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Assessment of Genetic Variability and Heritability in Indian Mustard (Brassica juncea L.)

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ABSTRACT: The present study involved 48 Indian mustard genotypes which were assessed for seed yield and its associated traits across 11 characters during the rabi season of 2022-23 at CCS HAU, Hisar. The analysis of variance indicated highly significant genotypic differences for all traits examined. The highest variability was observed in test weight (29.64%), while days to maturity showed the least variability (1.95%). Notably, secondary branches per plant (91.43%) and main shoot length (89.04%) exhibited very high broad sense heritability. Genetic advance was also notably high for test weight (36.54%), secondary branches per plant (35.54%), and primary branches per plant (26.65%). While high heritability coupled with high genetic advance was depicted by secondary branches per plant, seed yield per plant and thousand seed weight. This knowledge empowers breeders to develop new varieties that are not only higher-yielding but also more resilient to environmental challenges, thereby contributing to sustainable agricultural practices and food security.

Keywords: genotypes, heritability, seed yield, variability.

INTRODUCTION

Brassica juncea, commonly referred to as Indian mustard, is a significant oilseed crop globally recognized for its economic importance. It is an amphidiploid species with the genome configuration AABB (2n = 36). The unique genetic background and adaptability of Indian mustard make it a critical component of agricultural practices and an essential source of edible oil. Indian mustard oil, in particular, is known for its high content of monounsaturated fatty acids, which make up about 70% of its composition. This includes significant amounts of eicosenoic, oleic, and erucic acids. Additionally, the oil contains around 22% polyunsaturated fatty acids which contain linoleic and linolenic acids, while saturated fatty acids, including stearic and palmitic acids, comprise only about 8% of the total fatty acid content.

With its adaptability to diverse climatic conditions, it contributes significantly to the global edible oil market. India stands as the fourth-largest oilseed producer globally, covering about 20.8% of the world's oilseed Naresh et al..

area and contributing 10% of the global production (IBEF, 2022). Within the Indian context, Indian mustard ranks first and constitutes approximately 32.04% of the total production among nine oilseed crops (GOI, 2024) and cover roughly 90% of the oilseed area in India (Singh et al., 2021b). India imports up to 60% of its total domestic consumption whose cost is of approximately 1.22 trillion Indian rupees annually (Anonymous, 2021). Given India's continuous increasing population and increasing per capita consumption of vegetable oil, domestic demand is expected to increase further. This low productivity is largely due to the crop's susceptibility to different biotic and abiotic stresses, including diseases, pests, and extreme weather conditions, which are expected to worsen with ongoing climate change (Singh et al., 2021a). So, there is need for development of high yielding mustard varieties to combat growing needs of population.

The development of high-yielding cultivars of Indian mustard heavily relies on effective breeding techniques,

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which are influenced by the type and extent of genetic variation present in the crop. Key genetic parameterssuch as the phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), broad-sense heritability (h²bs), and genetic advance (GA %)-are crucial for guiding selection processes aimed at improving yield traits. Seed yield is a complex, polygenic trait that is highly susceptible to environmental variations, unlike specific yieldcontributing traits like the number of branches per plant, seeds per siliqua, main shoot length, seed count per siliqua, and 1000-seed weight. This complexity necessitates a comprehensive selection approach that takes into account both seed yield and its component traits.

Despite the existing knowledge about genetic variability within Indian mustard, it's well established that genetic correlation coefficients can differ significantly across various genotypes. To enhance yield potential and develop high-performing cultivars suited to specific agricultural regions, current research focuses on assessing the nature and magnitude of genetic variability, alongside the inter-relationships between various traits contributing to seed yield.

MATERIALS AND METHOD

The present study was carried out at Oilseeds Research Farm, CCS HAU, Hisar with the help of 48 Indian mustard genotypes. The genotypes were assessed in timely sown condition (15th Oct) in 2022-23 in two replications. Randomized block design was used to evaluate the genotypes for genetic variability parameters.

Randomly five plants per genotypes were selected for the examination of 12 morphological traits *i.e.* days to 50% flowering, days to maturity, plant height (cm), number of primary branches per plant, number of secondary branches per plant, main shoot length (cm), number of siliqua on main shoot, siliqua length (cm), number of seeds per siliqua, thousand seed weight (g), seed yield per plant (g) and oil content (%).

Morphological data was subject to statistical analysis through R and OPSTAT software. Analysis of Variance was conducted on the mean data based on the methodology outlined by Panse and Sukhatme (1967). To evaluate the genotypic and phenotypic coefficients of variation (GCV and PCV), the techniques recommended by Burton and Devane (1953) were applied. Broad-sense heritability was calculated using the formula established by Allard (1960). For estimating the genetic advance, the approach suggested by Johnson *et al.* (1955) was utilized.

RESULTS AND DISCUSSION

Mean sum of squares due to genotypes showed significant differences at 1 % level of significance for

all the morphological traits (Table 1), suggesting the presence of sufficient genetic variability among the genotypes. However, mean sum of squares due to replications exhibited non-significant differences for all the traits under study. Any program to improve crops must have variability; if there was little to no variability among the accessions, ineffective selection would take place. Results are in agreement with previous studies reported by Sharma et al. (2022b); Choudhary et al. (2023); Sowmya et al. (2024). The genetic variability parameters were estimated for different morphological traits recorded for 48 Indian mustard genotypes. For a crop breeder to achieve successful outcomes with experimental material, understanding and effective use of variability is crucial. The type of variability and gene action help in deciding suitable breeding methods. When environmental factors have minimal impact and additive variance is predominant, methods such as mass selection and pure line selection are beneficial. Conversely, if dominance effects are significant, crossing programs offer greater potential.

The estimates of PCV were somewhat higher than those of GCV, suggesting that environmental factors had a minimal impact. This indicates that the accessions were more reflective of their genotypic potential, with environmental effects being relatively minor. The results of PCV, GCV, heritability (broad sense) and genetic advance have been presented in Table 2. Maximum PCV and GCV were found for thousand seed weight (30.58% and 29.64%, respectively), number of secondary branches per plant (28.97% and 27.68%, respectively) and siliqua length (27.95% and 25.46%, respectively). This indicates a significant genetic influence on the expression of these traits, with minimal impact from environmental factors. Such a strong genetic contribution suggests that there is considerable potential for enhancing these genotypes through selective breeding and other improvement strategies. This could lead to the development of varieties with optimized traits, ultimately benefiting agricultural productivity. Similar findings were noted by Gupta et al. (2021); Shrivastava et al. (2023), who highlighted the importance of directly considering these traits for selection. While moderate PCV and GCV were observed for number of siliqua on main shoot (18.67%) and 17.45%, respectively), seed yield per plant (18.12%) and 17.65%, respectively), number of primary branches per plant (15.23% and 14.68%, respectively), days to 50% flowering (11.66% and 10.12%, respectively) and main shoot length (10.78% and 10.05%, respectively). The results indicate that the traits evaluated displayed moderate levels of phenotypic and genotypic coefficients of variation (PCV and GCV). The moderate levels of variation observed across these traits suggest a strong potential for genetic improvement through targeted breeding strategies.

Table 1: Analysis of variance for morphological traits of 48 Indian mustard genotypes under timely sown conditions.

Source of Variation	Replication	Genotype	Error
D.F.	1	47	47
DF	4.203	68.245**	1.456
DM	2.213	15.632**	1.989
PH	180.7	390.240**	29.666
PB	0.144	1.456**	1.234
SB	2.332	16.324**	0.345
MSL	55.234	80.324**	10.243
NOS/MS	27.60	57.654**	5.245
SL	0.076	0.289**	0.057
NOS/SQ	0.345	4.234**	0.213
Y	7.213	24.654**	1.143
TSW	0.354	2.765**	0.046
OC	0.134	0.987**	0.653

*Significant at p = 0.05,**Significant at p = 0.01

DF-Days to 50% flowering; DM-Days to maturity; PH-Plant height (cm); PB-Number of primary branches/plant; SB-Number of secondary branches/plant; MSL-Main shoot length (cm), NOS/MS-Number of siliquae on main shoot; SL-Siliqua length (cm); NOS/SQ-Number of seeds/siliqua; TSW-1000-seed weight (g); Y-Seed yield/plant (g); OC- Oil content (%)

Table 2: Genetic parameters under timely and late sown conditions for morphological traits.

TRAIT	PCV	GCV	Heritability	GA (%mean)
DF	11.66	10.12	87.23	21.05
DM	2.23	1.95	68.45	4.76
PH	8.75	7.96	80.54	18.65
PB	15.23	14.68	86.45	26.65
SB	28.97	27.68	91.43	35.54
MSL	10.78	10.05	89.04	14.65
NOS/MS	18.67	17.45	61.86	12.87
SL	27.95	25.46	45.65	26.24
NOS/SQ	5.87	4.08	55.65	10.92
Y	18.12	17.65	80.64	23.46
TSW	30.58	29.64	76.45	36.54
OC	6.64	5.98	51.23	7.76

DF-Days to 50% flowering; DM-Days to maturity; PH-Plant height (cm); PB-Number of primary branches/plant; SB-Number of secondary branches/plant; MSL-Main shoot length (cm), NOS/MS-Number of siliquae on main shoot; SL-Siliqua length (cm); NOS/SQ-Number of seeds/siliqua; TSW-1000-seed weight (g); Y-Seed yield/plant (g); OC- Oil content (%)

Breeders can focus on selecting individuals with desirable traits to enhance yield and overall plant performance in future generations. The results of Sharma *et al.* (2022b) are in conformity for number of primary branches per plant and seed yield.

Low PCV and GCV recorded for days to maturity (2.23% and 1.95%, respectively), number of seeds per siliqua (5.87% and 4.08%, respectively), oil content (6.64% and 5.98%, respectively) and plant height (8.75% and 7.96%, respectively). This suggests that environmental factors may play a more significant role in influencing these traits, making it more challenging to achieve substantial genetic improvement through selection. Choudhary *et al.* (2023) also reported low values of GCV and PCV for days to maturity and plant height in his study.

Highest heritability (broadsense) was shown by number of secondary branches per plant (91.43%) followed by main shoot length (89.04%), days to 50% flowering (87.23%), number of primary branches per plant (86.45%), seed yield per plant (80.64%), plant height (80.54%), thousand seed weight (76.45%), days to maturity (68.45%) and number of siliqua on main shoot (61.86%). Patel *et al.* (2021) in Indian mustard also reported high broad-sense heritability for most of the yield contributing traits. This consistency across studies underscores the potential for targeted breeding strategies to enhance important agronomic traits in Indian mustard, ultimately contributing to improved productivity and sustainability in oilseed production. Moderate heritability was expressed by siliqua length (45.65%), oil content (51.23%) and number of seeds per siliqua (55.65%).

Genetic advance measures the extent of improvement in a trait under specific selection pressure. When high heritability estimates are combined with high genetic advance, the results are more reliable due to predominance of additive gene action and little influence of environment on the trait's expression which offers better opportunities for effective selection in early segregating generations, leading to significant improvements in the trait. Genetic advance as percent of mean indicated a good scope of improvement for thousand seed weight (36.54%), number of secondary branches per plant (35.54%), number of primary branches per plant (26.65%), siliqua length (26.24%), yield per plant (23.46%) and days to 50% flowering (21.05%). High heritability coupled with high genetic advance was depicted by days to 50% flowering, number of primary branches per plant, number of secondary branches per plant, seed yield per plant and thousand seed weight. The combination of high heritability and high genetic advance in Indian mustard highlights the crop's potential for improvement through selective breeding. This knowledge empowers breeders to develop new varieties that are not only higheryielding but also more resilient to environmental challenges, thereby contributing to sustainable agricultural practices and food security. Choudhary *et al.* (2023) also reported high heritability coupled with high genetic advance for number of primary branches, number of secondary branches and siliqua length in his study. The results are in agreement with previous studies reported by Singh *et al.* (2017).

CONCLUSIONS

The evaluated genotypes exhibited considerable variability across all traits, with the highest variability observed in thousand seed weight and the lowest in days to maturity. Notably, heritability estimates were high for almost all traits, indicating a strong genetic influence on their expression. Furthermore, the genetic advance was particularly significant for test weight, the number of secondary branches per plant, and seed yield per plant. The results indicate a favourable additive gene action for traits such as number of primary branches per plant, number of secondary branches per plant, seed yield per plant and 1000 seed weight as evidenced by the high heritability and significant genetic advance observed. This suggests that these traits are primarily influenced by genetic factors, making them reliable targets for selection in breeding programs. By prioritizing the selection of these high-performing traits, breeders can develop new mustard varieties that not only enhance yield but also improve the efficiency of resource use and adaptability to diverse environmental conditions. Such strategic breeding approaches will contribute significantly to the sustainability and productivity of mustard cultivation, ultimately benefiting farmers and the agricultural sector as a whole.

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Conflict of Interest. None.

REFERENCES

- Allard, R. W. (1960). Principals of Plant Breeding. John, Wiley and Sons, Inc. New York.
- Anonymous (2021). Directorate General of Commercial Intelligence and Statistics, Department of commerce.
- Burton, G. W., & Devane, E. H. (1953). Estimating heritability in tall fescue (*Festuca arundinacea*) from

replicated clonal material. *Agronomy Journal*, 45, 478-481.

- Choudhary, R. R., Singh, R. A. M., & Bishnoi, M. (2023). Genetic parameters and correlation studies in Indian mustard (*Brassica juncea* L.). *Journal of Oilseed Brassica*, 14(1), 68-72.
- GOI (2024).Third advance estimates of production of major agricultural crops for the year 2023-24. Ministry of agriculture, department of agriculture and farmer's welfare.

https://agriwelfare.gov.in/en/AgricultureEstimates.

- Gupta, N., Gupta, M., Akhatar, J., Goyal, A., Kaur, R., Sharma, S., Goyal, P., Mukta, A., Kaur, N., Mittal, M., Singh, M. P., Bharti, B., Sardhana, V. K. & Banga, S. S. (2021). Association genetics of the parameters related to nitrogen use efficiency in *Brassica juncea* (L.). *Plant Molecular Biology*, *105*(1), 161-175.
- IBEF (2022). Indian brand equity foundation, https://www.ibef.org/states/haryana.
- Johnson, H. W., Robinson, H. F. & Comstock, R. E. (1955). Estimates of Genetic and Environmental Variability in Soybeans. Agronomy Journal, 47(7), 314-318.
- Panse, V. G. & Sukhatme, P. V. (1967). Statistical methods for agricultural workers. ICAR, New Delhi.
- Patel, P. B., Patel, P. J., Patel, J. R. & Patel, P. C. (2021). Elucidation of genetic variability and interrelationship studies for seed yield and quality traits in Indian mustard [*Brassica juncea* (L.) Czern and Coss]. *Electronic Journal of Plant Breeding*, 12(2), 589-596.
- Sharma, H. K., Singh, V. V., Kumar, A., Meena, H. S., Meena, B. L., Sharma, P. & Rai, P. K. (2022b). Genetic study of terminal heat stress in indigenous collections of Indian mustard (*Brassica juncea L.*) germplasm. *Journal of Environmental Biology*, 43(1): 161-169.
- Shrivastava, A., Tripathi, M. K., Tiwari, S., Tripathi, N., Tiwari, P. N., Bimal, S. S., & Chauhan, S. (2023). Evaluation of genetic diversity in Indian mustard (*Brassica juncea* var. rugosa) employing SSR molecular markers. *Plant Cell Biotechnol Mol Biol*. 2023b, 24, 10-21.
- Singh, M., Avtar, R., Lakra, N., Hooda, E., Singh,V. K., Bishnoi, M., Kumari, N., Punia, R., Kumar, N. & Choudhary, R. R., (2021a). Genetic and Proteomic Basis of Sclerotinia Stem Rot Resistance in Indian Mustard [*Brassica juncea* (L.) Czern and Coss.]. *Genes*, 12(11), p.1784.
- Singh, V. K., Avtar, R., Kumari, N. & Kumar, R. (2021b). Assessment of genetic diversity and population structure in Indian mustard (*Brassica juncea* L.) using SSR markers. *Journal of Environmental Biology*, 42, 396-405.
- Singh, V., Bhajan, R. & Pant, U. (2017). Genetic analysis for yield under seedling and terminal heat stress in Indian mustard. *Electronic Journal of Plant Breeding*, 8(1), 1-9.
- Sowmya, D., Delvadiya, I. R., & Ginoya, A. V. (2024). Genetic variability, correlation, path coefficient and cluster analysis in Indian mustard (*Brassica juncea* L.). *Electronic Journal of Plant Breeding*, 15(1), 201-208.

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