16.60	45.27	216.60	20.89	18.65	5.25	13.07
V ₁₀	11.6	102.1	195.80	60.33	4.09	1.093	17.80	43.13	223.27	27.03	21.84	4.57	11.47
V ₁₁	10.0	105.1	199.00	56.00	3.83	1.057	18.27	43.47	238.53	27.70	21.15	5.91	16.27
V ₁₂	16.3	99.7	204.00	60.33	3.63	0.92	18.00	40.80	205.27	25.26	18.43	5.10	12.80
V ₁₃	13.8	103.7	182.27	54.67	3.58	0.88	15.93	38.27	270.53	25.10	17.54	4.84	15.53
V ₁₄	13.3	106.9	204.20	55.67	3.35	0.957	17.67	39.60	234.07	28.35	19.10	5.50	16.20
V ₁₅	13.1	101.9	203.80	57.00	3.42	0.923	19.00	45.40	221.20	27.21	17.43	4.70	18.73
V ₁₆	14.7	101.8	211.13	57.67	3.59	0.92	28.07	40.87	262.07	25.98	18.45	4.91	19.13
V ₁₇	14.8	104.2	193.20	57.67	3.69	1.04	18.00	44.20	213.53	28.31	21.60	5.18	14.07
V ₁₈	15.7	101.6	186.00	58.00	4.24	1.103	22.27	44.87	309.13	26.32	22.12	5.03	15.40
V ₁₉	12.7	91.1	200.07	56.33	3.05	0.923	17.40	41.67	184.33	30.26	18.49	5.62	11.73
V ₂₀	10.2	111.0	199.20	56.67	4.50	1.083	18.13	44.67	172.27	24.40	21.69	5.22	13.53
Mean	13.5	103.1	201.65	57.93	3.97	1.0428	18.90	41.54	236.23	26.68	20.87	5.13	15.34
SEd	1.89	4.16	5.95	0.74	0.62	0.141	3.26	5.20	41.07	2.60	2.91	0.72	2.23
CD5%	3.82	8.42	5.04	1.50	1.25	0.286	6.59	10.52	83.15	5.26	5.89	1.46	4.52
CV	17.16	4.94	3.61	1.57	19.03	16.51	21.10	15.32	21.29	11.93	17.09	18.35	17.83
Max	16.5	111.0	214.33	62.33	5.976	1.277	28.07	49.00	353.33	30.35	27.05	5.91	19.13
Min	10.0	91.1	182.27	54.67	2.95	0.83	15.93	26.33	172.27	20.89	16.51	4.12	11.47

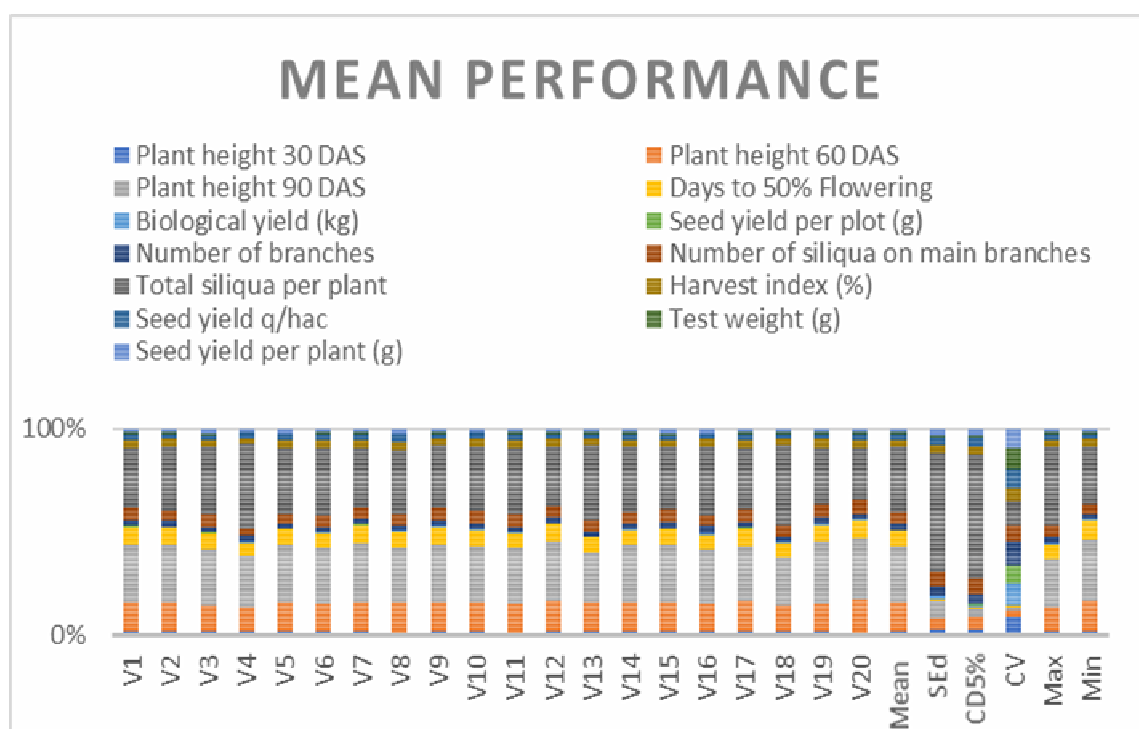
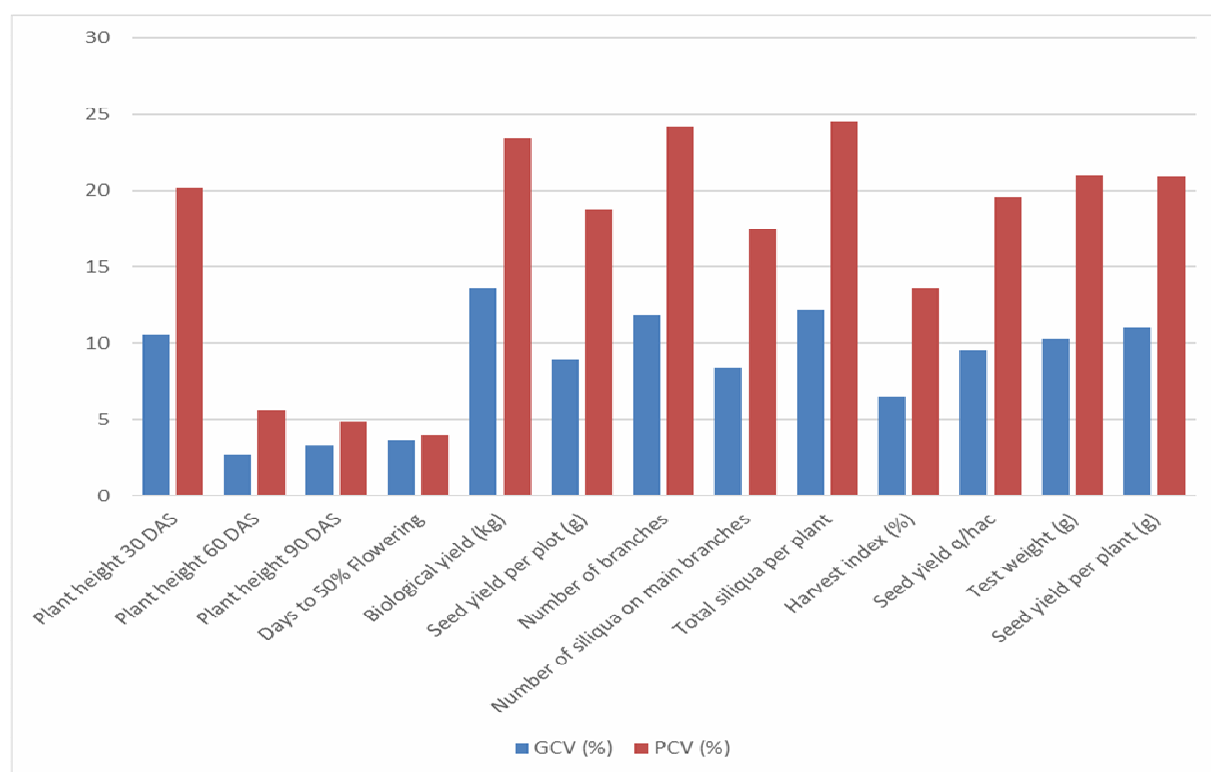
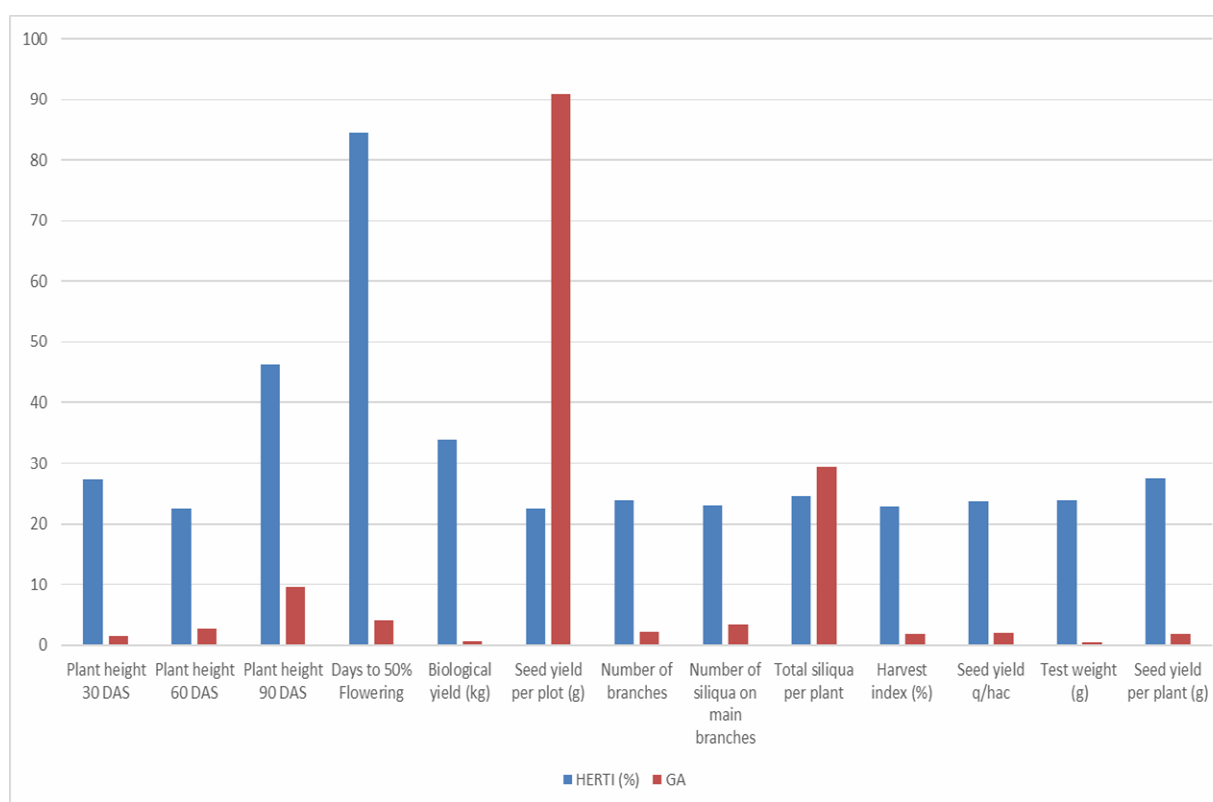


Fig. 1 : Mean Performance

Table 3 : Estimation of components of variance and genetic parameters for different quantitative characters.

Traits	V _g	V _p	GCV (%)	PCV (%)	HERTI (%)	GA	GA AS %
Plant height 30 DAS	2.02	7.36	10.54	20.14	27.42	1.53	11.37
Plant height 60 DAS	24.90	50.85	2.67	5.62	22.66	2.70	2.62
Plant height 90 DAS	81.10	134.16	3.35	4.92	46.29	9.47	4.7
Days to 50% Flowering	5.05	5.87	3.66	3.98	84.54	4.02	6.93
Biological yield (kg)	0.67	1.24	13.58	23.38	33.76	0.64	16.26
Seed yield per plot (Kg)	28393.87	58040.31	8.90	18.76	22.54	90.86	8.71
Number of branches	15.61	31.52	11.84	24.19	23.95	2.25	11.94
Number of siliqua on main branches	39.18	79.69	8.4	17.47	23.11	3.45	8.31
Total siliqua per plant	2514.71	5045.55	12.17	24.53	24.64	29.41	12.45
Harvest index (%)	9.77	19.91	6.50	13.59	22.88	1.71	6.40

Seed yield q/hac	12.44	25.16	9.52	19.56	23.70	1.99	9.55
Test weight (g)	2.30	3.08	10.27	21.03	23.86	0.49	10.34
Seed yield per plant (g)	7.84	15.33	11.00	20.95	27.57	1.82	11.90

**Fig. 2 : GCV&PCV****Fig. 3 : Heritability & Genetic advance**

Heritability and Genetic Advance

Heritability in broad sense and genetic advance were estimated using standard statistical methods.

- **Heritability (h^2)** was calculated by using statistical formula.

$$h^2 = (\text{Genotypic Variance} / \text{Phenotypic Variance}) \times 100$$

- **Genetic Advance (GA)** was calculated by using statistical formula.

$$GA = k \times \sqrt{(\text{Phenotypic Variance}) \times h^2}$$

Where:

- k = selection differential
- Genetic Advance as % of Mean was also calculated to assess the extent of variability.

Results and Discussion

Analysis of variance

The analysis of variance (ANOVA) indicated significant differences among the genotypes for all the traits studied. Traits such as plant height at 30, 60 and 90 DAS, days to 50% flowering, biological yield, seed yield per plot, number of branches, and siliqua-related characters showed statistical significance at 5% and 1% levels. For instance, plant height at 90 DAS and days to 50% flowering were highly significant at the 1% level, confirming strong genetic differences among genotypes. The presence of significant variation for all characters clearly indicates the existence of substantial genetic variability in the experimental material. Moreover, relatively lower error mean squares for most traits suggest good experimental precision and reliability of the data. These results highlight that the genotypes possess sufficient variability, which can be effectively utilized for selection and crop improvement programs.

Mean Performance of Genotypes

The mean performance of the genotypes revealed wide variability for all studied traits. Among the genotypes, Genotype 4 recorded the highest plant height at 90 DAS (214.33 cm), maximum total siliqua per plant (353.33), highest number of branches (26.80), and maximum seed yield per plot (1275.67 g), indicating its superior yield potential. Genotype 16 showed the highest number of branches (28.07) and seed yield per plant (19.13 g), while Genotype 8 exhibited the highest harvest index (30.35%). Early flowering was observed in Genotype 13 (54.67 days),

whereas Genotype 9 was the latest (62.33 days). The overall mean seed yield per plot was 1042.73 g, with a wide range from 825.33 g to 1275.67 g, indicating considerable variability among genotypes. These findings suggest that certain genotypes possess desirable combinations of traits and can be effectively utilized for yield improvement and breeding purposes.

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

The estimates of mean, range, standard error [SE(d)], critical difference (CD), and coefficient of variation (CV). Days to 50% flowering ranged from 54.67 to 62.33 days with a mean of 57.93 days, indicating moderate variability. Plant height at 90 DAS varied from 182.27 cm to 214.33 cm with an average of 201.65 cm. Total siliqua per plant exhibited a wide range (172.27–353.33), reflecting high variability for this important yield trait. The coefficient of variation was highest for total siliqua per plant (21.29%) and number of branches (21.10%), indicating greater environmental influence on these traits. In contrast, days to 50% flowering showed the lowest CV (1.57%), suggesting greater stability. The relatively narrow CD values at 5% level for most traits indicate that the differences among genotypes were statistically reliable. Overall, the results suggest that effective selection can be practiced for traits showing high variability and stability.

Table 4: Analysis of variance

Traits	Mean sum of squares		
	Replications	Genotypes	Error
	(d.f=2)	(d.f=19)	(d.f=38)
Plant height 30 DAS	21.173	11.405*	5.345
Plant height 60 DAS	72.338	48.765*	25.949
Plant height 90 DAS	436.789	190.262**	53.059
Days to 50% Flowering	5.017	14.337**	0.824
Biological yield (kg)	2.454	1.451**	0.574
Seed yield per plot (Kg)	209717.217	55535.6*	29646.445
Number of branches	7.064	30.938*	15.905
Number of siliqua on main branches	116.216	77.04*	40.509
Total siliqua per plant	3294.909	5013.292*	2530.837
Harvest index (%)	0.031	19.172*	10.142
Seed yield q/hac	73.386	24.585*	12.723
Test weight (g)	0.336	1.515*	0.781
Seed yield per plant (g)	21.986	16.038*	7.486

* indicates significance at 5% level,

** indicates significance at 1% level

Table 5: Genotypic correlation coefficient

Traits	Plant height 30 DAS	Plant height 60 DAS	Plant height 90 DAS	Days to 50% Flowering	Biological yield (kg)	Seed yield per plot (g)	Number of branches	Number of siliqua on main branches	Total siliqua per plant	Harvest index (%)	Seed yield q/hac	Test weight (g)	Seed yield per plant (g)
Plant height 30 DAS	1.00	-0.669**	0.016	-0.067	-0.147	-0.271*	0.995**	-0.446**	1.190**	-0.031	-0.282*	-0.395**	0.111
Plant height 60 DAS		1.00	-0.163	-0.164	0.879**	1.190**	-0.24	-0.276*	0.002	-0.188	1.185**	-0.083	0.368**
Plant height 90 DAS			1.00	0.161	0.295*	0.316*	0.650**	-0.349**	-0.019	-0.04	0.258*	0.604**	0.426**
Days to 50% Flowering				1.00	0.159	0.123	-0.303*	0.559**	-0.486**	-0.297*	0.167	-0.477**	-0.202
Biological yield (kg)					1.00	0.809**	0.642**	-0.281*	0.849**	-0.740**	0.765**	0.530**	-0.162
Seed yield per plot (g)						1.00	0.094	-0.244	0.368**	-0.187	1.000**	0.778**	-0.197
Number of branches							1.00	-0.945**	0.922**	-0.894**	-0.069	-0.023	0.222
Number of siliqua on main branches								1.00	-1.200**	-0.039	-0.03	0.109	-0.276*
Total siliqua per plant									1.00	-0.920**	0.185	0.061	0.403**
Harvest index (%)										1.00	-0.14	0.114	-0.065
Seed yield q/hac											1.00	0.778**	-0.347**
Test weight (g)												1.00	-0.280*
Seed yield per plant (g)													1.00

* indicates significance at 5% level, ** indicates significance at 1% level

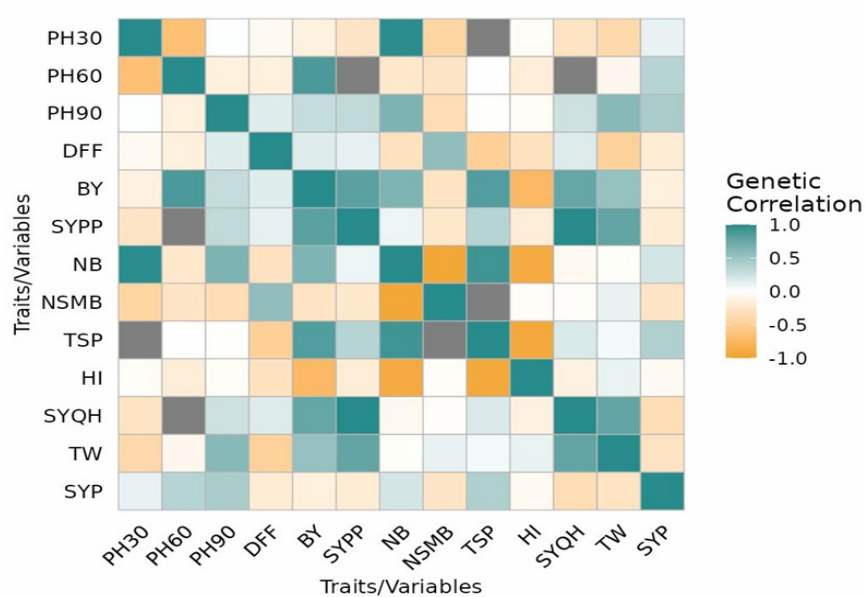
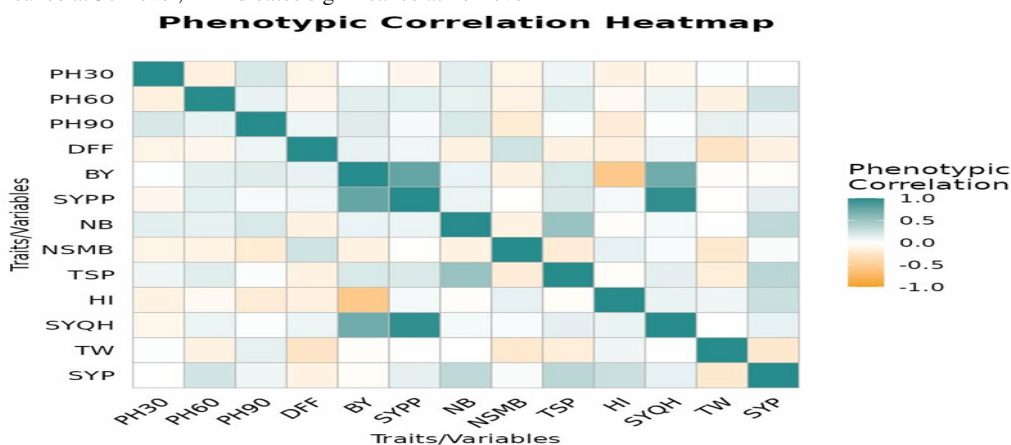
Genotypic Correlation Heatmap**Fig. 4:** Genotypic Correlation Heatmap

Table 6: Phenotypic correlation coefficient

Traits	Plant height 30 DAS	Plant height 60 DAS	Plant height 90 DAS	Days to 50% Flowering	Biological yield (kg)	Seed yield per plot (g)	Number of branches	Number of siliqua on main branches	Total siliqua per plant	Harvest index (%)	Seed yield q/hac	Test weight (g)	Seed yield per plant (g)
Plant height 30 DAS	1.00	-0.15	0.196	-0.112	0.016	-0.084	0.138	-0.114	0.087	-0.126	-0.089	0.018	0.006
Plant height 60 DAS		1.00	0.108	-0.084	0.141	0.134	0.131	-0.122	0.15	-0.059	0.1	-0.131	0.227
Plant height 90 DAS			1.00	0.089	0.157	0.043	0.19	-0.201	0.029	-0.196	0.02	0.129	0.082
Days to 50% Flowering				1.00	0.108	0.075	-0.133	0.241	-0.137	-0.149	0.089	-0.277	-0.135
Biological yield (kg)					1.00	0.773**	0.103	-0.139	0.189	-0.568**	0.717**	-0.027	-0.044
Seed yield per plot (g)						1.00	0.097	-0.02	0.183	0.058	0.974**	-0.011	0.126
Number of branches							1.00	-0.128	0.512**	-0.026	0.058	0.000	0.323*
Number of siliqua on main branches								1.00	-0.195	0.116	0.036	-0.229	0.031
Total siliqua per plant									1.00	-0.035	0.132	-0.179	0.349**
Harvest index (%)										1.00	0.105	0.082	0.267*
Seed yield q/hac											1.00	0.009	0.115
Test weight (g)												1.00	-0.223
Seed yield per plant (g)													1.00

* indicates significance at 5% level, ** indicates significance at 1% level

**Fig. 5:** Phenotypic Correlation Heatmap**Table 7:** Genotypic path

Traits	Plant height 30 DAS	Plant height 60 DAS	Plant height 90 DAS	Days to 50% Flowering	Biological yield (kg)	Seed yield per plot (Kg)	Number of branches	Number of siliqua on main branches	Total siliqua per plant	Harvest index (%)	Seed yield q/hac	Test weight (g)
Plant height 30 DAS	-0.04858	-0.04591	-0.00399	0.01051	-0.57658	1.45627	1.08779	0.2386	-1.30688	-0.06874	-0.87009	0.23848
Plant height 60 DAS	0.03249	0.06865	0.04085	0.02573	3.44083	-6.40469	-0.26213	0.14754	-0.00256	-0.41894	3.65066	0.04994
Plant height 90 DAS	-0.00077	-0.0112	-0.25042	-0.02523	1.1562	-1.70107	0.71073	0.18632	0.02061	-0.089	0.79428	-0.36475
Days to 50% Flowering	0.00326	-0.01127	-0.04031	-0.15674	0.62256	-0.66365	-0.33176	-0.29867	0.53363	-0.66119	0.51396	0.28847
Biological yield (kg)	0.00716	0.06034	-0.07397	-0.02493	3.91438	-4.35074	0.70173	0.15003	-0.93221	-1.6499	2.35622	-0.32034
Seed yield per plot (Kg)	0.01315	0.08171	-0.07916	-0.01933	3.16485	-5.38113	0.10255	0.13051	-0.40383	-0.41627	3.08028	-0.47039
Number of branches	-0.04834	-0.01646	-0.1628	0.04757	2.5126	-0.50476	1.09322	0.50507	-1.01274	-1.99303	-0.21258	0.0139
Number of siliqua on main branches	0.02168	-0.01894	0.08727	-0.08756	-1.09849	1.13157	-1.03279	-0.53462	1.31782	-0.08651	-0.09199	-0.06582
Total siliqua per plant	-0.05783	0.00016	0.0047	0.07618	3.32369	-1.97935	1.00844	0.64173	-1.09788	-2.0508	0.57122	-0.03692
Harvest index (%)	0.0015	-0.0129	0.01	0.04649	-2.89741	1.00494	-0.97748	0.02075	1.01011	2.229	-0.43149	-0.06877
Seed yield q/hac	0.01372	0.08135	-0.06457	-0.02615	2.99405	-5.38076	-0.07544	0.01597	-0.20358	-0.31222	3.08049	-0.47026
Test weight (g)	0.01917	-0.00567	-0.15114	0.07482	2.07488	-4.18842	-0.02514	-0.05823	-0.06706	0.25366	2.39701	-0.60434
Seed yield per plant (g)	-0.049	0.069	-0.25	-0.157	3.914	-5.381	1.093	-0.535	-1.098	2.229	3.08	-0.604

In this table, direct effects are denoted by diagonal values, whereas indirect effects are shown by the off-diagonal entries at the Genotypic level. GC: Genotypic Correlations. R effect = 1.307

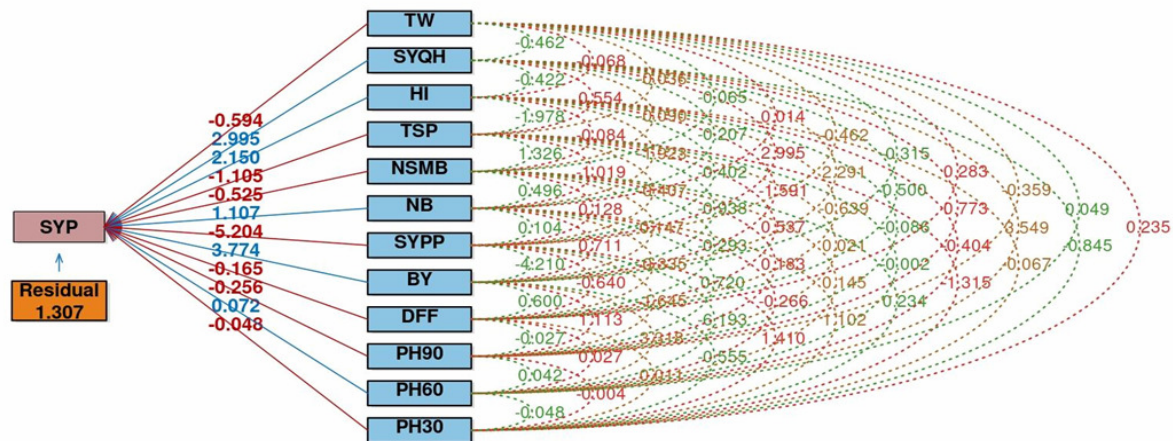


Fig. 6 Genotypic Path Analysis

Table 8: Phenotypic path

Traits	Plant height 30 DAS	Plant height 60 DAS	Plant height 90 DAS	Days to 50% Flower-ing	Biological yield (kg)	Seed yield per plot (Kg)	Number of branches	Number of siliqua on main branches	Total siliqua per plant	Harvest index (%)	Seed yield q/hac	Test weight (g)
Plant height 30 DAS	0.00078	-0.02275	0.02884	0.01133	0.01411	0.06694	0.02515	-0.01262	0.01599	-0.10755	-0.01003	-0.00452
Plant height 60 DAS	-0.00012	0.15186	0.01586	0.00852	0.1265	-0.10692	0.02389	-0.01356	0.02751	-0.04998	0.01133	0.0323
Plant height 90 DAS	0.00015	0.01639	0.14694	-0.00898	0.14018	-0.03398	0.03464	-0.02233	0.00529	-0.16646	0.00229	-0.03196
Days to 50% Flowering	-0.00009	-0.01281	0.01306	-0.10101	0.09685	-0.05965	-0.02419	0.02675	-0.02505	-0.12693	0.01002	0.06849
Biological yield (kg)	0.00001	0.02146	0.02301	-0.01093	0.89498	-0.61521	0.01886	-0.01538	0.03452	-0.48328	0.08112	0.00679
Seed yield per plot (Kg)	-0.00007	0.0204	0.00628	-0.00757	0.69199	-0.79568	0.01778	-0.00223	0.03341	0.04893	0.11016	0.0028
Number of branches	0.00011	0.0199	0.02791	0.0134	0.09258	-0.07758	0.18234	-0.01415	0.09375	-0.02203	0.00659	-0.00002
Number of siliqua on main branches	-0.00009	-0.01858	-0.02959	-0.02437	-0.12413	0.01603	-0.02328	0.11086	-0.03571	0.09885	0.00408	0.05656
Total siliqua per plant	0.00007	0.02282	0.00425	0.01382	0.16877	-0.14522	0.09339	-0.02163	0.18305	-0.02976	0.01488	0.0443
Harvest index (%)	-0.0001	-0.00892	-0.02875	0.01507	-0.50837	-0.04576	-0.00472	0.01288	-0.0064	0.85081	0.01186	-0.02031
Seed yield q/hac	-0.00007	0.01522	0.00297	-0.00895	0.64197	-0.77508	0.01063	0.004	0.02408	0.0892	0.11309	-0.00224
Test weight (g)	0.00001	-0.01986	0.01902	0.02802	-0.0246	0.00901	0.00001	-0.0254	-0.03284	0.06997	0.00102	-0.24689
Seed yield per plant (g)	0.001	0.152	0.147	-0.101	0.895	-0.796	0.182	0.111	0.183	0.851	0.113	-0.247

In this table, direct effects are denoted by diagonal values, whereas indirect effects are shown by the off-diagonal entries at the phenotypic level. PC: Phenotypic Correlations. R effect = 0.812 .

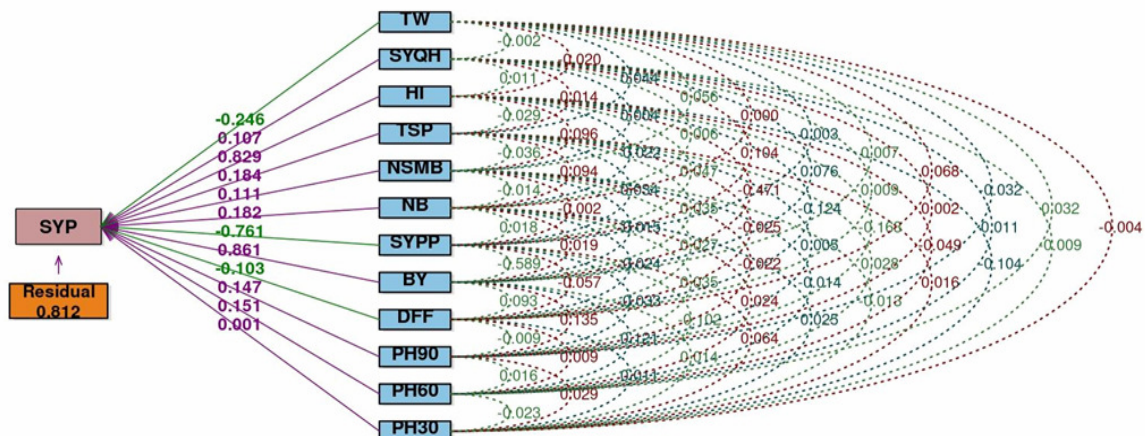


Fig. 7 : Phenotypic Path Analysis

Table 9: List of genotypes under various cluster.

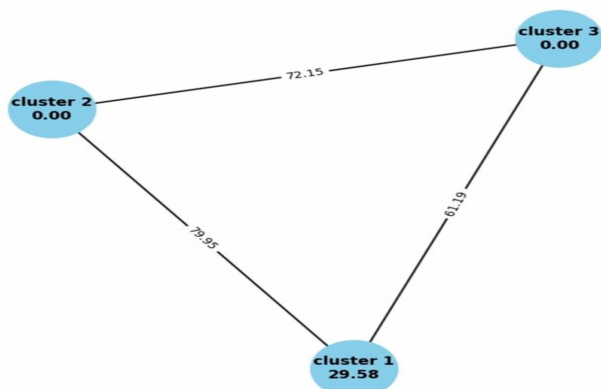
Cluster	Total Genotypes	Genetic_Material
cluster 1	18	Anmol, Arawali, Bhagirathi, Blackgold, C-724, CS-58, Krishna, Local-1, Local-2, Maya, ND-2005-1, PM-28, PM-29, PusaTarak, RH-749, RH-819, Sarson-444, Sona-4646
cluster 2	1	Local-3
cluster 3	1	Local-4

Table 10: Intra and Inter cluster distance

Cluster Number	cluster.1	cluster.2	cluster.3
cluster 1	29.58171706	79.94846249	61.19308688
cluster 2		0	72.14972309
cluster 3			0

Table 11: Table representing Cluster means :Tocher method

Trait	cluster 1	cluster 2	cluster 3
Plant height 30 DAS	13.33703704	15.6	13.8
Plant height 60 DAS	102.862963	105.7333333	103.7333333
Plant height 90 DAS	202.0259259	214.3333333	182.2666667
Days to 50% Flowering	58.25925926	55.33333333	54.66666667
Biological yield (kg)	3.890740741	5.966666667	3.6
Seed yield per plot (Kg)	1039	1275.666667	877
Number of branches	18.62592593	26.8	15.93333333
Number of siliqua on main branches	42.56666667	26.33333333	38.26666667
Total siliqua per plant	227.8222222	353.3333333	270.5333333
Harvest index (%)	27.04611111	21.68333333	25.10333333
Seed yield q/hac	20.86111111	24.38666667	17.54
Test weight (g)	4.823148148	5.61	3.876666667
Seed yield per plant (g)	15.33703704	15.2	15.53333333

**Fig. 8 :** Cluster distances by Tocher method

Regarding inference of the distribution of genotypes in the clusters

cluster 1 had the highest number of genotypes 18 followed by cluster 2, cluster 3 with 1 genotypes. The cluster 2, cluster 3 had the least number of genotypes 1. Inference regarding the contribution of the traits in the diversity of the genetic material. As per Singh (1981), the trait with highest contribution to genetic diversity was DFF with contribution of 25.9808 % followed by with contribution of 14.5012 % Inference

regarding the means of the traits for clusters, For the trait PH30, the maximum value was observed for cluster 2 (15.6) while the minimum value was observed for cluster 1 (13.337). The values for the trait PH60, ranged from 105.7333 (cluster 2) to 102.863 (cluster 1). The trait PH90 exhibited its highest value in cluster 2 (214.3333), whereas its lowest value was observed in cluster 3 (182.2667). For the trait DFF, the maximum value was observed for cluster 1 (58.2593) while the minimum value was observed for cluster 3 (54.6667). The values for the trait BY, ranged from 5.9667 (cluster 2) to 3.6 (cluster 3). The trait SYPP exhibited its highest value in cluster 2 (1275.6667), whereas its lowest value was observed in cluster 3 (877.0). For the trait NB, the maximum value was observed for cluster 2 (26.8) while the minimum value was observed for cluster 3 (15.9333). The values for the trait NSMB, ranged from 42.5667 (cluster 1) to 26.3333 (cluster 2). The trait TSP exhibited its highest value in cluster 2 (353.3333), whereas its lowest value was observed in cluster 1 (227.8222). For the trait HI, the maximum value was observed for cluster 1 (27.0461) while the minimum value was observed for cluster 2 (21.6833). The values for the trait SYQH, ranged from 24.3867 (cluster 2) to 17.54 (cluster 3). The

trait TW exhibited its highest value in cluster 2 (5.61), whereas its lowest value was observed in cluster 3 (3.8767). For the trait SYP, the maximum value was observed for cluster 3 (15.5333) while the minimum value was observed for cluster 2 (15.2).

Analysis of variance

The analysis of variance revealed the presence of significant differences among the genotypes for all the traits studied, indicating considerable genetic variability in the experimental material. This suggests the predominance of additive genetic effects and indicates that simple selection could be effective for improvement, which aligns with previous reports (Maurya *et al.*, 2018) and (Khulbe *et al.*, 2000). The mean sum of squares due to genotypes was found to be significant for traits such as plant height at 30 DAS (11.405), 60 DAS (48.765), and 90 DAS (190.262), with the latter showing highly significant variation at the 1% level. Similarly, days to 50% flowering (14.337) and biological yield (1.451) also exhibited highly significant differences, suggesting strong genetic control over these traits. Yield-related parameters, including seed yield per plot (55535.6), number of branches (30.938), number of siliqua on main branches (77.04), and total siliqua per plant (5013.292), were significant at the 5% level, indicating their importance in differentiating the genotypes. Other traits such as harvest index (19.172), seed yield (24.585 q/ha), test weight (1.515), and seed yield per plant (16.038) also showed significant variation among genotypes. In contrast, the error mean squares were comparatively lower for most traits, reflecting good experimental precision. The results of the present study are consistent with earlier reports in Indian mustard, where significant variability was observed for flowering and yield-related traits (Singh & Lallu, 2004; Chaurasiya *et al.*, 2019).

Path Coefficient Analysis

The path coefficient analysis at both genotypic and phenotypic levels provided a clearer understanding of the direct and indirect effects of different traits on seed yield per plant. Path coefficient analysis was performed using the approach originally suggested by (Wright 1921) and later refined by (Dewey and Lu 1959), which enables the partitioning of correlation coefficients into direct and indirect effects of component traits on seed yield. At the genotypic level, biological yield exhibited the highest positive direct effect (3.914), followed by number of branches (1.093), indicating that these traits are the most important contributors to seed yield. Similarly, seed yield per hectare also showed a strong positive

direct effect (3.080), reinforcing its close association with overall productivity. In contrast, seed yield per plot (-5.381) and harvest index (-2.229) showed negative direct effects, suggesting that their influence on yield is mainly indirect through other traits. Among indirect effects, biological yield influenced seed yield positively through number of branches and total siliqua per plant, while number of branches also contributed indirectly via siliqua-related traits. Total siliqua per plant, despite having some negative direct effects, showed important indirect contributions through branching traits and biological yield. At the phenotypic level, a similar trend was observed, though the magnitude of effects was comparatively lower due to environmental influence. Biological yield (0.895) and harvest index (0.851) showed strong positive direct effects on seed yield per plant, followed by total siliqua per plant (0.183) and number of branches (0.182). Seed yield per plot again exhibited a negative direct effect (-0.796), indicating that its apparent correlation with yield is largely due to indirect influences.

Correlation Analysis

The correlation analysis at both genotypic and phenotypic levels revealed similar trends among the studied traits, although genotypic correlations were generally higher in magnitude than phenotypic ones, indicating a stronger genetic association. The correlation coefficients among traits were computed at both genotypic and phenotypic levels as described by (Searle 1961), and their significance was evaluated using the t-test. At both levels, biological yield showed a strong and significant positive correlation with seed yield (genotypic: 0.809**, phenotypic: 0.773**) and seed yield per hectare (genotypic: 0.765**, phenotypic: 0.717**), highlighting its major contribution to productivity. Total siliqua per plant also exhibited a positive association with seed yield per plant (genotypic: 0.403**, phenotypic: 0.349**), while number of branches showed a strong positive relationship with total siliqua per plant (genotypic: 0.922**, phenotypic: 0.512**) and seed yield per plant (phenotypic: 0.323*). These results indicate that branching and siliqua production are key determinants of yield. Days to 50% flowering showed negative association with total siliqua per plant (genotypic: -0.486**, phenotypic: -0.137) and number of branches (genotypic: -0.303*, phenotypic: -0.133), suggesting that early flowering genotypes tend to perform better in yield-related traits. In addition, number of siliqua on main branches showed a strong negative association with total siliqua per plant at the genotypic level (-1.200**), indicating a compensatory relationship.

Conclusion

The present study revealed the existence of considerable genetic variability among the Indian mustard genotypes for all the traits studied, as confirmed by the analysis of variance. The significant differences observed among genotypes indicate the presence of sufficient scope for selection and improvement. The genetic divergence analysis grouped the genotypes into three clusters, with cluster I containing the maximum number of genotypes, while clusters II and III each consisted of a single genotype, indicating their distinct genetic nature. The highest contribution towards genetic divergence was observed for days to 50% flowering (25.98%), followed by biological yield (14.50%), suggesting that these traits played a key role in differentiating the genotypes. Cluster mean analysis revealed that cluster II possessed superior values for most yield-contributing traits such as plant height, biological yield, number of branches, total siliqua per plant, and seed yield per plot, indicating its potential for use in breeding programs. Correlation analysis at both genotypic and phenotypic levels indicated that biological yield, number of branches, and total siliqua per plant had strong positive associations with seed yield. Path coefficient analysis further confirmed that biological yield and number of branches exerted the highest positive direct effects on seed yield, emphasizing their importance as reliable selection criteria.

References

- Chaurasiya, J. P., Singh, M. and Tomar, P. (2019). Genetic variability, heritability, genetic advance and character association of Indian mustard (*Brassica juncea* L.). *Journal of Oilseed Brassica*, **10**(2), 129–135.
- Dewey, D. R. and Lu, K. H. (1959). A correlation and path-coefficient analysis of components of crested wheatgrass seed production. *Agronomy Journal*, **51**(9), 515–518.
- Gadi J, Chakraborty NR, Imam Z (2019). Genetic diversity analysis in Indian mustard (*Brassica juncea* L.). *Journal of Pharmacognosy and Phytochemistry*, **9**(1), 952–955.
- Khulbe, R. K., Pant, D. P. and Saxena, N. (2000). Variability, heritability and genetic advance in Indian mustard (*Brassica juncea* L.). *Crop Research*, **19**(3), 400–404.
- Kumar, A., Dharamvir, Kumar, M., Jangra, M. and Kumar, N. (2018). Growth and development of rapeseed–mustard and other field crops under different sowing dates. *International Journal of Pure and Applied Bioscience*, **6**(6), 144–156.
- Kumar, R. and Verma, A. (2023). Effect of sowing time and varieties on growth and yield of Indian mustard (*Brassica juncea* L.) under Prayagraj agro-climatic conditions. *International Journal of Agriculture Sciences*, **15**(1), 112–118.
- Meena, H. S., Kumar, A., Ram, B., Singh, V. V., Meena P. D., Singh, B. K. and Singh, D. (2018). Genetic variability and heritability studies in Indian mustard (*Brassica juncea* L. Czern & Coss). *Journal of Oilseed Brassica*, **9**(1), 61–67.
- Nagda R, Dubey N, Avinash H, Tamatam D. (2018). Assessment of genetic diversity in Mustard genotypes. *Plant Archives*, **18**(2), 1466–1470.
- Nandi Santanu, Rout Sanghamitra, Sur Bijaya, Chakraborty Moumita, Hijam Lakshmi, Roy Suvendu Kumar and Gupta (2021), Archi. Assessment of genetic parameters, trait association and diversity analysis in Indian Mustard [*Brassica juncea* L. Czern & Coss]. *An International Journal*, **13**(2), 95–109.
- Prakash, S., Wu, X. M. and Bhat, S. R. (2011). History, evolution, and domestication of Brassica crops. *Plant Breeding Reviews*, **35**, 19–84.
- Prasad, R. (2015). *Textbook of field crops production, Commercial crops*. Indian Council of Agricultural Research (ICAR), New Delhi, India.
- Rakow, G. (2004). Species origin and economic importance of Brassica. In *Biotechnology in Agriculture and Forestry* (Vol. 54, pp. 3–11). Springer, Berlin, Heidelberg.
- Rout S, Das A, Sur B, Umamaheswar Sadhu NS, Ghimiray TS, Mondal HA, Hijam L, Chakraborty M, Roy SK (2019). Genetic divergence in Indian mustard [*Brassica juncea* L. Czern & Coss] under sub-himalayan region. *Journal of Crop and Weed*, **15**(2), 18–24.
- Saleem, M., Zafar, A., Ahsan, M. and Asalam, M. (2017). Interrelationships and variability studies for grain yield and its various components in Indian mustard (*Brassica juncea* L.) Czern & Coss. *Journal of Agricultural & Social Sciences*, **3**(29), 266–269.
- Searle, S.R. (1961). Phenotypic, genotypic and environmental correlations. *Biometrics*, **17**(3), 474–480.
- Singh, M. and Lallu. (2004). Heterosis in relation to combining ability for seed yield and its contributing traits in Indian mustard (*Brassica juncea* L.). *Journal of Oilseeds Research*, **21**(2), 325–328.
- Singh, R., Singh, A. and Yadav, S. K. (2022). Economics and productivity of mustard cultivation in Prayagraj district of Uttar Pradesh. *Journal of Agricultural Economics and Extension*, **5**(2), 45–50.
- Wright, S. (1921). Correlation and causation. *Journal of Agricultural Research*, **20**, 557–585.