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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 contributes greatly to rapeseed-mustard production globally and is the largest grower of rapeseed-mustard, occupying the first position in the area and second position in production after China. Rapeseed-mustard are important crops that help meet the demand for domestic oil seeds. Given India's high population, there is a pressing need to increase the production of oil seed in the country. Therefore, the current study aims to analyze different genetic parameters in mustard to plant strategies for the development of high-yielding varieties of Indian mustard. Given this, an experiment was planned and sowing of the experimental material was done at the Oilseed Research Farm of the Chandra Shekhar Azad University of Agriculture & Technology (CSAUA&T), Kanpur. The experimental material comprising 100 treatments (10 parents + 45 F₁'s + 45 F₂'s) were grown in Randomized Block Design in three replications during rabi season (2021-22) following standard agronomic practices. The observations on seventeen quantitative characters were recorded. Significant differences were observed among the treatments (parents, F_1 's and F_2 's) for all the 17 characters under study in the combined analysis of variance (ANOVA). High heritability along with high genetic advance was recorded for main axis height (cm), total siliqua per plant, biological yield per plant, and seed yield per plant in F_1 and F_2 generations. Main axis height (cm), number of secondary branches per plant, total siliqua per plant, siliqua length(cm), biological yield per plant (g), and seed yield per plant showed high to moderate PVC and GCV. This showed the preponderance of additive gene action in the inheritance of test weight hence, selection based on test weight i.e., seed size would be rewarding.

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

INTRODUCTION

Brassica juncea (L.) Czern and Coss. belongs to the family Cruciferae (Brassicaceae), and is one of the most important edible oil seed crops in India. Rapeseed mustard are among the major contributors to India's edible oil seed production accounting for about 27% of the total area under various oil seed crops. Brassica juncea shares more than 80% of the total rapeseedmustard production in the country. Vavilov (1949) suggested Afghanistan and its adjoining regions (Central Asia) were the primary centres of its origin, while central and western China, Eastern India, and Asia Minor comprising Iran were the secondary centres of origin. The B. juncea and its wild forms and progenitor's species B. rapa and B. nigra are found in abundance in the Middle East (Olsson, 1960a, b; Mizushima and Tsunda 1967; Prakash and Hinata 1980). Later, it was widespread to different geographies such as Europe, Africa, North America, and Asia. Several authors believe that Eastern India, the

Caucasus, and China are the main genetic centres for *Brassica juncea*.

India is a significant contributor to the global production and consumption of rapeseed-mustard in the world in fact it is the largest grower of rapeseedmustard, occupying the first position in area and second position in production after China. Rapeseed and mustard production has increased by 40% from 91.24 to 128.18 lakh tonnes in the last 3 years. The productivity has also witnessed an increase of 11% from 1331 to 1447 kg/ha. The area under rapeseed and mustard was up by 29% from 68.56 lakh ha in 2019-20 to 88.58 lakh ha in 2022-23. (PIB 2023). Though there has been an increase in the production and productivity of this crop, indigenous production of rapeseed and mustard is not sufficient to meet domestic demand. Therefore, sincere efforts for the development of high-yielding varieties are the need of the day.

The success of any breeding programme depends on the variability present for the targeted traits and their exploitation systematically. The knowledge of genetic parameters helps in planning of an effective

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hybridization programme and selection strategy. The breeding plans to develop high-yielding varieties in crop plants; requires basic information for selecting parents to be used in hybridization programme. Parents with effective variability and storehouse of desirable genes for various traits are needed to be used in a breeding programme. Hence, the prerequisite of planning a breeding programme is knowledge about the genetic architecture, the extent of variability, transferability of any trait to the progenies (heritability), and expected genetic advance. Thus, in the present study the extent of variability present, heritability, and expected genetic advance due to selection of desirable types in Indian mustard has been estimated.

MATERIAL AND METHOD

Experimental details: The experiment was carried out at Oilseed Research Farm, (CSAUA&T), Kanpur (Uttar Pradesh) which is located at an altitude of 127 meters above the mean sea level and the altitude and longitude with 26.40°N and 80.10°E, respectively. The basic experimental material for the present investigation comprised ten varieties/ strains of Indian mustard namely, Varuna, Urvashi, Azad Mahak, RH-749, Maya, IJ-31, KMR 17-3, KMR 17-4, RH-406 and NRC-DR-2 which were collected from the germplasm maintained at Oilseed Section, Department of Genetics and Plant Breeding, CSAUA&T, Kanpur. All 10 genotypes were crossed in diallel mating design (excluded reciprocal crosses) in all possible combinations to produce sufficient F₁ seeds of 45 cross combinations during 2019-20 and the mature seeds were harvested separately and procured individually. Half of the F_1 seeds from each cross were procured during 2019-20 were grown in order to obtain source seed for F₂ generation and the parents were selfed during 2020-21 and mature seeds were harvested separately and procured.

In the final trial 100 treatments (10 parents + 45 F_1 's + 45 F_2 's) were grown in Randomized Block Design in three replications during rabi season (2021-22) following standard agronomic practices for raising a good crop. Each parent and F_1 's were planted in one row, and F_2 's in two rows 5m long and 45cm apart, Plant to plant distance was maintained 15cm by thinning

Observation recorded: Ten plants in parents and F_1 's and 20 plants in F_2 's were taken randomly for each treatment in each replication and tagged for recording observations for the following characters plant height (cm), main axis height (cm), leaf area index, chlorophyll content, number of primary branches per plant, number of secondary branches per plant, number of secondary branches per plant, siliqua length(cm), number of seeds per siliqua, biological yield per plant (g), 1000-seed weight (g), harvest index (%), oil content (%) and seed yield per plant (g)for seventeen agronomic traits.

Statistical Analyses: The mean values from the five competitive plants were calculated and data were subjected to various statistical analyses such as Analysis of Variance (ANOVA) for Randomized Block

Design following Panse and Shukhatme (1965), heritability in broad sense as per procedure suggested by Kempthorne and Curnow (1961), genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV) as per Burton and de Vane (1953) and genetic advance in percent of mean following Johnson *et al.* (1955) respectively.

RESULTS AND DISCUSSION

Analysis of variance: The combined analysis of variance (ANOVA) was performed using mean values of seventeen agronomic traits of the parents and their 45 F_1 's and 45 F_2 's. Significant differences were observed among the treatments (parents, F_1 's, and F_2 's) for all the 17 attributes under study. Parents vs. F_1 's exhibited significant differences for all the characters except days to maturity and seeds per siliqua. Parents vs. F_2 's significant differences for all the characters except days to 50% flowering and leaf area index. Similar observations were also reported by Yadav *et al.* (2021) in Table 1.

Mean performance of Parents, F₁'s and F₂'s: The mean values for all the seventeen characters for parents, F₁'s and F₂'s, and variability expressed in terms of mean and ranges are presented in Table 2. The variation amongst the parents, F₁'s and F₂'s was found highly significant for all 17 characters including seed yield. However, the magnitude varied from character to character. The values of mean differed from 71days for days to 50% flowering, 78days for days to reproductive maturity, 173.10 cm for plant height, 62.90 cm in main axis height, 1.61 for leaf area index, 49.29 mg/gm to 41.83mg/g for chlorophyll content, 6.35 for number of primary branches/plant, 9.54 for number of secondary branches/plant, 35.46 for siliqua on main axis, 234.03 for total siliqua per plant, 3.21cm for siliqua length, 14.04 for number of seeds/siliqua, 56.05 g for biological yield/plant, 5.06 g for 1000-seed weight, 26.99 percent for harvest index, 39.00 percent oil content and 14.39 g for seed yield/plant in parents.

Among the F₁'s, the mean was 72 days for days to 50% flowering, 77days for days to reproductive maturity, 207.99 cm for plant height, 69.73 cm in main axis height, 1.77 for leaf area index, 40.11 mg/g for chlorophyll content, 8.86 for number of primary branches/plant, 14.51 for number of secondary branches/plant, 42.06 for siliqua on main axis, 386.03 for total siliqua per plant, 3.70 cm for siliqua length, 14.17 for number of seeds/siliqua, 54.59 g for biological yield/plant, 5.58 for 1000-seed weight, 28.19 per cent for harvest index, 39.64 per cent for oil content and 16.17 g for seed yield/plant.

Among F₂'s, the mean was 71 days for days to 50% flowering, 76 days for days to reproductive maturity, 201.68 cm for plant height, 66.93 cm in main axis height, 1.61 for leaf area index, 40.70 mg/gm for chlorophyll content, 6.30 for number of primary branches/ plant, 12.40 for number of secondary branches/plant, 41.34 for siliqua on main axis, 284.07 for Total siliqua per plant, 3.52 cm for siliqua length, 14.72 for number of seeds/siliqua, 60.22 g for biological yield/plant, 5.28 g for 1000-seed weight,

26.77 per cent for harvest index, 37.75 per cent for oil content and 17.13 g for seed yield/plant.

In parents, the range of mean lies between 65.07 to 73.46 days for days to 50% flowering, 71.12 to 81.35 days for days to reproductive maturity, 156.01 to 188.87 cm for plant height, 52.24 cm to 72.12 cm in main axis height, 1.35 to 1.88 for leaf area index, 39.27 mg/gm to 41.83 mg/g for chlorophyll content, 5.06 to 7.05 for number of primary branches/plant, 8.01 to 11.41 for number of secondary branches/plant, 32.07 to 40.21 for siliqua on main axis, 195.53 to 264.83 for Total siliqua per plant, 3.08 cm to 3.41 cm for siliqua length, 13.62 to 14.42 for number of seeds/siliqua, 48.55 to 65.69 g for biological yield/plant, 4.58 to 5.82 g for 1000-seed weight, 24.42 to 28.73 percent for harvest index, 37.88 to 40.70 percent for oil content, 13.99 to 14.78g for seed yield/plant.

Among the F_1 's, the range of mean lies between 65 to 77 days for days to 50% flowering, 70.67 to 80.67 days for days to reproductive maturity, 176.67 to 233.83 cm for plant height, 50.67 cm to 93.33 cm in main axis height, 1.52 to 1.98 for leaf area index, 39.03 mg/gm to 41.53 mg/g for chlorophyll content, 6.00 to 12.03 for number of primary branches/plant, 8.75 to 20.06 for number of secondary branches/plant, 34.50 to 49.00 for siliqua on main axis, 184.67 to 515.37 for Total siliqua per plant, 3.11 cm to 4.53 cm for siliqua length, 11.11 to 16.72 for number of seeds/siliqua, 26.15 to 87.34 g for biological yield/plant, 3.24 to 7.84 g for 1000-seed weight, 26.35 to 30.03 percent for harvest index, 31.30 to 47.60 percent for oil content, 6.52 g to 25.14 g for seed yield/plant.

Among F₂'s, the range of mean lies between 63 to 79 days for days to 50% flowering, 69 to 83 days for days to reproductive maturity, 172.33 to 242.00 cm for plant height, 47 cm to 92 cm in main axis height, 1.31 to 1.79 for leaf area index, 39.17 mg/gm to 42.20 mg/g for chlorophyll content, 4.33 to 8.67 for number of primary branches/plant, 8.67 to 16.00 for number of secondary branches/plant, 30.33 to 53.33 for siliqua on main axis, 208.33 to 475 for Total siliqua per plant, 2.72 cm to 4.12 cm for siliqua length, 12.24 to 18.11 for number of seeds/siliqua, 25.68 g to 88.52 g for biological yield/plant, 3.38 g to 6.52 g for 1000-seed weight, 24.25 to 29.12 percent for harvest index, 32.34 to 44.21 percent for oil content, 6.46 g to 26.02 g for seed yield/plant.

Heritability and genetic advance: The estimates of heritability (broad sense) and genetic advance in percent over mean of the trait for all the 17 characters in F_1 and F_2 generations were determined. The findings of these parameters are given in Table 2.

High heritability in F_1 's for all the characters in order of ranking namely biological yield /plant (98.93%) followed by numbers of secondary branches (98.66%), seed yield/plant (97.48%), 1000-Seed weight (96.96%), number of primary branches (94.92%), total siliqua

(94.64%), leaf area index (93.18%), main axis height (85.23%), chlorophyll content (94.92%), plant height (70.30%), oil content (%) (70.05%), seed per siliqua (69.45%), harvest index (%) (68.51%), siliqua length (cm) (69.45%), pods on main axis (47.28%), days to 50% flowering (46.31%) and days to reproductive maturity (41.55%).

In F₂'s high heritability for leaf area index (99.36%), biological yield/plant (98.61%), seed yield/plant (92.66%), days to reproductive maturity (91.83%), 1000-Seed weight (91.28%), main axis height (cm) (89.28%), harvest index (%) (87.56%), oil content (%) (85.74%), chlorophyll content (81.20%), days to 50% flowering (69.69%), pods on main axis (68.97%), seed per siliqua (62.15%), plant height (60.68%) and numbers of secondary branches (47.33%) revealed that these attributes exhibited greater contribution of additive genetic variance and marginal role of nonadditive variance in their inheritance while medium heritability estimates were observed for two attributes for number of primary branches per plant (28.48%) and siliqua length (24.09%). In agreement with the findings of previous researchers such as Roy et al. (2015); Samahegn and Tesfaye (2015); Singh et al. (2018); Raut et al. (2019).

The estimates of genetic advance in percent over mean were calculated for all 17 characters. The arbitrary scale for genetic advance suggested that if the estimated value of genetic advance, if less than 10%, it is low, if it ranges between 10 to 20 percent, it is medium, and above 20%, it is high. High estimates for genetic advance were recorded for main axis height (43.14 in F_1 and 33.00 in F_2), total siliqua per plant (79.67 in F_1 and 44.15 in F₂), 1000-seed weight (78.20 in F₁and 28.24 in F_2), biological yield per plant (93.48 in F_1 and 48.31 in F₂) and seed yield per plant (99.13 in F₁ and 53.81 in F₂). The rest of the traits exhibited moderate to low genetic advance in percent over mean in most of the generations. As a result, for future enhancement of Brassica juncea genotypes, direct selection of germplasm can be done using these features. Lakra et al. (2020); Yadav et al., (2021); Kumar et al. (2022); Anjali et al. (2022) have also reported high to medium estimates for expected genetic advance.

Genotypic and phenotypic coefficient of variation: High to moderate PCV and GCV were observed for days Main axis height, leaf area index, chlorophyll content, number of primary branches per plant, number of secondary branches per plant, number of siliqua on main axis, total siliqua per plant, siliqua length, number of seeds per siliqua, biological yield per plant and seed yield per plant in both the generations (F₁ and F₂) as presented in Table 2. Akabari and Niranjana (2015); Singh *et al.* (2016) have also reported high to medium estimates for genotypic and phenotypic coefficient of variation.

Sourced of variation	df	Days to 50% flowering	Days to reproductive maturity	Plant Height (cm)	Main axis height (cm)	Leaf area index	Chlorophyll content	Primary Branches	Secondary Branches	Pods on Main Axis
Replication	2	0.12	8.81	51.37	3.69	0.001	0.04	1.11	0.01	8.08
Treatment	54	20.29**	20.45**	992.65**	177.95**	0.071**	1.76**	8.24**	36.24**	61.23**
Parents	9	17.80**	26.84**	261.49**	146.31**	0.117**	3.12**	1.33**	4.00**	25.07**
F ₂ `s	44	19.77**	19.32**	485.65**	162.43**	0.049**	1.50**	6.34**	29.87**	45.71**
PvF1	1	65.20**	12.81	29879.54**	1145.60**	0.663**	0.80**	154.29**	606.71**	1069.73**
F2`s	44	38.15**	48.74**	642.76**	401.73**	0.048**	1.80**	3.06**	11.05**	71.66**
PvF ₂	1	0.27	98.43**	20054.66**	397.24**	0.000	4.21**	0.05	201.43**	849.34**
Error	198	5.43	4.77	79.21	11.19	0.001	0.13	0.68	1.42	9.80

Table 1: Combined analysis of variance of parents, F1 and F2 for 17 characters in 10 × 10 diallel cross of Indian mustard (*Brassica juncea* L.) for various agronomic traits.

Sourced of variation	df	Total siliqua	Siliqua Length (cm)	Seeds/ Siliqua	Biological yeild/plant	1000- Seed weight (g)	Harvest index (%)	Oil content (%)	Seed Yield/Plant (g)
Replication	2	543.95	0.141	1.73	6.39	0.30	0.23	23.83	2.19
Treatment	54	22723.41**	0.409**	3.07**	659.80**	2.55**	4.26**	22.78**	55.91**
Parents	9	1342.56**	0.026	0.27	87.78**	0.50**	6.75**	2.43	1.45
F2`s	44	14725.15**	0.362**	3.71**	790.62**	2.87**	3.04**	27.23**	66.55**
PvF1	1	567077.49**	5.942**	0.41	52.18**	6.58**	35.60**	10.18**	77.80**
F2`s	44	12147.83**	0.279**	3.98**	609.76**	1.30**	4.04**	28.25**	66.53**
PvF ₂	1	61457.28**	2.381**	11.18**	427.55**	1.15**	1.17**	38.43**	184.57**
Error	198	248.84	0.107	0.52	2.74	0.03	0.27	2.40	1.04

 $PvF_1 = Parents versus F_1, PvF_2 = Parents versus F_2$

 Table 2: Genetic variability, Mean, range and coefficient of variation for 17 characters derived from 10 parental diallel crosses in Indian mustard (*Brassica juncea* L.) in F1 and F2.

	Mean		Minimum Ma		Maxi	vimiim		ability 6) Genetic ad		advance	GA%		PCV%		GCV%	
Genotypes	F1	F2	F1	F2	F1	F2	F1	F2	F1	F2	F1	F2	F1	F2	F1	F2
Days to 50% flowering	72.72	71	65.67	63.67	77.67	79	46.31	69.69	6.76	5.73	9.29	8.07	6.63	4.69	9.74	5.62
Days to reproductive maturity	77.67	76.39	70.67	69.67	82.67	83.67	41.55	91.83	6.15	7.84	7.92	10.27	5.96	5.2	9.25	5.43
Plant Height (cm)	207.99	201.68	176.67	172.33	233.83	242	70.3	60.68	45.49	21.3	21.87	10.56	12.66	6.58	15.1	8.45
Main axis height (cm)	69.73	66.93	50.67	47	93.33	92	85.23	89.28	30.08	22.09	43.14	33	22.68	16.95	24.57	17.94
Leaf area index	1.77	1.61	1.52	1.31	1.98	1.79	93.18	99.36	0.55	0.26	31.18	16.09	15.68	7.83	16.24	7.86
Chlorophyll content	40.11	40.7	39.03	39.17	41.53	42.2	81.39	81.1	2.8	1.39	6.98	3.41	3.76	1.84	4.16	2.04
Primary Branches	8.86	6.3	6	4.33	12.03	8.67	94.92	28.48	6.39	0.82	72.19	12.99	35.97	11.82	36.92	22.14
Secondary Branches	14.51	12.4	8.75	7.67	20.06	16	98.66	47.33	14.24	2.32	98.19	18.74	47.99	13.22	48.31	19.22
siliqua on Main Axis	42.06	41.34	34.5	30.33	49	52.33	47.28	68.97	10.44	7.8	24.82	18.86	17.52	11.02	25.48	13.27
Total siliqua	386.03	284.07	184.67	208.33	515.37	475	94.64	93.63	307.6	125.4	79.67	44.15	39.76	22.15	40.87	22.89
Siliqua Length (cm)	3.7	3.52	3.11	2.72	4.53	4.12	52.92	24.09	1.01	0.22	27.29	6.11	18.21	6.04	25.03	12.31
Seeds/ Siliqua	14.17	14.72	11.11	12.24	16.72	18.11	69.45	62.15	3.94	1.71	27.8	11.59	16.2	7.14	19.43	9.06
Biological yield/plant	54.59	60.22	26.15	25.68	87.34	88.52	98.93	98.61	73.42	29.1	99.48	48.31	65.63	23.62	65.99	23.78
1000-Seed weight (g)	5.58	5.28	3.24	3.38	7.85	6.52	96.96	91.28	4.36	1.27	78.2	24.14	38.55	12.27	39.15	12.84
Harvest index (%)	28.19	26.77	26.35	24.25	30.03	29.12	68.51	87.56	3.53	2.19	12.53	8.16	7.35	4.23	8.88	4.53
Oil content (%)	39.64	37.75	31.3	32.34	47.6	44.21	70.05	85.74	10.74	5.7	27.1	15.09	15.72	7.91	18.78	8.55
Seed Yield/Plant (g)	16.17	17.13	6.52	6.46	25.14	26.02	97.48	92.66	21.09	9.22	99.43	53.81	64.13	27.13	64.95	28.19

GA% mean = Genetic advance percent over mean, GCV (%) = Genotypic coefficient of variation and PCV (%) = Phenotypic coefficient of variation

CONCLUSIONS

FUTURE SCOPE

High heritability and high genetic advance for main axis height, total siliqua per plant, biological yield per plant, and seed yield per plant in F_1 and F_2 generations. It was mainly due to additive gene effects and selection would be effective for these traits. Main axis height, number of secondary branches per plant, siliqua per plant, siliqua length, biological yield per plant, and seed yield per plant also showed high to moderate GCV along with PCV indicating the additive gene action so the selection of genotypes would be rewarding for the aforesaid traits. A significant amount of variability was discovered in all the characters under study. Therefore, it is important to consider these characteristics when selecting for seed yield in rapeseed-mustard. To identify genotypes that exhibit stable performance for desirable traits, we can evaluate them in various agroclimatic regions in Uttar Pradesh known for their extreme weather conditions.

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