



ISSN (E): 2277-7695

ISSN (P): 2349-8242

NAAS Rating: 5.23

TPI 2022; 11(7): 557-560

© 2022 TPI

[www.thepharmajournal.com](http://www.thepharmajournal.com)

Received: 20-04-2022

Accepted: 25-06-2022

**Tarkeshwar**

Department of Genetics and Plant Breeding, Acharya Narendra Deva University of Agriculture and Technology, Kumarganj, Ayodhya, Uttar Pradesh, India

**Shiva Nath**

Department of Genetics and Plant Breeding, Acharya Narendra Deva University of Agriculture and Technology, Kumarganj, Ayodhya, Uttar Pradesh, India

**SC Vimal**

Department of Genetics and Plant Breeding, Acharya Narendra Deva University of Agriculture and Technology, Kumarganj, Ayodhya, Uttar Pradesh, India

**Ravi Prakash Chaudhary**

Department of Genetics and Plant Breeding, Acharya Narendra Deva University of Agriculture and Technology, Kumarganj, Ayodhya, Uttar Pradesh, India

**Govind Mishra**

Department of Genetics and Plant Breeding, Acharya Narendra Deva University of Agriculture and Technology, Kumarganj, Ayodhya, Uttar Pradesh, India

**Anand Mohan Chaudhary**

Department of Genetics and Plant Breeding, Acharya Narendra Deva University of Agriculture and Technology, Kumarganj, Ayodhya, Uttar Pradesh, India

**Vikash Kumar Singh**

Department of Vegetable Science, Acharya Narendra Deva University of Agriculture and Technology, Kumarganj, Ayodhya, Uttar Pradesh, India

**Corresponding Author:**

**Tarkeshwar**

Department of Genetics and Plant Breeding, Acharya Narendra Deva University of Agriculture and Technology, Kumarganj, Ayodhya, Uttar Pradesh, India

## Genetic variability for seed yield and its components in Indian mustard [*Brassica juncea* (L.) Czern and Coss.] Genotypes

**Tarkeshwar, Shiva Nath, SC Vimal, Ravi Prakash Chaudhary, Govind Mishra, Anand Mohan Chaudhary and Vikash Kumar Singh**

### Abstract

The present investigation was carried out at Students Instructional Farm of Acharya Narendra Deva University of Agriculture and Technology, Kumarganj, Ayodhya consisting of 60 Indian mustard genotypes including three checks sown in Augmented Block Design during *rabi* 2021-2022 to estimate the variability and heritability for various traits. All genotypes differed significantly among themselves for all 12 characters studied. The variance due to checks were highly significant for all the traits. The plant height (cm) (139.25-208.52) recorded the highest range of variation followed by days to maturity (121-141), while it was minimum in case of 1000 seed weight (g) (2.58-6.56). The highest estimates (>20%) of PCV and GCV were not recorded for any traits, whereas, moderate estimates (10-20%) of PCV and GCV was recorded for 1000-seeds weight (12.13 and 12.11 respectively). The heritability ranged from 27.54% (biological yield per plant) to 99.66% (1000-seeds weight). Generally higher estimates of heritability in broad sense (>75%) were recorded for 1000-seeds weight (99.66%) followed by plant height (cm) (98.44%). The Genetic advance in percent of mean ranged from 3.04% (3.04) to 24.91% (1000-seeds weight). Test weight (1000-seeds weight) showed high estimates (>20%) of genetic advance in percent of mean *i.e.*, 24.91.

**Keywords:** *Brassica*, variability, heritability, genetic advance, GCV, PCV

### Introduction

Indian mustard [*Brassica juncea* (L.) Czern and Coss.] belongs to the genus *Brassica* of the family *Brassicaceae* (former *Crucifereae*), is mainly a self-pollinating crop, although on an average 7.5-30% out-crossing occurs under open or natural field conditions (Abraham, 1994; Rakow and Woods, 1987) <sup>[1, 14]</sup>. Cytologically it is an amphidiploid (2n=36), derived from interspecific cross of *Brassica campestris* (2n=20) and *Brassica nigra* (2n=16) followed by natural chromosome doubling (Tomar *et al.*, 2017) <sup>[17]</sup>.

*Brassica* are economically of prime important genus comprising of oilseeds, vegetables and forage crops. Indian mustard is the second most important oilseed crop of the country next to groundnut, sharing 27.8% in the Indian oilseed economy. *Brassica napus*, *B. campestris* and *B. juncea* are the three chief species of mustard which produce edible oil. The major mustard producing regions are China, Indian subcontinent, Canada and Northern Europe (Ram and Hari, 1998) <sup>[15]</sup>. According to an estimate, the area, production and yield of rapeseed-mustard in the world was 36.59 million hectares (mha), 72.37 million tonnes (mt) and 1980 kg/ha, respectively, during 2018-19. The area under rapeseed-mustard increased from 5.98 mha (2017-18) to 6.12 mha (2018-19), production increased from 8.43 mt (2017-18) to 9.26 mt (2018-19), and productivity got increased from 1840 kg/ha in 2010-11 to 1980 kg/ha in 2018-19 in India (DRMR, annual report 2019-20) <sup>[3]</sup>. However, the production and productivity of Indian mustard is still low as compared to current demand of edible oils of the country (Jat *et al.*, 2019) <sup>[9]</sup>. Therefore, productivity of Indian mustard must be boost up in order to fulfil the increasing demand of edible oils in country.

Genetic parameters aid in the recognition of gene action which helps the breeder in selecting a suitable breeding approach which can suit to the experimental material. Generally, the heritability and environmental factors are influenced by the genotypic and phenotypic variances (Bisne *et al.*, 2009) <sup>[5]</sup>. Selection is effective only when there is an enough extent of variability found in the breeding population.

A precise understanding of variability present in a population is important in regard to opt out the most appropriate breeding method for improvement of various traits. The development of an intensive breeding and improvement program needs detailed biological information and an understanding of genetic variation for yield and its components.

Keeping the above facts in view, the present investigation was carried out to estimate the genetic variability present in the germplasm in order to plan a reliable breeding programme.

### Materials and Methods

The present investigation was carried out at Students Instructional Farm of Acharya Narendra Deva University of Agriculture and Technology, Kumarganj, Ayodhya consisting of 60 Indian mustard genotypes including three checks taken from the Department of Genetics and Plant Breeding. Geographically, this place is located at an altitude of 113 meters above from mean sea level in between 26.47°N latitude, 82.12°E longitude. This area falls in sub-tropical zone (Indo-gangatic plain) and the soil texture is characterized by silty loam in nature having 0.40% organic carbon 2.21dSm<sup>-1</sup> EC, and 45 ESP, 9.2 pH. The climate of district Ayodhya is semi-arid with hot summer and cold winter. The genotypes along with checks were sown in Augmented Block Design during *rabi* 2021-2022 to estimate the variability and heritability for various traits. Each genotype was planted in two rows of 5m long and 45cm apart; plant to plant distance was maintained 15cm by thinning. All the recommended cultural practices were followed to raise a healthy crop.

Five plants in each genotype were taken randomly for each treatment in each replication and tagged for recording observations for twelve metric characters *viz.*, days to 50% flowering, days to maturity, plant height (cm), number of primary branches per plant, number of secondary branches per plant, length of main raceme (cm), number of siliquae on main raceme, number of seeds per silique, biological yield per plant (g), harvest index (%), 1000-seed weight (g) and seed yield per plant (g).

The mean value of selected plants was undertaken to do statistical analyses as genetic variability, heritability and genetic advance as suggested by Panse and Shukhatme (1967)<sup>[13]</sup>, Hanson (1963)<sup>[18]</sup> and Johnson *et al.* (1955)<sup>[10]</sup> respectively.

### Results and Discussion

#### Analysis of variance

The analysis of variance (ANOVA) for the augmented block design used for sixty genotypes involving three checks was done for all 12 characters and presented in (Table 1). The variance analysis indicated that the presence of adequate variability. All genotypes differed significantly among themselves for all 12 characters studied. The variance due to checks were highly significant for all the traits.

#### Range, mean, coefficient of variability, heritability (broad sense) and genetic advance

The mean, range, phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability in broad sense ( $h^2b$ ) and genetic advance (GA) of sixty genotypes for

different characters have been shown in Table 2.

The plant height (cm) (139.25-208.52) recorded the highest range of variation followed by days to maturity (121-141), biological yield per plant (g) (41.55-68.55), number of siliquae on main shoot (35.95-75.12), harvest index (23.93-40.73) and days to 50% flowering (48-69) while it was minimum in case of 1000 seed weight (g) (2.58-6.56), number of primary branches per plant (4.63-8.85), number of seeds per silique (11.13-18.85), and number of secondary branches per plant (10.44-24.10).

The phenotypic and genotypic coefficient of variability (PCV and GCV) for all the twelve characters is given in Table 2. Usually phenotypic coefficient of variability (PCV) was more than genotypic coefficient of variability (GCV) for all the twelve metric characters. The highest estimates (>20%) of PCV and GCV were not recorded for any traits, whereas, moderate estimates (10-20%) of PCV and GCV was recorded for 1000-seeds weight (12.13 and 12.11 respectively). The lowest estimates (<10%) of PCV and GCV were recorded for rest of the traits. A similar pattern of results was also noted by the earlier worker Verma (2021)<sup>[18]</sup>.

The heritability gives an idea to estimate the heritability of characters from parents to their offspring (upcoming generations). The heritability estimates in broad sense were calculated for all 12 characters and have been illustrated in Table 2. The heritability ranged from 27.54% (biological yield per plant) to 99.66% (1000-seeds weight). Generally higher estimates of heritability in broad sense (>75%) were recorded for 1000-seeds weight (99.66%) followed by plant height (cm) (98.44%), number of seed per silique (96.20%), number of siliquae on main raceme (86.07), days to 50% flowering (78.28%), number of secondary branches per plant (75.50%), harvesting index (%) (76.95%) and seed yield per plant (76.40%). Number of primary branches and days to maturity had moderate estimates (50-75%) heritability in broad sense *i.e.*, 58.42% and 71.30% respectively. Comparatively low estimate of heritability (<50%) observed for biological yield per plant (27.54%) and length of main raceme (47.50%). These results are more similar to Devi (2018), Akabari and Niranjana (2015)<sup>[2]</sup> and Mishra *et al.* (2022)<sup>[12]</sup>.

The genetic advance (GA) gives a thought of expected advancement through selection in the next generation. The higher estimate of GA coupled with higher heritability without a doubt indicates the possibility of improvement through selection. Genetic advance (GA) in % of mean shows significant variations for different traits. The GA in percent of mean ranged from 3.04% (3.04) to 24.91% (1000-seeds weight). Test weight (1000-seeds weight) showed high estimates (>20%) of genetic advance in percent of mean *i.e.*, 24.91; and moderate estimates (10-20%) were noted in primary branches (13.20), secondary branches per plant (13.66), number of siliquae on main raceme (15.70), number of seed per silique (14.29) and harvest index (11.61) while, rest traits showed low estimates of genetic advance. These findings are in close agreement with the finding of Mahala *et al.* (2003)<sup>[11]</sup>, Bind *et al.* (2014)<sup>[4]</sup>, Rout *et al.* (2019)<sup>[16]</sup> and Gadi *et al.* (2020)<sup>[7]</sup>.

**Table 1:** ANOVA for Augmented Block Design for 12 traits in Indian mustard

Source of variation	Blocks	Checks	Error
DF	2	2	4
Days to 50% flowering	16.03	16.00**	1.24
Days to maturity	42.49	49.00**	2.14
Plant height (cm)	52.27	20.83**	0.98
Number of primary branches per plant	0.67	0.57**	0.24
Number of secondary branches per plant	10.61	18.90**	0.64
Length of main raceme (cm)	16.33	62.50**	18.08
Number of siliquae on main raceme	66.24	102.17**	3.12
Number of seeds per siliqua	2.04	0.82**	0.05
1000-seed weight (g)	1.21	0.35**	0
Biological yield per plant (g)	79.03	108.37**	15.63
Harvest index (%)	24.05	15.17**	1.17
Seed yield per plant	1.01	1.21**	0.11

\*,\*\*Significant at 5% and 1% level of probability

**Table 2:** Estimates of range, mean, coefficient of variability, heritability (broad sense) and genetic advance in percent of mean

Characters	Range			Variance			GA	GA% mean	GCV (%)	PCV (%)	ECV (%)
	Mean	Min	Max	Var (g)	Var (p)	h <sup>2</sup> bs (%)					
Days to 50% flowering	55.83	48.00	69.00	4.48	5.72	78.28	3.86	6.91	3.79	4.28	2.00
Days to maturity	131.70	121.00	141.00	5.30	7.44	71.30	4.01	3.04	1.75	2.07	1.11
Plant height (cm)	179.52	139.25	208.52	61.72	62.70	98.44	16.06	8.94	4.38	4.41	0.55
Number of primary branches per plant	6.94	4.63	8.85	0.34	0.58	58.42	0.92	13.20	8.38	10.97	7.07
Number of secondary branches per plant	18.34	10.44	24.10	1.96	2.60	75.50	2.51	13.66	7.63	8.79	4.35
Length of main raceme (cm)	70.06	50.99	89.73	16.36	34.43	47.50	5.74	8.20	5.77	8.38	6.07
Number of siliquae on main raceme	53.47	35.95	75.12	19.30	22.42	86.07	8.40	15.70	8.22	8.86	3.31
Number of seeds per siliqua	15.35	11.13	18.85	1.18	1.23	96.20	2.19	14.29	7.07	7.21	1.40
1000-seed weight (g)	4.53	2.58	6.56	0.30	0.30	99.66	1.13	24.91	12.11	12.13	0.71
Biological yield per plant (g)	56.71	41.55	68.55	5.94	21.57	27.54	2.64	4.65	4.30	8.19	6.97
Harvest index (%)	30.75	23.93	40.73	3.90	5.07	76.95	3.57	11.61	6.43	7.32	3.52
Seed yield per plant	17.15	14.56	19.74	0.35	0.46	76.40	1.07	6.22	3.46	3.95	1.92

## Conclusion

High heritability accompanied with high genetic advance for any trait gives an ample scope of selection to improvement of that trait. Hence, 1000-seeds weight followed by plant height (cm), number of seed per siliqua, number of siliquae on main raceme were the traits which fulfil criteria of selection for the improvement in these traits as well as seed yield.

## References

1. Abraham V. Rate of out-crossing in Indian mustard, *Brassica juncea*. *Cruciferae Newsl.* 1994;16:69-70.
2. Akabari VR, Niranjana M. Genetic variability and traits association studies in Indian mustard (*Brassica juncea* L. Czern & Coss). *International J Agri. Sci.* 2015;11(1):35-39.
3. Anonymous. ICAR-DRMR, annual report, 2019-20.
4. Bind D, Singh D, Dwivedi VK. Genetic variability and character association in Indian mustard [*Brassica juncea* (L.) Czern & Coss]. *Agric. Sci. Digest.* 2014;34(3):183-188.
5. Bisne R, Sarawgi AK, Verulkar SB. Study of heritability, genetic advance and variability for yield contributing characters in rice. *Bangladesh Journal of Agricultural Research.* 2009;34(2):175-179.
6. Devi B. Correlation and path analysis in Indian mustard (*Brassica juncea* L.). In agro-climatic conditions of Jhansi (U.P.). *Electronic J of Plant Breeding.*, 2017;1(4):407-413.
7. Gadi J, Chakraborty NR, Imam Z. To study the genetic variability, heritability and genetic advance for different quantitative characters in Indian Mustard (*Brassica juncea* L. Czern & Coss). *Int. J Curr. Microbiol. App. Sci.* 2020;9(10):1557-1563.
8. Hanson WD. Heritability. *Statistical genetics and plant breeding NAS\_NRC, Washington, Publ., 1963, 1982, 125-140.*
9. Jat RS, Singh VV, Sharma P, Rai PK. Oilseed brassica in India: Demand, supply, policy perspective and future potential, OCL. 2019;26:8.
10. Johnson HW, Robinson HF, Comstock RE. Estimates of genetic and environmental variability in soybean. *Agron. J.* 1955;47:314-318.
11. Mahala HR, Jambhulkar SJ, Yadav DK, Sharma R. Genetic variability and path analysis in Indian mustard [*Brassica juncea* (L.) Czern & Coss]. *Indian J Genet.* 2003;63(2):171-172.
12. Mishra G, Nath S Tarkeshwar. Analysis of genetic variability, heritability and genetic advance for seed yield and its contributing traits in Indian mustard [*Brassica juncea* (L.) Czern and Coss.] Under timely and late sown conditions. *The Pharma Innovation Journal.* 2022;11(6):1354-1357.
13. Panse VG, Sukhatme PV. *Statistical methods for agricultural workers, II Edn, 1967, 152-157.*
14. Rakow G, Woods DL. Outcrossing in rape and mustard under Saskatchewan prairies conditions. *Canadian J Plant Sci.* 1987;67:147-151.
15. Ram HH, Hari GS. *Crop Breeding and Genetics.* Kalyani Publishers, New Delhi-110002, 1998, 381p.
16. Rout S, Kerkhi SA, Gupta Archi. Estimation of genetic variability, heritability and genetic advance in relation to seed yield and its attributing traits in Indian mustard

- [*Brassica juncea* (L.) Czern and Coss.]. Journal of Pharmacognosy and Phytochemistry. 2019;8(3):4119-4123.
17. Tomar A, Singh M, Singh SK. Genetic analysis of yield and its components based on heterotic response and combining ability parameters in Indian mustard (*B. juncea*) Prog. Agric. 2017;15:85-91.
  18. Verma AK. Studies on genetic variability, path analysis and genetic divergence for quantitative traits in Indian mustard [*Brassica juncea* L. Czern & Coss]. Thesis, M.Sc. ANDUAT, Ayodhya, 2021, 27p.