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# **Evaluation of Heritability and Genetic Advance for Morphological Traits of Indian Mustard Germplasms**

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### Authors' contributions

This work was carried out in collaboration among all authors. Author DA designed the study, performed field experiments, collected the data, performed the statistical analysis and wrote the manuscript. Author VKT rechecking the statistical analysis, revised the manuscript and made suggestions to improve manuscript. Author VSK tabulated the data, managed the literature search and improved the final manuscript. All authors read and approved the final manuscript.

### Article Information

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### ABSTRACT

Genotypic source of variations were significant for all characters in 168 genotypes including 7 checks of Indian mustard at 5% level of significance. Maximum seed yield per plant (g) and harvest index was recorded in MRNJ-82; whereas, the minimum days to 50% flowering and maturity were recorded in RVM-1 and MRNJ-5 respectively. In genotypes viz; MRNJ-36, RVM-2, MRNJ-59, JM-1, MRNJ-53 and MRNJ-35 had maximum plant height (cm), number of primary branches per plant, number of secondary branches per plant, number of siliqua per plant, number of seeds per siliqua and 1000 seed weight (g). Highest GCV and PCV were recorded for seed yield per plant which indicates for improvement through selection among these genotypes. High heritability along with high genetic advance as percentage of mean has been noticed for seed yield per plant and harvest index indicating less influence of environment and also the presence of additive, dominance and interaction among genes in the expressions of these characters. Low genetic advance along with

low heritability estimate were observed for number of primary branches per plant and number of seeds per siliqua. This indicates the involvement of additive and non-additive gene actions in their inheritance.

Keywords: Genetic variability; heritability (h<sup>2</sup>); genetic advance; genotypic coefficient of variation (GCV); phenotypic coefficient of variation (PCV).

### 1. INTRODUCTION

Indian mustard (Brassica juncea L. Czern & Coss) is an important crop among the crops of oilseeds in the world. Mustard oil is widely used as cooking oil. Among oilseeds, Indian mustard covers about 80% cropped area in the country. But the productivity of this crop is low in India as compared to other mustard growing countries. Madhya Pradesh is the third most important rapeseed mustard growing state in the country with an area of 0.54 million ha and production of 0.88 million tones with an average productivity of 1639 kg/ha during the year 2015-16 [1]. In order to fulfil consumer demand, introduction of high grain and oil yielding varieties are needed. In this connection, efforts have been made to collect genetic germplasm for their vield potential evaluation and pest-disease resistance.

Therefore, it is necessary to partition the overall variability into genetic and environmental components which enables the breeders to adapt suitable breeding procedure for further improvement of genetic stocks. Generally, the estimates of broad sense heritability alone will not provide idea about expected gains in the desired trait over successive generations. Hence, in addition to heritability, estimates of genetic advance should also be considered. The large continuum of genetic variability in population depends on the amount of genetic variability among genotypes and offer better scope for selection. The large amounts of genetic variability and heritable variation in the characters have huge value in accepting the potential of the genotype for further breeding programme.

A wide variability for economic traits of germplasm is necessary for exploitation of selections. Thus. assessment of genetic parameter like phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability  $(h^2)$  and genetic advance which is a pre-requisite for making effective selection.

### 2. MATERIALS AND METHODS

### 2.1 Experimental Materials

168 germplasm lines including 07 checks namely: Rohini, Maya, RVM-1, RVM-2 JM-1, JM-2 and JM-3 of Indian mustard were sown in the Randomized Complete Block Design with row to row 30 (cm) and plant to plant 10 (cm) distance with 2 replications at research farm of Department of Plant Breeding and Genetics, Raimata Vijavaraje Scindia Krishi Vishwa Vidyalaya, Gwalior (M.P.) during 2016-17 and 2017-18.

### 2.2 Observations

Five plants were randomly selected from each germplasm in order to record observations on 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, number of seeds per siliqua, seed weight (g), harvest index, seed yield per plant (g) and seed oil content (%). Harvest index was calculated by following formula proposed by Donald and Hamblin [2].

### 2.3 Statistical Procedures

The data collected on the quantitative characters were subjected for statistical analysis as suggested by Panse and Sukhatme [3].

### 2.4 Genotypic and Phenotypic Variances

To estimate the phenotypic and genotypic variance, genotypic and phenotypic coefficients of variation were estimated based on formula given by Syukur et al. [4].

These were calculated as follows:

- (a) Genotypic variance=  $(\sigma^2 g) = (V_g V_e) / r$ (b) Phenotypic variance= $(\sigma^2 p) = \sigma^2 g + \sigma^2 e$
- (c) Environmental variance= $(\sigma^2 e) = V_{e}$

The genotype mean sum of square was tested against error mean sum of square by 'F' test for  $n_1$  (t-1) and  $n_2$  (r-1) (t-1) degree of freedom both at 0.05 and 0.01probability levels. Any significant variation was marked as one asterisk for 0.05 and two asterisks for 0.01 against the corresponding mean square in the analysis of variance table.

### 2.5 Estimation of Phenotypic and Genotypic Coefficients of Variation

The phenotypic and genotypic coefficients of variation in per cent were computed by the following formulae given by Burton [5].

- a) Phenotypic Coefficient of Variation  $(PCV \%) = \frac{Phnotypic SD}{Mean} \times 100$
- b) Genotypic Coefficient of Variation (GCV %) =  $\frac{\text{Genotypic SD}}{\text{Mean}} \times 100$

The PCV and GCV values are ranked as low (0-10%), medium (10-20%) and high (>20%)

### 2.6 Heritability (%)

The ratio of genetic variance to the total variance, i.e. phenotypic variance is known as heritability. Heritability (H) in broad sense was calculated as reported by Lush [6].

 $H^2$  (%) = Genotypic variance / Phenotypic variance x100

Heritability values are categorized as low, moderate and high by Robinson et al. [7] and are given below:

<30% - Low 30-60% - Moderate >60%- High

### 2.7 Genetic Advance (GA)

It was estimated by the formula suggested by Lush [6]

GA = Genotypic variance / phenotypic variance X k.  $\sigma$  p

Where,

 $\sigma$  p = Phenotypic standard deviation K constant at 5% selection intensity = 2.06

#### 2.8 The Test of Homogeneity

Prior pooling the data, the test of homogeneity for error variance was applied by appropriate method of analysis of variance described by Panse and Sukhatme [3].

### **3. RESULTS AND DISCUSSION**

The results obtained from the pooled data (2016-17 and 2017-18) under present study as well as the relevant discussions have been summarized under the following heads:

#### 3.1 Analysis of Variance

The analysis of variance revealed that component of variance for genotypes was significant for all characters namely days to 50% flowering, days to maturity, plant height (cm), number of primary branches per plant, number of secondary branches per plant, number of siliqua per plant, number of seeds per siliqua, 1000seed weight (g), seed yield per plant (g) and harvest index which has been shown in Table 1. This suggests that there is an opportunity for the genetic improvement in mustard for these traits.

In the present study, number of days taken to 50% flowering ranged from 45.50 to 61.13 days with a mean of 56.20 days. In RVM-1, minimum days were recorded for 50% flowering (45.50 %), while genotype Maya recorded maximum days taken to 50% flowering (61.13 days). Number of days to maturity among the genotypes ranged from 103.13 to 135.25 days with a general mean of 128.97 days. The genotype MRNJ-5 recorded the minimum days to maturity (102.25 days), while MRNJ-56 recorded maximum days to maturity (135.75 days). Khulbe et al. [8] and Rout et al. [9] have found variability in mustard and toria genotypes for characters related to maturity duration and seed yield which is in agreement with recent study.

Plant height among the genotypes ranged from 85.15 cm to 214.90 cm with a general mean of 194.84 cm. Maximum plant height was recorded in MRNJ-36 (214.90 cm), while minimum plant height was recorded in RVM-1 (85.15 cm). Primary branches among the genotypes ranged from 4.00 to 6.35 with a general mean of 5.13. Moreover, the maximum primary branches were recorded in RVM-2 (6.35), while minimum primary branches recorded in MRNJ-6 (4.00 cm).

Secondary branches among the genotypes ranged from 4.25 to 16.63 with a general mean of 7.87. The maximum secondary branches were recorded in MRNJ-59 (4.25), while minimum secondary branches were observed in MRNJ-74 (16.63 cm). Number of siliqua per plant among the genotypes ranged from 49.38 to 349.88 with a general mean of 187.13. Maximum number of siligua per plant was recorded in JM-1 (349.88), while minimum number of siliqua per plant was recorded in MRNJ-6 (49.38). Tiwari [10] has noticed high genetic variation for characters namely length of siliqua, seed yield per plant, number of siliqua per plant and 1000 seed weight (g) which supports the present results. Number of seed per siliqua among the genotypes ranged from 11.25 to 15.38 with a general mean of 13.09. Maximum number of seed per siliqua was recorded in MRNJ-53 (15.38), while minimum number of seed per siligua plant was recorded in MRNJ-29 (11.25). 1000 seed weight among the genotypes ranged from 2.22 (g) to 5.65 (g) with a general mean of 4.24 (g). Maximum 1000 seed weight was recorded in MRNJ-35 (5.65 g), while minimum 1000 seed weight was recorded in MRNJ-6 (2.22 g). Poonam and Singh [11] reported the varietal differences and found highly significant for plant height, days to 50% flowering, seeds per siligua, days to maturity. 1000-seed weight and seed yield per plant. It showed that seed yield per plant among the genotypes ranged from 6.23 (g) to 24.20 (g) with a general mean of 12.84 (g). Maximum seed yield per plant was recorded in MRNJ-82 (24.20 g), while minimum seed yield per plant was recorded in MRNJ-118 (6.23 g). It showed that harvest index among the genotypes ranged from 11.35 to 43.16 with a general mean of 22.65. Maximum harvest index was recorded in MRNJ-82 (43.16), while minimum harvest index was recorded in MRNJ-122 (11.35). In Table 2, percentage of oil content over two year's mean revealed that out of 168 germplasms, 48 germplasms including 04 checks were found promising for oil content and they had oil content which ranged from 37.75% to 40.53%. Among them RVM 2 (check) gave highest oil content (40.53%) followed by Rohini (40.10%) and Maya (40.07%). In another study which supports the contemporary results by Pant and Singh [12] who observed genetic variability in nine characters of twenty-five Indian mustard genotypes. Analysis of variance revealed highly significant genotypic differences for all traits studied, except days to flower, number of primary branches and oil content.

### 3.2 Coefficient of Variation

Estimates of phenotype coefficient of variation (PCV) and genotype coefficients of variation (GCV) were worked out and are depicted in Table 3. The maximum GCV was recorded for seed yield per plant (33.36%) followed by harvest index (33.14%), number of siliqua per plant (19.99%), number of secondary branches per plant (9.63%) and 1000 seed weight (8.41%), while minimum GCV was recorded for number of primary branches per plant (2.10%) followed by days to maturity (3.69%), number of seeds per siliqua (3.79%), days to 50% flowering (4.08%) and plant height (4.42%).

The maximum PCV was recorded for seed yield per plant (33.39 %) followed by harvest index (33.16 %), number of siliqua per plant (22.59 %), number of secondary branches per plant (14.77%) and 1000 seed weight (9.32%), indicates the prevalence of environmental effect for the phenotypic expression of these traits. while minimum PCV was recorded for days to maturity (3.70%) followed days to 50% flowering (4.15%), plant height (5.32%), Number of seeds per siliqua (6.80 %) and 1000 seed weight (9.32%). Rauf and Rahim [13] demonstrated that phenotypic variances were higher than the genotypic variances for most of the characters in their experiment.

Existing result of genotypic and phenotypic variability was supported by the findings of Tiwari [10] where it was stated that the maximum genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) was exhibited by number of secondary branches per plant followed by seed yield per plant and number of primary branches per plant. Contrary to present findings, Rout et al. [9] reported moderate PCV and GCV for the quantitative traits. This showed that there was least influence of environment in the expression of traits. High GCV and PCV were earlier reported Srivastava et al. [14] and Rauf and Rahim [13].

### 3.3 Heritability

Heritability estimates in broad sense were worked out for ten characters and are illustrated in Table 3. High heritability estimates was recorded for harvest index (99.86%) followed by seed yield per plant (99.82%), days to maturity (99.41%), days to 50% flowering (96.77%) and 1000 seed weight (81.52%). However, low

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Source of variation	DF	Days to 50% flowering	Days to maturity	Plant height (cm)	No. of primary branches per plant	No. of secondary branches per plant	No. of Siliqua per plant	No. of seed per plant Siliqua	Seed yield per plant(g)	1000 seed weight(g)	Harvest index(%)
Year (Y)	1	414.07**	0.11	136.22**	0.48	7.73**	1719.68**	3.43**	0.06	0.24**	1.27**
Rep within year	2	0.54	1.64*	93.02	4.15	3.32	26586.99	0.09	0.01	0.01	0.26
Varieties (V)	167	21.43**	90.59**	367.20**	0.66	3.79**	6455.47**	2.08**	73.45**	0.57**	225.58**
Y*V	167	2.98**	1.47**	29.58	0.60	2.39**	411.01	1.07	0.05	0.03	0.63**
Pooled error	334	0.27	0.23	35.43	0.58	1.43	652.33	0.94	0.05	0.05	0.11

### Table 1. Pooled analysis of variance (ANOVA) for ten characters in the germplasm of Indian mustard

\*Significant at 5% level of probability \*\*Significant at 1% level of probabilit

1 2 3 4 5 6 7 8 9 10	Entry MRNJ-82 MRNJ-90 MRNJ-93 MRNJ-120 MRNJ-4 MRNJ-86 MRNJ-89 MRNJ-55 MRNJ-55	<b>2016-17</b> 40.01 39.80 38.78 38.50 39.01 38.45 39.40	Oil content (% 2017-18 39.86 38.80 38.40 38.44 38.44 38.40	Mean 39.93 39.30 38.59 38.47
2 3 4 5 6 7 8 9	MRNJ-90 MRNJ-93 MRNJ-120 MRNJ-4 MRNJ-86 MRNJ-89 MRNJ-55	39.80 38.78 38.50 39.01 38.45	38.80 38.40 38.44	39.30 38.59 38.47
3 4 5 6 7 8 9	MRNJ-93 MRNJ-120 MRNJ-4 MRNJ-86 MRNJ-89 MRNJ-55	38.78 38.50 39.01 38.45	38.40 38.44	38.59 38.47
4 5 6 7 8 9	MRNJ-120 MRNJ-4 MRNJ-86 MRNJ-89 MRNJ-55	38.50 39.01 38.45	38.44	38.47
4 5 6 7 8 9	MRNJ-4 MRNJ-86 MRNJ-89 MRNJ-55	39.01 38.45		
5 6 7 8 9	MRNJ-86 MRNJ-89 MRNJ-55	38.45	38.40	
6 7 8 9	MRNJ-89 MRNJ-55			38.70
7 8 9	MRNJ-89 MRNJ-55		38.48	38.46
8 9	MRNJ-55		38.43	38.91
9		37.90	38.42	38.16
	MRNJ-84	37.50	38.44	37.97
	MRNJ-94	38.10	38.07	38.08
11	MRNJ-92	38.20	39.00	38.60
12	MRNJ-81	39.15	38.05	38.60
13	MRNJ-88	37.90	37.69	37.75
14	MRNJ-25	38.50	37.90	38.20
15	MRNJ-20	39.30	38.45	38.87
16	MRNJ-85	37.80	38.00	37.90
17	MRNJ-34	39.60	38.80	39.20
18	MRNJ-57	37.75	38.20	37.97
19				
	MRNJ-18	38.70	39.07	38.88
20	MRNJ-91	39.08	38.90	38.99
21	MRNJ-83	36.90	37.50	37.20
22	MRNJ-31	40.20	39.90	40.05
23	MRNJ-80	38.50	37.80	38.15
24	MRNJ-87	39.00	39.06	39.03
25	RVM-2(165)	41.07	40.00	40.53
26	MRNJ-76	38.70	39.07	38.88
27	MRNJ-79	38.30	38.60	38.45
28	MRNJ-78	39.40	39.00	39.20
29	MRNJ-21	36.90	37.09	36.99
30	IMD-69(161)	38.74	39.00	38.87
31	JM-2(167)	39.90	39.50	39.70
32	MRNJ-35	40.00	39.80	39.90
33	MRNJ-77	38.68	38.90	38.79
34	MRNJ-68	38.50	39.02	38.76
35	IMD -8(146)	37.89	38.07	37.98
36	MRNJ-61	36.70	37.01	36.85
37	MRNJ-30	39.08	39.00	39.04
38	MRNJ-66	38.40	38.00	38.20
39	MRNJ-17	39.20	39.00	39.10
40	IMD-41(154)	38.42	38.20	38.31
41	Maya(163)	40.06	40.08	40.07
42	MRNJ-14	38.70	38.50	38.60
43	MRNJ-48	39.80	39.60	39.70
44	IMD-(155)	39.80	39.90	39.85
45	MRNJ-33	37.90	38.01	37.95
46	IMD-66(159)	38.90	39.00	38.95
47	MRNJ-75	39.10	39.00	39.05
48	Rohini (162)	40.00	40.20	40.10 s
	Mean	38.79	38.70	38.76

Table 2. Selected 48	germplasm for oil c	content (%) in Ir	ndian mustard

	GCV %			PCV %			h2 (%)			GA (% of mean)		
	Year		Mean	Year		Mean		Year	Mean	Year		Mean
	16-17	17-18		16-17	17-18		16-17	17-18	16-17	17-18		
Days to 50% flowering	4.89	4.43	4.08	4.99	4.51	4.15	96.01	96.58	96.77	9.86	8.98	8.28
Days to maturity	3.73	3.70	3.69	3.74	3.71	3.70	99.13	99.37	99.41	7.65	7.60	7.57
Plant height (cm)	7.31	4.92	4.42	8.43	5.74	5.32	75.23	73.51	69.00	13.06	8.69	7.57
No. of primary branches/plant	5.49	4.01	2.10	15.14	12.20	11.05	13.13	10.79	3.61	4.10	2.71	0.82
No. of secondary branches/plant	13.49	11.27	9.63	23.31	18.58	14.77	33.48	36.82	42.47	16.08	14.09	12.92
No. of siliqua per plant	21.95	20.65	19.99	28.45	25.02	22.59	59.50	68.14	78.27	34.88	35.12	36.43
No. of seeds per siliqua	5.93	4.86	3.79	9.58	7.88	6.80	38.31	38.10	31.04	7.56	6.18	4.35
1000 seed weight (g)	8.96	8.69	8.41	11.10	10.14	9.32	65.14	73.53	81.52	14.89	15.36	15.65
Seed yield per plant (g)	33.52	33.44	33.36	33.55	33.47	33.39	99.79	99.83	99.82	68.97	68.83	68.66
Harvest index (%)	33.39	33.25	33.14	33.41	33.28	33.16	99.83	99.86	99.86	68.72	68.45	68.21

## Table 3. Genetic parameters for ten characters of germplasm in Indian mustard

heritability estimates were recorded for number of primary branches per plant (3.61%) followed by number of seeds per siliqua (31.04%), number of secondary branches per plant (42.47%), plant height (69.00%) and number of siliqua per plant (78.27%). The high heritability estimate was observed for harvest index followed by seed yield per plant, days to maturity and days to 50% flowering. However, the harvest index, number of siligua per plant and number of secondary branches per plant showed high heritability with high genetic advance in percentage of mean. This suggests that these traits are under additive genetic control and selection might be effective for these traits. High heritability estimates for most of the characters studied have been reported earlier also by Vermai et al. [15]. Tiwari [10] reported that number of secondary branches per plant, number of siliqua per plant, length of siliqua, 1000 seed weight (g), oil content and seed yield per plant possessing high heritability. Thus, the heritability estimates together with genetic advance are more authentic for selecting the leading genotype.

### 3.4 Genetic Advance

Genetic advance as percentage of mean was estimated for all the characters and are demonstrated in Table 3.

Estimates of genetic advance as per cent of mean was high for seed yield per plant (68.66%) followed by harvest index (68.21%). number of siliqua per plant (36.43%), 1000 seed weight (15.65%) and number of secondary branches per plant (12.92%), while, low estimates of genetic advance as per cent of mean was observed for number of primary branches per plant (0.82%) followed by number of seeds per siligua (4.35%), days to maturity (7.57%), plant height (7.57%) and days to 50% flowering (8.28%). Singh et al. [16] studied variability, heritability and genetic advance of forty Indian mustard cultivars. High heritability along with high genetic advance in per cent of mean was observed for secondary branches per plant, seed yield per plant and number of siliquae per plant, indicating preponderance of additive gene action. High genetic advance in concurrence with high heritability estimates for a certain trait is believed to be the most successful state in breeding programs. High heritability and high genetic advance was a signal of additive gene effects Akbar et al. [17] while high heritability associated with low genetic advance was an indication of dominance and epistatic effects. Genetic advance as percentage of mean was highest for seed yield per plant, followed by plant height and number of branches as reported by Mondal and Khajuria [18]. In another study, Afrin et al. [19] found that low heritability with high genetic advance in percentage of mean for plant height whereas, low broad sense heritability for siliqua length was observed by Zare and Sharafzadeh [20].

In support to existing study, Khan et al. [21] has found high heritability coupled with high genetic advance for number of secondary branches per plant; whereas Bibi et al. [22] reported high heritability with high genetic advance for number of siliquae per plant. High heritability along with considerable genetic advance in percentage of mean was reported by Afrin et al. [19] for thousand seed weight it was due to additive gene action control of length of siliqua, seed yield per plant, 1000 seed weight, number of secondary branches per plant and number of siliqua per plant which support recent study

### 4. CONCLUSION

A wide rang of genetic variability was observed for seed yield and its attributing characters in the germplasm of Indian mustard. The highest genotypic coefficient of variation was noticed for seed yield per plant. High heritability along with high genetic advance as percentage of mean was found in seed yield per plant and harvest index indicating less influence of environment.

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### **COMPETING INTERESTS**

Authors have declared that no competing interests exist.

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