

## Genetic Variability Studies on Yield and its Related Traits in Indian Mustard [*Brassica juncea*]

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**ABSTRACT:** Existing nature and magnitude of genetic variability, heritability and genetic advance determines the potential of a crop for being responsive to a breeding programme. It is necessary to study the direct and indirect effects of various components on yield also. An experiment was conducted with 10 parents and their 45 crosses in half diallel fashion in Indian mustard for fourteen quantitative characters. Analysis of variance showed significant variation among the genotypes for all the studied yield and yield contributing characters. The phenotypic co-efficient of variation was higher than the genotypic co-efficient of variation for all the characters measured, indicating that there was major influence of environment. High heritability coupled with high genetic advance as per cent of mean was observed for the characters like harvest index, biological yield per plant, grain yield per plant, number of secondary branches, thousand seed weight, pod length and number of siliqua on the main shoot. Yield is a complicated trait that is governed by a number of supplementary characters or traits. So the traits which are high heritable or have a positive association or correlation with yield can be used for selection in an indirect way. Hence these traits could be considered as the best for exploiting the higher yields in further breeding programmes.

**Keywords:** Variability, heritability, genetic advance, yield and Indian mustard.

### INTRODUCTION

The oilseed crops *Brassica napus*, *Brassica rapa* and *Brassica juncea* are one of the most important sources of vegetable oil globally. In many countries, canola quality (low erucic acid, low glucosinolates) *B. rapa* and *B. napus* are the main Brassica oilseed crops. Indian mustard (*Brassica juncea*) is an important oil seed crop of the world. It is popularly known as rai, raya or laha in India. It belongs to family Cruciferae. Cytologically, *Brassica juncea* is a natural amphidiploid (2n= 36) derived from interspecific cross of *Brassica campestris* (2n= 20) and *Brassica nigra* (2n= 16) (Nagaharu, 1935). The major rapeseed producing countries are Canada, China, Germany and France. The area, production and productivity of rapeseed-mustard in the world was 36.59 million hectares (M ha), 72.37 million tonnes (M t) and 1980 kg/ha, respectively, during 2018-19. India occupies the first position in area and second position in production of mustard after China. Globally, India account for 19.8 % and 9.8% of the total acreage and production (USDA). In India, Soybean, groundnut and rapeseed-mustard contributes nearly 84% and 88% to its total acreage and production, respectively (Average of 2014-15 to 2018-19). The major rapeseed-mustard growing states in India are Rajasthan (44.97% area), Uttar Pradesh (10.60%), Madhya Pradesh (11.32%) and

Haryana (12.44%)

([https://www.drmr.res.in/about\\_rmcrop.php](https://www.drmr.res.in/about_rmcrop.php)).

For measurement of genetic variability, several biometric tools such as genetic parameters like the genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability and genetic advance (GA) are being used (Manjunath *et al.*, 2017). Coefficient of variation is helpful in exposing and understanding the clear picture of existing variability within the population. An estimate of genetic advance along with heritability is helpful in assessing the reliability of character for selection. By intermating of superior genotypes of segregating population (developed from combination breeding), the character showing high heritability along with low genetic advance can be improved (Synrem *et al.*, 2014). The biological method of nanoparticle synthesis is a relatively simple, cheap and environmentally friendly method (Kumar *et al.*, 2017). Chakraborty *et al.* (2021) conclude that significant genetic variation among the genotypes and the traits. The study of contributing characters of the yield can prove to be beneficial in studying the genetic architecture of yield. As a result, a plant breeder would be able to breed for high yielding genotypes with desired combination of traits (Khan and Dar 2010).

## MATERIALS AND METHODS

Forty five crosses were made among ten parents during *rabi* season 2020-2021 and a set of 55 genotypes comprising of ten parents and their 45 F<sub>1</sub> s were sown in randomized block design (RBD) with three replications. Each genotype was sown in three rows each of 5 meter length with a spacing 45 × 15 cm at CRC, SVPUAT, Meerut. All recommended package of practices has been followed to retain a good crop. Five competitive plants were randomly selected for each genotype from each replication. Data on several observations *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 pods on main shoot, length of main shoot, pod length (cm), number of seeds per pod, test weight (g), biological yield per plant (g), harvest index (%), oil content (%), grain yield per plant (g) was recorded. The characters *viz.*, days to 50% flowering and days to maturity were recorded on per plot basis. Means were computed and data were analysed for variances by Panse and Sukhatme (1967) and

coefficient of variation as suggested by Burton (1952) and heritability (broad sense) as the ratio of genotypic to phenotypic variance. The expected genetic advance and genetic advance as per cent of mean was calculated as per the procedure of Johnson *et al.* (1955). All the statistical analysis was conducted by IBM SPSS 22 statistical package (IBM Cooperation, 2019).

## RESULTS

Analysis of variance (ANOVA) for different characters is being presented in Table 1. The results revealed highly significant differences among the material used in the current investigation for all yield related traits *viz.*, days to 50% flowering, days to maturity, plant height, number of primary branches per plant, number of secondary branches per plant, numbers of pods on main shoot, length of main shoot, pod length, number of seeds per pod, test weight, biological yield per plant, harvest index, oil content and grain yield per plant components, among parents, crosses and parents vs crosses, which showed significant differences for all the traits.

**Table 1: Analysis of variance for fourteen characters in Indian mustard.**

Source of variation	Replication (df 2)	Treatments (df 54)	Error (df 108)	Total (df 164)
Days to 50 % flowering	8.95	69.03**	5.61	26.53
Days to maturity	21.24	57.13**	5.28	22.55
Plant height (cm)	94.51	573.35**	55.6	226.55
Number of primary branches	0.91	1.60**	0.09	0.59
Number of Secondary branches	0.09	20.12**	0.53	6.97
Numbers of pods on main shoot	19.36	102.03**	4.25	36.63
Main shoot length	1.14	177.67**	9.79	64.97
Pod length	0.2	1.45**	0.05	0.51
Number of seeds per pod	0.1	3.85**	0.21	1.41
Thousand seeds weight	0.08	1.30**	0.04	0.46
Biological yield per plant	1422.19	57767.73**	523.27	19383.02
Harvest index	1.3	74.79**	0.61	25.04
Oil content	0.076	0.688**	0.055	0.264
Grain yield per plant	16.63	1262.69**	16.8	427.03

\*, \*\* significant at 5% and 1% level, respectively.

The results of variability, heritability and genetic advance as percentage of mean are presented in Table 2. In the present study, the genotypic coefficients of variation (GCV) for all the characters studied were found to be lesser than the phenotypic coefficients of variation (PCV) indicating the modifying effect of the environment in association with the characters at genotypic level. The difference between magnitude of genotypic and phenotypic coefficient of variation showed low difference for all the characters studied that indicated that there was good correspondence between genotypic and phenotypic expression of traits with low effect of environmental factors operating on the traits. The highest estimate of coefficient of variation was registered for harvest index (GCV = 27.34%; PCV = 27.67%) followed by biological yield per plant (GCV = 24.30%; PCV = 24.64%), grain yield per plant (GCV = 20.52%; PCV = 20.93%), which indicated that the vast inherent variability, that remained unaffected by environmental conditions among the genotypes, was present there, which in turn can be more useful for exploitation in hybridization and/or selection. Our results are in line as per findings for high variance in

biological yield per plant was reported by Bind *et al.* (2014), Seed yield per plant was observed by Singh *et al.* (2018), Kumar *et al.* (2018) and Singh *et al.* (2019) and harvest index was reported by Swetha *et al.* (2019). Moderate estimates of coefficients of variation were observed for number of secondary branches (GCV = 15.36%; PCV = 15.97%) followed by pod length (GCV = 13.59%; PCV = 14.28%), thousand seed weight (GCV = 13.40%; PCV = 14.06%), number of pods on the main shoot (GCV = 12.03%; PCV = 12.79%) and number of primary branches (GCV = 10.06%; PCV = 10.90%). These results showed that sufficient variability was present there for attempting selections to improve these traits in the genotypes studied. On the other side, moderate PCV and low estimates of GCV were recorded for number of seeds per pod (GCV = 9.90%; PCV = 10.74%) followed by main shoot length (GCV = 9.79%; PCV = 10.61%), Whereas low GCV and PCV was seen for days to 50% flowering (GCV = 7.96%; PCV = 8.96%), plant height (GCV = 7.09%; PCV = 8.16%), days to maturity (GCV = 3.07%; PCV = 3.51%) and oil content (GCV = 1.19%; PCV = 1.34%) indicating a narrow range of variability for

these traits there by restricting or limiting the scope for selection which were also reported by Gadi *et al.* (2020).

In the present study, the heritability ranged from 75.63% (plant height) to 97.61% (harvest index). High heritability (> 80%) was observed for characters such as harvest index (97.61%) followed by the biological yield per plant (97.33), grain yield per plant (96.11), number of secondary branches (92.52), thousand seed weight (90.89), pod length (90.63), number of siliqua on the main shoot (88.46). Singh *et al.* (2018) Kumar *et al.* (2018) Ray *et al.* (2019) corroborates the similar finding. While number of primary branches (85.15), main shoot length (85.11) and number of seeds per pod (84.94), while oil content (79.36) followed by the days to flowering (79.04), days to maturity (76.60) and plant height (75.63) showed moderate heritability (60 – 80%).

High genetic advance as percent of mean (> 20%) was recorded for harvest index (55.64) followed by biological yield per plant (49.40), grain yield per plant (41.43), number of secondary branches (30.44), pod length (26.65), thousand seed weight (26.32) and number of pods on the main shoot (23.31). Moderate genetic advance as percent of mean (10 -20%) is for in

number of primary branches per plant (19.12) followed by number of seeds per siliqua (18.80), the main shoot length (18.60), days to 50 % flowering (14.59) and plant height (12.71), whereas days to maturity (5.54) and oil content (2.19) exhibited low genetic advance as percent of mean (>10%).

High heritability coupled with high genetic advance as per cent of mean was observed for the characters like harvest index, biological yield per plant, grain yield per plant, number of secondary branches, thousand seed weight, pod length and number of siliqua on the main shoot. On the other side, High heritability coupled with moderate genetic advance as per cent of mean was found for number of primary branches and main shoot length. While moderate heritability coupled with moderate genetic advance as per cent of mean was observed days to 50 % flowering, plant height whereas, moderate heritability coupled with low genetic advance as per cent of mean was observed for oil content and days to maturity. In a study conducted by Kaur *et al.* (2022), High heritability along with high genetic advance (GA) was observed for siliquae/ plant, biological yield/ plant and test weight (TW). Singh *et al.* (2018) Kumar *et al.* (2018) Ray *et al.* (2019) and Tiwari (2019) have also reported the same results.

**Table 2: Mean, range, coefficient of variation, heritability (broad sense) and genetic advance as per cent of mean for yield and its attributes of Indian mustard and in their crosses.**

Sr. No.	Character	Mean	Range		Variance		Coefficient of variation		Heritability (broad sense) (%)	Genetic advance (GA)	Genetic advance as per cent of mean (%)
			Min	Max	Genotypic	Phenotypic	Genotypic	Phenotypic			
1.	Days to 50 % flowering	57.73	46.00	68.00	21.14	26.75	7.96	8.96	79.04	8.42	14.59
2.	Days to maturity	135.23	123.00	141.67	17.28	22.56	3.07	3.51	76.60	7.50	5.54
3.	Plant height	185.21	145.33	216.80	172.58	228.18	7.09	8.16	75.63	23.54	12.71
4.	Number of Primary branches	7.05	5.60	8.73	0.50	0.59	10.06	10.90	85.15	1.35	19.12
5.	Number of Secondary branches	16.64	10.67	22.60	6.53	7.06	15.36	15.97	92.52	5.06	30.44
6.	Number of pod on main shoot	47.44	33.87	62.53	32.59	36.85	12.03	12.79	88.46	11.06	23.31
7.	Length of Main shoot	76.45	56.87	97.20	55.96	65.75	9.79	10.61	85.11	14.22	18.60
8.	Pod length	5.03	2.49	6.55	0.47	0.52	13.59	14.28	90.63	1.34	26.65
9.	Number of seeds per pod	11.12	8.53	13.27	1.21	1.43	9.90	10.74	84.94	2.09	18.80
10.	1000-grain weight (g)	4.83	3.17	6.57	0.42	0.46	13.40	14.06	90.89	1.27	26.32
11.	Biological yield per plant (g)	568.35	345.69	885.34	19081.48	19604.76	24.30	24.64	97.33	280.74	49.40
12.	Harvest index (%)	18.19	10.96	34.04	24.73	25.34	27.34	27.67	97.61	10.12	55.64
13.	Oil content	38.55	37.47	40.12	0.21	0.27	1.19	1.34	79.36	0.84	2.19
14.	Grains per plant	99.33	52.37	142.46	415.30	432.10	20.52	20.93	96.11	41.16	41.43

Heritability is the heritable portion of phenotypic variance. It is a good index of transmission of characters from parents to their offspring. The estimates of heritability can prove to be useful for plant breeders in selection of elite genotypes from divergent population. Heritability does not provide any indication towards the amount of genetic progress that would result in selecting best individual rather it depends upon the amount of genetic advance. Hence, for selection of elite genotypes, high heritability coupled with high genetic advance as percent of mean could be considered. In the present investigation, high heritability coupled with high genetic advance as percent of mean were recorded for harvest index,

biological yield per plant, grain yield per plant, number of secondary branches, thousand seed weight, pod length and number of pods on the main shoot which indicated that the traits were controlled majorly by the predominance of additive gene effects thus suggesting the early and simple selection could be exercised due to fixable additive gene effects. High heritability coupled with moderate genetic advance was registered for number of primary branches and main shoot length, indicating that the character is governed by additive genes and may express consistently in succeeding generations, leading to greater efficiency of breeding programme. Moderate heritability coupled with moderate genetic advance as percent of mean was

observed for days to 50 % flowering, plant height indicating that both additive and non-additive gene actions had a role in inheritance and phenotypic selection would be effective.

By and large, in the present study, higher GCV, high heritability and high genetic advance as percent of mean were observed for harvest index, biological yield per plant, grain yield per plant revealed that simple directional selection would be effective for improving these traits with connotation that genetic variation was mainly due to the presence of additive gene effects.

## CONCLUSION

By and large, in the present study, higher GCV, high heritability and high genetic advance as percent of mean were observed for harvest index, biological yield per plant, grain yield per plant revealed that simple directional selection would be effective for improving these traits with connotation that genetic variation was mainly due to the presence of additive gene effects.

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**Conflict of Interest.** None.

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