

Original Research Article

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Genetic Analysis for Quantitative Traits in Indian Mustard (*Brassica juncea* L. Czern and Cos)

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ABSTRACT

Keywords

Genetic variability, genetic advance, heritability, Indian mustard (*Brassica juncea* L. Czern and Cos)

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The present investigation was carried out with 10 genotypes of Indian mustard for 11 quantitative traits to examine the genetic variability, heritability and genetic advance as per cent of mean at Field Experiment Centre, Department of Genetics and Plant Breeding, SHUATS, Prayagraj in Randomized Block Design with three replications during Rabi, 2021-22. Phenotypic Coefficient of Variation (PCV) was higher than Genotypic Coefficient of Variation (GCV) indicating that these characters are influenced by environment for all the traits. High estimates of PCV and GCV were observed for number of secondary branches/plant, biological yield/plant and number of siliqua/plant. High heritability was recorded for number of siliqua/plant, number of secondary branches/plant, biological yield/plant, number of seeds/siliqua, number of primary branches/plant, harvest index, seed yield/plant and high genetic advance as percentage of mean for number of secondary branches/plant, number of siliqua/plant, biological yield/plant, number of seeds/siliqua and harvest index. High heritability coupled with high genetic advance in percent of mean was observed for number of siliqua/plant, number of secondary branches/plant, biological yield/plant, number of seeds /siliqua, harvest index and number of primary branches/plant. High heritability coupled with high genetic advance indicated that most likely the heritability is due to additive gene effect and selection directly based on these traits would be effective.

Introduction

Indian mustard is cultivated throughout the world. Brassica is the world's third most important oil seed crop. It is popularly known as Indian Mustard (*Brassica juncea* L. Czern and Coss.) also known as brown mustard and Chinese mustard belongs to the genus Brassica of Brassicaceae family (Cruciferae) which is a natural amphidiploid with chromosome number (2n=36). Common names are rai & brown mustard. *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. Globally India accounts for 19.80% and 9.8% of the total acreage and production respectively (USDA). Mustard, rai (*B. juncea*) is very popular among the farmers due to higher yield and greater tolerance against lodging, shattering, drought condition, and relative diseases as well as the saline sodic conditions. It is cultivated over an area of 6.07 million hectares with a production of 7.92 million

tones giving an average productivity of 1304kg/ ha. Rajasthan is the highest mustard producing state which accounts 40.82% of total mustard in the country followed by Haryana (11.73 %), Madhya Pradesh (10.82%), Uttar Pradesh (9.73%), and West Bengal (6.69%) respectively. The estimated area, production and yield of rapeseed-mustard in the world was 36.59 million hectares (mha), 72.37 million tones (mt) and 1980 kg/ha, respectively, during 2018-19. Canada is the world's leading producer of mustard seed followed by India (Directorate of Economics and Statistics). It is the premier oilseed Brassica which covers over 80% of the total area under rapeseed-mustard crops (Rao *et al.*, 2017 and Meena *et al.*, 2017a).

Study of variability, heritability and genetic advance in germplasm will help to ascertain the real potential of the genotype. For efficient selection, estimation of parameters like phenotypic and genotypic coefficients of variation, heritability and genetic advance is pre-requisite. Heritability estimates coupled with genetic advance is helpful in judging the reliability of character for selection. Character with high heritability accompanied by low genetic advance can be improved by intermating superior genotypes of segregating population developed from combination breeding. In the present investigation an attempt has been made to estimate the heritability in broad sense by variance component analysis. The heritability estimates would be dependable if it is limited in a broad sense; additive and non-additive gene effects are accompanied with high genetic advance. The heritability value alone however, provides no indication of the amount of genetic improvement that would result from selection of superior genotypes. To facilitate the comparison of progress in various characters of different genotypes, genetic advance was calculated as percentage of mean.

Materials and Methods

The field trial was carried out at field Experimentation Centre of Department of Genetics and Plant Breeding, Sam Higginbottom University

of Agriculture, Technology and Sciences, Prayagraj, U.P during *Rabi*, 2021-22. The experimental materials comprising of 10 diverse genotypes grown under Randomized Block (RBD) with three replications. The experimental area was divided into 3 blocks of equal size and cash plot size was 1×1m spacing of 45cm between rows and 15 cms between plants. An irrigation channel of 1m maintained between adjacent blocks. All cultural practices essential for the good crop of mustard were applied for obtaining healthy and competitive crop stand. The observations were recorded on five randomly competitive in each entry of each replication for all the characters except days to flowering, days to maturity as these were recorded on plot basis. The data was recorded for 11 quantitative traits viz; days to 50 % flowering, days to maturity, number of primary branches/plant, number of secondary branches/plant, number of siliqua /plant, number of seeds /siliqua, plant height (cm), biological yield/plant (g), harvest index (%), Seed yield/plant (g) and 1000 seed weight (g). Analysis of variance (ANOVA) for Randomized Block Design for all traits 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 (1978). The Phenotypic Coefficient of Variation (PCV), Genotypic Coefficient of Variation (GCV) and heritability in broad sense were calculated using the formula. Genetic advance was calculated by the method suggested by Johnson *et al.*, (1955). The data generated were subjected to statistical analysis to assess the objectives and to identify the high yielding lines besides divergent parents for future hybridization programme.

Results and Discussion

The analysis of variance exhibited highly significant difference among the genotypes for all the traits. This indicates that there was an ample scope for selection of promising lines from the present gene pool for quantitative traits for Indian mustard

improvement. The mean performance of 10 mustard genotypes for 11 quantitative traits is presented in (Table 2).

The existence of genetic variability in the population provides sample opportunities for selection being effective. 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. In general, estimates of phenotypic coefficient of variation (PCV) were found to be higher than their corresponding genotypic coefficient of variation (GCV), this was due to environmental component, which could be attributable to a high degree of genotype-environmental interaction.

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 (>20%) were observed in the case of number of secondary branches/plant, biological yield/plant and number of siliqua/plant. Moderate estimates of PCV as well as GCV (10-20%) were recorded for harvest index, number of seeds/siliqua and number of primary branches/plant. Low estimates of PCV as well as GCV (<10%) were recorded for 1000 seed weight, days to 50% flowering and days to maturity.

Similar findings were reported by Tripathi *et al.*, (2015); Maurya *et al.*, (2018) for high PCV and GCV for number of secondary branches/plant, biological yield /plant. Rout *et al.*, (2019) reported low PCV and GCV for days to maturity and days to 50% flowering.

Knowledge of heritability of a character is important as it indicates the possibility and extent to which improvement is possible through selection. The efficiency of selection depends upon the magnitude of heritability of traits, because it measures the transmissibility of characters from parents to off-

spring. The traits with high heritability estimates showed that variation in these traits was predominately governed by heritable factors, where both genetics and environment play an equivalent roles in the expression ratio of traits. The high heritable values of the considered traits in the present study indicated that those were less influenced by the environment and thus help in effective selection of the traits based on the phenotypic expression by adopting simple method and thereby it enhances the scope of genetic improvement.

The high heritability (>60%) was observed for number of siliqua/plant (91.771%) followed by number of secondary branches/plant (90.181%), biological yield/plant (88.469%), number of seeds/siliqua (84.209%), number of primary branches/plant (83.386%), harvest index (80.835%), and seed yield/plant (62.074%), whereas the moderate heritability (31-60%) was observed for plant height (49.479%) followed by 1000 seed weight (44.02%), days to maturity (40.118%) and days to 50% flowering (37.255%).

The heritability value alone however, provides no indication of the amount of genetic improvement that would result from selection of superior genotypes. The heritability estimates would be dependable if it is limited in a broad sense; additive and non-additive gene effects are accompanied with high genetic advance. To facilitate the comparison of progress in various characters of different genotypes, genetic advance was calculated as percentage of mean. Genetic advance as percent of mean was observed high (>20%) for number of siliqua/plant (42.813%), biological yield/plant (41.779%), number of seeds/siliqua (33.096%), harvest index (32.043%) and number of primary branches/plant (30.823%).

Moderate genetic advance (10-20%) was recorded for seed yield/plant (16.196%) and plant height (11.868%) and low magnitude of genetic advance was recorded for 1000 seed weight (6.762%) followed by days to 50% flowering (2.019%) and days to maturity (1.486%).

Table.1 Analysis of variance for 11 quantitative traits in mustard (*Brassica juncea* L. Czern and Cos.)

| Source of variation | d. f. | Days to 50% percent flowering | Days to maturity | No. of primary branches /plant | No. of secondary branches/ plant | No. of siliqua/ plant | No of seeds/sili qua | Plant height (cm) | Biologic al yield / plant | Seed yield/pl ant | Harvest index (%) | 1000 seed weight (g) |
|---------------------|-------|-------------------------------|------------------|--------------------------------|----------------------------------|-----------------------|----------------------|-------------------|---------------------------|-------------------|-------------------|----------------------|
| Replication | 2 | 3.3990 | 8.3630 | 0.2630 | 0.8520 | 2.7210 | 1.410 | 36.7610 | 336.7580 | 29.7050 | 13.0570 | 0.0370 |
| Treatment | 9 | 4.741* | 8.374* | 2.113** | 12.194** | 4946.187** | 12.009** | 628.695** | 4050.833** | 87.947* | 89.395** | 0.14* |
| Error | 18 | 1.705 | 2.782 | 0.132 | 0.427 | 143.548 | 0.707 | 159.641 | 168.669 | 14.881 | 6.547 | 0.042 |

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

Table.2 Estimates of mean, range, coefficients of variation (%), heritability and genetic advance for 11 characters in Indian mustard (*Brassica juncea* L. Czern & Coss)

| Sl. No. | Traits | Grand mean | Range | | Coefficient of variance(%) | | Heritability (Broad Sense) | Genetic Advance | Genetic Advanceas percent of Mean |
|---------|---|------------|--------|--------|----------------------------|--------|----------------------------|-----------------|-----------------------------------|
| | | | Min | Max | GCV | PCV | | | |
| 1 | Days to fifty percent flowering | 62.67 | 61.33 | 65.33 | 1.605 | 2.63 | 37.255 | 1.265 | 2.019 |
| 2 | Days to maturity | 119.9 | 117.67 | 123.67 | 1.139 | 1.798 | 40.118 | 1.781 | 1.486 |
| 3 | No of primary branches / plant | 4.96 | 4.13 | 6.93 | 16.386 | 17.944 | 83.386 | 1.529 | 30.823 |
| 4 | No of secondary branches / plant | 8.61 | 5.067 | 12 | 23.011 | 24.231 | 90.181 | 3.874 | 45.015 |
| 5 | No of siliqua / plant | 184.43 | 113.6 | 252.87 | 21.695 | 22.647 | 91.771 | 78.959 | 42.813 |
| 6 | No of seeds / siliqua | 11.09 | 7.67 | 13.73 | 17.508 | 19.079 | 84.209 | 3.669 | 33.096 |
| 7 | Plant height (cm) | 152.67 | 135.87 | 180.13 | 8.19 | 11.643 | 49.479 | 18.119 | 11.868 |
| 8 | Biological yield / plant | 166. 83 | 122 | 261.67 | 21.562 | 22.924 | 88.469 | 69.701 | 41.779 |
| 9 | Seed yield / plant | 49.46 | 40.9 | 59.2 | 9.979 | 12.665 | 62.074 | 8.01 | 16.196 |
| 10 | Harvest index (%) | 30.37 | 19.84 | 38.67 | 17.301 | 19.243 | 80.835 | 9.733 | 32.043 |
| 11 | 1000 seed weight (g) | 3.66 | 3.33 | 3.9 | 4.948 | 7.457 | 44.02 | 0.248 | 6.762 |

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 percent of mean was observed for number of siliqua/plant, number of secondary branches/plant, biological yield/plant, number of seeds /siliqua, harvest index and number of primary branches/plant. High heritability coupled with high genetic advance indicated that most likely the heritability is due to additive gene effect and selection directly based on these traits would be effective. Similar results were also observed by Singh *et al.*, (2004); Upadhyay and Kumar (2009); 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 number of secondary branches/plant, biological yield/plant and number of siliqua/plant 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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