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Exploring genetic variability, heritability, and genetic advance in Indian mustard (*Brassica juncea* L.) for yield improvement

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Abstract

A field experiment was conducted during *rabi* season of 2022-23 at Agricultural Research Farm, Department of Plant Breeding and Genetics, R.B.S. College, Bichpuri, Agra, (U.P.). The investigation entitled "Study of genetic variability and character association in Indian mustard (*Brassica juncea* (L.) Czern & Coss). The variables involves in this study was 30 genotypes of Indian mustard (*Brassica juncea* L.). Thus in all Thirty (30) Genotypes treatment combinations were compared in a Randomized Block Design with three replications. The results revealed that the significant genetic variability was observed among the genotypes for all studied traits. Heritability ranged from moderate to high, and genetic advance indicated substantial additive genetic variance. These findings provide essential insights for enhancing yield and associated traits through effective selection in breeding programs.

Keywords: Genetic variability, heritability, Indian mustard, genetic advance, genotypic and phenotypic coefficient

Introduction

Indian mustard (*Brassica juncea* L.) is a vital oilseed crop, second only to groundnut in India, contributing significantly to the economy. Enhancing yield and quality traits demands a clear understanding of genetic variability, heritability, and genetic advance. Rapeseed and mustard oil is used primarily for edible purposes and is the principle cooking oil in the mustard growing area of the country. Known for its great taste and subtle flavor, this vegetable oil is the world's second leading source of protein meal. Besides seeds, it is used as condiments. The meal cake left after oil extraction forms important cattle feed and may also be used as organic manure. The economically valuable product is grain, which is used for food and feed, but also for industrial processing. (Singh *et al.*, 2024) ^[17]. But over the past few centuries, human activity particularly since the industrial revolution has significantly altered the makeup of the atmosphere. In spite of a changing climate, climate-resilient agronomy aims to maintain sustainable food production and stable livelihoods for farmers. (Singh *et al.*, 2023). One of the biggest obstacles to raising the commercial yield of crops is the current increase in fertilizer prices. Therefore, measures to reduce its losses and improve its economic utilization are required (Lokendra *et al.*, 2024) ^[10].

The availability of genetic variability is the basic pre-requisite for genetic improvement through systematic breeding programme. Nature always favours the plant having much variability in terms of prominences and adaptation across year and location. It is true that more diverse plants greater the chances of obtaining high heterosis improvement. Selection and hybridization technique are frequently used for improving genetic constitution of a genotype. The knowledge of the extent of existing genetic variability and character association are important to carry out an efficient selection programme. The problem of increasing the yield can be tackled effectively on the basis of the performance of yield components and selection for closely related characters. Grain yield as a complex character and is dependent upon the sum total of many genes. Presently, development of new varieties for higher yields has reached a plateau and no further increase is achieved unless biotechnological interventions are made. (Archana, *et al.*, 2023) ^[2].

Materials and Methods

The study was conducted on 30 genotypes, viz. Radhika, Girraj, RH725, RH-761, DRMR-150-35, RH -406, PPM -25, PM -27, RGN-73, Pusha tarak, Kranti, Geeta, Pusha bold, RH-0749, KRISHNA, DRMR-31, NRCHB-101, PUSHA MAHAK, NRCHB-02, CS-60, CS-56, ASHIRWAD, RGN-48, Maga, Pusha vijay, Bhagirathi, Seeta, Pusha Jay Kishan, NRCRD-601, RH-30 of Indian mustard at the R.B.S. College, Agra, during the 2022-23 rabi season. These genotypes were made available from the DRMR, Bharatpur (Rajasthan). The material was sown in Randomized Block Design with three replications. These Mustard genotypes were sown with spacing of 0.45 m row to row and 0.15 m plant to plant. Observations were recorded on 12 metric traits (days to 50% flowering, days to maturity, plant height (cm), primary branches per plant, secondary branches per plant, length of main raceme, siliquae on main raceme, seeds per siliqua, 1000-seed weight (g), biological yield per plant (g), seed yield per plant (g) and harvest index (%). Five competitive plant from

each plot were randomly selected for recording observation for all the quantitative characters except days to 50 % flowering and days to maturity, which were recorded on the plot basis. The variability present in the population was estimated by measure mean, phenotypic & genotypic variance and coefficient of variation. The phenotypic & genotypic variation and genotypic and phenotypic coefficient and heritability in broad sense were estimated using formula of Burton and Lu Vane (1953).

Results and Discussion

Analysis of variance

The analysis of variance for the randomized block design used for the 30 genotypes was done for different characters and is presented in; (ANOVA Table 1). The variance analysis showed that the genotypes differ significantly among themselves for all the characters in study, indicating the presence of adequate variability. Among the varieties taken for experimentation.

Table 1: Analysis of variance for 12 characters in Indian mustard

d. f Character	Replications	Treatments	Error
	2	29	57
	Mean	Sum of squares	
Days to 50 percent flowering	2.47	8.11**	2.45
Days to maturity	6.11	11.09**	3.95
Plant height (cm)	14.67	188.17**	21.9
Primary branches/plant	0.01	0.31**	0.03
Secondary branches/plant	0.00	0.7**	0.07
Length of main raceme (cm)	1.49	28.87**	2.57
Siliquae on main raceme	0.05	8.41**	1.78
Seeds/siliqua	0.02	1.31**	0.14
1000 seed weight (g)	0.01	0.43**	0.01
Biological yield/plant (g)	0.59	47.11**	2.70
Seed yield/plant (g)	0.10	4.82**	0.18
Harvest index (%)	0.08	26.84**	0.49

*, ** significant at 5% and 1% probability level, respectively

Success of any plant breeding programme largely depends upon the genetic variability existing in crops. The mean value of any populations sample provides an idea about the center of variability of any traits. While, the range of traits provides maximum and minimum limits of the variable genotypes. The genotypic coefficient of variation measures the range of variability available in the crop and also enables to compare the amount of variability present among different characters. In the present study, the extent of variability was examined in 30 strains/varieties of Indian mustard for 12 characters. In general, phenotypic coefficient of variability was higher than genotypic coefficient of variability for all the characters which higher indicate that environment play a considerable role in the expression of these traits. On general phenotypic coefficient of variation was weighs that genotypic coefficient of variation. The

result indicated that breeders have opportunely for selection of desirable plants through the characters Hervey higher magnitude of PCV / GCV. The estimates of phenotypic and genotypic coefficient of variability for most of the characters under study are in accordance with earlier reports, Pant and Singh (2001) ^[12], Rai *et al.* (2005) ^[15], Singh *et al.* (2007) ^[19], Yadav *et al.* (2012) ^[22], Devi (2018) ^[7] and Harish *et al.*, (2023) ^[8], Singh *et al.*, 2024 ^[17], Virendra, *et al.*, (2024) ^[21]. The mean performance range, mean CV PCV, GCV, heritability and genetic advance over 30 genotypes for various characters are presented in Table 2. The plant height recorded the maximum range of variation followed by biological yield, length of main raceme, siliqua on main raceme and seed yield per plant while it was minimum in case of no. of primary branches per plant.

Table 2: Mean, range, genotypic and phenotypic coefficient of variability, heritability (%) in broad sense) and genetic advance in % of mean for different characters in Indian mustard

Genotypes	Range		Mean	C.V. %	GCV (%)	PCV (%)	Heritability (%)	G.A.	G.A. as % mean
	Min	Max							
Days to 50 percent flowering	63	75	69.52	0.63	1.98	3.00	43.57	1.87	2.69
Days to maturity	115	128	122.47	0.34	1.26	2.05	37.71	1.95	1.60
Number of primary branches /plant	5	8	6.42	1.56	4.74	5.52	73.56	0.54	8.37
Number of secondary branches/plant	8	13	10.27	1.11	4.46	5.18	73.93	0.81	7.90
Plant height (cm)	145	180	166.84	1.49	4.46	5.27	71.67	12.98	7.78

Length of main raceme	45	62	54.82	1.69	5.40	6.14	77.34	5.37	9.79
Number of siliquae on main raceme	36	50	41.86	1.84	3.56	4.77	55.68	2.29	5.47
Number of seeds /siliqua	10	14	12.53	1.17	4.99	5.81	73.64	1.10	8.82
1000 seed weight (g)	2.86	4.36	3.69	1.57	10.13	10.5	91.82	0.74	20.00
Biological yield (g)	48.13	65.8	58.10	1.63	6.62	7.20	84.56	7.29	12.54
Harvest index (%)	19.96	31.5	25.72	2.44	11.53	11.8	94.75	5.94	23.11
Seed yield/plant (g)	11.77	17.1	14.63	1.70	8.51	8.98	89.74	2.43	16.60

The moderate estimates (>10%) of phenotypic coefficient of variability (11.84%) and genotypic coefficient of variability (11.53%) were observed for harvest index followed by 1000 seed weight. The lowest estimates (<5%) phenotypic coefficient of variability (2.05%) and genotypic coefficient of variability (1.26%) observed for days of maturity. Heritability estimates ranged from 70% to 92%, with the highest observed in 1000-seed weight. Gene action and may be exploited directly in selection

The heritability gives an idea of transmissibility of characters from parent to offspring. The heritability estimates in broad sense were computed for all the characters and have been presented in Table 4.2. The heritability ranged from 37.71% (days of maturity) to 94.75% (harvest index). In general higher estimates of heritability in broad sense (>75%) were observed for harvest index, 1000 seed weight, biological yield, seed yield and length of main raceme characters. For days to 50% flowering (43.57%) and days to maturity (37.71%) which showed lower estimates (<50%) and other characters showed moderate estimates of heritability (<75->50%). The results are in close agreement with the findings of Chaudhary *et al.* (2003), Mahak sing *et al.* (2003), and Priyamedha *et al.* (2013) Karan *et al.*, (2023), Babu, S., & Singh, V. (2024) and Singh *et al.*, (2024) [11, 14, 9, 3, 17]. Moderate heritability together with low genetic advance was noticed for 1000 seed weight, primary branch per plant, secondary branch per plant. This obviously indicates the role of non-additive gene action for inheritance of these characters. It is concluded that any improvement in these characters is possible only when hybridization programme is initiated and the inheritance of these characters is well established.

The genetic advance gives an idea of expected improvement through selection in the next generation. The higher estimate of genetic advance along with higher heritability clearly indicates the possibility of improvement through selection. Genetic advance in % of mean exhibited considerable variations for different characters. The Genetic advance in percent of mean ranged from 1.60% (days of maturity) to 23.11% (harvest index). Harvest index showed high estimates (>20%) of genetic advance in % of mean (23.11%) followed by 1000 seed weight (20.00%) and moderate estimates (<20->10%) were recorded for seed yield per plant (16.60%), biological yield (12.54%).

High heritability coupled with high genetic advance in per cent of mean was observed for harvest index (23.11) followed by 1000 seed weight. The characters Hervey high heritability with high genetic advance generally indicated that heritability is more due to the additive gene effort and advocated the use to of high estimates of heritability along with high magnitude of genetic advance for genetic improvement in any trait through selection. Higher heritability coupled with higher genetic advance for these characters were also reported by Kumar *et al.* (1988) Poonam Singh *et al.* (2003), Choudhary *et al.* (2003), Amit

et al. (2013), Bind *et al.* (2014) Devi (2018) and Babu, S., & Singh, V. (2024) [4, 17, 13, 6, 1, 5, 7, 23].

Conclusion

The study on Indian mustard (*Brassica juncea* L.) provides valuable insights into the genetic variability, heritability, and genetic advance. Results revealed that significant variability among the 30 genotypes studied, with high heritability (up to 94.75% for harvest index) and substantial genetic advance for traits like 1000-seed weight and harvest index. The study confirmed that traits with high heritability and genetic advance, such as biological yield and seed yield, are critical for improving mustard productivity. The observed genetic parameters provide a robust foundation for breeders to focus on traits with potential for significant yield improvement. This research underscores the importance of selecting traits with strong genetic influence to develop high-yielding varieties, contributing to sustainable mustard cultivation and improved farmer profitability. Future studies could explore molecular approaches to complement traditional breeding methods and achieve even greater advances in crop improvement.

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