

Original Research Article

<https://doi.org/10.20546/ijcmas.2018.711.002>

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

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ABSTRACT

An experiment was made to assess extant of genetic variability among fifty germplasm accessions of Indian mustard with three check varieties for various quantitative characters, heritability and genetic advance also estimated for such characters. Analysis of variance revealed highly significant differences for all the characters. The genotypes showed moderate to high level of genotypic coefficient of variance (GCV) and phenotypic coefficient of variance (PCV). In general phenotypic coefficient of variance was found to be higher than their genotypic coefficient of variance but the extent was quite small, indicating very less environmental influence on the expression of the characters. Genotypic coefficient of variation (GCV) was found to be higher for 1000-seed weight (24.33), biological yield per plant (22.47), secondary branches plant (22.41), seed yield per plant (19.75). Heritability and genetic advance are important selection parameters. High heritability estimates were observed for biological yield, plant height, oil content, main raceme length, 1000-seed weight, siliqua on main raceme, secondary branches per plant, seed yield per plant and days to maturity. The expected genetic advance as percent of mean was high for 1000-seed weight, biological yield, secondary branches plant, seed yield per plant. High heritability coupled with high genetic advance in per cent of mean as well as high GCV observed for yield components such as 1000-seed weight, biological yield per plant, secondary branches per plant, seed yield per plant, harvest index and siliqua on main raceme, indicates that most likely the heritability is due to additive gene effects so selection may be effective and it would be helpful in predicting the gain under selection.

Keywords

Indian mustard (*Brassica juncea* L. Czern & Coss.), Selection parameters, Genetic variability, Heritability and genetic advance

Article Info

Accepted:

04 October 2018

Available Online:

10 November 2018

Introduction

Brassica juncea is the second most important oilseed crop in the country after groundnut which accounts for nearly 30.7% of the total oilseed production in the country. India's share in global production of mustard oil was

around 9.0 percent in 2015-16. India was the 7th largest oil importing country in 2014-15 (Anonymous 2016). Indian mustard [*Brassica juncea* L. Czern & Coss.], which is cultivated throughout the world belongs to the family Cruciferae (*Brassicaceae*) under the genus *Brassica*, cultivated all over India and it is the

major *rabi* oilseed crop of northern India. It has 38 to 42% oil and 24% protein. Since, *Brassica juncea* is the second most important oilseed crop in the country, it should be emphasized to increase quality and quantity of oil in *Brassica juncea* to provide best diet to our Indians. For the fulfilment of this objective it is essential that the breeding material must contain sufficient amount of genetic variability since, the success of any breeding programme depends upon the genetic variability engraved in the breeding material.

The assessment of parameters including phenotypic and genotypic coefficients of variation, heritability in broad sense, and genetic advance as % of mean is a prerequisite for making effective selection. Information on the nature and magnitude of variability and heritability in a population is one of the prerequisite for successful breeding programme in selecting genotypes with desirable characters. It is therefore, of great importance for breeder to know the heritability of the agronomical characters to improve the yield of the crop effectively. Keeping these point under consideration the present investigation is carried out.

Materials and Methods

An experiment on Indian mustard (*Brassica juncea* L. Czern & Coss) was conducted in Randomized Block Design (RBD) accommodating 50 germplasm accessions along with three check varieties *viz.*, Kranti, Narendra Rai and Vardan during *Rabi 2016-17* at the research farm of Narendra Deva University of Agriculture and Technology, Kumarganj, Faizabad. These genotypes were obtained from various Rapeseed and Mustard centres located across the country. The length of the rows was kept 3 meter with a spacing of 45cm between the rows and 15cm between the plants. All the cultural practices were followed to raise a good crop.

Five competitive plants were randomly selected from each entry in each replication and were tagged for recording detailed field and laboratory observations. Data on various quantitative characters such as plant height(cm), number of primary branches per plant, number of secondary branches per plant, length of main raceme (cm), number of siliqua on main raceme, number of seeds per siliqua, 1000-seed weight(g), biological yield per plant(g), harvest index(%), oil content (%), seed yield per plant(g) were recorded on the basis of five randomly selected plants, while data on two characters such as days to 50percent flowering, days to maturity were recorded on plot basis.

Analysis of variance (ANOVA) for Randomized Block Design for all attributes (major and minor) was done using statistical software. Analysis of variance and the genetic parameters were computed by following standard statistical procedure (Table 1). The mean data were subjected to analysis of variance as per standard procedure outlined by Panse and Sukhatme (1967). The Phenotypic Coefficient of Variation (PCV), Genotypic Coefficient of Variation (GCV) and heritability in broad sense were calculated using the formula suggested by Burton and de Vane (1953). Genetic advance was calculated by the method suggested by Johnson *et al.*, (1955).

Results and Discussion

The analysis of variance exhibited highly significant difference among the genotypes for all the characters indicating the presence of adequate amount of genetic variability among the genotypes. The mean performance of 50 entries of mustard genotypes for 13 characters is presented in (Table 2). The existence of genetic variability in the population provides sample opportunities for selection being effective.

Table.1 Analysis of variance for 13 characters in mustard (*Brassica juncea* L. Czern & Coss)

Source of variation	d. f.	Days to 50% flowering	Days to maturity	Plant height (cm)	Primary branches/Plant	Secondary branches/plant	Main raceme length (cm)	Siliqua on main raceme	Seeds/siliqua	1000-seed weight (g)	Biological yield (g)	Harvest index (%)	Oil content %	Seed yield/plant (g)
Replications	2	0.9866	5.0866	3.12	0.4066	5.0866	1.1266	5.9266	0.14	0.3244	14.6866	0.1667	0.161	5.82
Treatments	49	16.1904**	30.2352**	492.944**	1.5668*	24.296**	128.28**	70.1808**	5.8787**	3.0788**	631.12**	38.23**	3.1634**	28.75**
Error	98	2.3472	3.005	7.2288	1.0121	1.8213	3.4531	3.9334	0.9155	0.1262	4.9859	6.0733	0.071	2.47

*, **Significant at 5% and 1% probability levels, respectively.

Table.2 Estimates of mean, range, coefficients of variation (%), heritability and genetic advance for 13 characters in Indian mustard (*Brassica juncea* L. Czern & Coss)

S. No.	Characters	Mean	Range	Coefficient of variation (%)		Heritability in broad sense (%)	Genetic advance	Genetic advance in (%) of mean
				PCV	GCV			
1.	Days to 50% flowering	41.86	37.00 - 49.00	6.30	5.13	66.30	3.603	8.605
2.	Days to maturity	135.07	119.00 - 139.00	2.57	2.23	75.10	5.379	3.983
3.	Plant height (cm)	188.02	156.33 - 227.66	6.91	6.76	95.70	25.646	13.640
4.	Primary branches/plant	5.81	4.33 - 7.33	18.82	7.39	15.40	0.348	5.989
5.	Secondary branches/plant	12.21	6.00 - 19.33	24.98	22.41	80.40	5.057	41.406
6.	Main raceme length (cm)	64.23	46.66 - 73.66	10.45	10.04	92.30	12.769	19.880
7.	Siliqua on main raceme	44.40	34.66 - 62.66	11.48	10.58	84.90	8.919	20.084
8.	Seeds/siliqua	13.86	11.33 - 17.00	11.56	9.28	64.40	2.126	15.339
9.	1000-seed weight (g)	4.07	2.16 - 6.26	25.84	24.33	88.60	1.924	47.188
10.	Biological yield (g)	64.29	28.33 - 98.66	22.73	22.47	97.70	29.411	45.746
11.	Harvest index (%)	23.65	16.83 - 34.79	17.32	13.83	63.80	5.389	22.778
12.	Oil content%	39.27	37.46 - 41.39	2.67	2.58	93.60	2.023	5.151
13.	Seed yield/plant (g)	14.98	8.00 - 22.33	22.37	19.75	78.00	5.384	35.943

For any sound breeding programme, it is essential to have a large variation in the material at the hand of breeder. The characters of economic important are generally quantitative in nature and exhibited a considerable degree of interaction with the environment.

The phenotypic coefficients of variation (PCV) were invariably slightly higher than their corresponding genotypic coefficients of variation (GCV) due to environmental influence (Table 2). The higher estimates of phenotypic (PCV) and genotypic (GCV) coefficient of variation were observed in the case of 1000-seed weight, secondary branches per plant, biological yield and seed yield per plant can be considered as high because of being very close to 20%. Moderate estimates of PCV as well as GCV were recorded for, Primary branches/plant, harvest index, seeds per siliqua, siliqua on main raceme, main raceme in length. Generally the phenotypic coefficient of variation was higher than genotypic coefficient of variation which indicated that environment played a considerable role in expression of these traits. Relatively smaller values of environmental coefficients of variation (ECV) for these traits suggested that their phenotypic expression is less influenced by environments. Highest genetic variability was observed in Indian mustard for 1000-seed weight, secondary branches per plant as reported by Khan *et al.*, (2006), Roy *et al.*, (2011), Lohia *et al.*, (2013) and Tele *et al.*, (2014).

Knowledge of heritability of a character is important as it indicates the possibility and extent to which improvement is possible through selection Robinson *et al.*, (1949). The efficiency of selection depends upon the magnitude of heritability of traits, because it measures the transmissibility of characters from parents to off-spring. Through the estimates of heritability in biometrical studies

are influenced by method of estimation, generation of study, sample size and environment even through it helps the breeders during selection. The present study revealed that estimates of high heritability for different traits under study viz., biological yield, plant height, oil content, main raceme length, 1000-seed weight, siliqua on main raceme, secondary branches per plant, seed yield per plant and days to maturity, exhibited high estimates of heritability(>75%), while the lowest value by primary branches per plant.

The highest value of genetic advance in per cent of mean was shown by 1000-seed weight (47.18%) while days of maturity (3.98%) had lowest value for this parameter. The character exhibiting high estimates (>20%) of genetic advance in per cent of mean were biological yield (45.74%), secondary branches per plant (41.40%), seed yield per plant (35.94%), harvest index (22.77%) and siliqua on main raceme (20.08%) indicating that direct selection for these traits would be effective for the improvement. Moderate estimates of genetic advance in per cent of mean (10-20%) were recorded for main raceme length (19.88%), seed per siliqua (15.339%), plant height (13.64%) and its low estimate (<10%) was recorded for days of 50% flowering (8.60%), primary branches per plant (5.98%), oil content (5.15%) and days to maturity (3.98%). The character having high heritability with high genetic advance generally indicates that heritability is more due to the additive gene effect and advocated the use of high estimates of heritability along with high magnitude of genetic advance for genetic improvement in any trait through selection. Higher heritability does not always ensure an increased genetic advance. Heritability estimates together with genetic advance are generally regarded to be more useful in predicting the grain through selection (Johnson *et al.*, 1955). High

heritability coupled with high genetic advance in per cent of mean was observed for yield components such as 1000-seed weight, biological yield, secondary branches per plant, seed yield per plant, harvest index and siliqua on main raceme and similar results were also observed by Singh *et al.*, (2004), Upadhyay and Kumar (2009), Amit Singh *et al.*, (2013), Tele *et al.*, (2014), and Akabari and Niranjana (2015).

From all over the analysis, it can be concluded that the experimental material possess sufficient amount of genetic variability for most of the economic traits and a combination of various traits contributing to seed yield. In this study it is found that 1000-seed weight, secondary branches plant, biological yield per plant, Seed yield per plant, length of main raceme and siliqua on main raceme showed maximum potential for effectiveness of selection, since these traits show high GCV, heritability and genetic advance. This would help us in designing the selection methodology which can further be utilized in the breeding programme for improvement of seed yield.

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How to cite this article:

Sarvesh Kr. Maurya, K.N. Maurya, Kanhaiya Lal, Yogendra Singh, Sujit Singh, Brijesh Dixit and Soni Singh. 2018. Assessment of Genetic Variability, Heritability and Genetic Advance in Indian Mustard [*Brassica juncea* L. Czern & Coss.]. *Int.J.Curr.Microbiol.App.Sci*. 7(11): 13-18. doi: <https://doi.org/10.20546/ijcmas.2018.711.002>