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GENETIC VARIABILITY, HERITABILITY AND GENETIC ADVANCE FOR SEED YIELD AND ITS COMPONENT TRAITS IN INDIAN MUSTARD (*Brassica juncea* L. CZERN & COSS) UNDER DIFFERENT GROWING ENVIRONMENTS

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ABSTRACT

An investigation was undertaken to estimate the magnitude of genetic variability, heritability and genetic advance for seed yield and twelve component traits in a set of 157 genotypes of Indian mustard (*Brassica juncea* (L.) Czern & Coss), comprising 30 lines, 4 testers, their 120 line × tester cross combinations, and 3 check varieties. The genotypes were evaluated in a randomized block design with three replications across four environments generated by two locations (Sri Ganganagar and Bikaner) and two sowing dates (timely and late sown) during the 2024-25 *rabi* season. Analysis of variance revealed significant differences among genotypes for most of the characters studied, indicating the presence of considerable genetic variability in the material. In all four environments, phenotypic coefficient of variation (PCV) was consistently higher than the corresponding genotypic coefficient of variation (GCV) for every trait, reflecting a modulating influence of environment on trait expression. Seed yield per plant recorded the highest GCV (21.55-23.45%) and PCV (22.92-24.85%) together with high heritability (88.4-89.1%) and very high genetic advance as per cent of mean (41.73-45.59%) across all environments, followed closely by number of siliquae per plant and biological yield per plant, indicating predominance of additive gene effects and good scope for improvement through direct phenotypic selection. Harvest index, 1000-seed weight, siliqua length and number of primary branches per plant also exhibited moderate to high GCV coupled with high heritability and high genetic advance as per cent of mean in all the environments. In contrast, days to maturity and oil content displayed very low genotypic coefficients of variation together with negligible or negative heritability estimates in three of the four environments, suggesting these traits were governed largely by non heritable environmental variance in the material evaluated and offer limited scope for improvement through simple selection. The consistency of high heritability coupled with high genetic advance for seed yield, siliqua number, biological yield and harvest index across contrasting environments indicates that these traits are under strong additive genetic control and may be relied upon as reliable selection indices for yield improvement in Indian mustard breeding programmes.

Key words: GCV, PCV, genetic variability, heritability and genetic advance.

Introduction

Rapeseed-mustard (*Brassica* spp.) ranks among the most important oilseed groups of the world, providing edible oil, protein-rich meal and industrial raw material. India occupies the second position globally in area and third in production of rapeseed-mustard, with the crop

covering about 8.86 million hectares and contributing 12.67 million tonnes of production at an average productivity of 1463 kg/ha (Economics, Statistics & Evaluation Division, DA&FW, 2024-25). Indian mustard [*Brassica juncea* (L.) Czern & Coss], a natural amphidiploid ($2n = 4x = 36$, AABB) derived from *Brassica campestris* and

Brassica nigra, is the most widely cultivated species of this group in the country, and Rajasthan alone accounts for nearly 3.49 million hectares of area and 5.42 million tonnes of production (Ministry of Agriculture & Farmers Welfare, 2025). Seed yield in Indian mustard is a complex quantitative trait, resulting from the interplay of several component characters and their interaction with the environment (Ghosh *et al.*, 2002; Singh *et al.*, 2013). Direct selection for yield per se is often unrewarding because of its low heritability and marked environmental sensitivity; hence, breeders rely on the partitioning of observed phenotypic variability into its heritable and non-heritable components to design efficient selection strategies. The phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV), first proposed by Burton (1952) and refined by Burton and De Vane (1953), provide a standardized measure of the extent of variability present for a character, while heritability in broad sense (Hanson *et al.*, 1956) indicates the proportion of this variability that is transmissible to the offspring. However, heritability estimated alone, without genetic advance, may not always be able to predict the effective response to selection, since it does not account for the magnitude of genetic gain (Johnson *et al.*, 1955). A trait with high heritability coupled with high genetic advance as per cent of mean (GAM) is generally governed by additive gene action and responds well to simple mass selection, whereas high heritability accompanied by low genetic advance points towards non-additive gene action, warranting alternative breeding approaches such as heterosis breeding or recurrent selection. A large number of workers have reported the presence of substantial genotypic variability for seed yield and its component traits in Indian mustard, but the magnitude and ranking of genetic parameters have varied considerably with the germplasm evaluated and the environment under which it was tested (Chaurasiya *et al.*, 2019; Kumar *et al.*, 2023; Meena *et al.*, 2024). Since genotype x environment interaction is a major impediment to accurate estimation of these parameters, evaluation across more than one environment is essential before a character can be recommended as a dependable selection criterion (Yadava *et al.*, 2011). Keeping this in view, the present investigation was carried out to estimate the genetic variability, heritability and genetic advance for seed yield and twelve related traits in a large panel of Indian mustard genotypes evaluated across four distinct environments created through variation in location and date of sowing, with the objective of identifying traits amenable to direct phenotypic selection for varietal improvement.

Material and Methods

The experimental material comprised 157 genotypes of Indian mustard, consisting of 30 lines, 4 testers, their 120 line × tester cross combinations obtained through crossing at ARS, Sri Ganganagar during 2023-24 *rabi* season, and 3 standard check varieties. The genotypes were evaluated in a randomized block design (RBD) with three replications, each genotype being sown as a single-row plot, during the 2024-25 *rabi* season. Four environments were created by growing the material at two locations, ARS Sri Ganganagar and ARS Bikaner, under two dates of sowing, namely, timely sown and late sown conditions, viz., Environment-I (Timely sown, Sri Ganganagar), Environment-II (Late sown, Sri Ganganagar), Environment-III (Timely sown, Bikaner) and Environment-IV (Late sown, Bikaner). Data were recorded on five randomly selected competitive plants per genotype per replication in each environment for thirteen quantitative characters, viz., days to 50% flowering, days to maturity, plant height (cm), number of primary branches per plant, number of secondary branches per plant, number of siliquae per plant, siliqua length (cm), number of seeds per siliqua, 1000-seed weight (g), biological yield per plant (g), seed yield per plant (g), harvest index (%) and oil content (%).

Analysis of variance was carried out separately for each environment as per the standard procedure for randomized block design (Panse and Sukhatme, 1961) to test the significance of differences among genotypes. From the resultant mean squares, genotypic (σ^2_g), phenotypic (σ^2_p) and environmental (σ^2_e) variances were partitioned as:

$$\sigma^2_g = (Mg - Me) / r$$

$$\sigma^2_p = \sigma^2_g + \sigma^2_e$$

$$\sigma^2_e = Me$$

Where,

Mg and Me are the mean sums of squares due to genotypes and error, respectively, and r is the number of replications.

Genotypic and phenotypic coefficients of variation were computed following Burton (1952) and Burton and De Vane (1953) as:

$$GCV (\%) = (\sqrt{\sigma^2_g} / \bar{x}) \times 100$$

$$PCV (\%) = (\sqrt{\sigma^2_p} / \bar{x}) \times 100$$

Where,

$\bar{x}$ is the general mean of the character. The GCV and PCV estimates were classified as low (<10%), moderate (10-20%) and high (>20%) following

Table 1: Estimates of genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), broad-sense heritability [h^2 (bs)], genetic advance (GA) and genetic advance as per cent of mean (GAM, at 5% selection intensity) for thirteen characters in Indian mustard under Environment-I (Timely sown, Sri Ganganagar).

Character	GCV (%)	PCV (%)	h^2 (bs) (%)	GA (5%)	GAM (%)
Days to 50% flowering	6.29	9.98	39.7	4.72	8.16
Days to maturity	2.12	7.72	7.5	1.67	1.20
Plant height (cm)	8.10	10.67	57.7	24.62	12.68
Number of primary branches/plant	13.52	15.66	74.5	1.67	24.03
Number of secondary branches/plant	16.41	18.04	82.8	5.15	30.77
Number of siliquae/plant	15.13	16.90	80.1	216.37	27.89
Silique length (cm)	13.68	15.61	76.8	1.27	24.69
No. of seeds/silique	10.15	12.65	64.4	2.76	16.78
1000-seed weight (g)	16.25	18.11	80.6	1.59	30.05
Biological yield/plant (g)	18.57	20.07	85.6	57.08	35.39
Seed yield/plant (g)	21.55	22.92	88.4	17.07	41.73
Harvest index (%)	12.99	15.41	71.0	5.75	22.55
Oil content (%)	2.29	7.33	-9.8	-0.57	-1.47
GCV = Genotypic coefficient of variation; PCV = Phenotypic coefficient of variation; h^2 (bs) = Heritability in broad sense; GA = Genetic advance; GAM = Genetic advance as per cent of mean.					

Sivasubramanian and Menon (1973).

Heritability in broad sense (h^2 bs) was estimated as the ratio of genotypic to phenotypic variance (Hanson *et al.*, 1956) and expressed as a percentage:

$$h^2 \text{ (bs)} = (\sigma^2_g / \sigma^2_p) \times 100$$

and categorized as low (<30%), moderate (30-60%) and high (>60%) as suggested by Robinson (1966). Expected genetic advance under selection was calculated following Johnson *et al.*, (1955) as:

$$GA = k \times \sigma_p \times h^2(\text{bs})$$

$$GAM (\%) = (GA / \bar{x}) \times 100$$

Where,

k is the standardized selection differential ($k = 2.06$ at 5% selection intensity), σ_p is the phenotypic standard deviation and $\bar{x}$ is the general mean. GAM was classified as low (<10%), moderate (10-20%) and high (>20%) following Johnson *et al.*, (1955).

Results and Discussion

Analysis of variance revealed highly significant differences among genotypes for most of the characters studied in all four environments, confirming the existence of substantial genetic variability in the experimental material and providing scope for further genetic analysis and selection. The estimates of GCV, PCV, heritability (broad sense), genetic advance and genetic advance as per cent of mean for the thirteen characters under the four environments are presented in Tables 1 to 4.

Phenotypic and genotypic coefficients of variation

In agreement with the general expectation, the

phenotypic coefficient of variation was higher in magnitude than the corresponding genotypic coefficient of variation for every character in all four environments, indicating that the apparent phenotypic variability was influenced, to varying degrees, by the environment in addition to the genotype. This trend is consistent with earlier reports in Indian mustard by Chaurasiya *et al.*, (2019), Kumar *et al.*, (2023) and Meena *et al.*, (2024). However, the difference between PCV and GCV was narrow for seed yield per plant, number of siliquae per plant, biological yield per plant and harvest index across all the environments, suggesting a comparatively lower environmental influence and a greater role of genetic factors in the expression of these traits.

Seed yield per plant recorded the highest genotypic coefficient of variation among all the characters studied, ranging from 21.55% in Environment-I to 23.45% in Environment-IV, and was consistently categorized as high across all environments. Similarly high GCV was recorded for number of siliquae per plant (15.13-20.11%) and biological yield per plant (10.28-19.41%), the latter falling in the moderate category only in Environment-III. Harvest index also exhibited high to moderately high GCV (11.38-18.84%) in all environments. These findings corroborate the results of Ganesh Prasad and Patil (2018), who reported high genotypic coefficient of variance for secondary branches per plant, biological yield, harvest index and seed yield in Indian mustard, and Kumar *et al.* (2023), who observed high PCV and GCV for number of siliquae per plant and seed yield per plant across four sowing date and spacing environments. Moderate GCV was recorded for 1000-seed weight (14.03-16.25%),

Table 2: Estimates of genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), broad-sense heritability [h^2 (bs)], genetic advance (GA) and genetic advance as per cent of mean (GAM, at 5% selection intensity) for thirteen characters in Indian mustard under Environment-II (Late sown, Sri Ganganagar).

Character	GCV (%)	PCV (%)	h^2 (bs) (%)	GA (5%)	GAM (%)
Days to 50% flowering	7.69	10.91	49.7	5.87	11.16
Days to maturity	1.54	7.67	-4.0	-0.83	-0.64
Plant height (cm)	13.85	16.11	73.9	41.27	24.53
Number of primary branches/plant	13.58	15.63	75.4	1.44	24.30
Number of secondary branches/plant	12.23	14.41	72.0	2.59	21.38
Number of siliquae/plant	19.68	21.16	86.5	246.91	37.72
Silique length (cm)	12.94	15.10	73.5	1.09	22.86
No. of seeds/silique	11.25	13.59	68.5	2.75	19.19
1000-seed weight (g)	14.03	16.14	75.6	1.23	25.14
Biological yield/plant (g)	14.15	16.25	75.9	33.48	25.39
Seed yield/plant (g)	22.19	23.54	88.8	13.74	43.08
Harvest index (%)	18.84	20.57	83.9	8.65	35.56
Oil content (%)	3.33	6.56	-25.7	-1.33	-3.48
GCV = Genotypic coefficient of variation; PCV = Phenotypic coefficient of variation; h^2 (bs) = Heritability in broad sense; GA = Genetic advance; GAM = Genetic advance as per cent of mean.					

silique length (12.94-13.68%), number of primary branches per plant (12.19-14.38%) and number of seeds per silique (10.15-12.47%) in all four environments, a pattern also reported by Chaurasiya *et al.*, (2019) and Yadava *et al.*, (2011) for the same set of traits. In contrast, days to maturity (1.54-3.75%) and oil content (1.74-3.33%) recorded consistently low GCV across all environments, indicating a narrow genetic base for these two characters in the material evaluated, a finding also noted by Ray *et al.*, (2019) and Lakra *et al.*, (2020) for oil content in Indian mustard. Days to 50% flowering behaved inconsistently, ranging from low (2.10-7.69%) in Environments I to III to moderate (10.48%) in Environment-IV, while plant height and number of secondary branches per plant showed low to moderate GCV that varied appreciably between the Sri Ganganagar and Bikaner locations, reflecting the influence of genotype $\times$ environment interaction on these traits, as also reported for stability behaviour in Indian mustard by Gupta *et al.*, (2021) and Prasad *et al.*, (2015).

Heritability (broad sense)

High heritability (>60%) was recorded for the majority of the characters across all four environments, particularly for seed yield per plant (88.4-89.1%), biological yield per plant (63.9-86.1%), number of siliquae per plant (73.7-86.5%), harvest index (66.1-83.9%), 1000-seed weight (75.6-80.6%), silique length (73.5-76.8%), number of primary branches per plant (70.9-77.5%) and number of seeds per silique (64.4-71.2%). Such consistently high heritability across contrasting environments indicates that these characters were relatively less influenced by environmental fluctuations

and that the observed phenotypic variation was largely attributable to genotypic differences, a conclusion also drawn by Kumar *et al.*, (2023) and Meena *et al.*, (2024) for the same traits in Indian mustard. Plant height and number of secondary branches per plant recorded high heritability in Environments I, II and IV (52.2-82.8%) but fell to the moderate (Environment-IV plant height, 57.5%) and low category in Environment-III (22.8% and 47.3%, respectively), again reflecting a pronounced genotype $\times$ environment interaction for these two traits under the more stressful late-sown or Bikaner conditions.

Days to 50% flowering exhibited moderate to high heritability in Environments I, II and IV (39.7-66.6%) but very low heritability in Environment-III (7.3%). Days to maturity and oil content, on the other hand, recorded negligible or negative heritability estimates in three of the four environments (Environments II, III and IV), and only a low positive value in Environment-I (7.5% and -9.8%, respectively, oil content being negative even in Environment-I). A negative or near-zero heritability estimate arises when the environmental component of variance exceeds or closely approximates the total phenotypic variance, effectively indicating an absence of exploitable genetic variance for the trait in the panel under study; such estimates are conventionally treated as heritability approaching zero rather than being biologically meaningful negative values (Falconer, 1985). Similar low heritability for days to maturity and oil content has been reported by Ray *et al.*, (2019) and Lakra *et al.*, (2020), and is generally attributed to the strong modulating effect of temperature and photoperiod on maturity duration and of post-anthesis environmental conditions

Table 3: Estimates of genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), broad-sense heritability [h^2 (bs)], genetic advance (GA) and genetic advance as per cent of mean (GAM, at 5% selection intensity) for thirteen characters in Indian mustard under Environment-III (Timely sown, Bikaner).

Character	GCV (%)	PCV (%)	h^2 (bs) (%)	GA (5%)	GAM (%)
Days to 50% flowering	2.10	7.77	7.3	0.60	1.16
Days to maturity	3.75	7.13	-27.6	-5.40	-4.05
Plant height (cm)	4.32	9.06	22.8	7.84	4.25
Number of primary branches/plant	12.19	14.48	70.9	1.23	21.15
Number of secondary branches/plant	7.09	10.32	47.3	1.31	10.05
Number of siliquae/plant	12.91	15.04	73.7	158.64	22.83
Silique length (cm)	13.32	15.39	74.9	1.08	23.74
No. of seeds/silique	10.87	13.19	67.9	2.74	18.44
1000-seed weight (g)	15.83	17.70	79.9	1.35	29.15
Biological yield/plant (g)	10.28	12.86	63.9	22.57	16.92
Seed yield/plant (g)	15.23	16.98	80.5	9.84	28.14
Harvest index (%)	11.38	13.99	66.1	5.00	19.06
Oil content (%)	1.74	7.68	-5.1	-0.31	-0.81
GCV = Genotypic coefficient of variation; PCV = Phenotypic coefficient of variation; h^2 (bs) = Heritability in broad sense; GA = Genetic advance; GAM = Genetic advance as per cent of mean.					

on oil accumulation in Brassica juncea.

Genetic advance and genetic advance as per cent of mean

Genetic advance as per cent of mean, considered jointly with heritability, is regarded as a more reliable indicator of the expected response to selection than heritability alone (Johnson *et al.*, 1955). High heritability coupled with high GAM was consistently recorded for seed yield per plant (41.7-45.6%), number of siliquae per plant (22.8-38.2%), biological yield per plant (16.9-37.1%), harvest index (19.1-35.6%), 1000-seed weight (25.1-30.0%), silique length (22.9-24.7%) and number of primary branches per plant (21.1-26.1%) across all four

environments, indicating that these traits are governed predominantly by additive gene action and that direct phenotypic selection would be effective for their improvement. This finding is in close agreement with Ganesh Prasad and Patil (2018), Chaurasiya *et al.*, (2019), Kumar *et al.*, (2023) and Meena *et al.*, (2024), all of whom reported high heritability with high genetic advance for seed yield, biological yield, harvest index and silique number in Indian mustard, and points to the predominance of additive gene effects governing these economically important traits.

Number of seeds per silique showed high heritability coupled with moderate to high GAM (16.8-21.7%), while

Table 4: Estimates of genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), broad-sense heritability [h^2 (bs)], genetic advance (GA) and genetic advance as per cent of mean (GAM, at 5% selection intensity) for thirteen characters in Indian mustard under Environment-IV (Late sown, Bikaner).

Character	GCV (%)	PCV (%)	h^2 (bs) (%)	GA (5%)	GAM (%)
Days to 50% flowering	10.48	12.84	66.6	8.94	17.63
Days to maturity	3.67	7.05	-27.1	-4.89	-3.93
Plant height (cm)	9.14	12.05	57.5	22.51	14.29
Number of primary branches/plant	14.38	16.34	77.5	1.27	26.07
Number of secondary branches/plant	7.56	10.46	52.2	1.11	11.25
Number of siliquae/plant	20.11	21.79	85.1	210.98	38.22
Silique length (cm)	13.41	15.51	74.7	1.05	23.88
No. of seeds/silique	12.46	14.77	71.2	2.93	21.67
1000-seed weight (g)	14.67	16.71	77.1	1.11	26.53
Biological yield/plant (g)	19.41	20.92	86.1	38.02	37.10
Seed yield/plant (g)	23.45	24.85	89.1	11.58	45.59
Harvest index (%)	13.05	15.22	73.6	5.74	23.07
Oil content (%)	2.23	7.42	-9.0	-0.51	-1.38
GCV = Genotypic coefficient of variation; PCV = Phenotypic coefficient of variation; h^2 (bs) = Heritability in broad sense; GA = Genetic advance; GAM = Genetic advance as per cent of mean.					

plant height and number of secondary branches per plant displayed high heritability with high GAM in Environments I, II and IV, but comparatively low GAM in Environment-III (4.3% and 10.0%, respectively), consistent with the low heritability recorded for these traits under that environment. Days to 50% flowering showed low to moderate GAM (1.2-17.6%) that mirrored its inconsistent heritability across environments. Days to maturity and oil content recorded negative or negligible GAM in all four environments, corroborating their negligible heritability and confirming that these two characters offer little scope for improvement through simple selection in the present material; their improvement, if desired, would require alternative approaches such as biparental mating, recurrent selection over multiple cycles, or exploitation through marker-assisted or mutation breeding, as also suggested by Ray *et al.*, (2019) for oil content in Indian mustard.

Implications for selection

Taken together, the consistency of high GCV, high heritability and high genetic advance as per cent of mean for seed yield per plant, number of siliquae per plant, biological yield per plant, harvest index, 1000-seed weight, siliqua length and number of primary branches per plant across all four environments, spanning two contrasting locations and two sowing dates, establishes these traits as dependable and environmentally stable selection indices for improving seed yield in Indian mustard. This concurs with the general conclusion of Yadava *et al.*, (2011), Patel *et al.*, (2021) and Kaur *et al.*, (2022) that yield-contributing traits with a strong additive genetic basis provide the most reliable criteria for indirect selection when direct selection for yield alone proves difficult on account of its complex polygenic inheritance. Conversely, the very low genetic variability and negligible heritability recorded for days to maturity and oil content in the present study indicate that these traits, at least within this genetic base, are strongly governed by environmental and non-additive factors, and that widening the genetic base through introduction of exotic or diverse germplasm may be necessary before meaningful genetic gain can be expected for these characters.

Conclusion

The present investigation, conducted across four diverse environments generated by two locations and two dates of sowing, revealed the presence of considerable genetic variability for seed yield and its component traits in a large panel of Indian mustard genotypes. Seed yield per plant, number of siliquae per plant, biological yield per plant, harvest index, 1000-seed weight, siliqua length

and number of primary branches per plant consistently exhibited high GCV, high heritability and high genetic advance as per cent of mean across all environments, indicating predominance of additive gene action and reliable scope for their improvement through simple phenotypic selection. Days to maturity and oil content, on the other hand, showed very low genetic variability and negligible heritability throughout, suggesting that improvement of these traits in the present material would require broadening of the genetic base or the adoption of alternative breeding strategies. The environmental stability of the genetic parameters for the major yield-contributing traits across both timely and late-sown conditions at Sri Ganganagar and Bikaner underscores their utility as dependable selection criteria for the development of high-yielding and widely adapted Indian mustard varieties.

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