Journal of Oilseed Brassica, 15 (2) : 252-255, July 2024

Studies on genetic variability for morpho-phenological traits in diversity fixed foundation set of Indian mustard (*Brassica juncea* L)

Sunayana[1]*, Manpreet Singh[1] and Priyanka[2]

[1]*Dr JC Bakhshi PAU Regional Research Station, Abohar 152116, Fazilka, Punjab, India*
[2]*Department of Plant Breeding and Genetics, Punjab Agricultural University, Ludhiana 141004, Punjab, India*
**Corresponding author: sunayanapunia19@pau.edu*

(Received: 30 April 2024; Revised: 30 May 2024; Accepted: 31 May 2024)

Abstract

Indian mustard diversity fixed foundation set of 280 genotypes was undertaken to study the genetic variability, heritability and genetic advance for seed yield and its component traits during 2020-21. The genotypes were evaluated for nine characters to study the extent of genetic variability. Analysis of variance revealed significant genotypic differences for all the nine characters under study which indicate wide range of variation was apparent for all the characters. The genotypic coefficient of variation (GCV) was observed moderate to high for the characters viz., seed yield per plant, 1000-seed weight, main shoot length, number of siliqua on main shoot, primary branches, secondary branches and siliqua length. Number of seeds per siliqua and plant height had lower values of GCV. Low heritability with low genetic advance was noted for number of seeds per siliqua which may be due to low value of estimated phenotypic variance for these traits. Plant height, main shoot length, number of primary branches, number of secondary branches, number of siliquae on main shoot, siliqua length, 1000-seed weight and seed yield per plant possessed substantial to high heritability and genetic advance in the genotypes studied. This variability was due to moderate to high differences in the genetic makeup of genotypes and controlled by additive gene action which revealed that direct selection would be effective for those above mentioned traits. Therefore, due weightage should be given to these characters while selection for improving seed yield in Indian mustard.

Keywords: *Genetic advance, genetic variability, heritability, Indian mustard*

Introduction

On a global scale, India holds the fourth position in the oilseed production economy, following the USA, China, and Brazil. The country contributes to 10% of the world's oilseed production, 6-7% of its vegetable oil output, and approximately 7% of its protein meal production (http://www.icfa.org.in). Rapeseed-mustard stands as one of the principal oilseed crops globally. Following China and Canada, India holds the third spot in rapeseed-mustard production. These crops play a pivotal role, constituting one-third of the overall vegetable oil production and ranking as the second most crucial edible oilseed crop in India, surpassed only by soybean. In the agricultural year 2020-21, rapeseed-mustard cultivation spanned 6.69 million hectares, resulting in a production of 10.11 million tonnes and a productivity of 1511 kg/ha (https://eands.dacnet.nic.in). Rapeseed-mustard share nearly 24% area and 27% production of total oilseeds in the country (https://www.drmr.res.in). Though in trade, rapeseed-mustard is known by single name but they include three *Brassica* species viz., *Brassica juncea*, *B. rapa* and *B. napus*. Among these, Indian mustard (*B. juncea* L. Czern & Coss, 2n = 4x = 36, genome AABB) is a pivotal oilseed crop in Asia. It is mostly cultivated under semi-arid to arid tropical and subtropical regions with nearly 16.8% area under rainfed cultivation (https://eands.dacnet.nic.in).

Information on the nature and magnitude of variability and irritability is one of the prerequisites for a successful breeding program in selecting genotypes with desirable characters (Dudly and Moll, 1969). The effectiveness of any breeding program relies on the genetic variability present in the breeding material. Germplasm, an essential component of breeding programs, serves as valuable source material, offering opportunities for the development of genetic variability. Evaluating variability parameters such as phenotypic and genotypic coefficients of variation, heritability in broad sense, and genetic advance is crucial. It is, therefore, of great importance for breeders to know the heritability of the agronomic characters to improve the yield of the crop effectively. According to Falconer and Mackay (1996), heritability is defined as the measure of the correspondence between breeding values and phenotypic values. Thus, heritability plays a predictive role in breeding, expressing the reliability of phenotype as a guide to its breeding value (Tazeen *et al.,* 2009). There is a direct relationship between heritability and response to selection, which is referred to as genetic advance. High genetic advance with high heritability estimates offers the most effective condition for selection (Larik *et al.,* 2000). The utility of heritability therefore increases when it is used to calculate genetic advance, which indicates the degree of gain in a character obtained under a particular selection pressure. Thus, genetic advance is another important selection parameter that aids breeder in a selection program. With the virtue of this fact the present investigation was undertaken to determine genetic variability, heritability and genetic advance of grain yield and some of its related components to select a more desired trait that may contribute for the improvement of a set of 280 genotypes of Indian mustard.

Material and Methods

The current investigations were carried out at Punjab Agricultural University, Regional Research Station, Abohar Fazilka, Punjab, India during *Rabi* season of 2020-21. The plant material under investigation was an association panel consisting of a diversity fixed foundation set of *B.juncea* (BjDFFS) with very wide genetic base of about 280 lines. It includes historical varieties; exotic *B. juncea* resynthesized *B. juncea*, alloplasmic lines and alien introgression lines. They were characterized for yield and yield related attributes in alpha lattice design with two replications in paired rows of two meters. The sowing was carried out by hand drilling. The experiment and other post-sowing operations were carried out in accordance with the practices recommended for the mustard crop. The data were recorded from five randomly selected plants from each entry in each replication for the characters; plant height (PH in cm), main shoot length (MSL in cm), number of primary branches (PB), number of secondary branches (SB), number of siliquae on main shoot (NSMS), number of seeds/siliqua (NSPS), siliqua length (SL), 1000-seed weight (TSW) and seed yield/plant.

The mean over replication of each character was subjected to statistical analysis. Genotypic and phenotypic variances were computed according to method suggested by (Johnson *et al.,* 1955). Genotypic and phenotypic coefficient of variation (GCV and PCV) were estimated based on formula given by (Burton,1952) and heritability and genetic advance as per cent mean were calculated according to (Allard, 1960) and (Singh and Chaudhury,1985). The analysis was done by using meta-R software.

Results and Discussion

The analysis of variance for different characters is presented in Table 1. Analysis of variance revealed significant genotypic differences for all the nine characters under study, which indicate the presence of high amount of genetic variability was apparent for all the characters studied. The estimates of genotypic (σ^2g) and phenotypic (σ^2p) variances were obtained from analysis of variance. The mean values and variance components were used to compute other genetic parameters *viz.*, heritability in broad sense (H^2 (bs)), genotypic co-efficient of variance (GCV), phenotypic coefficient of variance (PCV) and genetic advance as percent of mean (GA as % of mean) which are presented in Table 2. The perusal of data revealed that there is an ample scope to identify desirable genotypes to improve different characters.

Table 1: Analysis of variance for different nine characters in Indian mustard

Source of Variation	Degree of freedom	Yield (g)	TSW (g)	PH (cm)	MSL (cm)	NSMS (no.)	NSPS (no.)	PB (no.)	SB (no.)	SL (no.)
Replication	1	22.64	0.39	48.44	41.26	8.064	1.06	0.85	0.06	0.02
Genotype	279	16.51**	0.78**	360.78**	105.91**	80.11**	3.55**	0.44**	1.89**	0.57**
Blocks	26	7.64	0.15	50.90	26.04	11.85	1.64	0.19	0.52	0.08
Residual	253	6.80	0.19	63.22	26.70	15.17	2.19	0.14	0.49	0.08

Significant at *5%=1.22; and **1%=1.33 level of probability

A wide range of phenotypic variability was present in respect of plant height, main shoot length and number of siliqua on main shoot. Moderate level of phenotypic variability was found for seed yield per plant, while low level found in 1000-seed weight, number of seeds per siliqua, primary branches, secondary branches and length of siliqua. The phenotypic variation is not the precise criterion for estimation of the amount of genetic variability present in breeding population. The other genetic parameters such as genotypic co-efficient of variation, heritability and genetic advance are important to study the extent of genetic variability more precisely.

Further, the phenotypic variance was partitioned into its genotypic and environmental components to know the genetic variability present in each character. Simple measures of variability, such as phenotypic and genotypic coefficients of variation, are often employed to examine variability. The level of variability present in the population on genetic basis can be estimated using the relative values of coefficient. As a result, components of variation such as the PCV and GCV were computed. The fact that the phenotypic coefficients of variation were slightly greater than the genotypic coefficients of variation indicated that the environment had a significant impact on the expression of the character included in the study. For categorization of PCV and GCV, (Sivasubramanium and Madhavamenon, 1973) suggested a scale as low (less than 10%), moderate (10-20%) and high (more than 20%). For all the character under study higher magnitude of phenotypic coefficient of variation was recorded over genotypic coefficient of variation. The high GCV as well as high PCV were observed for seed yield per plant (20.33%, 31.70%). The moderate GCV as well as moderate PCV was recorded for 1000-seed weight (14.54%, 18.64%), main shoot length (10.50%, 13.58%), number of siliqua on main shoot (13.96%, 16.84%), primary branches (11.67%, 16.39%), secondary branches (14.92%, 19.53%) and siliqua length (10.29%, 11.86%). While the present study indicated that plant height (7.46%, 8.88%) and number of seeds per siliqua (5.78%, 11.60%) showed low coefficient of variability at both genotypic and phenotypic levels. High value of genetic co-efficient of variation indicates the presence of high amount of variability and thereby much more effective for selection. Lower values suggesting that these characters were more influenced by environment and the selection of these characters will not be much effective. Similar findings were also reported by (Bineeta Devi, 2018) and (Trivedi *et al.*, 2016) for number of branch per plant, (Akabari *et al.*, 2015) for 1000-seed weight, (Arpna *et al.*, 2018) for seed yield per plant, (Sushil Kumar, 2013) for palmitic acid, eicosenoic acid and erucic acid, (Bineeta Devi, 2018) and (Akabari *et al.,* 2015) for days to flowering, days to maturity and plant height, (Trivedi *et al.,* 2016) for seeds per siliqua, (Bineeta Devi, 2018) for length siliqua and (Trivedi *et al.,* 2016), (Akabari *et al.,* 2015) and (Sushil Kumar, 2013) for oil content.

Table 2: Mean, range, genotypic, phenotypic and environmental variance, GCV, PCV, heritability (broad sense) and GA as percent of mean for different characters in Indian mustard

Characters	Mean	Range	Genotypic variance	Phenotypic variance	Environmental variance	GCV (%)	PCV (%)	H2 (%)	GA (%)
Yield (g)	10.8	2.8-22.9	4.8	11.7	6.9	20.3	31.7	41.2	26.9
TSW (g)	3.7	1.8-5.8	0.3	0.5	0.2	14.5	18.6	60.8	23.4
PH (cm)	163.7	117.9-216.7	149.4	211.4	62.1	7.5	8.9	70.6	12.9
MSL (cm)	59.9	36-88.3	39.6	66.3	26.7	10.5	13.6	59.8	16.7
NSMS (No.)	40.9	23-61.3	32.6	47.5	14.9	13.9	16.8	68.7	23.8
NSPS (No.)	14.6	10-19.1	0.7	2.9	2.1	5.8	11.6	24.8	5.9
PB (No.)	3.3	1.9-4.9	0.2	0.3	0.1	11.7	16.4	50.7	17.1
SB (No.)	5.6	3-9	0.7	1.2	0.5	14.9	19.5	58.4	23.5
SL (cm)	4.8	3.4-6.3	0.2	0.3	0.1	10.3	11.9	75.3	18.4

Heritability and genetic advance

Coefficient of variation just gives us information about the variability of data for that character but doesn't provide us information about what part of it is heritable. As a result, it is necessary to identify the heritable portion of the total variability, which will enhance the selection effectiveness. If the occurrence of the variance is mostly attributable to additive gene action and assessed in terms of heritability, the breeder can achieve maximal selection response. Using variance component analysis, an attempt was made to quantify heritability in broad sense in the current study. (Johanson *et al.,* 1955) suggested a scale for categorization of heritability *viz;* low (less than 50%), medium (50-70%) and high (more than 70%). In case of the current study highest heritability was observed for siliqua length (75.27%). Moderate heritability was observed for plant height (70.64%) followed by number of siliqua on main shoot (68.70%), 1000 seed weight (60.83%), main shoot length (59.80%), secondary branches (58.40%) and primary branches (50.66%). Low heritability was observed for seed yield (41.17%) followed by number of seeds per siliqua (24.79%). The heritability value is not the clear-cut indicator of genetic improvement that could be achieved by selecting promising lines. The estimates of heritability would be reliable when restricted in terms of broad sense, additive and non-additive gene effects coupled with substantial genetic advance. Genetic advance was estimated as a percentage of mean to make it easier to compare improvement in different traits of various genotypes. The magnitude of genetic advance as percentage of mean was categorized as high (>20%), moderate (10%-20%) and low (<10%). Higher magnitude of genetic advance as percentage of mean was recorded for the character seed yield/ plant (26.87%) followed by number of siliqua on main shoot (23.84 %), secondary branches (23.49%) and 1000-seed weight (23.36%). Moderate genetic advance as percentage of mean was recorded for the siliqua length (18.40%), primary branches (17.11%), main shoot length (16.73%) and plant height (12.92%). While it was observed that genetic advance as percentage of mean was low for the trait number of seeds per siliqua (5.92%). The estimates of heritability and genetic advance are important for the expression of seed yield. These parameters are also helpful in designing breeding programme. Panse (1957) stated that high heritability coupled with high genetic advance indicates the additive gene effects for their inheritance and improvement could be brought about by phenotypic selection. These results are in conformity with (Sushil Kumar, 2013) for oleic acid, (Trivedi *et al.,* 2016) and (Akabari *et al.,* 2015) for 1000-seed weight, (Roy *et al.,* 2018), (Trivedi *et al.,* 2016) and (Akabari *et al.,* 2015) for seed yield per plant. High heritability accompanied with moderate genetic advance indicated the involvement of both additive and non-additive gene action. These results were supported by (Trivedi *et al.,* 2016), (Akabari *et al.,* 2015) and (Bind *et al.,* 2014) for days to flowering and (Roy *et al.,* 2018), (Akabari *et al.,* 2015) and (Bind *et al.*, 2014) for length of siliqua. While high heritability coupled with low genetic advance indicates the non-additive gene effects for control of the particular character are supported by (Akabari *et al.,* 2015) and (Bind *et al.,* 2014) for days to maturity and (Trivedi *et al.,* 2016) and (Bind *et al.,* 2014) for oil content.

Conclusion

It can be concluded that the characters *viz.,* plant height, main shoot length, number of primary branches, number of secondary branches, number of siliquae on main shoot, siliqua length, 1000-seed weight and seed yield/plant possessed substantial to high genetic variability in the genotypes studied. This variability was due to moderate to high differences in the genetic makeup of genotypes and controlled by additive gene action which revealed that direct selection would be effective for those above mentioned traits. Therefore, due weightage should be given to these characters while selection for improving seed yield in Indian mustard.

References

Akabari VR and Niranjana M. 2015. Genetic variability and trait association studies in Indian mustard (*B. juncea*). *Int J Agric Sci* **11**: 35-39.

Allard RW. 1960. Principles of Plant Breeding. John Wiley and Sons, Inc., New York.

Arpna K and Vedna K. 2018. Genetic variability and divergence studies for seed yield and component characters in Indian mustard (*B. juncea*) over environments. *Int J Curr Microbiol Appl Sci* **7**: 3376-3388.

Bind D, Singh D and Dwivedi VK. 2014. Genetic variability and character association in Indian mustard (*B. juncea*). *Agric Sci Dig* **34**: 183-188.

Bineeta Devi. 2018. Correlation and path analysis in Indian mustard (*B. juncea*) in agro-climatic conditions of Jhansi (UP). *J Pharm Phytochem* **7**: 1678-1681.

Burton GW. 1952. Quantitative inheritance in grasses. *Proc 6th Int Grassld Congr* **1**: 227-283.

Comstock RR and Robinson HF. 1952. Genetic parameters, their estimation and significance. *Proc 6th Int Grassld Congr* **1**: 248-291.

Dudly JW and Moll RH. 1969. Interpretation and use of estimates of heritability and genetic variance in plant breeding. *Crop Sci* **9**: 257-267.

Falconer DS and Mackay FC. 1996. Introduction to Quantitative Genetics. Longman, New York. p. 464.

Johnson HW, Robinson HF and Comstock RE. 1955. Estimates of genetic and environmental variability in soybean. *J Agron* **47**: 314-318.

Larik AS, Malik SI, Kakar AA and Naz MA. 2000. Assessment of heritability and genetic advance for yield and yield components in *Gossypium hirsutum*. *Sci Khyber* **13**: 39-44.

Panse VG. 1957. Genetics of quantitative characters in relation to plant breeding. *Ind J Genet Plant Breed* **28**: 225-229.

Roy RK, Kumar A, Kumar S, Kumar A and Kumar RR. 2018. Correlation and path analysis in Indian mustard (*B. juncea*) under late sown condition. *Env Eco* **36**: 247-254.

Singh RK and Chaudhary BD. 1985. Biometrical Methods in Quantitative Analysis. Kalayani Publishers. New Delhi.

Sivasubramanian J and Madhavamenon P. 1973. Genotypic and phenotypic variability in rice. *J Mad Agric* **12**:15-16.

Sushil K. 2013. Genetic analysis of oil content and quality parameters in Indian mustard (*B. juncea*). *J Agric Sci* **3**: 299-304.

Tazeen M, Nadia K and Farzana NN. 2009. Heritability, phenotypic correlation and path coefficient studies for some agronomic characters in synthetic elite lines of wheat. *J Food Agric Env* **7**: 278-282.

Trivedi SD, Singh SK and Kumar R. 2016. Genetic variability, character association and path analysis in Indian mustard (*B. juncea*). *Technofame- J Multidisc Adv Res* **5**: 50-58.