



Exploring Genetic Variability and Mutational Parameters for Selection toward Combined Improvement of Stress Resilience and Nutritional Composition in Mustard (*Brassica juncea* L.)

Harsh Kumar ^a and Divya Singh ^{a*}

^a Department of Genetics and Plant Breeding, Department of Soil Science and Agricultural Chemistry, Faculty of Agriculture, Prof. Rajendra Singh (Rajju Bhaiya) University, Prayagraj, Uttar Pradesh (211010), India.

Authors' contributions

This work was carried out in collaboration between both authors. Both authors read and approved the final manuscript.

Article Information

DOI: <https://doi.org/10.9734/ijpss/2026/v38i86238>

Open Peer Review History:

This journal follows the Advanced Open Peer Review policy. Identity of the Reviewers, Editor(s) and additional Reviewers, peer review comments, different versions of the manuscript, comments of the editors, etc are available here: <https://pr.sdiarticle5.com/review-history/163623>

Original Research Article

Received: 03/06/2026

Accepted: 30/07/2026

Published: 03/08/2026

Abstract

Background: Indian mustard (*Brassica juncea* L.) is one of the most important oilseed crops, contributing significantly to edible oil production and nutritional security. However, its productivity and quality are frequently constrained by abiotic stresses, necessitating the identification of genetically diverse and stress-resilient genotypes for sustainable crop improvement. The present investigation was conducted during the Rabi 2025–2026 season at the Department of Genetics and Plant Breeding, Prof. Rajendra Singh (Rajju Bhaiya) University, Prayagraj, India. Ten mustard genotypes, comprising nine test entries and one check

*Corresponding author: E-mail: divyamaltisingh@gmail.com;

variety, were evaluated in a Randomised Complete Block Design (RCBD) with three replications. Observations were recorded for growth, yield, quality, physiological, and stress tolerance traits. Genetic variability was assessed through analysis of variance, genotypic and phenotypic coefficients of variation, heritability, genetic advance, correlation, and path coefficient analyses. Significant ($P \leq 0.01$) genetic variation was observed among the genotypes for all studied traits, indicating substantial scope for genetic improvement. Genotype G₉ consistently exhibited superior performance for growth, yield, nutritional quality, physiological efficiency, and antioxidant activity, recording the highest seed yield (19.33 q ha⁻¹), oil content (45.48%), protein content (23.05%), oil yield (651.25 kg ha⁻¹), relative water content (85.05%), membrane stability index (68.05%), proline accumulation, catalase activity, and peroxidase activity, while exhibiting the lowest glucosinolate content (22.80 $\mu\text{mol g}^{-1}$). Genotype G₆ ranked second for most agronomic and physiological traits. High heritability coupled with high genetic advance was observed for seed yield, biological yield, oil yield, branching traits, and antioxidant enzyme activities, suggesting the predominance of additive gene action. Correlation and path coefficient analyses identified biological yield, number of siliquae per plant, test weight, oil content, relative water content, membrane stability index, and antioxidant enzyme activities as major contributors to seed yield and stress resilience. The study demonstrated considerable genetic variability among the evaluated mustard genotypes and identified G₉, followed by G₆ and G₄, as superior genotypes combining high productivity, improved nutritional quality, and enhanced stress tolerance. These genotypes represent valuable genetic resources for breeding programmes aimed at developing climate-resilient, high-yielding, and nutritionally superior mustard cultivars.

Keywords: *Brassica juncea*; genetic variability; heritability; genetic advance; seed yield; nutritional quality; physiological traits; antioxidant enzymes; stress resilience; path coefficient analysis.

1. Introduction

Mustard (*Brassica juncea* L. Czern & Coss.) is one of the most important oilseed crops cultivated worldwide and constitutes a major source of edible oil, protein-rich meal, and industrial raw materials. As an amphidiploid species (AABB, $2n = 36$), *B. juncea* possesses broad adaptability to diverse agro-climatic conditions, making it one of the predominant oilseed crops in South Asia, particularly in India. The crop contributes significantly to food security, rural livelihoods, and the edible oil economy due to its comparatively short duration, drought tolerance, and multiple end uses. Despite continuous improvements in production technologies, mustard productivity remains substantially below its genetic potential because of various environmental constraints and limited availability of superior cultivars. Climate change has intensified the occurrence of drought, heat, salinity, and oxidative stresses, which adversely affect plant growth, flowering, seed development, oil accumulation, and ultimately crop productivity. These abiotic stresses alter physiological and biochemical processes, including photosynthesis, membrane stability, antioxidant metabolism, and nutrient uptake, thereby reducing yield stability and seed quality. Consequently, the development of stress-resilient mustard genotypes has become one of the major objectives of modern breeding programmes aimed at sustaining productivity under changing environmental conditions (Prakash *et al.*, 2011; Sujata *et al.*, 2023).

Recent physiological screening has shown that Indian mustard genotypes differ in relative water content, membrane stability, and growth responses under water deficit, underscoring the value of these traits in selecting drought-tolerant material (Rani *et al.*, 2024).

Genome-wide expression analysis has also identified drought-responsive growth-regulating factor genes in *Brassica juncea*, supporting the integration of physiological assessment with genetic evidence when identifying stress-resilient material (Zhang *et al.*, 2024).

Genetic variability serves as the foundation of crop improvement because the efficiency of selection depends upon the extent of heritable variation available within breeding populations. Quantitative genetic parameters such as genotypic and phenotypic coefficients of variation, heritability, genetic advance, correlation, and path coefficient analysis provide valuable information regarding the inheritance of economically important traits and assist breeders in designing efficient selection strategies. Although considerable variability has been reported for agronomic and quality traits in mustard, the existing genetic diversity within cultivated germplasm is often insufficient for simultaneous improvement of stress tolerance, yield, and nutritional quality. Induced mutagenesis has emerged as an effective complementary approach for generating novel genetic variation beyond

the limits of naturally available diversity. Physical and chemical mutagens, particularly ethyl methane sulphonate (EMS), have been widely employed to induce point mutations that create useful allelic variation with relatively low chromosomal damage. Mutation breeding has successfully contributed to the development of improved crop varieties possessing enhanced yield, early maturity, disease resistance, and abiotic stress tolerance. Evaluation of mutagenic effectiveness, efficiency, and induced variability enables the identification of optimal mutagen doses and promising mutant lines suitable for crop improvement. Nutritional enhancement has also become an important breeding objective in mustard due to increasing consumer demand for healthier edible oils. Improvement of fatty acid composition, reduction of undesirable compounds such as erucic acid and glucosinolates, and enhancement of seed protein and antioxidant content are increasingly emphasised in breeding programmes. However, the simultaneous improvement of stress resilience and nutritional quality remains challenging because these complex traits are governed by multiple genes and are strongly influenced by environmental interactions (Bhat *et al.*, 2001; Ministry of Agriculture and Farmers Welfare, 2024; Rakow, 2004).

Multivariate divergence analysis can complement variability estimates by identifying genetically distinct parental combinations with potential value for broadening selection gains in Indian mustard (Yadav *et al.*, 2025).

Multi-environment diallel analysis has further shown that 1000-seed weight and oil content may differ in their genetic control, indicating that parental selection for combined yield and quality improvement should consider both traits simultaneously (Sharma *et al.*, 2024).

Despite substantial advances in mutation breeding, relatively limited information is available regarding the integration of genetic variability analysis with mutational parameters for the combined improvement of stress resilience and nutritional composition in Indian mustard. A comprehensive evaluation of induced variability and genetic parameters is therefore essential for identifying superior genotypes that can be effectively utilised in future breeding programmes. Accordingly, the present investigation was undertaken to evaluate genetic variability, estimate mutational parameters, and identify promising mustard genotypes possessing enhanced stress resilience and improved nutritional attributes. The findings are expected to contribute to the development of climate-resilient, nutritionally superior mustard cultivars and provide valuable information for future genetic improvement programmes (Gupta *et al.*, 2025).

However, integrated evaluation of genetic variability and mutational parameters alongside agronomic, physiological, stress-related, and nutritional traits remains limited for selecting Indian mustard genotypes with a balanced combination of these attributes.

1.1 Objective of the Study

The objective of the present study was to evaluate genetic variability and mutational parameters and to identify Indian mustard genotypes combining favourable agronomic performance, nutritional composition, physiological efficiency, and stress resilience.

2. Material and Methods

2.1 Experimental Site and Plant Material

The experiment was conducted during the Rabi season (2025–2026) at the experimental farm of the Department of Genetics and Plant Breeding, Prof. Rajendra Singh (Rajju Bhaiya) University, Prayagraj, Uttar Pradesh, India (25°21'33.1" N, 81°53'41.0" E; 98 m above mean sea level). The experimental site experiences a tropical semi-arid climate characterised by cool winters and hot summers. During the crop growing period, maximum temperature ranged from 20.8 to 32.4°C, minimum temperature from 5.4 to 18.7°C, and relative humidity from 44.5 to 98.1%. Ten Indian mustard (*Brassica juncea* L.) genotypes, including nine test genotypes (Pusa Mustard-27, Jagannath, Basant-I, Pusa Bold, Pusa Mustard-26, NRCDR-601, Pusa Mustard-28, RRC-9, and NRCDR-101) and one check cultivar (SBH-618), were obtained from SHUATS, Prayagraj, and used as experimental material.

2.2 Experimental Design and Crop Management

The experiment was laid out in a Randomised Complete Block Design (RCBD) with three replications. Each genotype was grown in a plot measuring 1.5 × 1.0 m, maintaining a spacing of 30 cm between rows and 10 cm

between plants. Recommended agronomic practices, including fertiliser application (80:40:40 kg N:P₂O₅:K₂O ha⁻¹), irrigation, weed management, and plant protection measures, were followed uniformly throughout the crop growth period.

2.3 Data Recording

Observations were recorded on five randomly selected plants from each replication. Data were collected for growth and yield-related traits, including days to germination, plant height (cm), number of primary and secondary branches, days to 50% flowering, days to maturity, siliquae per plant, siliqua length (cm), number of seeds per siliqua, 1000-seed weight (g), and seed yield per plant (g), biological yield, seed yield per hectare, and harvest index (Akkenapally & Chetariya, 2022).

2.4 Biochemical and Physiological Analysis

Oil content was estimated by Soxhlet extraction using petroleum ether, while protein content was determined following the method of Lowry et al. (1951). Oil yield was calculated from seed yield and oil percentage. Erucic acid was quantified by gas chromatography with flame ionisation detection (GC-FID) after preparation of fatty acid methyl esters according to AOCS Official Method Ce 1h-05 (American Oil Chemists' Society [AOCS], 2017). Glucosinolate content was estimated by the sodium tetrachloropalladate colourimetric method described by Thies (1982). Physiological parameters, including total chlorophyll content, relative water content (RWC), membrane stability index (MSI), proline accumulation, catalase (CAT) activity, and peroxidase (POD) activity, were determined using standard protocols described by Arnon (1949), Barrs and Weatherley (1962), Blum and Ebercon (1981), Bates et al. (1973), and Chance and Maehly (1955), respectively.

2.5 Statistical Analysis

Analysis of variance (ANOVA) was performed using the Randomised Complete Block Design following the procedure of Panse and Sukhatme (1967). Genotypic and phenotypic coefficients of variation (GCV and PCV), broad-sense heritability, genetic advance, and genetic advance as a percentage of the mean were estimated according to Burton (1952), Hanson et al. (1956), and Johnson et al. (1955). Genotypic and phenotypic correlation coefficients were computed following Miller et al. (1958), while path coefficient analysis was carried out according to the method of Dewey and Lu (1959). Statistical significance was tested at the 5% and 1% probability levels.

3. Results and Discussion

3.1 Performance of Mustard Genotypes for Growth, Yield, Quality, and Physiological Traits

Significant differences were observed among the ten Indian mustard (*Brassica juncea* L.) genotypes for all evaluated agronomic, physiological, biochemical, and quality traits, indicating substantial genetic diversity within the experimental material. The observed variability reflects the potential for effective selection and genetic improvement through conventional breeding.

Among the evaluated genotypes, G₉ consistently outperformed the remaining entries for most growth, yield, and quality parameters. It recorded the highest oil content (45.48%), protein content (23.05%), oil yield (651.25 kg ha⁻¹), fatty acid composition (65.48%), relative water content (85.05%), membrane stability index (68.05%), proline accumulation (52.05 µg g⁻¹ FW), catalase activity (26.53 U mg⁻¹ protein min⁻¹), and peroxidase activity (2.203 ΔA470 min⁻¹ g⁻¹ FW), while exhibiting the lowest glucosinolate content (22.80 µmol g⁻¹). Genotypes G₆ and G₄ also performed consistently well for several yield and physiological traits, whereas G₃ recorded comparatively lower values for most characters. The superior performance of G₉ indicates that this genotype possesses enhanced physiological efficiency and stronger antioxidant defence mechanisms, resulting in improved biomass accumulation, seed production, and seed quality. Similar observations have been reported in *Brassica* breeding programmes, where superior physiological performance has been positively associated with higher productivity under diverse environmental conditions (Sujata *et al.*, 2023).

3.2 Analysis of Variance

Analysis of variance revealed highly significant ($P \leq 0.01$) differences among genotypes for all studied traits, confirming the existence of considerable genetic variability for growth, yield, physiological, and quality

parameters. In contrast, replication effects were generally non-significant, indicating uniform experimental conditions and high precision of the field experiment. The significant treatment effects demonstrate that the observed variation among genotypes is primarily attributable to genetic differences rather than environmental fluctuations. This wide variability provides an excellent opportunity for identifying elite genotypes and selecting desirable traits for future breeding programmes. Similar findings have been reported by several researchers working on Indian mustard, who emphasised that significant genotypic variation forms the basis for efficient crop improvement (Gupta *et al.*, 2025; Tiwari *et al.*, 2025).

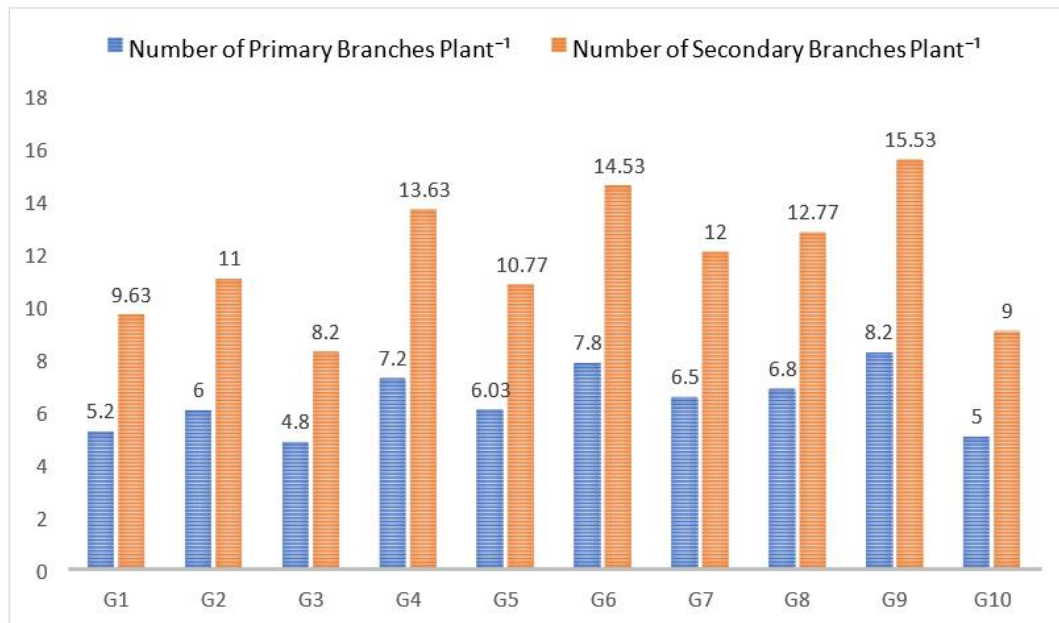


Fig. 1. Number of Primary and Secondary Branches Plant⁻¹ among Different Black Mustard Genotypes.

3.3 Genetic Variability, Heritability and Genetic Advance

Estimates of genetic parameters revealed the presence of substantial genetic variability among the evaluated genotypes for all studied traits, indicating considerable scope for genetic improvement through selection. The phenotypic coefficient of variation (PCV) was consistently higher, although only slightly, than the corresponding genotypic coefficient of variation (GCV) for almost all characters. This close correspondence between PCV and GCV suggests that environmental factors had only a minor influence on the expression of these traits, whereas most of the observed variation was attributed to genetic differences among the genotypes. Therefore, the phenotypic performance of the genotypes can be considered a reliable indicator of their genetic potential, making selection based on phenotypic observations more dependable.

Broad-sense heritability estimates were generally high (>95%) for most of the evaluated traits, indicating that a large proportion of the total phenotypic variation had a genetic basis rather than being environmentally induced. High heritability alone, however, does not necessarily guarantee effective selection because it does not distinguish between additive and non-additive gene effects. Therefore, heritability was interpreted together with genetic advance expressed as a percentage of the mean (GAM), which provides a more reliable indication of the expected response to selection.

High heritability coupled with high genetic advance as a percentage of the mean was recorded for several economically important traits, including the number of primary branches per plant, the number of secondary branches per plant, siliquae per plant, test weight, seed yield per plant, biological yield per plant, oil yield, catalase activity, and peroxidase activity. This favourable combination suggests that these traits are predominantly governed by additive gene action, where the effects of individual genes are cumulative and can be effectively transmitted from one generation to the next. Consequently, these traits are expected to respond well to simple phenotypic selection, making them valuable targets in breeding programmes aimed at improving seed yield, productivity, oil content, and antioxidant defence mechanisms.

Table 1. Mean Performance of Different Black Mustard Genotypes for Growth and Phenological Traits

Genotype	Days to Germination	Plant Height at 30 DAS (cm)	Plant Height at 60 DAS (cm)	Plant Height at 90 DAS (cm)	Number of Primary Branches Plant⁻¹	Number of Secondary Branches Plant⁻¹	Days to 50% Flowering	Days to Maturity
G1	5.90	18.35	72.50	140.50	5.20	9.63	49.00	115.50
G2	6.47	19.05	78.17	150.27	6.00	11.00	53.33	118.50
G3	5.30	20.20	70.10	138.10	4.80	8.20	47.00	121.50
G4	7.10	17.10	85.10	162.10	7.20	13.63	56.00	112.50
G5	6.00	19.65	76.10	148.10	6.03	10.77	50.00	119.50
G6	7.40	22.55	88.57	168.50	7.80	14.53	58.00	125.00
G7	6.80	19.90	80.10	155.10	6.50	12.00	53.00	118.50
G8	6.90	21.35	82.10	160.10	6.80	12.77	56.00	123.50
G9	7.80	23.25	90.50	172.50	8.20	15.53	60.00	130.00
G10	5.60	21.15	74.10	145.10	5.00	9.00	47.00	122.50
Mean	6.53	20.26	79.53	154.03	6.35	11.71	52.93	120.10
SE(m)	0.057	1.043	0.052	0.056	0.011	0.045	0.568	2.547
SE(d)	0.081	1.476	0.073	0.079	0.015	0.063	0.803	3.602
CD (P=0.05)	0.171	3.385	0.155	0.168	0.032	0.134	1.700	8.264
CV (%)	1.514	7.285	0.113	0.063	0.288	0.664	1.857	2.98

Table 2. Mean performance of different black mustard genotypes for yield and yield attributing traits

Genotype	Number of Siliquae Plant ⁻¹	Siliqua Length (cm)	Number of Seeds Siliqua ⁻¹	Test Weight (g)	Seed Yield Plant ⁻¹ (g)	Biological Yield Plant ⁻¹ (g)	Seed Yield (q ha ⁻¹)	Harvest Index (%)
G1	147.67	4.50	15.00	3.80	16.00	46.00	12.63	34.78
G2	160.00	5.10	17.00	4.30	18.47	53.00	14.67	34.85
G3	135.00	4.20	14.33	3.60	14.50	41.00	11.50	35.37
G4	187.67	6.00	18.33	5.10	21.77	65.00	17.33	33.49
G5	154.67	5.00	15.33	4.00	17.13	50.00	13.63	34.26
G6	200.00	6.50	20.33	5.60	23.50	72.00	18.67	32.64
G7	176.33	5.50	17.33	4.80	19.50	58.00	15.50	33.62
G8	182.00	5.80	18.33	5.00	20.33	62.00	16.17	32.79
G9	210.00	6.80	22.33	6.00	24.27	75.00	19.33	32.36
G10	149.67	4.60	14.33	3.90	15.63	43.00	12.17	36.35
Mean	170.10	5.40	17.63	4.61	19.11	56.50	15.76	34.05
SE(m)	0.869	0.036	0.387	0.048	0.111	0.483	0.037	0.048
SE(d)	1.228	0.052	0.547	0.068	0.156	0.683	0.052	0.068
CD (P=0.05)	2.600	0.109	1.157	0.145	0.331	1.446	0.109	0.145
CV (%)	0.883	1.170	3.877	1.815	1.002	1.481	0.288	1.815

Table 3. Mean performance of different black mustard genotypes for quality and physiological parameters

Genotype	Oil Content (%)	Protein Content (%)	Oil Yield (l ha ⁻¹)	Erucic Acid Content (%)	Glucosinolate Content (μmol g ⁻¹)	Relative Water Content (%)	Membrane Stability Index (%)
G1	38.25	19.25	424.50	58.25	28.25	68.25	55.25
G2	40.15	20.55	483.25	60.18	26.55	72.05	58.05
G3	36.48	18.85	391.25	56.53	30.70	65.53	52.53
G4	42.75	21.85	561.25	62.75	24.25	78.25	62.05
G5	39.53	20.05	451.25	59.53	27.03	70.05	57.05
G6	44.25	22.55	601.25	64.25	23.55	82.53	65.53
G7	41.03	21.05	521.25	61.03	25.03	75.05	60.05
G8	42.05	21.55	541.25	62.05	24.53	76.53	61.53
G9	45.48	23.05	651.25	65.48	22.80	85.05	68.05
G10	37.80	19.05	411.25	57.80	29.03	67.05	54.05
Mean	40.78	20.78	503.75	60.98	26.17	74.03	59.41
SE(m)	0.098	0.006	0.848	0.073	0.058	0.012	0.012
SE(d)	0.139	0.009	1.199	0.104	0.083	0.017	0.017

The presence of additive genetic variance for these traits indicates that superior genotypes identified in the present investigation can be directly utilised as parents in hybridisation programmes or selected for advancement in breeding populations. Improvement through conventional selection methods is likely to be highly effective, as the favourable alleles controlling these traits can be accumulated over successive generations. Overall, the observed pattern of high GCV, high heritability, and high genetic advance confirms that these characters possess substantial genetic variability and are amenable to genetic improvement through selection, thereby contributing significantly to the development of high-yielding and physiologically superior genotypes.

Conversely, traits exhibiting relatively moderate genetic advance despite high heritability may be influenced by non-additive gene effects and genotype × environment interactions. Therefore, these characters may require recurrent selection or hybridisation approaches to achieve sustained genetic improvement. The genetic parameter estimates revealed the presence of substantial, exploitable genetic variability among the evaluated

genotypes and highlighted the potential of direct phenotypic selection for the simultaneous improvement of seed yield, quality attributes, and stress tolerance in Indian mustard (Tiwari *et al.*, 2025).

Table 4. Mean Performance of Different Black Mustard Genotypes for Stress Tolerance Parameters

Genotype	Proline Content ($\mu\text{g g}^{-1}$ FW)	Catalase Activity (U mg^{-1} protein min^{-1})	Peroxidase Activity ($\Delta\text{A470 min}^{-1} \text{g}^{-1}$ FW)
G1	42.53	18.25	1.453
G2	45.05	20.53	1.605
G3	40.25	17.05	1.353
G4	48.53	23.53	1.853
G5	44.03	19.83	1.553
G6	50.25	25.53	2.053
G7	46.53	22.05	1.753
G8	47.80	22.83	1.803
G9	52.05	26.53	2.203
G10	41.53	18.05	1.403
Mean	45.85	21.42	1.703
SE(m)	0.018	0.012	0.001
SE(d)	0.025	0.016	0.001

Table 5. Estimates of genetic parameters for growth, yield, quality, physiological and stress tolerance traits in mustard

Trait	Mean	GV	PV	GCV (%)	PCV (%)	Heritability (%)	GA (% Mean)
Days to Germination	6.53	0.659	0.669	12.44	12.53	98.54	25.44
Plant Height (30 DAS)	20.62	5.133	5.134	10.99	10.99	99.97	22.63
Plant Height (60 DAS)	79.73	46.776	46.782	8.58	8.58	99.99	17.67
Plant Height (90 DAS)	154.04	135.501	135.509	7.56	7.56	99.99	15.57
Number of Primary Branches Plant ⁻¹	6.35	1.360	1.361	18.37	18.38	99.93	37.82
Number of Secondary Branches Plant ⁻¹	11.71	5.871	5.877	20.71	20.72	99.90	42.61
Days to 50% Flowering	52.93	20.685	21.652	8.60	8.80	95.53	17.31
Days to Maturity	120.10	12.126	25.104	2.90	4.17	48.30	4.15
Number of Siliquae Plant ⁻¹	170.10	606.763	609.026	14.49	14.52	99.63	29.80
Siliqua Length (cm)	5.40	0.759	0.763	16.15	16.20	99.48	33.21
Number of Seeds Siliqua ⁻¹	17.63	6.907	7.355	14.91	15.39	93.91	29.77
Test Weight (g)	4.61	0.663	0.670	17.68	17.77	98.96	36.23
Seed Yield Plant ⁻¹ (g)	19.11	11.310	11.347	17.62	17.65	99.67	36.24
Biological Yield Plant ⁻¹ (g)	56.50	141.378	142.078	21.05	21.10	99.51	43.28
Seed Yield (q ha ⁻¹)	15.76	8.570	8.571	18.59	18.59	99.99	38.31
Harvest Index (%)	34.05	3.790	3.803	5.72	5.73	99.66	11.77
Oil Content (%)	40.78	8.371	8.409	7.10	7.11	99.55	14.58
Protein Content (%)	20.78	2.193	2.193	7.13	7.13	100.00	14.68
Oil Yield (kg ha ⁻¹)	503.75	9917.679	9920.556	19.78	19.79	99.97	40.76
Fatty Acid Composition	60.98	8.325	8.347	4.73	4.74	99.74	9.73
Glucosinolate Content	26.17	6.641	6.655	9.85	9.86	99.79	20.28
Relative Water Content (%)	74.03	39.375	39.376	8.48	8.48	99.99	17.47
Membrane Stability Index (%)	59.41	21.875	21.876	7.88	7.88	99.99	16.24
Proline Content	45.85	17.896	17.897	9.23	9.23	99.99	19.01
Catalase Activity	21.42	12.861	12.862	16.74	16.74	99.99	34.47
Peroxidase Activity	1.703	0.079	0.079	16.50	16.51	99.97	33.99

Table 6. Genotypic correlation for growth and yield

Traits	Germination Percent age (%)	Plant Height at 30 DAS (cm)	Plant Height at 60 DAS (cm)	Plant Height at 90 DAS (cm)	Number of Primary Branches Plant ⁻¹	Number of Secondary Branches Plant ⁻¹	Days to 50% Flowering	Days to Maturity	Number of Siliqua e Plant ⁻¹	Siliqua Length (cm)	Number of Seeds Siliqua ⁻¹	1000Seed Weight (g)	Seed Yield Plant ⁻¹ (g)	Biological Yield Plant ⁻¹ (g)	Seed Yield (q ha ⁻¹)	Harvest Index (%)	Chlorophyll Content (mg g ⁻¹ FW)
G%	1	0.9836 **	0.9815 **	0.9755 **	0.9832 **	0.992 **	0.9894 **	0.9906 **	0.9884 **	0.9839 **	0.983 **	0.9814 **	0.9918 **	0.9893 **	0.9882 **	0.9884 **	0.9972 **
PH30	0.9836 **	1	0.9942 **	0.9908 **	0.9865 **	0.9904 **	0.9749 **	0.9854 **	0.989 **	0.9927 **	0.9749 **	0.9786 **	0.99 **	0.9863 **	0.9831 **	0.9861 **	0.9884 **
PH60	0.9815 **	0.9942 **	1	0.9962 **	0.9885 **	0.9901 **	0.9789 **	0.9919 **	0.9932 **	0.9977 **	0.9854 **	0.9878 **	0.9964 **	0.9924 **	0.9899 **	0.9905 **	0.9887 **
PH90	0.9755 **	0.9908 **	0.9962 **	1	0.9854 **	0.9856 **	0.9818 **	0.9886 **	0.9939 **	0.9983 **	0.9868 **	0.9912 **	0.9989 **	0.9905 **	0.9904 **	0.9872 **	0.9859 **
NPB/P	0.9832 **	0.9865 **	0.9885 **	0.9854 **	1	0.9969 **	0.9847 **	0.9944 **	0.9848 **	0.9949 **	0.9826 **	0.9789 **	0.9925 **	0.9955 **	0.9943 **	0.9949 **	0.9941 **
NSB/P	0.992 **	0.9904 **	0.9901 **	0.9856 **	0.9969 **	1	0.9873 **	0.9942 **	0.9903 **	0.9952 **	0.9837 **	0.9828 **	0.9956 **	0.9967 **	0.9943 **	0.9962 **	0.9984 **
DFF	0.9894 **	0.9749 **	0.9789 **	0.9818 **	0.9847 **	0.9873 **	1	0.992 **	0.9818 **	0.9875 **	0.987 **	0.9789 **	0.9862 **	0.9892 **	0.9917 **	0.99 **	0.9936 **
DM	0.9906 **	0.9854 **	0.9919 **	0.9886 **	0.9944 **	0.9942 **	0.992 **	1	0.99 **	0.9963 **	0.9923 **	0.9865 **	0.9965 **	0.9965 **	0.9941 **	0.998 **	0.9962 **
NSP/P	0.9884 **	0.989 **	0.9932 **	0.9939 **	0.9848 **	0.9903 **	0.9818 **	0.99 **	1	0.9969 **	0.9892 **	0.9984 **	0.993 **	0.9942 **	0.9912 **	0.9893 **	0.9914 **
SL	0.9839 **	0.9927 **	0.9977 **	0.9983 **	0.9949 **	0.9952 **	0.9963 **	0.9963 **	1	0.9914 **	0.9935 **	0.9935 **	0.996 **	0.9979 **	0.9963 **	0.996 **	0.9945 **
NSS/S	0.983 **	0.9749 **	0.9854 **	0.9868 **	0.9826 **	0.9837 **	0.987 **	0.9923 **	0.9892 **	0.9914 **	1	0.9915 **	0.986 **	0.9873 **	0.9896 **	0.9928 **	0.9888 **
TW	0.9814 **	0.9786 **	0.9878 **	0.9912 **	0.9789 **	0.9826 **	0.9789 **	0.9865 **	0.9984 **	0.9935 **	0.9915 **	1	0.9873 **	0.9903 **	0.9894 **	0.9849 **	0.9855 **
SY/P	0.9918 **	0.99 **	0.9964 **	0.9925 **	0.9955 **	0.9962 **	0.9862 **	0.9965 **	0.993 **	0.996 **	0.986 **	0.9873 **	1	0.9976 **	0.9948 **	0.9937 **	0.9953 **
BY/P	0.9893 **	0.9863 **	0.9924 **	0.9905 **	0.9955 **	0.9967 **	0.9892 **	0.9965 **	0.9942 **	0.9979 **	0.9873 **	0.9903 **	0.9976 **	1	0.9974 **	0.9948 **	0.9961 **
SY	0.9882 **	0.9831 **	0.9899 **	0.9904 **	0.9943 **	0.9943 **	0.9917 **	0.9941 **	0.9912 **	0.9963 **	0.9896 **	0.9894 **	0.9948 **	0.9974 **	1	0.9925 **	0.9952 **
HI	0.9884 **	0.9861 **	0.9905 **	0.9872 **	0.9949 **	0.9962 **	0.99 **	0.998 **	0.9893 **	0.996 **	0.9923 **	0.9849 **	0.9937 **	0.9948 **	0.9925 **	1	0.9967 **
CLO	0.9972 **	0.9884 **	0.9887 **	0.9859 **	0.9941 **	0.9984 **	0.9936 **	0.9962 **	0.9914 **	0.9945 **	0.9888 **	0.9855 **	0.9953 **	0.9961 **	0.9952 **	0.9967 **	1

Table 7 Phenotypic Correlation Coefficients for Growth and Yield Traits

Traits	Germination Percent age (%)	Plant Height at 30 DAS (cm)	Plant Height at 60 DAS (cm)	Plant Height at 90 DAS (cm)	No of Primary Branches Plant ⁻¹	No of Secondary Branches Plant ⁻¹	Days to 50% Flowering	Days to Maturity	Number of Siliqua e Plant ⁻¹	Siliqua Length (cm)	Number of Seeds Siliqua ⁻¹	1000-Seed Weight (g)	Seed Yield Plant ⁻¹ (g)	Biological Yield Plant ⁻¹ (g)	Seed Yield (q ha ⁻¹)	Harvest Index (%)	Chlorophyll Content
G%	1	0.9765 **	0.9744 **	0.9682 **	0.9757 **	0.9843 **	0.9822 **	0.9834 **	0.9792 **	0.977 **	0.9756 **	0.974 **	0.9849 **	0.9821 **	0.9813 **	0.9816 **	0.99 **
PH30	0.9765 **	1	0.994 **	0.9906 **	0.9864 **	0.99 **	0.9747 **	0.9853 **	0.9875 **	0.9905 **	0.9747 **	0.9783 **	0.9883 **	0.9862 **	0.9829 **	0.9859 **	0.9883 **
PH60	0.9744 **	0.994 **	1	0.9962 **	0.9884 **	0.9895 **	0.9789 **	0.9919 **	0.9912 **	0.9951 **	0.9853 **	0.9877 **	0.9948 **	0.9923 **	0.9899 **	0.9904 **	0.9886 **
PH90	0.9682 **	0.9906 **	0.9962 **	1	0.9853 **	0.985 **	0.9818 **	0.9886 **	0.992 **	0.9955 **	0.9868 **	0.9912 **	0.9882 **	0.9904 **	0.9904 **	0.9871 **	0.9858 **
NPB/P	0.9757 **	0.9864 **	0.9884 **	0.9853 **	1	0.9962 **	0.9845 **	0.9942 **	0.9826 **	0.9925 **	0.9824 **	0.979 **	0.9911 **	0.9954 **	0.9941 **	0.9948 **	0.9939 **
NSB/P	0.9843 **	0.99 **	0.9895 **	0.985 **	0.9962 **	1	0.9868 **	0.9937 **	0.9883 **	0.9919 **	0.9831 **	0.982 **	0.9931 **	0.9962 **	0.9938 **	0.9956 **	0.9977 **
DFF	0.9822 **	0.9747 **	0.9789 **	0.9818 **	0.9845 **	0.9868 **	1	0.992 **	0.9799 **	0.9949 **	0.987 **	0.9788 **	0.9846 **	0.9892 **	0.9916 **	0.99 **	0.9935 **
DM	0.9834 **	0.9853 **	0.9919 **	0.9886 **	0.9942 **	0.9937 **	0.992 **	1	0.9882 **	0.9936 **	0.9923 **	0.9864 **	0.9949 **	0.9965 **	0.9941 **	0.9979 **	0.9962 **
NSP/P	0.9792 **	0.9875 **	0.9912 **	0.992 **	0.9826 **	0.9883 **	0.9799 **	0.9882 **	1	0.9929 **	0.9873 **	0.9966 **	0.9894 **	0.9924 **	0.9895 **	0.9874 **	0.9897 **
SL	0.977 **	0.9905 **	0.9951 **	0.9955 **	0.9925 **	0.9919 **	0.9849 **	0.9936 **	0.9929 **	1	0.9889 **	0.9906 **	0.9926 **	0.9953 **	0.9935 **	0.9929 **	0.9919 **
NSS/S	0.9756 **	0.9747 **	0.9853 **	0.9868 **	0.9824 **	0.9831 **	0.987 **	0.9923 **	0.9873 **	0.9889 **	1	0.9913 **	0.9843 **	0.9873 **	0.9896 **	0.9927 **	0.9888 **
TW	0.974 **	0.9783 **	0.9877 **	0.9912 **	0.979 **	0.982 **	0.9788 **	0.9864 **	0.9966 **	0.9906 **	0.9913 **	1	0.9856 **	0.9904 **	0.9896 **	0.985 **	0.9855 **
SY/P	0.9849 **	0.9883 **	0.9948 **	0.9882 **	0.9911 **	0.9931 **	0.9846 **	0.9949 **	0.9894 **	0.9926 **	0.9843 **	0.9856 **	1	0.996 **	0.9932 **	0.9918 **	0.9936 **
BY/P	0.9821 **	0.9862 **	0.9923 **	0.9904 **	0.9954 **	0.9962 **	0.9892 **	0.9965 **	0.9924 **	0.9953 **	0.9873 **	0.9904 **	0.996 **	1	0.9974 **	0.9947 **	0.9961 **
SY	0.9813 **	0.9829 **	0.9899 **	0.9904 **	0.9941 **	0.9938 **	0.9916 **	0.9941 **	0.9895 **	0.9935 **	0.9896 **	0.9896 **	0.9932 **	0.9974 **	1	0.9924 **	0.9952 **
HI	0.9816 **	0.9859 **	0.9904 **	0.9871 **	0.9948 **	0.9956 **	0.99 **	0.9979 **	0.9874 **	0.9929 **	0.9927 **	0.985 **	0.9918 **	0.9947 **	0.9924 **	1	0.9966 **
CLO	0.99 **	0.9883 **	0.9886 **	0.9858 **	0.9939 **	0.9977 **	0.9935 **	0.9962 **	0.9897 **	0.9919 **	0.9888 **	0.9855 **	0.9936 **	0.9961 **	0.9952 **	0.9966 **	1

3.4 Correlation and Path Coefficient Analysis

Correlation analysis revealed strong positive associations among most growth, yield, and physiological traits, indicating their close genetic relationship. Seed yield per plant showed highly significant positive correlations with biological yield ($r = 0.9976$), days to maturity ($r = 0.9965$), siliqua length ($r = 0.9960$), number of siliquae per plant, branching traits, and chlorophyll content, suggesting that these characters contribute substantially to yield improvement. Similarly, oil content exhibited significant positive correlations with protein content, oil yield, fatty acid composition, relative water content, membrane stability index, proline accumulation, and antioxidant enzyme activities, whereas glucosinolate content showed significant negative associations with these quality and physiological traits. The positive relationships among physiological traits indicate that improved photosynthetic efficiency, maintenance of cellular water status, and enhanced antioxidant defence collectively contribute to greater biomass accumulation and seed production (Table 6 and Table 7).

Therefore, these traits may serve as reliable indirect selection criteria for developing high-yielding and stress-tolerant Indian mustard cultivars. In *Brassica* breeding, seed yield is a complex quantitative trait governed by the interaction of several morphological, physiological, and biochemical components. Since direct selection for yield is often influenced by environmental fluctuations, selection based on strongly associated component traits is considered more efficient and reliable. The significant positive associations of biological yield, number of siliquae per plant, test weight, oil content, and chlorophyll content with seed yield indicate that these characters contribute substantially to the overall productivity of the crop. Increased biological yield reflects greater biomass production and assimilate availability, while a higher number of siliquae per plant directly increases sink capacity. Similarly, greater test weight contributes to heavier seeds and improved economic yield, whereas enhanced chlorophyll content promotes photosynthetic efficiency, resulting in greater assimilate production and translocation to developing seeds. Oil content is an economically important quality trait in Indian mustard, and its positive association with seed yield suggests the possibility of simultaneously improving both productivity and oil quality through appropriate selection strategies (Singh *et al.*, 2022a, 2022b).

Path coefficient analysis further confirmed the importance of these traits by revealing that biological yield, number of siliquae per plant, test weight, oil content, and chlorophyll content exerted strong positive direct effects on seed yield, whereas several other characters contributed indirectly through these primary yield components. This indicates that the influence of many secondary traits on seed yield is mediated through their effects on these major determinants of productivity. Such information is particularly valuable in *Brassica* improvement programmes because path coefficient analysis partitions correlation into direct and indirect effects, thereby identifying the most effective traits for selection. Consequently, simultaneous improvement of these key attributes is expected to enhance yield potential, oil productivity, and adaptability under diverse agro-climatic conditions, making them valuable targets in breeding programmes aimed at developing high-yielding and stress-resilient Indian mustard cultivars (Dwivedi *et al.*, 2023; Shubham *et al.*, 2026; Srivastav *et al.*, 2026).

Conversely, several traits exhibited significant negative correlations with seed yield and its major contributing characters, indicating potential trade-offs among growth, reproductive development, and resource allocation. Negative associations imply that improvement of one trait may inadvertently reduce the expression of another, necessitating careful selection to avoid undesirable genetic linkages. In *Brassica juncea*, such antagonistic relationships are common due to competition for assimilates between vegetative growth, reproductive structures, and seed filling. Therefore, breeders should adopt a balanced selection strategy that maximises favourable trait combinations while minimising the adverse effects of negatively correlated characters, thereby achieving sustained genetic gains in both yield and quality (Ali *et al.*, 2026).

3.5 Breeding Implications and Identification of Superior Genotypes

The present investigation demonstrated the existence of substantial genetic variability among the evaluated mustard genotypes for agronomic, physiological, biochemical, and quality traits. The close agreement between GCV and PCV estimates, together with high heritability and genetic advance for most economically important traits, indicates that additive genetic effects predominantly govern these characters, making them amenable to direct phenotypic selection. Among the tested genotypes, G₉ emerged as the most promising genotype owing to its superior seed yield, oil content, protein content, physiological efficiency, and antioxidant capacity, followed by G₆ and G₄. These genotypes also exhibited favourable associations among yield components and stress-related traits, indicating their potential as valuable parental lines for future breeding programmes aimed at

improving productivity, nutritional quality, and abiotic stress tolerance. The significant positive correlations among yield, physiological, and quality traits further suggest that simultaneous selection for branching ability, silique number, biological yield, chlorophyll content, oil content, and antioxidant enzyme activities could accelerate the development of high-yielding and climate-resilient mustard cultivars. Consequently, the identified elite genotypes provide an important genetic resource for future breeding strategies focused on developing nutritionally superior and stress-tolerant Indian mustard varieties (Singh *et al.*, 2020; Akkenapally & Chetariya, 2022; Dwivedi *et al.*, 2023, Singh *et al.*, 2023).

The present study evaluated ten Indian mustard (*Brassica juncea* L.) genotypes to investigate genetic variability, agronomic performance, nutritional quality, physiological responses, and stress tolerance under field conditions during the Rabi 2025–2026 season. Significant variability was observed among the genotypes for growth, yield, quality, physiological, and antioxidant traits, demonstrating the availability of sufficient genetic diversity for selection and genetic improvement. Among the evaluated genotypes, G₉ consistently exhibited superior performance for most agronomic and quality traits, including plant height, branching, siliques per plant, seed yield, oil content, protein content, and oil yield. It also maintained higher relative water content, membrane stability index, proline accumulation, catalase activity, and peroxidase activity while recording the lowest glucosinolate content, indicating enhanced nutritional quality and greater stress resilience. Genotype G₆ ranked second for most of these characteristics, followed by G₄, whereas G₃ showed comparatively poor performance.

Analysis of variance confirmed highly significant differences among genotypes for nearly all evaluated traits, indicating that the observed variation was primarily genetic. Estimates of genetic parameters revealed high heritability coupled with moderate to high genetic advance for most economically important traits, suggesting the predominance of additive gene action and the effectiveness of direct phenotypic selection. Correlation and path coefficient analyses further demonstrated that biological yield, siliques per plant, test weight, oil content, relative water content, membrane stability index, and antioxidant enzyme activities contributed positively to seed yield and may serve as reliable selection criteria in mustard improvement programmes. The study identified G₉, followed by G₆ and G₄, as promising genotypes combining high productivity, improved nutritional quality, and enhanced stress tolerance. These genotypes constitute valuable genetic resources for breeding climate-resilient and high-yielding Indian mustard cultivars (Akkenapally & Chetariya, 2022; Dwivedi *et al.*, 2023).

4. Conclusion

The present investigation demonstrated substantial genetic variability among ten Indian mustard (*Brassica juncea* L.) genotypes for agronomic, yield, nutritional, physiological, and stress-related traits, indicating considerable scope for genetic improvement through selection. The close agreement between genotypic and phenotypic variability estimates, together with high heritability and genetic advance for most economically important traits, confirmed that additive genetic effects predominantly govern these characters, making them suitable targets for direct phenotypic selection. Among the evaluated genotypes, G₉ emerged as the most promising genotype because of its superior yield potential, enhanced oil and protein content, lower glucosinolate concentration, and stronger physiological and antioxidant responses under stress conditions. G₆ and G₄ also demonstrated favourable agronomic performance and stress tolerance, indicating their potential as valuable parental materials for future breeding programmes. The superior performance of these genotypes suggests that combining high productivity with improved nutritional quality and stress resilience is achievable within the available genetic resources.

The strong positive associations of seed yield with biological yield, siliques per plant, oil content, relative water content, membrane stability index, and antioxidant enzyme activities indicate that these traits can be effectively used as indirect selection criteria for improving yield and stress tolerance. Furthermore, the identified elite genotypes provide a strong foundation for developing climate-resilient mustard cultivars capable of maintaining productivity under variable environmental conditions. In conclusion, G₉, followed by G₆ and G₄, represents promising breeding material for the simultaneous improvement of yield, nutritional quality, and abiotic stress tolerance in Indian mustard. Future multi-location evaluation and integration of molecular breeding approaches, including marker-assisted selection and genomic tools, will facilitate the development of stable, high-yielding, and nutritionally superior mustard cultivars adapted to diverse agro-climatic environments.

5. Limitation

The study evaluated only ten genotypes at one location during a single Rabi season. Consequently, genotype × environment effects and the stability of trait expression across seasons and production environments could not

be fully assessed. The physiological and stress-related measurements were obtained under the reported field conditions rather than across multiple controlled stress treatments. Multi-location and multi-season testing is therefore required to confirm the repeatability of the observed performance and the suitability of the identified genotypes for broader breeding use.

Acknowledgement

All necessary facilities and resources are provided by the authors and Prof. Rajendra Singh (Rajju Bhaiya) University Prayagraj, UP, India and are gratefully Acknowledged.

Declaration of AI Use

This manuscript was prepared through the combined contributions of all author(s), including contributions to the study design, data, content development, results, interpretation, and related scholarly work. The author(s) acknowledge the use of Grammarly and ChatGPT to assist with grammar checking, language refinement, and reference formatting. These AI-assisted tools were not used as authors and did not replace the intellectual contributions or scholarly judgment of the author(s). All AI-assisted outputs, including content, references, and interpretations, were carefully reviewed, revised, verified, and approved by the author(s). The author(s) accept full responsibility for the accuracy, integrity, and final content of the manuscript.

Competing Interests

Authors have declared that they have no known competing financial interests or non-financial interests or personal relationships that could have appeared to influence the work reported in this paper.

References

- Akkenapally, J. S., & Chetariya, C. P. (2022). Variability, correlation, path coefficient and genetic diversity analysis in Indian mustard. *International Journal of Environment and Climate Change*, 12(10), 1116–1125. <https://doi.org/10.9734/ijecc/2022/v12i1030907>
- Ali, T., Singh, D., & Srivastava, R. (2026). Foxtail Millet (*Seteria italica* L.) A Climate-Resilient Functional Food for Nutritional Security and Health Promotion. *International Journal of Biochemistry Research & Review*, 35(3), 71–91. <https://doi.org/10.9734/ijberr/2026/v35i31125>
- American Oil Chemists' Society. (2017). *Official methods and recommended practices of the AOCS* (7th ed.; Official Method Ce 1h-05). <https://www.aocs.org/laboratory-proficiency-program/trans-fatty-acid-content-laboratory-proficiency-testing/>
- Arnon, D. I. (1949). Copper enzymes in isolated chloroplasts: Polyphenol oxidase in *Beta vulgaris*. *Plant Physiology*, 24(1), 1–15. <https://doi.org/10.1104/pp.24.1.1>
- Barrs, H. D., & Weatherley, P. E. (1962). A re-examination of the relative turgidity technique for estimating water deficits in leaves. *Australian Journal of Biological Sciences*, 15(3), 413–428. <https://doi.org/10.1071/B19620413>
- Bates, L. S., Waldren, R. P., & Teare, I. D. (1973). Rapid determination of free proline for water-stress studies. *Plant and Soil*, 39(1), 205–207. <https://doi.org/10.1007/BF00018060>
- Bhat, S. R., Haque, A., & Chopra, V. L. (2001). Induction of mutations for cytoplasmic male sterility and some rare phenotypes in Indian mustard (*Brassica juncea* L.). *Indian Journal of Genetics and Plant Breeding*, 61(4), 335–340. <https://www.isgpb.org/journal/index.php/IJGPB/article/view/1801>
- Blum, A., & Ebercon, A. (1981). Cell membrane stability as a measure of drought and heat tolerance in wheat. *Crop Science*, 21(1), 43–47. <https://doi.org/10.2135/cropsci1981.0011183X002100010013x>
- Burton, G. W. (1952). Quantitative inheritance in grasses. In *Proceedings of the 6th International Grassland Congress* (Vol. 1, pp. 277–283). Pennsylvania State College. https://www.si.edu/object/siris_sil_404212
- Chance, B., & Maehly, A. C. (1955). Assay of catalases and peroxidases. In S. P. Colowick & N. O. Kaplan (Eds.), *Methods in enzymology* (Vol. 2, pp. 764–775). Academic Press. [https://doi.org/10.1016/S0076-6879\(55\)02300-8](https://doi.org/10.1016/S0076-6879(55)02300-8)
- Dewey, D. R., & Lu, K. H. (1959). A correlation and path-coefficient analysis of components of crested wheatgrass seed production. *Agronomy Journal*, 51(9), 515–518. <https://doi.org/10.2134/agronj1959.00021962005100090002x>
- Dwivedi, S., Singh, M., Yadav, R. K., Saini, P. K., & Tripathi, H. (2023). Correlation and path analysis for seed yield and its component traits in Indian mustard (*Brassica juncea* L. Czern and Coss.). *International*

- Journal of Environment and Climate Change*, 13(11), 1044–1054. <https://doi.org/10.9734/ijecc/2023/v13i113253>
- Gupta, K. K., Singh, M. K., Singh, S. M., & Raghuvanshi, A. K. (2025). Genetic variability, heritability, correlation and path analysis of quantitative traits in Indian mustard (*Brassica juncea* L.). *Journal of Experimental Agriculture International*, 47(6), 27–33. <https://doi.org/10.9734/jeai/2025/v47i63467>
- Hanson, C. H., Robinson, H. F., & Comstock, R. E. (1956). Biometrical studies of yield in segregating populations of Korean lespedeza. *Agronomy Journal*, 48(6), 268–272. <https://doi.org/10.2134/agronj1956.00021962004800060008x>
- Johnson, H. W., Robinson, H. F., & Comstock, R. E. (1955). Estimates of genetic and environmental variability in soybeans. *Agronomy Journal*, 47(7), 314–318. <https://doi.org/10.2134/agronj1955.00021962004700070009x>
- Lowry, O. H., Rosebrough, N. J., Farr, A. L., & Randall, R. J. (1951). Protein measurement with the Folin phenol reagent. *Journal of Biological Chemistry*, 193(1), 265–275. [https://doi.org/10.1016/S0021-9258\(19\)52451-6](https://doi.org/10.1016/S0021-9258(19)52451-6)
- Miller, P. A., Williams, J. C., Robinson, H. F., & Comstock, R. E. (1958). Estimates of genotypic and environmental variances and covariances in upland cotton and their implications in selection. *Agronomy Journal*, 50(3), 126–131. <https://doi.org/10.2134/agronj1958.00021962005000030004x>
- Ministry of Agriculture and Farmers Welfare. (2024). *Agricultural statistics at a glance 2024*. Government of India. <https://desagri.gov.in/document-report/agricultural-statistics-at-a-glance-2024/>
- Panse, V. G., & Sukhatme, P. V. (1967). *Statistical methods for agricultural workers* (2nd ed.). Indian Council of Agricultural Research. <https://catalog.hathitrust.org/Record/009171831>
- Prakash, S., Wu, X. M., & Bhat, S. R. (2011). History, evolution, and domestication of *Brassica* crops. *Plant Breeding Reviews*, 35, 19–84. <https://doi.org/10.1002/9781118100509.ch2>
- Rakow, G. (2004). Species origin and economic importance of *Brassica*. In E. C. Pua & C. J. Douglas (Eds.), *Biotechnology in agriculture and forestry: Vol. 54. Brassica* (pp. 3–11). Springer. https://doi.org/10.1007/978-3-662-06164-0_1
- Rani, P., Rani, J., Mittal, A., & Sheoran, N. (2024). Assessment of drought tolerance of two cultivars of Indian mustard (*Brassica juncea*) using morphological and physiological parameters. *Archives of Current Research International*, 24(5), 437–450. <https://doi.org/10.9734/acri/2024/v24i5721>
- Sharma, M., Vasisth, P., Dhanasekaran, G., Meena, M. L., Limbalkar, O. M., Sahoo, B. C., Kumar, N., Nanjundan, J., Singh, R., Avtar, R., Watts, A., & Singh, N. (2024). Breeding *Brassica juncea* hybrids with higher seed weight and oil content: Defining criteria for selection of parents. *Heliyon*, 10(23), e40555. <https://doi.org/10.1016/j.heliyon.2024.e40555>
- Shubham, Singh, D., Choudhary, R., Verma, K., Srivastav, R., & Ali, T. (2026). Assessment of Genetic Variability Divergence, Biochemical Influence on Growth and Yield Parameter in Linseed (*Linum usitatissimum* L.). *Journal of Advances in Biology & Biotechnology*, 29(5), 865–878. <https://doi.org/10.9734/jabb/2026/v29i53963>
- Singh, D., & Verma, S. B. (2020). Pre-sowing treatments of maize (*Zea mays* L.) effect on seed treatments in growth and seed quality on different parameters. *Journal of Xidian University*, 14(6), 2878–2894.
- Singh, D., Lawrence, K., Bhattacharjee, I., Lawrence, R., Choudhary, R., Ercişli, S., & Karunakaran, R. (2023). Rainfed assessment of foxtail millet (*Setaria italica* (L.) Beauv.) germplasms through genotyping and principal component analysis. *Frontiers in Plant Science*, 14, 1017652. <https://doi.org/10.3389/fpls.2023.1017652>
- Singh, D., Lawrence, K., Singh, S., Ercişli, S., & Choudhary, R. (2022). In-vivo hyperglycemic, antioxidant, histopathological changes, and simultaneous measurement of kaempferol verified by high-performance thin layer chromatography of *Setaria italica* in streptozotocin-induced diabetic rats. *Saudi Journal of Biological Sciences*, 29(5), 3772–3790. <https://doi.org/10.1016/j.sjbs.2022.03.009>
- Singh, D., Marker, S., Suresh, B. G., & Lawrence, K. (2022). Under rainfed effect of foxtail millet [*Setaria italica* (L.) Beauv.] germplasms evaluation on genotypic variance, correlation and path analysis. *Indian Journal of Agricultural Research*, 56(2), 141–146. <https://doi.org/10.18805/IJARE.A-5862>
- Srivastav, R., Singh, D., & Ali, T. (2026). Wheat genotype improvement evolution of selection strategies for stress and nutrition. *International Journal of Biochemistry Research & Review*, 35(4), 14–34. <https://doi.org/10.9734/ijberr/2026/v35i41131>
- Sujata, Goyal, V., Baliyan, V., Avtar, R., & Mehrotra, S. (2023). Alleviating drought stress in *Brassica juncea* (L.) Czern & Coss. by foliar application of biostimulants—orthosilicic acid and seaweed extract. *Applied Biochemistry and Biotechnology*, 195, 693–721. <https://doi.org/10.1007/s12010-022-04085-2>

- Thies, W. (1982). Complex formation between glucosinolates and tetrachloropalladate(II) and its utilization in plant breeding. *Fette, Seifen, Anstrichmittel*, 84(9), 338–342. <https://doi.org/10.1002/lipi.19820840903>
- Tiwari, A., Kumar, A., Singh, D., Tripathi, P., Singh, S., Singh, S., Kumar, A., & Kumar, A. (2025). Genetic variability and improvement in Indian mustard (*Brassica juncea* L.). *Journal of Advances in Biology & Biotechnology*, 28(10), 591–606. <https://doi.org/10.9734/jabb/2025/v28i103085>
- Yadav, D., Singh, L., Jafri, S. K. F., & Mishra, U. K. (2025). Studies on genetic divergence in different genotypes of Indian mustard [*Brassica juncea* (L.) Czern and Coss]. *Plant Cell Biotechnology and Molecular Biology*, 26(5–6), 76–84. <https://doi.org/10.56557/pcbmb/2025/v26i5-69293>
- Zhang, Y., Jiang, H., Liang, F., Yang, B., Wang, L., Tang, R., Lei, S., Xiao, H., & Zhang, C. (2024). Genome-wide identification and expression analysis of growth-regulating factors under drought in *Brassica juncea*. *Scientific Reports*, 14, 29835. <https://doi.org/10.1038/s41598-024-80941-x>

Disclaimer/Publisher's Note: The statements, opinions and data contained in all publications are solely those of the individual author(s) and contributor(s) and not of the publisher and/or the editor(s). This publisher and/or the editor(s) disclaim responsibility for any injury to people or property resulting from any ideas, methods, instructions or products referred to in the content.

© Copyright (2026): Author(s). The licensee is the journal publisher. This is an Open Access article distributed under the terms of the Creative Commons Attribution License (<http://creativecommons.org/licenses/by/4.0>), which permits unrestricted use, distribution, and reproduction in any medium, provided the original work is properly cited.

Peer-review history:

The peer review history for this paper can be accessed here:

<https://pr.sdiarticle5.com/review-history/163623>