Genetic Variability Studies in Indian Mustard (*Brassica juncea L.*)

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Abstract: The study centered around Brassica juncea, commonly known as Indian Mustard, renowned for its edible leaves, seeds, and oil. Focusing on nineteen mustard genotypes, the research aimed to assess genetic diversity and trait connections. Conducted during the Rabi season 2022-23 at Sam Higginbottom University's Central Research Farm, Prayagraj, the experiment adhered to a Randomized Block Design with three replications. Data collection from five plants per genotype unveiled Pusa Bold and DRMR 150-35 as top performers in seed yield per plant compared to DRMR IJ-31, the check variety. Genotype analysis showcased significant variance across all traits. Mustard germplasm displayed considerable Genetic Coefficient of Variation (GCV) and Phenotypic Coefficient of Variation (PCV), notably in secondary branch count. Traits like siliquae number and seed yield boasted high heritability. Several traits exhibited moderate GCV, high heritability, and genetic advancement, especially siliquae number and seed yield.

Keywords: *Brassica juncea*, Heritability, Variability, PCV, GCV.

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1. Introduction

Indian mustard (*Brassica juncea* L.) commonly known as rai, raya or laha is important oil seed crop in India. It is second most important edible oilseed crop of India after groundnut. Mustard seed contains about 38 to 43 percent oil which is considered to be the healthiest and nutritious cooking medium (Patel *et al.*, 2012) as compared to other edible oils because it has lowest amount of harmful saturated fatty acids and adequate amount of linoleic and linolenic acid which are essential fatty acids (Porter and Crompton, 2008). India ranks third in terms of acreage (19.29%) after Canada (24.55%) and China (20.58%); however, it accounts for only 11.27% of total production next to China and Canada that contributes nearly 22.08% and 21.77% of total production respectively (www.drmr.org.in). Mustard is produced in around 6.82 million tons from area of 5.76 million hectare in 2015-16, with the productivity of 1,184 kg/ha (Anonymous, 2016). The major Rapeseed-mustard growing states in India are Rajasthan (43% area), Uttar Pradesh (14%), Madhya Pradesh (11%) and Haryana (8%).

The assessment of parameters including phenotypic and genotypic coefficients of variation, heritability in broad sense, and genetic advance as % of mean is a prerequisite for making effective selection (Manjunath *et al.*, 2017). An estimate of genetic advance along with heritability is helpful in assessing the reliability of character for selection (Meena *et al.*, 2017). The character showing high heritability along with low genetic advance can be improved by intermating superior genotypes of segregating population developed from combination breeding. The proper evaluation of important crop species helps in the identification and utilization of improved genotypes. The present investigation was planned to access heritability, association between traits and defines suitable selection criteria for mustard yield improvement. Availability of sufficient genetic variability is very important in crop improvement programme. Therefore, it is essential for a breeder to measure the variability with the help of parameters like phenotypic coefficient of variation, genotypic coefficient of variation, heritability and genetic advance. Hence these parameters give the information regarding the availability of genetic variability for different characters in available germplasm which provides a strong basis for selection of desirable genotypes.

2. materials and methods

The experiment was conducted during *Rabi* 2022-13 at Central Research Farm, Department of plant Breeding and Genetics, SHUATS, Prayagraj. Nineteen Indian mustard genotypes were sown under Randomized Block Design in three replications. The observations were recorded on five randomly selected plants for thirteen traits *viz.* days to 50% flowering, days to maturity, plant height (cm), number of primary branches / plants, number of secondary branches/plant, average siliqua length(cm), length of main raceme(cm), number of siliquae on main raceme, number of siliqua/plant, seeds/siliqua, 1000 seed weight (g), oil content (%), and seed yield/plant (gm). Test of significance for each character were analyzed as per methodology advocated by Panse and Sukhatme (1967). Genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were calculated by the formula given by Al-Jibouri *et al.*, (1958), heritability in broad sense (h2) by Burton and De Vane (1953) and genetic advance *i.e.* the expected genetic gain were calculated by using the procedure proposed by Johnson *et al*. (1955).

3. Result and discussion

ANOVA for randomized block design, carried out for thirteen traits revealed significant differences for genotypes (treatments) (table 1). It indicates the presence of sufficient genetic variation among the genotypes tested for all the morphological traits. Mean, range, estimates of GCV, PCV, heritability and genetic advance for seed yield and component traits of Indian mustard is presented in table 2. Mean for days to 50% flowering (ranging from 61.67 to 71.67 days), days for maturity (ranging from 126.67 to 142.33 days), plant height (ranging from 142.43 to 194.13 cm), primary branches per plant (ranging from 4.07 to 6.60), secondary branches per plant (ranging from 9.23 to 20.73), siliquae length (ranging from 4.92 to 6.43 cm), main raceme length (ranging from 50.60 to 70.33 cm), siliqua count on the main shoot (ranging from 35.33 to 55.43), seeds per siliqua (ranging from 10.50 to 14.57), siliquae per plant (ranging from 171.07 to 273.13), test weight (ranging from 3.33 to 4.43 g), oil content (ranging from 36.10 to 39.40%), and seed yield per plant (ranging from 12.20 to 25.20 g). These findings align with research conducted by Roy *et al.* (2011)

The GCV ranged from 2.19% (Days to maturity) to 20.47% (Number of secondary branches), while the PCV ranged from 3.31% (oil content) to 28.31% (Number of secondary branches). The attribute with both high GCV and PCV was the number of secondary branches. The number of siliquae per plant, siliquae on the main shoot, and the number of primary branches showed a moderate GCV and PCV in the mustard germplasm. Seed yield per plant exhibited moderate GCV and high PCV. In contrast, seeds per siliquae, main raceme length, and plant height demonstrated low GCV and moderate PCV. These attributes, in comparison to others, indicated substantial genetic variability, implying a promising potential for enhancing crops through hybridization and selection methods.

On the contrary, characteristics like days to 50% flowering, days to maturity, siliquae length, test weight, and oil content exhibited low GCV and PCV values. The heritability (broad sense) in the study ranged from 42.05% (days to maturity) to 77.04% (number of siliquae on the main shoot). High heritability was observed for the number of siliquae on the main shoot and seed yield per plant. Moderate heritability was noted for the number of secondary branches, followed by plant height, number of seeds per siliquae, siliquae length, number of siliquae per plant, test weight, oil content, number of primary branches, and days to 50% flowering. These characteristics are likely governed by additive gene actions and can be improved through individual plant selection due to their high heritability values. Similar findings were reported previous

sly by Yadava *et al.* (2011).

The genetic advance ranged from 0.34 (test weight) to 35.69 (number of siliquae per plant). A high genetic advance was observed only for the number of siliquae per plant. Moderate genetic advance was seen for plant height and the number of siliquae on the main shoot. The rest of the characters displayed low genetic advance values. High or moderate genetic advance values suggest additive gene action, whereas low genetic advance values indicate non-additive gene actions. Similar results were found in the studies of Akbari and Niranjana (2015) and Yadav and Pandey (2018)

Expressed as a percentage of the mean, genetic advance varied from 2.92% (days to maturity) to 31.52% (seed yield per plant). High genetic advance as a percentage of the mean was found for seed yield per plant, followed by the number of secondary branches and number of siliquae on the main shoot. Moderate genetic advance was noted for the number of siliquae per plant, followed by the number of primary branches, number of seeds per siliquae, plant height, main raceme length, test weight, siliquae length, days to 50% flowering, oil content, and days to maturity. The remaining attributes had low genetic advance as a percentage of the mean. These results are similar to findings of Chaurasiya *et al.* (2018) and Nishad *et al.* (2022).

Table 1: Mean sum of squares for different characters in Indian mustard germplasm

Sl. No.	**Source**	**Replication**	**Treatment**	**Error**
	Degrees of freedom	**n=2**	**n=18**	**n=36**
1	Days to 50% flowering	14.23	36.20**	10.69
2	Days to maturity	22.33	38.30*	12.06
3	Plant height	93.91	666.28*	163.73
4	Number of primary branches	0.68	1.35**	0.39
5	Number of secondary branches	2.36	27.47**	6.41
6	Siliquae length	0.20	0.46*	0.14
7	Main Raceme length	0.65	81.14**	25.31
8	Siliqua on Main Raceme	8.55	122.83**	11.10
9	Number of seeds per siliquae	0.37	4.56*	1.13
10	Number of siliquae per plant	1173.00	2584.40*	693.30
11	Test weight	0.07	0.24**	0.06
12	Oil content	0.49	3.00**	0.82
13	Seed yield per plant ‘H-[	4.42	49.51**	8.64

****, * Significant at 1% and 5% level of significance respectively**

Table 2: Genetic Parameters for 13 characters of 19 genotypes

Sr. No.	Characters	GCV (%)	PCV (%)	h^2 (%)	Genetic Advance	Genetic Advance as Percentage of Mean (%)
1	**Days to 50% flowering**	4.37	6.57	44.30	3.99	5.99
2	**Days to maturity**	2.19	3.37	42.05	3.95	2.92
3	**Plant height**	7.60	10.81	50.57	18.96	11.26
4	**Number of primary branches**	10.15	15.09	45.21	0.78	14.06
5	**Number of secondary branches**	20.47	28.31	52.27	3.95	30.49
6	**Siliquae length**	5.64	8.57	43.33	0.44	7.65
7	**Main Raceme length**	7.09	10.89	42.36	5.78	9.50
8	**Siliqua on Main Shoot**	14.53	16.55	77.04	11.03	26.26
9	**Number of seeds per siliquae**	8.31	11.78	50.15	1.55	12.17
10	**Number of siliquae per plant**	11.59	16.80	47.62	35.69	16.48
11	**Test weight**	6.52	8.96	47.14	0.34	8.70
12	**Oil content**	2.27	3.31	47.05	1.20	3.21
13	**Seed yield per plant**	19.56	25.00	61.20	5.95	31.52

5. Conclusion

The findings of the present study lead to the conclusion that among the 18 mustard genotypes examined, two specific genotypes, namely Pusa Bold and DRMR 150-35, exhibited the highest seed yield per plant when compared to the control variety DRMR IJ-31. It is also established that the analysis of variance underscored notable disparities among different genotypes across all assessed traits. Notably, the number of secondary branches displayed both high GCV and PCV. A moderate level of GCV and PCV was noted for the number of siliquae per plant, siliquae on the main shoot, and the number of primary branches within the mustard germplasm. In terms of genetic attributes, high heritability (broad sense) was observed for the number of siliquae on the main shoot and seed yield per plant. However, a combination of moderate GCV with high heritability, alongside substantial genetic advancement as a percentage of the mean, was found for traits like siliquae on the main shoot and seed yield per plant.

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