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Studies on Genetic Variability, Heritability and Genetic Advance for Seed Yield and its Components in Indian Mustard [*Brassca juncea* (L.) Czern & Coss.]

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ABSTRACT: India is the second largest rapeseed–mustard cultivating country in the world after China and third in production after China and Canada, rapeseed-mustard holds a prominent place in the country's economy. The present investigation has been carried out to study the inter-relationships and direct and indirect effects of yield contributing traits toward seed yield. The experiment was carried out at the Research Farm, Institute of Agriculture Science, Bundelkhand University, Jhansi (U.P.). The experimental material comprising 100 treatments *viz*., (10 parents + 45 F_1's + 45 F_2's) were evaluated in Randomized Block Design with three replications during *rabi* 2021-2022 to assess the extent of variability present among genotypes and strains of Indian mustard. The data were recorded for fourteen quantitative characters. In F_1 generation estimates of heritability in broad sense were observed high for 1000-seed weight (95.27%) followed by number of primary branches per plant while in F_2, observed high for test weight (95.66%) followed by number of primary branches/plant (93.66%). High estimates for genetic advance were recorded for 1000-seed weight and number of primary branches per plant (23.02 and 28.15% in F_1 and F_2) respectively. High heritability and high genetic advance were observed for 1000-seed weight and number of primary branches per plant in both generations. This showed the preponderance of additive gene action in the inheritance of test weight hence, selection would be rewarding.

Keywords: Indian mustard, *Brassica juncea*, heritability, variability, genetic advance, GCV, PCV.

INTRODUCTION

Brassica juncea (L.) Czern & Coss (AABB) is the second most important edible oilseed crop in India after the soybean (Saroj *et al.,* 2021). Cytological studies have revealed that *B. juncea* is a natural allotetraploid or amphidiploid (2n=36), of two diploid species *viz*., *Brassica rapa* (also known as *Brassica campestris*) (AA) (2n=20) and *Brassica nigra* (BB) followed by natural chromosome doubling (2n=16) (Tomar *et al.,* 2017; Tarkeshwar *et al*., 2022a). The species has probably evolved in the Middle East, where its putative diploid progenitors are sympatric (Prakash and Hinata 1980; Singh *et al*., 2022).

India is the second-largest rapeseed–mustard-cultivating country in the world after China and third in production after China and Canada (Kumari *et al.,* 2019). During 2018–2019, rapeseed–mustard was cultivated over an area of 5.96 million hectares with production and productivity of 8.32 million tons and 1,397 Kg/ha, respectively in India (Directorate of Economics & Statistics, and Dac & Fw., 2019).

The existence of genetic variability in any plant population or genetic stock is the pre-requisite for any crop improvement programme. Available genetic stocks with effective variability are the store house of desirable genes for various traits. Hence, before planning a breeding programme, knowledge of important genes and extent of variability present among genotypes is utmost criteria. Thus, the present investigation has been conducted to estimate the extent of variability and heritability for various traits in Indian mustard.

MATERIALS AND METHODS

Experimental Details. The experiment was carried out at the Research Farm, Institute of Agriculture Science, Bundelkhand University, Jhansi (U.P.). The basic material in the present investigation comprised ten varieties/strains of Indian mustard namely, Urvashi, Azad Mahak, R.H.30, Pusa Mustard-25, Kranti, Pusa Mahak-7, NDR-8501, Bio-902, CS-52 and NRCDR-2 were taken from the germplasm maintained at Oilseed Section, Department of Genetics and Plant Breeding, Chandra Shekhar Azad University of Agriculture and Technology, Kanpur (U.P.). Ten genetically diverse genotypes of Indian mustard were subjected to diallel fashion mating design (excluding reciprocals) was attempted during *rabi* 2019–2020. The F_1 seeds of 45 crosses were advanced during the Rabi season of 2020-2021 to raise the F_1's and were selfed in order to obtain F_2's seeds. The parents were also maintained through selfing. The experimental material comprising 100 treatments *viz*., (10 parents + 45 F_1's + 45 F_2's) were evaluated in RBD with three replications during *rabi* 2021-2022. Each parent, F_1's and F_1's planted in one row of 5m long 45cm apart; plant to plant distance was maintained 15cm by thinning. All the recommended packages of practices were adopted for raising a good crop.

Observations Recorded. Five competitive plants in parents, F_1's as well as F_2's were taken randomly for each treatment in each replication and tagged for recording fourteen quantitative traits *viz*., days to 50% flowering, days to maturity, leaf area index (cm^2), plant height (cm), number of primary branches per plant, number of secondary branches per plant, length of main raceme (cm), number of siliquae on main raceme, number of seeds per siliqua, biological yield per plant (g), harvest index (%), 1000-seed weight (g), oil content (%) and seed yield per plant (g).

Statistical Analyses. Theaverage from the five competitive plants was calculated and data were then subjected to estimate the various statistical analyses as Analysis of variance (ANOVA) for R.B.D. (Panse and Shukhatme 1988), Heritability in broad sense (Hanson, 1963) and Genetic advance and genetic advance in percent of mean (Johnson *et al.,* 1955), genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) (Burton, 1952) respectively.

RESULTS AND DISCUSSION

Analysis of Variance. The combined analysis of variance (ANOVA) for parents and their forty-five each F_1's and F_2's for all the above fourteen characters' mean sum of squares are presented in Table 1. Significant differences were observed among the treatments (parents, F_1's and F_2's) for all the fourteen attributes under investigation. ANOVA for parents and hybrids showed significant differences among all the traits studied except length of main raceme in F_1 and plant height and oil content in F_2. Similar observations were also reported by Mahendra *et al.* (2020).

Table 1: ANOVA of Randomized block design for 14 traits of Indian mustard.

Characters	Replications	Treatments	Error
	2 d.f	**99 d.f**	**198 d.f**
Days to 50% flowering	0.05	18.78**	1.43
Days to maturity	0.19	32.37**	9.32
Plant height (cm)	0.51	244.62**	22.72
Length of main raceme (cm)	1.59	62.10**	3.01
Leaf area index	0.00	0.08**	0.005
Number of primary branches/plant	0.03	3.04**	0.07
Number of secondary branches/plant	0.12	11.78**	0.52
Number of siliquae/plant	15.66	2894.54**	158.4
Number of seeds/siliqua	0.85	3.32**	0.36
1000-seed weight (g)	0.00	2.03**	0.03
Biological yield/plant (g)	6.4	27.38**	1.38
Harvest index (%)	8.01	13.96**	1.36
Oil Content%	0.01	10.99**	2.24
Seed yield/plant (g)	1.08	7.57**	0.42

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

Mean performance of Parents, F_1's and F_2's. The mean values for all the fourteen characters for parents, F_1's and F_2's, and variability expressed in terms of mean and ranges are presented in Table 2. The variation amongst the parents, F_1's and F_2's was found highly significant for all the fourteen attributes. However, the magnitude varied from character to character.

In comparison with parents and F_1, the variation in parents was ranged from 51.00 to 56.00 days for days to 50% flowering with mean of 53.40 days, 124.67 to 132.67 days with mean value of 128.47 days for days to maturity, 172.97 to 204.41 cm with mean of 187.93 cm for plant height, 72.42 to 91.04 cm with mean of 80.60 cm for length of main raceme, 1.52 to 2.02 with mean of 1.80 for leaf area index, 5.76 to 8.29 with mean 6.89 for number of primary branches/ plant, 16.26 to 21.27 with mean of 18.92 for number of secondary branches/plant, 264.74 to 375.24 with mean of 333.96 for number of siliquae/plant, 13.46 to 16.45 with mean of 15.10 for number of seeds/siliqua, 3.16 to 4.94 with mean of 4.30 g for 1000-seed weight, 52.07 to 60.57 g with mean of 57.03 g for biological yield/plant, 25.46 to 29.19 with mean of 27.39 per cent for harvest index, 37.05 to 41.56 with mean of 39.62 per cent for oil content and 13.40 to 17.45g with mean of 15.62 g for seed yield/plant.

Among the F_1's, the range lies between 46.67 to 54.33 with mean of 50.82 days for days to 50% flowering, 117.33 to 130.67 with mean of 124.98 days for days to maturity, 162.65 to 200.71 with the mean of 183.12 cm for plant height, 73.83 to 87.34 with mean of 80.32 cm for length of main raceme, 1.64 to 2.13 with mean of 1.90 for leaf area index, 6.10 to 9.08 with mean of 7.35 for number of primary branches/plant, 17.64 to 22.92 with mean of 20.01 for number of secondary branches/plant, 288.38 to 392.98 with the mean of 349.85 for number of siliquae/plant, 14.36 to 17.54 with 15.92 for number of seeds/siliqua, 3.38 to 6.04 g with the mean of 4.68 for 1000-seed weight, 55.67 to 67.64 g with mean of 60.82 g for biological yield/plant, 24.18 to 33.44 with mean of 28.32 per cent for harvest index, 37.45 to 44.12 with mean of 40.47 per cent for oil content and 14.48 to 20.48 g with the mean of 17.21 g for seed yield/plant.

In comparison with parents and F_2, the variation in parents ranged from 52.67 to 57.67 days for days to 50% flowering with mean of 54.93 days, 126.33 to 134.33 days with mean value of 130.13 days for days to maturity, 168.00 to 199.44 cm with mean of 182.96 cm for plant height, 67.20 to 82.19 cm with mean of 74.56 cm for length of main raceme, 1.35 to 1.84 with mean of 1.865 for leaf area index, 4.60 to 7.12 with mean 5.72 for number of primary branches/ plant, 13.57 to 18.88 with mean of 16.23 for number of secondary branches/plant, 245.33 to 362.24 with mean of 312.12 for number of siliquae/plant, 12.51 to 15.17 with mean of 13.79 for number of seeds/siliqua, 3.05 to 4.86 with mean of 4.33 g for 1000-seed weight, 50.72 to 57.59 g with mean of 54.70 g for biological yield/plant, 23.86 to 28.15 with mean of 26.61 per cent for harvest index, 36.60 to 40.81 with mean of 39.27 per cent for oil content and 12.56 to 16.14g with mean of 14.56 g for seed yield/plant.

Among the F_1's, the range lies between 45.00 to 53.67 with mean of 49.53 days for days to 50% flowering, 116.00 to 127.33 with mean of 122.39 days for days to maturity, 159.32 to 195.87 with the mean of 178.66 cm for plant height, 73.20 to 90.85 with mean of 80.41 cm for length of main raceme, 1.62 to 2.19 with mean of 1.94 for leaf area index, 6.09 to 9.22 with mean of 7.42 for number of primary branches/plant, 17.96 to 23.38 with mean of 20.27 for number of secondary branches/plant, 292.14 to 401.75 with the mean of 355.53 for number of siliquae/plant, 14.13 to 17.86 with 15.99 for number of seeds/siliqua, 3.47 to 6.13 g with the mean of 4.73 for 1000-seed weight, 55.95 to 68.68 g with mean of 61.62 g for biological yield/plant, 23.56 to 33.09 with mean of 28.26 per cent for harvest index, 37.46 to 44.69 with mean of 40.62 per cent for oil content and 14.66 to 20.73 g with the mean of 17.41 g for seed yield/plant. When all the three populations *i.e.,* parents, F_1's and F_2's were considered simultaneously, the extent of variability differed from parents' *vis-a-vis* F_1 hybrids and parents' *vis-a-vis* F_2 progenies. Similarly, F_1 hybrids expressed greater variability in eleven attributes out of fifteen in comparison of the F_2 progenies in their investigation had also reported the almost similar results for most of these traits for parents and their F_1's.

Heritability and Genetic advance. The estimates of heritability (broad sense) and genetic advance in per cent over mean of the trait for all the 14 characters in F_1 and F_2 generations were determined. The findings on these parameters are given in Table 2.

Table 2: Mean, Range, heritability, genetic advance, genotypic and phenotypic coefficient of variation for 14 traits.

Characters	Mean		Min.		Max.		Heritability (%)		GA		GA% mean		GCV (%)		PCV (%)	
	F_1	F_2	F_1	F_2	F_1	F_2	F_1	F_2	F_1	F_2	F_1	F_2	F_1	F_2	F_1	F_2
Days to 50% flowering	51.29	49.53	46.67	45.00	56.00	53.67	79.30	79.75	4.27	4.55	8.32	8.62	4.54	4.68	5.09	5.25
Days to maturity	125.61	122.39	117.33	116.00	132.67	127.33	57.14	35.19	4.92	2.90	3.92	2.28	2.52	1.86	3.33	3.14
Plant height (cm)	184.00	178.66	162.65	159.32	204.41	195.87	85.01	69.30	19.13	12.75	10.39	6.98	5.47	4.07	5.94	4.89
Length of main raceme (cm)	80.37	80.41	72.42	73.20	91.04	90.25	88.01	82.35	7.95	7.56	9.89	9.94	5.12	5.32	5.45	5.86
Leaf area index	1.88	1.94	1.52	1.62	2.13	2.19	80.66	84.36	0.28	0.28	14.64	15.83	7.91	8.37	8.81	9.11
No. primary branches/plant	7.26	7.42	5.76	6.09	9.08	9.22	89.75	93.36	1.67	1.72	23.02	28.15	11.80	14.14	12.45	14.64
No. secondary branches/plant	19.81	20.27	16.26	17.96	22.92	23.38	78.93	85.66	2.79	2.95	14.07	17.23	7.69	9.04	8.66	9.76
Number of siliquae/plant	346.96	355.53	264.74	292.14	392.98	401.75	84.05	88.29	57.33	59.80	16.52	18.28	8.75	9.44	9.54	10.05
Number of seeds/siliqua	15.77	15.99	13.46	14.13	17.54	17.86	65.18	70.25	1.41	1.49	8.95	10.26	5.38	5.94	6.67	7.09
1000-seed weight (g)	4.61	4.73	3.16	3.47	6.04	6.13	95.27	95.66	1.62	1.60	35.05	35.33	17.43	17.54	17.86	17.93
Biological yield/plant (g)	60.13	61.62	52.07	55.95	67.64	68.68	86.51	79.09	5.81	3.89	9.66	6.85	5.04	3.74	5.42	4.21
Harvest index (%)	28.15	28.26	24.18	23.56	33.44	33.09	76.58	74.83	3.66	3.60	13.01	13.02	7.22	7.31	8.25	8.45
Oil Content%	40.32	40.62	37.05	37.46	44.12	44.69	54.15	54.84	2.55	2.48	6.32	6.26	4.17	4.10	5.67	5.54
Seed yield/plant (g)	16.92	17.41	13.40	14.66	20.04	20.73	83.11	86.83	2.83	2.80	16.74	17.85	8.91	9.30	9.78	9.98

The estimates of heritability in broad in sense varied from 54.15% (oil content) to 95.27% (1000-seed weight) in F1 and 35.15% (days to maturity) to 95.66% (1000-seed weight) in F_2 generation, respectively.

In F_1 generation estimates of heritability in broad sense were observed high for 1000-seed weight (95.27%) followed by number of primary branches per plant (89.77%), length of main raceme (88.01 %), biological yield/plant (86.51%), plant height (85.1%), number of siliquae/plant (84.05%), seed yield/plant (83.11%), leaf area index (80.66%), days to 50% flowering (79.30%), number of secondary branches/plant (78.93%) and harvest index (76.58%). Moderate values of heritability were observed for days to maturity (57.14%) and oil content (54.15%).

In F_2 generation estimates of heritability in broad sense were observed high for test weight (95.66%) followed by number of primary branches/plant (93.66%), number of siliquae/plant (88.29%), seed yield/plant (86.83%), number of secondary branches/plant (85.66%), leaf area index (84.36%), length of main raceme (82.35%), days to 50% flowering (79.75%), and biological yield/plant (79.09%). While, moderate values of heritability were observed for oil content (54.84%) and low values for days to maturity (35.15%).

The estimates of genetic advance in per cent over mean was calculated for all 14 characters. The arbitrary scale for genetic advance suggested that if estimated value of genetic advance if, less than 10%, it is low, if it is ranged between 10 to 20 per cent, it is medium and above 20%, it is high.

The estimates of genetic advance in per cent over mean of the character ranged from 3.92% (days to maturity) to 35.05% (1000-seed weight) in F_1's and 2.28% (days to maturity) to 35.33% (1000-seed weight) in F_2 generation. High estimates for genetic advance were recorded for 1000-seed weight and number of primary branches per plant (23.02 and 28.15% in F_1 and F_2) respectively. Moderate genetic gain was observed for number of leaf area index (14.54 and 15.83%), number of secondary branches per plant (14.07 and 17.23%), number of siliquae/plant (16.52 and 18.28%), harvest index (13.01 and 13.02%) and seed yield per plant (16.74 and 17.85%) in both F_1 and F_2 generations, and plant height (10.39%) in F1 generation only. Rest of the traits in both the generations exhibited low estimates of genetic advance in percent of mean. Similar findings were reported by Rout *et al.* (2019); Gadi *et al.* (2020).

Genotypic and Phenotypic coefficient of variation. The higher values of genotypic coefficient of variation (GCV) along with phenotypic coefficient (PCV) were recorded for 1000-seeds weight followed by number of primary branches per plant as presented in Table 2.

CONCLUSION

High heritability and high genetic advance were observed for 1000-seed weight and number of primary branches per plant in both generations. It was mainly due to additive gene effects and selection would be effective for these traits. The trait 1000-seed weight also showed the high GCV along with PCV indicates the additive gene action so selection of genotypes would be rewarding for the aforesaid trait.

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Conflict of Interest. None.

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