



# **Dissection of Genetic Parameters for Enhancing Yield and Yield Components in Indian Mustard (*Brassica juncea* L.)**

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## **Authors' contributions**

*This work was carried out in collaboration among all authors. All authors read and approved the final manuscript.*

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## **ABSTRACT**

A study was conducted to evaluate the genetic variability, heritability, and genetic advance of 13 quantitative traits in 55 mustard (*Brassica juncea*) genotypes. The traits assessed included days to 50% flowering, days to maturity, plant height, primary branches per plant, siliqua per plant, siliqua length, seeds per siliqua, seed yield per plant, 1000-seed weight, relative water content, membrane stability index, proline content, and oil content. Significant genetic variation was observed for all traits. Moderate phenotypic and genotypic coefficients of variation were noted for siliqua per plant and proline content. Both traits exhibited high heritability coupled with high genetic advance, indicating that additive gene action predominates. This suggests that selection for these traits could lead to substantial genetic gains in mustard breeding programs. In contrast, traits like days to 50%

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flowering and oil content showed lower genetic advance, suggesting limited scope for selection. The findings highlight the importance of focusing on traits with high variability and heritability for improving yield and stress tolerance in mustard.

**Keywords:** Genetic variability; heritability; additive gene action; seed yield.

## 1. INTRODUCTION

Indian mustard (*Brassica juncea*) is a major oilseed crop, widely cultivated in the Rabi season across India. Rajasthan is the largest producer of rapeseed mustard followed by Uttar Pradesh, Haryana, Madhya Pradesh, West Bengal, Gujarat and Assam. Oilseeds play a vital role in the Indian economy, as highlighted by the Yellow Revolution. Despite accounting for 21.10 per cent of the world's rapeseed-mustard area, India contributes only 12.60 per cent of global production [1], suggesting a gap between cultivated area and productivity. Identifying high-yielding genotypes remains a challenge. As part of the Brassicaceae family, *B. juncea* is a natural amphidiploid species derived from *B. rapa* and *B. nigra* [2,3]. Despite its adaptability to various agro-climatic conditions, improving yield remains a major challenge due to both biotic and abiotic stresses [4,5].

Enhancing the yield of Indian mustard is a major goal for plant breeders. Yield and its related traits are governed by complex interactions between genetic factors and the environment [6]. Dissecting the genetic parameters associated with yield can provide crucial insights into the nature of variability and inheritance, guiding the selection of superior genotypes [7]. For instance, genetic variability, heritability, and genetic advance are essential metrics that indicate the potential for genetic gain through selection [8,9]. Recent studies have highlighted the importance of dissecting genetic parameters to improve the yield of Indian mustard [10]. By understanding the genetic architecture of yield and related traits, breeders can make more informed decisions regarding selection and hybridization [11,12].

In light of these developments, the present study aims to dissect the genetic parameters influencing yield and its attributing components in Indian mustard. By evaluating a diverse set of 55 genotypes, this research seeks to provide insights into the genetic variability, heritability, and genetic advance of important yield and yield contributing traits in Indian mustard. The findings from this study will contribute to the ongoing efforts to develop high-yielding, stress-tolerant varieties of Indian mustard, ensuring enhanced productivity in mustard cultivation.

## 2. MATERIALS AND METHODS

The present study was conducted during the Rabi season of 2022-23 at the Instructional Farm, SKN College of Agriculture, Jobner, Jaipur, Rajasthan, to evaluate fifty-five genotypes i.e. 45 F<sub>1</sub> and 10 parents of Indian mustard for yield and yield-related traits. The experiment was designed using a randomized block design (RBD) with three replications, with each genotype planted at a spacing of 45x20 cm. To ensure optimal crop growth, recommended agronomic practices were meticulously followed, including appropriate fertilization, irrigation, and necessary plant protection measures.

The data was collected on thirteen yield and yield contributing characters viz., days to 50% flowering, days to maturity, plant height (cm), primary branches per plant, siliqua per plant, siliqua length (cm), seeds per siliqua, 1000- seed weight (g), seed yield per plant (g), relative water content at siliqua stage (%), membrane stability index at siliqua stage (%), proline content (mg/g) and oil content (%). Among different genotypes, five plants were randomly selected and tagged for taking observations except days to 50% flowering, days to maturity on plot basis and the mean value was calculated for analysis on three replications.

Statistical significance among the genotypes was assessed using analysis of variance (ANOVA), employing standard statistical methods. Genotypic and phenotypic variances were computed according to the methodology outlined by Johnson et al. [13], while the genotypic and phenotypic coefficients of variation (GCV and PCV) were estimated based on Burton [14] formula. Heritability in the broad sense and genetic advance as a percentage of the mean were determined following the approaches described by Allard [15] and Singh and Chaudhary [16]. Data analysis was conducted using the meta-R software package, allowing for precise calculations of variance components, coefficients of variation, heritability estimates, and genetic advance.

### 3. RESULTS AND DISCUSSION

#### 3.1 Analysis of Variance

The ANOVA results revealed significant variations for all traits under study (Table 1). The presence of these variations provides a solid foundation for initiating the selection process. According to Falconer and Mackay [6], the presence of significant genetic variance among traits indicates the potential for effective selection, ultimately facilitating the identification of superior genotypes. Similar pattern of results obtained by the Sharma et al. [17] and Choudhary et al. [1].

#### 3.2 Per Se Performance and Range

The evaluation of fifty-five genotypes of Indian mustard revealed significant variability in various agronomic traits (Table 2), which is crucial for breeding programs. Days to 50% flowering ranged from 42 to 51 days, with a mean of 47 days, while days to maturity varied from 113 to 129 days, average number of days to maturity 120 days [18,19]. Plant height showed considerable dispersion, with measurements ranging from 118.27 to 173.67 cm and an average of 142.20 cm. The number of primary branches averaged 3.87, varying between 3.00 and 4.60. The number of siliqua per plant was recorded between 146.33 and 273.00, with an average of 201.64, while siliqua length ranged from 4.75 to 6.03 cm, averaging 5.41 cm [17]. Seeds per siliqua varied from 10.57 to 13.53, with a mean of 12.19. The 1000-seed weight averaged 3.70 g, varying from 3.17 to 4.13 g, and seed yield per plant had an average performance of 45.43 g, ranging from 37.80 g to 51.07 g. The membrane stability index ranged from 59.67 to 74.67%, with an average of 68.69%, while proline content was between 5.55 and 9.18 mg/g, averaging 7.85 mg/g. Oil content ranged from 32.23% to 39.40%, averaging 36.31% [20,17]. The observed variability in these traits supports the selection process in breeding programs, as previous studies have highlighted the importance of these traits in improving yield and adaptability in mustard [21,22].

#### 3.3 Coefficient of Variation

The categorization of the range of variation was done as proposed by Sivasubramanian and Madhavamenon [23]: low (less than 10%), moderate (10-20%), and high (more than 20%). The phenotypic and genotypic coefficients of variation (PCV and GCV) are vital for assessing

the heritable and non-heritable components of variability among the genotypes of Indian mustard (*Brassica juncea*). The observed disparity between these coefficients indicates significant environmental influences on the traits measured, with PCV values consistently exceeding GCV values for all biometric features. This finding aligns with earlier studies that emphasize the importance of environmental factors in trait expression [24,25].

As detailed in Table 2, moderate PCV values were recorded for several major traits, including siliqua per plant (16.47%), proline content (13.85%), primary branches per plant (11.44%) and plant height (11.26%). These traits exhibited sufficient variability, suggesting potential for selection in breeding programs aimed at enhancing yield and resilience. Conversely, lower PCV values were noted for traits such as relative water content at the siliqua stage (4.72%), days to maturity (4.91%), oil content (5.67%), membrane stability index at the siliqua stage (6.01%), days to 50% flowering (6.12%), siliqua length (7.12%), seeds per siliqua (7.71%), seed yield per plant (7.96%) and 1000-seed weight (7.98%). These lower values suggest that these traits may be less responsive to environmental variations and more stable across different conditions, as supported by the findings of Akabari et al. [26] and Trivedi et al. [27]. The implications of these results indicate that breeding efforts should focus on traits with higher PCV to maximize genetic gain while also considering the environmental context [28,29].

Moderate genotypic coefficients of variation (GCV) were observed for several key traits in the study. Specifically, siliqua per plant demonstrated a GCV of 15.62%, while proline content showed a GCV of 12.78%. These moderate GCV values indicate significant potential for improvement through selective breeding [24]. In contrast, lower GCV values were recorded for traits such as relative water content at the siliqua stage (3.64%), days to maturity (4.03%) and the membrane stability index at the siliqua stage (4.45%). Other traits, including oil content (4.58%), days to 50% flowering (5.11%), siliqua length (5.54%), seeds per siliqua (5.95%), and 1000-seed weight (6.85%), exhibited low GCV values, suggesting limited genetic variability for these traits [25,26]. Seed yield per plant presented GCV of 6.94%, while plant height and primary branches per plant recorded GCV of 9.23% and 9.55%, respectively [28,27]. These findings underscore the

importance of selecting traits with higher GCV for effective breeding strategies aimed at improving yield and resilience in Indian mustard.

### 3.4 Heritability ( $h^2$ ) and Genetic Advance as a Percentage of Mean (GAM)

Estimates of heritability provide essential insights into inherited traits and the degree of similarity between parents and their offspring. High heritability is crucial for any selection program, ensuring that selected traits exhibit similar phenotypic expressions in progeny [19]. However, heritability alone is not sufficient for genetic improvement; it must be accompanied by a significant degree of genetic advance, reflecting how effectively a trait can be enhanced through appropriate selection [30]. Therefore, a combination of high heritability and strong genetic advance as a percentage of the mean is necessary for effective selection.

Heritability values were categorized as suggested by Johnson et al. [13] as follows: low (less than 30%), moderate (30-60%) and high (more than 60%). In this study, values for heritability and genetic advancement are summarized in Table 2, highlighting the potential for successful breeding strategies.

The highest heritability estimates were recorded for siliqua per plant (89.95%) and proline content (85.15%), indicating that these traits are predominantly influenced by genetic factors rather than environmental ones. This means they can be reliably selected in breeding programs, ensuring the development of new mustard varieties with improved yield and resilience to environmental stresses (Table 2). These findings are consistent with previous studies by Akabari et al. [26] and Roy et al. [31], who also reported high heritability for similar traits.

**Table 1. Analysis of variance for various characters of Indian mustard**

S.No.	Source of variation/Characters	Replication	Treatment (Genotypes)	Error
	Degrees of freedom	2	54	108
1	Days to 50% flowering	1.04	19.99**	2.55
2	Days to maturity	1.50	81.55**	11.36
3	Plant height (cm)	26.82	600.76**	84.44
4	Primary branches per plant	0.11	0.47**	0.06
5	Siliqua per plant	138.30	3087.62**	110.81
6	Siliqua length (cm)	0.11	0.33**	0.06
7	Seeds per siliqua	0.63	1.93**	0.36
8	1000-seed weight (g)	0.05	0.22**	0.02
9	Seed yield per plant (g)	1.73	1780.56**	339.57
10	Relative water content (%)	0.04	32.58**	6.03
11	Membrane stability index (%)	1.65	35.71**	7.68
12	Proline content (mg/g)	0.32	3.19**	0.18
13	Oil content (%)	0.16	9.78**	1.48

\*\* = Significant at 1%

**Table 2. Genetic variability parameters for yield and its component traits of Indian mustard**

S.No.	Characters	Mean	Range	GCV (%)	PCV (%)	$h^2$ (BS) (%)	GAM
1	Days to 50% flowering	47.00	42-51	5.11	6.12	69.52	8.77
2	Days to maturity	120.00	113-129	4.03	4.91	67.31	6.81
3	Plant height (cm)	142.20	118.27-173.67	9.23	11.26	67.08	15.57
4	Primary branches per plant	3.87	3.00-4.60	9.55	11.44	69.64	16.42
5	Siliqua per plant	201.64	146.33-273.00	15.62	16.47	89.95	30.52
6	Siliqua length (cm)	5.41	4.75-6.03	5.54	7.12	60.48	8.87
7	Seeds per siliqua	12.19	10.57-13.53	5.95	7.71	59.42	9.44
8	1000-seed weight (g)	3.70	3.17-4.13	6.85	7.98	73.65	12.10
9	Seed yield per plant (g)	45.43	37.80-51.07	6.94	7.96	75.98	12.46
10	Relative water content (%)	81.72	73.00-87.00	3.64	4.72	59.50	5.78
11	Membrane stability index (%)	68.69	59.67-74.67	4.45	6.01	54.89	6.79
12	Proline content (mg/g)	7.85	5.55-9.18	12.78	13.85	85.15	24.28
13	Oil content (%)	36.31	32.23-39.40	4.58	5.67	65.21	7.62

High heritability was observed for seed yield per plant (75.98%), days to 50% flowering (69.52%), primary branches per plant (69.64%), days to maturity (67.31%), plant height (67.08%), siliqua length (60.48%), and oil content (65.21%). In contrast, moderate heritability was recorded for the membrane stability index at the siliqua stage (54.89%), seeds per siliqua (59.42%), and relative water content at the siliqua stage (59.50%). These results are further supported by findings from Bind et al. [32], Devi et al. [28], and Trivedi et al. [27], who emphasized the significance of heritability in breeding programs.

The variance of genetic advance as a percentage of the mean was classified according to the guidelines of Johnson et al. [13] as follows: low (less than 10%), moderate (10-20%), and high (more than 20%). The expected genetic advance as a percentage of the mean was notably high for siliqua per plant (30.52%) and proline content (24.28%). These results align with findings from Singh et al. [18], Gupta et al. [19], Patel et al. (2019), Rout et al. [25], and Awasthi [29], who also reported significant genetic advances for these traits. Moderate genetic advance percentages were observed for primary branches per plant (16.42%), plant height (15.57%) and seed yield per plant. Additionally, the 1000-seed weight exhibited a genetic advance of 12.10%. Conversely, low genetic advance percentages were recorded for days to 50% flowering (8.77%), days to maturity (6.81%), siliqua length (8.87%), seeds per siliqua (9.44%), relative water content at the siliqua stage (5.78%), membrane stability index at the siliqua stage (6.79%) and oil content (7.62%).

Broad heritability and genetic advance as a percentage of the mean serve as crucial selection criteria, providing a transmissibility index for various traits and indicating the effectiveness of the selection process in enhancing individual characteristics. In the current study, siliqua per plant and proline content exhibited high heritability estimates alongside high genetic advances, suggesting that these traits are predominantly influenced by additive gene action and possess significant selective value. As these traits contribute to overall seed yield and stress tolerance (particularly proline content related to drought), breeders can prioritize them to develop mustard varieties with enhanced yield potential and adaptability to stressful conditions. Similar findings have been documented by Lodhi et al. [33] and Roy [31], further supporting the notion

that traits with high heritability and genetic advance are ideal candidates for targeted selection in crop improvement initiatives.

The study's findings on traits like proline content and membrane stability index provide direct pathways for improving stress tolerance. High proline content is associated with drought tolerance, while a stable membrane stability index reflects the plant's resilience under heat and moisture stress. Breeding for these traits can lead to mustard varieties capable of thriving in stressful environments, which is critical for maintaining yield stability in areas prone to water scarcity or temperature extremes.

The significant variability in traits such as proline content highlight the potential for integrating physiological and biochemical traits into breeding programs. By selecting for trait that stress resilience (e.g., proline), breeders can develop mustard varieties that are not only high-yielding but also better equipped to withstand environmental stresses like drought and high temperatures.

#### 4. CONCLUSION

The analysis of variance for all the traits included in the investigation showed significant results, indicating sufficient genetic variation for each trait. The high heritability and genetic advance observed for siliqua per plant and proline content. These traits are largely governed by additive gene action, making them ideal candidates for selection to achieve meaningful genetic improvement in both yield and stress tolerance. In contrast, traits like days to 50% flowering and oil content, which showed lower genetic advance, may offer limited opportunities for selection.

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Author(s) hereby declare that NO generative AI technologies such as Large Language Models (ChatGPT, COPILOT, etc) and text-to-image generators have been used during writing or editing of this manuscript.

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## COMPETING INTERESTS

Authors have declared that no competing interests exist.

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