J. Soils and Crops 34(1) 111-115, June 2024

ISSN 0971-2836 (Print)
ISSN 2582-2756 (Online)

GENETIC VARIABILITY STUDY IN INDIAN MUSTARD (*Brassica* species) FOR YIELD AND YIELD CONTRIBUTING TRAITS

P. S. Kalpande[1], M. P. Meshram[2], S. R. Kamdi[3], Snehal V. Pawar[4], M. N. Dhawne[5] and Anjali D. Sable[6]

ABSTRACT

The 23 Indian mustard genotypes along with a check (TAM 108-1) were planted in RBD with three replications in *rabi* 2021-22 and *rabi* 2022-23 at the Research farm of AICRP on Linseed and Mustard, College of Agriculture, Nagpur. The pooled data regarding analysis of variance reported highly significant genotypes for all the characters *viz.,* days to 50% flowering, days to maturity, plant height, number of branches plant^{-1}, point to first siliqua, siliqua length, number of seeds siliqua^{-1}, number of siliquae plant^{-1}, siliqua density on main branch, 1000 seed weight and seed yield plant^{-1}. The presence of higher value of PCV than GCV highlighted the importance of the environment in the expression of genotypes. Among the characters studied, high GCV and PCV along with high heritability coupled with high genetic advance reported for the seed yield plant^{-1}, days to 50% flowering, number of siliquae plant^{-1} and point to first siliqua that indicate predominance of additive gene action in the inheritance of these traits, which shows greater scope for improvement of these characters. Considering the above criteria, genotypes RE-11, CG-SARSON, NC-37362, NRCHB-101 and PC-6 reported as superior genotypes for further breeding programme.

(Key words: GCV, PCV, heritability, genetic advance, Indian mustard)

INTRODUCTION

Indian mustard [*Brassica juncea* (L.) Czern.and Coss] a natural amphidiploid (2n= 36, AABB genome) from Cruciferae family as important oilseed crop. India predominates other countries in terms of area under production of oilseeds but lack behind in terms of yield. On the other hand, the rapid increase in population is being reflected in the growing demand for edible oil. It is therefore necessary to develop and cultivate high-yielding varieties in order to meet this surge in demand, given the relatively lower production rates in the Vidarbha region when compared to the larger Indian context (Deshmukh *et al*., 2021).

The cultivation of high-yielding cultivars through breeding techniques relies on the nature and extent of variability observed in various yield components. The evaluation of genetic parameters, such as phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), broad-sense heritability (h^2) and genetic advance (GA%) is important as a preliminary step to facilitate effective selection of genotype (Chaudhary *et al*., 2023). Hence, the genotype having the character associated with high GCV, PCV, broad-sense heritability and genetic advance is identified as an important criterion in selection for crop improvement.

MATERIALS AND METHODS

The 23 Indian mustard genotypes alongwith check (TAM 108-1) were planted in RBD with three replications in *rabi* 2021-22 and *rabi* 2022-23 at Research farm of AICRP on Linseed and Mustard, College of Agriculture, Nagpur. All there commended cultural practices were followed to raise a good crop. The observations were recorded at the maturity for days to maturity, plant height, number of branches plant^{-1}, point to first siliqua, siliqua length, number of seeds siliqua^{-1}, number of siliquae plant^{-1}, siliqua density on main branch, 1000 seed weight and seed yield plant^{-1} except days to 50% flowering. Data were subjected to statistical analysis. Analysis of variance calculated as per procedure suggested by Panse and Sukhatme (1954), GCV and PCV by Burton and Devane (1953), heritability by Hanson *et al*. (1956) and genetic advance by Robinson *et al.* (1949).

RESULTS AND DISCUSSION

Analysis of variance for individual year and pooled analysis

The pooled data regarding analysis of variance are presented in Table 1. The mean sum of squares due to individual genotypes were highly significant for days to 50% flowering, days to maturity, plant height, number of branches plant^{-1}, point to first siliqua, siliqua length, number of siliquae plant^{-1}, 1000 seed weight and seed yield plant^{-1} except for second year for number of seeds siliqua^{-1} and

---

1, 4, 5 and 6. P. G. Students, Agril. Botany Section, College of Agriculture, Nagpur, India
2. Junior Rice Breeder, Agricultural Research Station on Rice, Sakoli, Maharashtra, India
3. Mustard Breeder, AICRP on Linseed and Mustard, College of Agriculture, Nagpur, India

siliqua density on main branch. For pooled analysis, genotypes differed significantly for all the characters under study. This reveals that the genotypes had significant amount of genetic variability among themselves, which allow the further estimation of different parameters for all characters. Results were supported by Sur *et al.* (2023), they observed the significant amount of genetic variability for plant height, height up to first fruiting branch, days to 50% flowering, primary branches plant^{-1}, penetration force and 1000 seed weight in pooled analysis and for rest of parameters differed significantly in individual year in Indian mustard.

The data regarding minimum, maximum and grand mean, GCV, PCV, heritability (h^2) and genetic advance as 5% of mean for all characters are presented in Table 2. The study revealed that estimates of phenotypic coefficient of variation (PCV) were higher than their corresponding values of genotypic coefficient of variation (GCV) for all the eleven characters under consideration indicating that, the significant variation was not only due to genotypes but also due to the influence of environment in the expression of genotypes. Similar results were observed by Choudhary *et al.* (2023) and Pandey *et al.* (2020) in Indian mustard, who also observed high value of PCV as compared to GCV due to the influence of environment. Among the characters studied, high GCV and PCV were obtained for seed yield plant^{-1} (27.157%, 28.677%) and number of siliquae plant^{-1} (24.107%, 26.441%) and GCV and PCV for point to first siliqua (14.643%, 16.795%) and days to 50% flowering (13.795%, 14.527%) which shows greater scope for improvement of these four characters. Similar results were reported by Chaudhary *et al.* (2023), Pandey *et al.* (2020) and Kumar *et al.* (2019) for seed yield plant^{-1} and number of siliquae plant^{-1} in Indian mustard.

Higher estimates of heritability coupled with high genetic advance were observed for seed yield plant^{-1} (89.68%, 52.98%), days to 50% flowering (90.17%, 26.98%), number of siliqua plant^{-1} (83.12%, 45.27%) and point to first siliqua (76.01%, 26.30%) indicated that heritability of the trait is mainly due to additive effect and selection will be effective for such traits. It also predicts the gain under selection than heritability estimates alone. This indicates that improvement in these traits could be made by simple selection. Similar to these results high genetic advance as percentage of mean were also reported by Pandey *et al.* (2020) for harvest index and secondary branches plant^{-1} in Indian mustard. A similar study conducted by Sapkal *et al.* (2023) on Indian mustard. They reported that high GCV and high heritability accompanied with high genetic advance as per-cent of the mean for a number of branches plant^{-1}, siliquae density on main branch, number of siliquae plant^{-1} and seed yield plant^{-1} can be effective for further selection. Uikey *et al.* (2018) observed a high heritability and significant genetic advance for number of mature pods plant^{-1}, number of immature pods plant^{-1}, dry pod yield plant^{-1}, hundred pod weight, shelling per cent, oil content and hundred kernel weight in groundnut, indicating potential of the traits in future breeding programs.

The pooled mean values for all the characters are presented in Table 3. For both the traits days to 50% flowering and days to maturity genotype DRMRMJB-35 was identified as earliest in maturity. Genotype PC-6 exhibited tallest plant height with maximum number of branches plant^{-1} and number of siliquae plant^{-1}. The highest number of seeds siliqua^{-1} and siliqua length was observed in genotype NPJ-112. The lowest point to first siliqua was reported by genotype NRCHB 101 and this genotype was found significantly superior over check TAM 108-1. The genotypes RE-8, DRMRIJ12-48 and DRMRIJ12-40 gave highest siliqua density on main branch at harvest, whereas highest 1000 seed weight observed in genotype RLC-3. The highest seed yield plant^{-1} exhibited by genotype CG-SARSON followed by NC-37362 and PC-6.

Based on high GCV, PCV and high heritability along with genetic advance, it is suggested that the characters *viz.*, seed yield plant^{-1}, days to 50% flowering, number of siliquae plant^{-1} and point to first siliqua were useful for selection of genotypes. Considering these characters, the genotypes RE-11, CG-SARSON, NC-37362, NRCHB-101 and PC-6 showed significant mean performance over check which are identified as superior for further breeding programme. Similar study was conducted by Barde *et al.* (2023) on soybean. They reported high GCV, PCV, heritability with genetic advance for number of pods plant^{-1}, number of branches plant^{-1} and number of cluster plant^{-1} along with seed yield plant^{-1} for mutants NSM 21-16 and NSM 21-18. Hence, these two mutants can be identified for further breeding programme.

Table 1. ANOVA for 11 traits in Indian mustard genotypes over two years

Year	Sources of variation	d. f.	Mean Sum of Square										
			Days to 50% flowering	Days to maturity	Plant height (cm)	Number of branches plant^{-1}	Point to first siliqua (cm)	Siliqua length	Number of seeds siliqua^{-1}	Number of siliquae plant^{-1}	Siliqua density on main branch (%)	1000 seed weight (g)	Seed yield plant^{-1} (g)
First Year	Replication	2	3.14	19.17	60.97	0.17	114.70	0.19	0.62	583.71	0.006	0.25	4.92
	Genotypes	22	119.41**	68.97**	1020.54**	1.19**	506.30**	0.52**	10.31**	22379.36**	0.010**	0.33**	156.63**
	Error	44	13.80	15.73	207.99	0.33	94.24	0.14	3.05	315.88	0.003	0.14	5.62
Second Year	Replication	2	3.71	11.26	62.79	0.19	368.39	0.35	3.93	3841.91	0.01	0.09	0.03
	Genotypes	22	138.24**	68.21**	936.40**	0.67**	512.02**	0.52**	2.12	7336.00**	0.01	0.37**	12.87**
	Error	44	2.45	7.41	242.80	0.10	122.55	0.13	1.37	1950.19	0.01	0.10	0.74
Pooled	Rep within year	4	3.43	15.22	62.047	0.18	241.53	0.192	2.28	2,212.58	0.008	0.168	2.47
	Year (Y)	1	183.20**	4.17	2061.89**	67.62**	67.99	0.001	143.25**	9,689.89	0.006	0.001	7070.50**
	Genotypes (G)	22	248.76**	134.57**	1550.82**	1.24**	999.35**	1.046**	7.14**	18,185.31**	0.015**	0.681**	83.57**
	Y X G	22	8.89	2.6	406.15**	0.62**	18.97	0.001	5.30**	11530.03**	0.001	0.013	85.93**
	Pooled Error	88	8.13	11.57	225.387	0.21	108.39	0.142	2.211	1,133.05	0.003	0.119	3.18

*, ** = Significance at 5% and 1% level of significance

Table 2. Estimation of GCV, PCV, heritability and genetic advance for different quantitative characters (Pooled mean)

Observations	Range		Grand Mean	Coefficient of variation		h^2(bs)	Genetic Advance as 5% of Mean
	Min	Max		GCV	PCV		
Days to 50% flowering	39	71	46	13.795	14.527	90.170	26.984
Days to maturity	102	123	109	3.976	4.966	64.117	6.559
Plant height (cm)	145.63	216.03	175.64	8.471	10.385	66.536	14.234
Number of branches plant^{-1}	3.67	5.37	4.26	9.534	12.668	56.638	14.781
Point to first siliqua (cm)	56.98	103.70	83.84	14.643	16.795	76.012	26.299
Siliqua length (cm)	3.16	4.52	3.90	9.975	12.037	68.676	17.029
Number of seeds siliqua^{-1}	11.97	16.23	13.60	6.538	10.361	39.819	8.499
Number of siliquae plant^{-1}	166.77	375.13	221.02	24.107	26.441	83.120	45.275
Siliqua density on main branch (%)	0.50	0.70	0.64	6.099	10.454	34.039	7.330
1000 seed weight (g)	4.01	5.21	4.75	5.510	9.313	35.006	6.716
Seed yield plant^{-1} (g)	7.46	20.58	13.49	27.157	28.677	89.684	52.980

Table 3 Pooled mean values of the genotypes for yield and yield contributing characters

Genotypes	Days to 50% flowering	Days to maturity	Plant height (at maturity) (cm)	Number of branches plant^{-1}	Point to first siliqua (at maturity)	Number of seeds siliqua^{-1}	Number of siliquae plant^{-1}	Siliqua length (at maturity) (cm)	Siliqua density on main branch (at maturity) (%)	1000 seed weight (g)	Seed yield plant^{-1} (g)
RE-11	51.00	113.50	166.77	4.40	69.67	11.97	335.53	3.33	0.64	4.41	15.42
NC-37362	47.00	110.50	177.00	4.57	82.40	12.87	302.33	3.57	0.67	4.79	18.83
RE-44	45.33	112.67	164.80	4.57	81.60	13.73	298.13	3.52	0.62	4.88	10.80
CN-105364	41.67	112.50	161.40	3.83	81.95	12.30	225.50	3.93	0.65	4.87	7.46
IC-597880	42.50	110.33	156.27	4.17	83.97	12.63	176.03	4.08	0.63	4.52	17.60
RLC-3	52.67	111.50	201.33	3.83	103.70	15.37	208.13	3.16	0.50	5.21	10.99
RE-8	43.83	111.17	172.40	4.20	100.22	13.57	228.50	3.47	0.70	4.81	12.65
DRMRMJB-35	39.17	102.33	168.57	4.13	90.12	14.20	227.40	4.40	0.55	4.39	10.41
DRMRIJ12-48	44.83	110.67	181.77	4.43	98.07	13.40	196.10	4.29	0.70	4.76	11.18
DRMRIJ12-40	46.00	112.67	175.53	4.13	96.55	13.20	178.07	3.27	0.70	4.65	13.16
DRMRIJ-31	43.33	106.33	159.20	4.33	85.40	13.87	194.83	3.84	0.61	4.75	15.93
LES-39	44.17	107.33	202.43	3.73	98.63	14.67	184.37	4.18	0.65	4.04	8.86
TN-3	41.00	105.00	169.70	5.20	96.95	14.63	202.13	3.87	0.63	4.91	16.25
NPJ-112	41.33	102.33	145.63	3.67	82.33	16.23	183.13	4.52	0.63	4.18	7.93
M-34	49.50	108.00	161.87	4.70	100.60	14.90	209.10	4.08	0.68	5.02	14.07
ACN-141	45.00	110.67	173.03	4.63	73.07	12.70	209.70	3.73	0.63	4.96	16.28
ACN-184	49.33	115.00	178.70	3.90	82.35	13.30	166.77	3.32	0.68	5.02	10.29
ACN-9	46.33	103.33	171.23	4.63	76.45	12.50	229.90	3.95	0.67	4.93	16.83
PC-6	71.00	122.67	216.03	5.27	71.27	13.07	375.13	4.31	0.68	4.01	18.00
CG-SARSON	41.83	102.50	183.60	4.30	59.60	12.77	192.07	4.38	0.64	5.04	20.58
NRCHB 101	40.83	108.50	176.40	3.80	56.98	15.00	167.50	4.17	0.68	4.96	15.26
TAM 108-1	43.67	107.83	188.33	3.73	80.07	12.93	211.80	4.49	0.60	5.03	12.64
BHAWANI	44.83	107.67	187.73	3.73	76.33	13.10	181.23	3.85	0.58	5.10	8.82
SE(m) ±	**1.17**	**1.88**	**6.10**	**0.21**	**3.98**	**0.63**	**13.86**	**0.15**	**0.03**	**0.14**	**0.71**
CD at 5%	**3.35**	**5.37**	**17.42**	**0.59**	**11.39**	**1.80**	**39.64**	**0.43**	**0.09**	**0.39**	**2.05**

REFERENCES

Barde, S. R., S. R. Kamdi, R. A. Jadhav, S. B. Baviskar, S. S. Pokale and A. P. Mate, 2023. Character association and path analysis studies for yield and yield contributing traits in soybean mutant progenies. J. Soils and Crops. **33**(1): 200-206.

Burton, G. W. and E. M. Devane, 1953. Estimating heritability in tall fescue (*Festuca circuncliaceae*) from replicated material. Agron. J. **45**:478-481.

Chaudhary, R. R., R. Avtar, M. Singh and M. Bishnoi, 2023.Genetic parameters and correlation studies in Indian mustard (*Brassica juncea* L.). J. Oilseeds Res. **14**(1): 68-72.

Deshmukh, A. S., S. R. Kamdi, B. Nair, S. R. Patil, S. S. Bhure and H. P. Ingole, 2021. Heterosis for seed and yield contributing characters in mustard (*Brassica* species). J. Soils and Crops. **31**(2): 371-376.

Hanson, G. H., H. F. Robinson and R. E. Comstock, 1956. Biometrical studies on yield in segregating population. Agron. J. **48**:268-272.

Kumar, R., R. Kaur and L. Kaur, 2019.Genetic variation for yield characters of F_1 hybrids in Indian mustard (*Brassica juncea* L.). J. Oilseed Brassica. **10**(2): 117-121.

Pandey, S. K., K. K. Srivastava, S. Negi, N. A. Khan and R. K. Singh, 2020. Variability, trait relationship and path analysis for seed yield and seed quality parameters in Indian mustard (*Brassica juncea* L.). J. Oilseed Brassica. **11** (1): 69-76.

Panse, V. G. and P.V. Sukhatme, 1954.Statistical method for agriculture worker I.C.A.R. publications, New Delhi.2nd edn. pp. 63-66.

Robinson, H.F., R.E. Comstock and V.H. Harvey, 1949. Estimates of heritability and degree of dominance in corn. Agron. J. **41**:353-359

Sapkal, A. D., S. R. Kamdi, R. A. Jadhav and M. P. Meshram, 2023.Genetic analysis of yield and its components in F_1 and F_2 population of Indian mustard [*Brassica juncea* (L.) Czern and Coss]. AATCC Rev. 28-39.

Sur, B., S. Rout, S. Singla, R. Mandal, S. Nath, B. Maying, S. Sandhu, M. Chakraborty, L. Hijam, M. K. Debnath and S. K. Roy, 2023. Evaluation of mustard genotypes [*Brassica juncea* (L.)Czern and Coss] for quantitative traits and character association of seed yield and yield components at sub-Himalayan region of West Bengal (India). Plant Sci. Today. **10**(1): 166-178.

Uikey, K. N., S. R. Kamdi, S. R. Patil, R. D. Deotale, N. V. Lande and V. S. Jayade, 2018. Genetic variability studies in local collections of groundnut (*Valencia botanical* type). J. Soils and Crops. **28**(1): 136-141.

Rec. on 25.11.2023 & Acc. on 13.12.2023