Estimation of Genetic Variability, Heritability and Genetic Advance in Indian Mustard [*Brassica juncea* (L.) Czern & Coss]

Abstract

Twenty seven genotypes of Indian mustard [*Brassica juncea* (L.) Czern & Coss] were evaluated for genetic variability, heritability and genetic advance for nine yield and yield attributing characters. The experiment was carried out during *Rabi* 2022 in Randomized Block Design (RBD) at Agricultural Research Station, Ummedganj-Kota, Rajasthan. ANOVA of nine quantitative characters revealed significant differences at 1% level of significance. Mean values of seed yield showed that NPJ 261 had highest seed yield (kg/ha) followed by RH 2199 and RB-110. Also, they were at par with each other. High genotypic and phenotypic coefficient of variation was found in number of secondary branches per plant. Phenotypic variance had higher values than genotypic variance indicating the influence of environment. High heritability estimates coupled with high GAM were reported for number of secondary branches per plant, number of siliquae per plant and 1000-seed weight. These characters are highly heritable as they are governed by additive gene action. Selection for these characters will be effective in future breeding programme. Hence, breeders should emphasize on these character in Indian mustard genotypes for higher yield or productivity.

Keywords: Genetic Variability, Heritability, Genetic Advance, Indian mustard [*Brassica juncea* (L.) Czern & Coss]

Introduction

Indian mustard [*Brassica juncea* (L.) Czern & Coss] is one of the most important oilseed crops of India which occupies considerably large area among the Brassica group of oilseed crops. Even after high productivity of Indian mustard, there is a wide fluctuation in area, production and productivity of this crop (Yadava *et al.,* 2011). This may be due to the cultivation of crop either in rainfed or with limited irrigation facilities, as well as due to climate change. The variability of a trait describes how much that trait tends to vary in response to environmental and genetic influences. Genetic variability for yield and yield attributing traits are the key components of breeding programmed for broadening the gene pool. The genetic variability in any breeding material is a prerequisite as it provides not only a basic for selection but also provide valuable information regarding selection of diverse parents for use in hybridization programme. For various targeted qualities in Indian mustard, heritability and genetic advance estimations assist the breeder in using proper breeding methodology in the crop improvement programme (Patel *et al.,* 2021). Though, primary goal of every crop enhancement effort is to increase production. As, yield is a complicated feature it is influenced by a number of different supplementary traits. Therefore, the present investigation was carried out to estimate genetic variability, heritability and genetic advance as per cent of mean in Indian mustard.

Materials and Methods

The study was conducted on 27 genotypes (including checks) of Indian mustard [*Brassica juncea* (L.) Czern & Coss], which were grown in Randomized Block Design (RBD) with 3 replications during *Rabi*, 2022 at the Agricultural Research Station, Ummedganj-Kota (Agriculture University, Kota), Rajasthan.

The observations were recorded for the nine seed yield contributing 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, 1000-seeds weight (g), oil content (%) and seed yield (kg/ha). Statistical measure, *i.e.*, mean, standard error of mean, range, coefficient of variation, heritability, and genetic advance for each quantitative characters were computed for the study of phenotypic and genotypic variability through Rstudio 4.2.3 (R Core Team, 2021).

Results and Discussion

Analysis of Variance and Mean

Analysis of variance for the nine quantitative traits has been presented in Table 1, which revealed that the genotypes exhibited highly significant differences among all the traits under study. Hence, there is an ample scope for the selection of promising lines from the present gene pool for yield and its components (Bishnoi *et al.*, 2021). Mean for twenty-seven genotypes has been illustrated in table 3, which depicted that NPJ 261 had highest seed yield (3,143 kg/ha) followed by RH 2199 (3,104 kg/ha), RB-110 (3,036 kg/ha), DRMR 2020-8 (3,025 kg/ha) and PBR 813-2 (3,001 kg/ha). The critical distance for twenty seven varieties for seed yield (kg/ha) character was found to be significantly higher than check varieties which indicated that top five genotypes were at par with each other. Table 3, suggested that all the genotypes under study showed high grain yield and quantitative parameters can be of immense use in the future breeding program.

Coefficient of variation

Table 2 represented the genetic parameters for all the nine characters under study. Phenotypic variances were found to be higher than genotypic variances indicating the influence of environment on the expression of characters in Indian mustard. Genotypic coefficient of variation was found to be high for number of secondary branches per plant (29.03). Moderate genotypic coefficient of variation was reported for number of siliquae per plant (13.78), number of primary branches per plant (11.26) and 1000-seed weight (10.94). Rest of the characters exhibited low genotypic coefficient of variation. Similar, trend was also reported for phenotypic coefficient of variation. However, seed yield reported moderate phenotypic coefficient of variation (11.85) among the genotypes of Indian mustard. High to moderate genotypic and phenotypic coefficient of variation indicate that the selection of these characters may be reported to be effective. Yadava *et al.* (2011), Lakra *et al.* (2020) and Kaur *et al.* (2022) also observed high PCV and GCV for seed yield and number of secondary branches per plant. These characters have been reported as main yield contributing traits. Results revealed presence of high amount of genetic variability in the evaluated genotypes for the major yield contributing characters along with seed yield which indicated that further improvement for these traits is possible. According to Ray *et al.* (2019), these results indicate that the breeders have opportunity for selection of desirable plants through the attributes had higher magnitudes of PCV/GCV.

Heritability, Genetic advance and Genetic Advance as percentage of mean (GAM)

The heritability in broad sense or the degree of genetic determination is the ratio genotypic and phenotypic variance, expresses the extent to which individual phenotypes are determined by their genotype (Falconer, 1985). From table 2, it was estimated that heritability (in broad sense) was high for most of the characters *viz*., days to 50% flowering (91.99 %), followed by oil content (90.76 %), days to maturity (87.06 %), 1000-seed weight (83.88 %), number of secondary branches per plant (72.95 %), number of siliquae per plant (70.42 %) and number of primary branches per plant (60.40 %), except for traits *viz.*, plant height (46.98 %) and seed yield (47.84 %), which reported moderate heritability. The fundamental requirement of selection is the heritable variation of genotypes. The characters which are more heritable and yield contributing can ameliorate the yield potential by their few cyclic selection (Ray *et al.*, 2019). Similar findings were also reported by Kaur *et al.* (2022), Kumar *et al.* (2019) and Rout *et al.* (2018).

The expected genetic advance is a prediction of breeders that is up to which extant, a character can be improved in coming generation after 9-10% of better heritable individual selection (Ray *et al.*, 2019). The perusal of genetic advance represented highest values for number of siliquae per plant (46.61) followed by, seed yield (17.95), plant height (15.55), days to 50% flowering (5.17), days to maturity (5.14), number of secondary branches per plant (4.23), oil content (1.90), 1000-seed weight (1.09) and number of primary branches per plant (0.99). Highest genetic advance for number of siliquae per plant was also reported by Patil *et al.*, in 2018. High GAM was exhibited by number of secondary branches per plant (51.07), number of siliquae per plant (23.82) and 1000-seed weight (20.64). Number of primary branches per plant (18.03), seed yield (11.68) and days to 50% flowering (10.70) showed moderate GAM. Rest of the characters reported low GAM.

Heritability estimates together with genetic advance are generally regarded to be more useful in predicting the grain through selection. High heritability coupled with high GAM was reported in number of secondary branches per plant, number of siliquae per plant and 1000-seed weight. These characters are highly heritable as they are governed by additive gene action. Moderate heritability coupled with moderate GAM was shown by seed yield and moderate heritability and low GAM was expressed by plant height. This indicated that these characters are regulated by non-additive gene/s. Similar findings were also observed by Kaur *et al.* (2022), Awasthi *et al.* (2020), Ray *et al.* (2019) and Yadava *et al.* (2011).

Conclusion

Analysis of variance reveled that all the nine quantitative characters of twenty seven genotypes of Indian mustard were significantly different. NPJ 261 had highest seed yield (kg/ha) followed by RH 2199 and RB-110. Also, they were at par with each other. High genotypic and phenotypic coefficient of variation was found in number of secondary branches per plant. Phenotypic variance had higher values than genotypic variance indicating the influence of environment. High heritability coupled with high GAM was reported in number of secondary branches per plant, number of siliquae per plant and 1000-seed weight. These characters are highly heritable as they are governed by additive gene action. Selection for these characters will be effective in future breeding programme. Hence, breeders should emphasize on these character in Indian mustard genotypes for higher yield or productivity.

References

Awasthi, D., Tiwari, V.K. and Kandalkar, V.S. (2020) Evaluation of heritability and genetic advance for morphological traits of Indian mustard germplasms. *Current Journal of Applied Science and Technology*, 39: 39-47.

Bishnoi, R., Marker, S., Kumar, K.V.Y. and Taranum, S.A. (2021) Genetic Variability Parameters for Quantitative Traits in Farmers' Pea (*Pisum sativum* var. *arvense* L.) Varieties. *Biological Forum – An International Journal*, 13(4): 320-325.

Falconer, D.S. (1985) Introduction to quantitative genetics. ELBS Second Ed. Longman Group Ltd., London, P., 113:281-290.

Kaur, S., Kumar, R., Singh, V. and Gupta, S. (2022) Genetic variability analysis in different F_1 combinations in Indian mustard (*Brassica juncea* L). *Journal of Oilseed Brassica*, 13 (1): 59-63.

Kumar, R., Kaur, S., Bala, K., Kaur, S. and Sharma, L. (2019) Assessment of genetic variability, correlation and path analysis for yield traits in F1 hybrids of Indian mustard [*B. juncea* (L) Czern & Coss.]. *Agriways* 7: 1-7.

Lakra, A., Tantuway, G., Tirkey, A.E. and Srivastava, K. (2020) Genetic variability and trait association studies in Indian mustard (*B. juncea* (L.) Czern & Coss). *International Journal of Current Microbiology and Applied Sciences*, 9: 2556-2563.

Patel, P.B., Patel, P.J., Patel, J.R. and Patel, P.C. (2021) Elucidation of genetic variability and inter-relationship studies for seed yield and quality traits in Indian mustard [*B. juncea* (L.) Czern & Coss]. *Electronic Journal of Plant Breeding*, 12: 589 – 596.

Patil, S., Kalamkar, V., Deotale, R.D., Kamdi, S.R., Kuchanwar, O. and Chopde, N. (2018) Genetic analysis of siliqua per plant and seed yield per plant in mustard (*B. juncea*). *International Journal of Current Microbiology and Applied Sciences*, 6: 1355-1360.

R Core Team. (2021) R: A language and environment for statistical computing. R Foundation for Statistical Computing, Vienna, Austria. URL https://www.R-project.org/.

Ray, J., Singh, O.P., Pathak, V.N. and Verma, S.P. (2019) Assessment of genetic variability, heritability, genetic advance and selection indices for yield contributing traits in Indian mustard [*Brassica juncea*]. *International Journal of Chemical Studies,* 7(4): 1096-1099.

Rout, S., Kerkhi, S.A. and Chauhan, C. (2018) Character association and path analysis among yield components in Indian mustard [*B. juncea* (L) Czern & Coss.]. *International Journal of Current Microbiology and Applied Sciences*, 7: 50-55.

Yadava, D.K., Giri, S.C., Vignesh, M., Vasudev, S., Yadav, A.K., Dass, B., Singh, R., Singh, N., Mohapatra, T. and Prabhu, K.V. (2011) Genetic variability and trait association studies in Indian mustard (*Brassica juncea*). *Indian Journal of Agricultural Sciences*, 81(8): 712-716.

Table 1. Analysis of variance for nine yield and yield attributing characters of Indian mustard genotypes during *Rabi,* 2022-23

Characters	Mean sum of square		
	Replications (df=2)	Treatments (df=26)	Error (df=52)
DF50	1.494	21.141**	0.596
DM	2.383	22.502**	1.062
PH	39.120	500.730**	136.870
NPBPP	0.764	1.392**	0.250
NSBPP	5.649	19.487**	2.143
NSP	392.960	2486.260**	305.320
1000 SW	0.142	1.061**	0.064
OC	0.574	2.920**	0.096
SY	8568.000	58877.000**	15693.000

**** 1% level of significance**

DF50: Days to 50% flowering, DM: Days to maturity, PH: Plant height (cm), NPBPP: Number of primary branches per plant, NSBPP: Number of secondary branches per plant, NSP: Number of siliquae per plant, 1000 SW: 1000-seeds weight (g), OC: Oil content (%), SY: Seed yield (kg/ha)

Table 2. Genetic parameters for nine quantitative characters in Indian mustard genotypes during *Rabi,* 2022-23.

	GV	PV	ECV	GCV	PCV	h^2 (bs)	GA	GAM
DF50	6.85	7.44	1.60	5.42	5.65	91.99	5.17	10.70
DM	7.15	8.21	0.78	2.03	2.17	87.06	5.14	3.90
PH	121.29	258.16	6.57	6.19	9.02	46.98	15.55	8.73
NPBPP	0.38	0.63	9.12	11.26	14.49	60.40	0.99	18.03
NSBPP	5.78	7.92	17.67	29.03	33.98	72.95	4.23	51.07
NSP	726.98	1032.30	8.93	13.78	16.42	70.42	46.61	23.82
1000 SW	0.33	0.40	4.80	10.94	11.94	83.88	1.09	20.64
OC	0.94	1.04	0.75	2.36	2.48	90.76	1.90	4.63

SY	14394.50	30087.83	8.56	8.20	11.85	47.84	170.95	11.68

GV: Genotypic Variance, PV: Phenotypic Variance, ECV: Environmental Coefficient of Variance, GCV: Genotypic Coefficient of Variance, PCV: Phenotypic Coefficient of Variance, GA: Genetic Advance, GAM: Genetic Advance as percentage of mean.

Table 3. Mean performance of twenty-seven genotypes for yield attributing characters in Indian mustard during *Rabi*, 2022-23.

S.No.	Genotypes	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/ plant	1000 seed weight (g)	Oil content (%)	Seed yield (kg/ha)
1	RMM-19-12	46.3	133.0	178.5	5.9	8.8	210.2	4.89	40.1	2,210
2	DRMRHT 18-141	42.7	124.7	175.5	5.4	11.2	229.5	4.40	41.8	2,384
3	Kranti (Check)	43.0	124.7	150.0	5.0	9.0	193.6	4.56	41.8	2,806
4	PR-2019-1	47.0	132.0	166.0	6.0	7.1	165.7	5.63	40.1	2,504
5	KMR 22-4	49.0	133.0	173.5	4.9	4.0	228.9	5.05	40.4	2,909
6	RH 2187	47.0	131.3	180.0	6.8	8.4	182.5	5.31	40.6	2,798
7	DRMRIJ 21-37	47.0	128.7	180.0	5.2	8.0	206.3	5.42	42.2	2,727
8	DRMRCI- 154	47.7	131.3	140.0	4.3	4.8	178.9	5.64	42.0	2,606
9	ACNMM- 3	49.3	131.3	181.5	5.7	8.3	198.0	4.53	42.4	2,723
10	RGN 528	52.7	136.7	195.0	5.3	8.9	177.3	6.07	40.5	2,878
11	Maya (Check)	48.3	130.7	176.5	6.0	10.8	215.1	5.39	41.8	2,176
12	NPJ 262	52.3	134.0	190.0	5.3	6.1	177.3	5.85	39.3	2,733
13	DRMR 2020-8	44.3	129.3	175.0	5.1	7.9	195.3	5.96	41.6	3,025
14	HUJM-21-4	48.0	132.7	168.5	6.3	11.3	169.7	5.02	41.6	2,754
15	DM 2020-3	50.0	134.0	191.0	5.8	10.4	221.4	5.90	41.7	2,644
16	RAURD 18-1	48.3	131.3	175.0	4.0	2.7	142.8	5.89	41.6	2,551
17	RGN 73	52.7	135.7	202.0	4.7	6.1	150.9	4.81	39.8	2,517
18	NPJ 261	48.0	133.3	178.5	5.7	8.1	217.9	5.47	42.1	3,143
19	RH 2199	47.0	130.0	173.5	6.3	9.7	245.1	5.85	41.7	3,104
20	PR-2020-14	48.7	130.7	185.0	5.1	4.4	164.0	5.73	39.9	2,656
21	SKM 1924	46.0	132.0	167.5	4.7	7.5	160.7	5.76	41.5	2,844
22	KMR 22-3	51.0	134.7	192.0	5.9	11.5	235.7	4.56	41.3	2,733
23	SKM 2012	52.0	133.7	180.0	5.4	9.4	188.1	4.52	41.7	2,759
24	TM316	46.7	131.3	179.0	5.2	7.3	165.1	4.29	38.6	2,738
25	DTM- 341	50.7	133.3	181.0	6.9	13.7	199.1	4.71	41.0	2,217
26	PBR 813-2	49.3	131.0	193.5	5.6	7.5	234.6	4.82	42.1	3,001
27	RB- 110	49.7	133.0	179.5	5.5	10.8	229.6	6.27	40.9	3,036
	Mean	**48.32**	**131.75**	**178.06**	**5.48**	**8.28**	**195.68**	**5.27**	**41.11**	**2710.21**
	CD (@ 5%)	**1.27**	**1.69**	**19.17**	**0.82**	**2.4**	**28.63**	**0.41**	**0.51**	**205.25**
	CV	**1.60**	**0.78**	**6.57**	**9.12**	**17.67**	**8.93**	**4.80**	**0.75**	**6.70**