UNDER PEER REVIEW

STUDIES ON GENETIC VARIABILITY, CORRELATION COEFFICIENT, HERITABILITY AND PATH ANALYSIS FOR QUANTITATIVE TRAITS IN INDIAN MUSTARD (*Brassica*

Abstract: An experiment was conducted to derived information on genetic variability, heritability and genetic advance gain in twelve genotypes of mustard (*Brassica juncea* L.) during rabi season of 2023-2024 at the field experimentation centre (Pilikothi) of the department of Genetics and Plant Breeding, Tilak Dhari Post Graduate College Jaunpur Uttar Pradesh. In experiment, analysis of variance showed significant differences among the genotypes for all the characters indicating the existence of wide spectrum of variability among the genotypes. The phenotypic coefficient of variation (PCV) was higher than corresponding genotypic coefficient of variation (GCV). The highest estimates (>20%) phenotypic coefficient of variability (29.889%) and genotypic coefficient of variability (29.776%) was recorded for number of secondary branches per plant fallowed by number of siliquae per plant. The lowest estimates (<5%) PCV (4.178%) and GCV (3.177%) observed for days of 50% flowering. Grain yield per plant (g), length of main raceme (cm), number of primary branches per plant, number of seeds per siliquae, 1000-seed weight showed high estimate (<20->10) of PCV and GCV. Days to maturity, plant height (cm), showed moderate estimate (<10->5%) of phenotypic and genotypic coefficient of variability. Days to 50% flowering showed lower values of phenotypic (PCV) and genotypic coefficients of variability. The higher estimates of heritability in broad sense(>75%) were recorded for number of siliquae per plant fallowed by plant height (cm), number of secondary branches per plant, 1000-seed weight (g), number of primary branches per plant, length of main raceme, days to maturity, seed yield per plant and number of seed per siliquae characters 91.454, 99.248, 96.098, 91.573, 91.087, 98.540, 71.001, and 88.231 (in percentage) respectively. Comparatively low estimate of heritability (<75) observed for days to 50% flowering (57.827). Seed yield per plant showed high estimates(>20%) of genetic advance in % of mean (27.430%) followed by number of primary branches per plant (28.234%), length of main raceme (24.484%), number of siliquae per plant(47.151),number of seeds per siliquae (22.761),1000-seeds weight (30.058) and moderate estimates (<20->5%) were days to maturity (16.825%), plant height (15.547) and days to 50% (4.977%) showed low estimates (<5%) of (GA) genetic advance. The character such as number of secondary branches, number of siliquae per plant, seed yield per plant, 1000-seed weight, number of primary branches, length of main raceme, number of seed per siliquae showed high GCV, heritability and genetic advance. Therefore, from the above obtained results it can be concluded that the characters studied are governed by additive gene effect. Hence, adoption for selection of elite genotype on the basis of attributing characters.
Keywords: Genetic variability, heritability, GCV, PCV and Genetic advance.

Introduction: Mustard and rapeseed are significant oil seed crops in India. Mustard and rapeseed belong to the Brassicaceae family. After soybeans, rapeseed-mustard is India's second-most important oil seed crop in terms of both acreage and production. Crop Brassicas are a group of many different kinds of plants that are grown for their vegetables, feed, oils, and condiments. One of the most important agricultural commodities for the economy is the oleiferous Brassica species, commonly referred to as rapeseed-mustard. 53 countries worldwide cultivate rapeseed- mustard, which includes eight distinct species: Indian mustard, Toria, yellow sarson, brown sarson, gobhi-sarson, Karan rai, black mustard, and taramira. India, Canada, China, the European Union, Pakistan, Poland, Bangladesh, and Sweden are the countries that grow rapeseed and mustard worldwide. In 2022–23, the world's rapeseed-mustard production, productivity, and area were 36.59 million hectares (mha), 72.37 million tons (mt), and 1980 kg/ha, respectively. India remains fourth after the

European Union, Canada, and China in terms of area (17.19%) and production (8.54%). India contributes 19.8% and 9.8% of global production and area, respectively. 12.25 lakh hectares, 17.10 lakh tons, and 11.85 q/ha, respectively, were the estimated area, production and productivity of rapseed mustard in uttar pradesh. In Agra, Mathura, Aligarh, Kanpur Auraiya, Unnao and Hathras rapseed mustard is grown. In terms of area, rapseed mustard production, and productivity Mathura is the leading district.

In southern and near-east Iran, wild relatives of *Brassica juncea* have been discovered. Divergent opinions exist on *B. juncea's* origin. It was thought in the late 19th century that*B. juncea* most likely came from China and entered India through a northeastern path unrelated to any Aryan invasion. Vavilov (1949) said that the primary center of origin was Afghanistan and the Central Asian countries that bordered it, while the subsidiary centers of origin were central and western China, Eastern India, and Asia Minor, which included Iran.. Others have suggested several *B. juncea* genesis sites where the probable progenitors, *B. nigra* and *B. campestris,* shared geographic sympatry. There is an evolutionary link between the six species of Brassica crops.Three fundamental diploid species—*B. rapa, B. nigra,* and *B. oleracea*—are involved. The evolution of the basic diploid level and the three amphiploid species *B. napus*, *B. carinata,* and *B. juncea* were caused by pair wise hybridization between these diploid species, which was followed by chromosome doubling. The F1 hybrids created as a result of artificial hybridization between these species demonstrated a high degree of similarity and frequent meiotic pairing among the comparable genomes. When *B. juncea* (AABB; 2n = 36) and *B. rapa* (AA; 2n = 20) are crossed, for example, 10 of *B. juncea's* chromosomes couple with the 10 of *B. rapa*, leaving the remaining 8 as univalent at metaphaseI. Similarly, eight bivalent sare frequently seen during meiosis when *B.nigra* (CC; 2n = 18) is crossed with *B.juncea*, while the remaining ten chromosomes show their identity as univalent. This data unequivocally indicates that hybridization between these two diploid parent species is how *B.juncea* originated.The amphidiploid origin of *B. carinata* and *B. napus* has been confirmed by similar cytogenetic research. A loose secondary link between two or more bivalents is observed in addition to pairing between homologous chromosomes of similar genomes from related species. The idea that the three basic genomes descended from a single parent has been supported by the secondary connection. Initially believed to be 5, the haploid number of this ancestral genome was eventually found to be n = 6.

Materials and Methods:

The present investigation was conducted at Genetics and Plant Breeding research farm of agriculture (Pilikothi), Tilakdhari Post Graduate College, Jaunpur, U.P. The experimental Material consists of 12 genotypes of mustard namely viz. Bhagirathi, Kranti, RH-406, Laxmi, Pusa-Mustard-24, Pusa-Tarak, Seeta, DRMR-IJ-31, RGN-48, Pusa-Mustard-21, BR-40 and Radhika which were obtained from Mustard Resarch Centre at Bharatpur, Rajasthan. All the genotypes were grown in a Randomized Block Design with 3 Replication during Winter season. Plant to Plant and Row to Row distance is maintained at 15 cm. and 30 cm. respectively. Observation were recorded on 5 randomly selected plants from each treatment on 10 characters viz. Days to 50% flowering, Days to maturity, Plant height (cm), Number of primary branches per plant, Number of secondary branches per plant, Length of main raceme(cm), Number of siliquae per plant, Number of seed per siliquae, 1000 Seed weight(gm) and Seed Yield (gm). The data were statistically analyzed for computation of genetic coefficient of variation using appropriate statistical analysis. ANOVA was carried out as per the procedure given [1]. The phenotypic and genotypic coefficient of variance was estimated [2] and heritability in broad sense was estimated as per formula given [3]. The expected genetic advance was calculated by using formula as suggested [4].

Results and Discussion: All ten characters underwent the analysis of variance (ANOVA) for the randomized block design utilized for twelve genotypes, which is shown in Table 1. According to the variance analysis, there was sufficient variability. For each of the ten characters, there were notable difference between the genotypes.

UNDER PEER REVIEW

Table: 1 Analysisofvariancefor10charactersinIndianMustard:

Sourceof variation	Degree of freedom	Days to50% flowering	Daysto maturity	Plant Height (cm)	Length of main raceme (cm)	Primary branches/ plant
Replication	2	4.861	2.694	23.111	4.166	0.049
Treatment	11	13.081**	357.240**	596.57**	153.32**	2.065**
Error	22	2.558	1.755	18.020	4.843	0.061

Sourceof variation	Degree of freedom	Secondary branches/ plant	Siliquae/ plant	Seeds/ siliquae	1000- seeds weight(g)	Seed yield/plant (g)
Replication	2	0.250	1.129	0.861	0.041	3.921
Treatment	11	21.853**	11004.4**	8.838**	1.515**	44.547**
Error	22	0.055	2.673	0.376	0.020	5.338

**,significant at1%probability level

Further, the mean performance (table-2) also showed high significant differences between the characters among the genotypes which show sufficient variability for all the characters.
The results are as follows, Genotype KRANTI take minimum time to 50 % flowering (55.00)days where was genotype DRME-IJ-31 takes maximum time (62.33)days. With respect to days to maturity minimum and maximum days taken by BR-40 (110.00)days and RADHIKA (141.667)days respectively. The genotype PUSA-TARAK obtained minimum plant height (150.00 cm) and maximum was observed for DRMR-IJ-31 (196.333 cm). Similarly, the data obtained from Number of siliquae per plant genotype DRMR-IJ-31 (181.243) minimum siliquae per plant where as KRANTI (373.967) maximum. Genotype RADHIKA (4.580) have minimum Number of primary branches per plant where as maximum for SEETA (7.640). In case of number of seed per siliquae, highest and lowest number of seed per siliquae were obtained by the genotype DRMR-IJ-31 (17.333) and PUSA-MUSTARD-21, LAXMI & SEETA (12.00) respectively. The maximum 1000-seed weight was obtained from PUSA-TARAK (5.90 gm) where as, minimum in BR-40 (4.00 gm). In addition, genotype KRANTI was recorded with maximum number of secondary branches (14.580) where as, minimum in DRMR-IJ-31 (4.770). Similarly, maximum seed yield was reported in genotype SEETA (27.267 gm), while minimum in RH-406 (16.60 gm) and maximum length of main raceme was found in DRMR-IJ-31 (68.733 cm) whereas, minimum in KRANTI (46.600 cm). Similar, findings were reported, which indicate the variability among the genotype for most of the characters under study.

All the variability among the genotype of mustard for all the characters under investigation were analyzed for genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability (broad sense) and genetic advance as per cent of mean given (table 2). In the present investigation, magnitude of GCV for all the characters were less than the corresponding PCV which indicate the influence of environmental components on the characters expression [5-7]. However, the difference between GCV and PCV was relatively small specifying the expression of the characters were highly controlled by genetic factors than the environmental causes. Thus, the selection could be based on the basis of phenotypic performance offering scope for the crop improvement. The phenotypic coefficient of variation (PCV) ranges from 4.178 % to 29.889 %. The high amount of PCV was recorded for number of secondary branches (29.889 %) followed by number of siliquae per plant (22.906 %), seed yield (18.754 %), 1000-seed weight (15.184 %), number of primary branches (14.967 %), length of main raceme (13.048 %) and number of seed per siliquae (12.523 %). And the low amount of PCV were recorded for days to maturity (8.288 %), plant height (8.252 %) and days to 50% flowering (4.178 %).

The amount of genetic coefficient of variation (GCV) ranged from 3.177 % to 29.776 %. Higher magnitude of GCV was recorded for number of secondary branches (29.776 %), followed by number of siliquae per plant (22.897%), seed yield (15.802 %), 1000-seed weight (14.885 %), number of primary branches (14.323 %), length of main raceme (12.453 %) and number of seed per siliquae (11.763 %). And the low amount of GCV were recorded for days to maturity (8.228 %), plant height (7.892 %) and days to 50% flowering (3.177 %).

Heritability estimate provides guide for the selection procedure to be followed by the breeder for improvement of these characters under given environment. The estimates of heritability per cent in broad sense for all the characters range from 57.872% (days to 50% flowering) to99.927% (number of siliquae per plant).Generally higher estimates of heritability in broad sense(>75%) were recorded for number of siliquae per plant fallowed by plant height(cm), number of secondary branches per plant, 1000-seed weight (g), number of primary branches per plant, length of main raceme, days to maturity, seed yield per plant and number of seed per siliquae characters 91.454, 99.248, 96.098, 91.573, 91.087, 98.540, 71.001 and 88.231(in percentage) respectively. Comparatively low estimate of heritability (<75) observed for days to 50% flowering (57.827). The characters such as number of secondary branches, number of siliquae per plant and days to maturity shows high heritability and these similar results are also reported [8-10].

Table 2: Mean, range, genotypic and phenotypic coefficient of variation, heritability (%) in broad sense for different characters in Indian mustard:

Variables	Mean	Range	GCV (%)	PCV(%)	Heritabiliy in broad Sense(%)	GA in % of mean
Days to50% flowering	58.944	55.00-62.33	3.177	4.178	57.827	4.977
Days to maturity	132.306	110-141.66	8.228	8.288	98.540	16.825
Plant height (cm)	174.972	150-196.33	7.892	8.252	91.454	15.547
Length of main raceme	56.492	46.60-68.7	12.453	13.048	91.087	24.484
No. of primary branches	5.706	4.58-7.640	14.323	14.967	91.573	28.234
No. of secondary branches	9.053	4.77-14.58	29.776	29.889	99.248	61.107
No. of siliquae/plant	264.476	181.243-373.967	22.897	22.906	99.927	47.151
No. of seed/siliquae.	14.278	12.0-17.33	11.763	12.523	88.231	22.761
1000-seed weight (gm)	4.742	4.00-5.900	14.885	15.184	96.098	30.058
Seed-yield/plant	22.878	16.6-27.267	15.802	18.754	71.001	27.430

The genetic advance (GA) gives a thought of expected advancement through selection in the next generation. The higher estimate of GA coupled with higher heritability without a doubt indicates the possibility of improvement through selection. Genetic advance (GA) in % of mean shows significant variations for different traits. The GA in percentage of mean ranged from 4.977% (days to 50% flowering) to 61.107% (number of secondary branches per plant). Seed yield per plant showed high estimates(>20%) of genetic advance in % of mean (27.430%) followed by number of primary branches per plant (28.234%), length of main raceme (24.484%), number of siliquae per plant(47.151),number of seeds per siliquae (22.761),1000-seeds weight (30.058) and moderate estimates (<20->5%) were days to maturity (16.825%), plant height (15.547) and days to 50% (4.977%) showed low estimates (<5%) of (GA) genetic advance. The characters such as number of secondary branches, number of siliquae per plant and seed yield coupled with high amount of GCV, hHeritability and Genetic advance as percent of mean. It also shows higher response for selection of high yielding genotypes as these characters are governed by additive gene action. The similar finding also reported in [11-13].

Conclusion:

High heritability coupled with high GCV and genetic advance as percent of mean was observed number of secondary branches, number of siliquae per plant, seed yield per plant, 1000-seed weight, number of primary branches, length of main raceme, number of seed per siliquae and these characters are governed by additive gene effects. Thus the selection for these characters would be quiet effective in enhancing grain yield per plant and also simultaneously its relative attributes. Therefore, emphasis should be paid on the above mentioned traits for improving the productivity during selection.

References:

1. Panse, V.G., Sukhtame, P.V. (1967). Statistical Methods for Agricultural Workers (2nd eds.).Indian Council of Agriculture Research, New Delhi.

2. Burton, G.W., de Vane, E.H. (1953). Estimating heritability in tall fiscue (Festuca arundinacea) from replicated clonal materials. J Agron.45:478- 481.

3. Singh, R.K. and Chaudhary, B.D. (1977). Biometrical methods in quantitative genetic analysis. Kalyani Publishers, New Delhi. 318 p.

4. Robinson, H.F., Comstock, R.E. and Harvey. P.H. (1949). Estimates of heritability and the degree of dominance in Corn. Agron. J.. 41: 353-359.

5. Ghosh, S.K. and Gulati, S.C. (2001). Genetic variability and association of yield components in Indian mustard. (Brassica juncea L.). Crop Res. Hisar. 21 (3): 345-349.

6. Lekh, Raj, Singh, H. and Singh, V.P. (1998). Variability studies in rapeseed and mustard. Ann. Agric. Res. 19 (1): 87-88.

7. Muhammad Akbar; Saleem Usman, Muhammad Tahira Yaqub and Iqbal Nasim (2007)/(2009). Utilization of genetic variability, correlation and path analysis for seed yield improvement in mustard Brassica juncea. L. Agril. Res. Lahore. 45(1): 25-31.

8. Mondal, S.K. and Khajuria, M.R. (2000). Genetic analysis for yield attributes in mustard. Environ. and Ecology. 18 (1): 1-5.

9. Prasad, Lalta, Singh, Mahak and Dixit, R.K. (2001). Analysis of heritability and genetic advance in Indian mustard [Brassica juncea (L.) Czern and Coss.]. Adv. in Pl. Sci. 14 (2): 577-581.

10. Singh, A., Yadav, T.P. and Gupta, V.P. (1975). Heritability and Correlations for oil content and yield components in raya (B. juncea Coss.) SABRAO J. 7(1): 85-89.

11. Das, K, Barua, P.K. and Hazarika, G.N. (1998). Genetic variability and correlation in Indian mustard. J. Agric. Sci. 11 (2): 262- 264.

12. Hussain, S., Hazarika, G.N. and Barua, P.K. (1998). Genetic variability, heritability and genetic advance in Indian rapeseed (Brassica campestris L.) and mustard (B. juncea Czern and Coss). 11 (2): 260-261.

13. Kumar, S. and Sangwan, R.S. (1994). Genetic variability, heritability and genetic advance in Brassica species under dryland conditions. Agric. Sci. Digest Karnal. 14 (3-4): 172-176.