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Assessment of genetic variability, heritability, and genetic advance in rapeseed-mustard (*Brassica spp.*) genotypes

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Abstract

The experiment consisting of 20 genotypes of rapeseed-mustard were carried out in a RBD with three replications during *Rabi* 2023-24 at Instructional Research Farm at IGKV, RMD CARS, Ambikapur (C.G.). The observations were recorded on seventeen metric traits. The analysis of variance estimates of all the characters were found highly significant. Coefficient of variation for GCV and PCV were found high for the following traits i.e. seed yield (q/ha), biological yield (q/ha). High Heritability in broad sense coupled with high genetic advance as percentage of mean was found for number of secondary branches per plant, siliqua on primary branch, siliqua on secondary branch, number of siliqua per plant, test weight (gm), biological yield (q/ha), seed yield (q/ha) and harvest index (%).

Keywords: GCV, PCV, genetic advance, heritability, variability

Introduction

Rapeseed-mustard (*Brassica spp.*) is the third important oil seed crop in the world after palm oil and soybean. It belongs to the family *Brassicaceae* (Cruciferae). Rapeseed-mustard crops are grown under a wide range of agro-climatic conditions. genus *Brassica*, which contributes 7% of the total oil seed production of the world (Vipin Kumar Malik *et al.*). Indian mustard (*Brassica juncea* L.) is a naturally amphidiploid. Indian mustard, popularly known as rai, raya, laha, etc. In rapeseed mustard groups, rapeseed is comprised of three ecotypes of *Brassica juncea compestris*, i.e., yellow sarson, brown sarson, and toria. The two main types of rapeseed mustard are (i) self-pollinated varieties such as raya and yellow sarson, of which Indian mustard is the most significant member, occupying 75–80% of the group's area, and (ii) cross-pollinated varieties such as brown sarson, toria, and taramira. Rapeseed and mustard play a significant role in the Indian oil economy, contributing about 27% to the total oil production (S.K. Roy *et al.*, 2011) [8]. The oil content ranges from 37 to 49%. In India, the crop is grown on an area of 8.06 million hectares with a production of 11.75 million metric tonnes and a productivity of 1458 kg ha⁻¹ (Anonymous, 2021-22). In Chhattisgarh, the crop is grown in an area of 36.87 thousand hectares, with a production of 42.21 thousand metric tonnes and a productivity of 1145 kg ha⁻¹ (Anonymous, 2021-22). This rapeseed and mustard group of oilseed crops is gaining wide acceptance among farmers because of their adaptability for both rainfed and irrigated environments, as well as their suitability for both mixed and solo cropping. In addition, it provides a higher yield with lower water consumption and a lower cost of production.

Materials and Methods

The experiment was carried out in *Rabi* 2023-24. experiment was conducted at IGKV, RMD CARS, Research and Instructional Farm, Ajirna, Ambikapur (C.G.) which is located at a latitude of 20°8'N, longitude of 83°15'E and altitude of 592.62 m MSL (mean sea level). The experimental material consists of 20 genotypes of rapeseed–mustard. genotypes are obtained from AICRP, Bharatpur Rajasthan. The genotypes were sown in randomized block

design (RBD) with three replications at IGKV, RMD CARS, research-cum instructional farm, Ambikapur during Rabi 2023-24. Each genotype was sown as row-to row 45 cm and plant to plant distance of 15 cm. The observations of quantitative characters were recorded based on five randomly selected plants from each genotype for some observations and for other observations recorded on whole plot basis. These characters were computed on basis of mean data after computing for each character was subjected to standard method of analysis of variance following Panse and Sukhatme phenotypic and genotypic coefficient of variation, heritability (Broad Sense) and genetic advance as percent of mean were estimated by the formula suggested by Burton and Johanson.

Results and Discussion

Analysis of variance

The analysis of variance revealed highly significant differences among genotypes for days to 50% flowering, days to maturity, plant height (cm), number of primary branches per plant, number of secondary branches per plant, total number of branches per plant, number of siliqua per plant, number of seed per siliqua, siliqua length (cm), number of siliqua on main branch, siliqua on secondary branch, biological yield (q/ha), harvest index (%), test weight (gm), seed yield (q/ha) and for length of main shoot (cm) it is significant. It is indicating the presence of sufficient amount of variability in the experimental materials.

Components of genetic variance

Different attributes of genetic parameters such as GCV, PCV, heritability, genetic advance and genetic advance as percent mean were measured. in this study the phenotypic coefficient of variance was higher than genotypic coefficient of variance indicating that genotype along with environment played prevalent role in the expression of the trait. High GCV and PCV is recorded for seed yield (q/ha) (31.51 and 32.87) followed by biological yield (q/ha) (29.11 and 30.36). Similar result recorded by Jagdish Prasad. For gcv and pcv for seed yield. The moderate estimate (10 to 20%) GCV and PCV were recorded for harvest index (15.50 and 17.08) followed by siliqua on secondary branch (14.74 and 16.48), number of secondary branches per plant (14.72 and 15.88), number of siliqua per plant (14.48 and 15.70), siliqua on primary branch (13.87 and 15.51), test weight (12.39 and 14.33), total number of branches per plant (10.45 and 12.07), number of seed per

siliqua (8.92 and 11.47), number of siliqua on main branch (7.62 and 10.07). Similar result recorded by Jarman for test weight. The lowest estimate (<10%) GCV and PCV were observed for days to maturity (7.77 and 9.70), plant height (6.68 and 9.45), number of primary branches per plant (6.92 and 9.15), siliqua length (5.46 and 9.11), days to 50% flowering (4.77 and 7.8) and length of main shoot (1.69 and 2.98). Similar result recorded by R.S. Sikarwar *et al* (2020)^[9] low gcv and pcv for days to flowering, plant height, and siliqua length Jarman.

Heritability and genetic advance

Table 2 revealed the highest estimate (>60) heritability were recorded for biological yield (91.891) maximum heritability, followed by seed yield (91.884), number of secondary branches per plant (85.899), number of siliqua per plant (85.001), harvest index (82.364), siliqua on secondary branch (80), siliqua on primary branch (79.996), total number of branches per plant (75.003), test weight (74.777), days to maturity (64.242) and number of seed per siliqua (60.486). similar findings were reported by Sudheer Singh *et al.* (2018)^[11], Joohi Ray *et al.* (2019)^[6], Govind Mishra *et al.* (2022)^[4]. moderate estimate (30 to 60%) of heritability were recorded for number of primary branches per plant (57.188), number of siliquae on main branch (57.148), plant height (49.99), days to 50% flowering (42.951), siliqua length (35.886) and length of main shoot (32.133). similar findings were reported by Govind Mishra *et al.* (2022)^[4].

The degree of genetic advance as a percentage of mean was classified as high (> 20%), moderate (20-10%) and low (<10%) according to the scale given by Johnson *et al.*, (1955). the highest estimate of genetic advance as a percentage of the mean were recorded for seed yield (62.22), followed by biological yield (57.48), harvest index (28.99), number of secondary branches per plant (28.10), number of siliqua per plant (27.50), siliqua on secondary branch (27.16), siliqua on primary branch (25.55), test weight (22.07). moderate estimate of genetic advance as a percentage of the mean were recorded for total number of branches per plant (18.64), number of seed per siliqua (14.29), days to maturity (12.83), number of siliquae on main branch (11.86), number of primary branches per plant (10.78). The plant height (9.74), siliqua length (6.73), days to 50% flowering (6.44), and length of main shoot (1.97) showed low genetic advance as a percentage of mean.

Table 1: Analysis of variance for seed yield and yield attributing traits

S. No.	Character	Source of variation		
		Replication	Treatments	Error
	Degrees of freedom	2	19	38
1	Days to 50% flowering	2.5810	23.684**	7.268
2	Days to maturity	3.0380	180.908**	28.312
3	Plant height (cm)	220.4870	411.205**	102.832
4	Number of primary branches /plants	0.1270	0.537**	0.107
5	Number of secondary branches/ plants	2.2520	13.527**	0.702
6	Total number of branches per plant	3.6130	11.65**	1.165
7	Number of siliquae per plant	814.80	6340.326**	352.209
8	Number of seed per siliqua	0.7470	5.467**	0.978
9	Siliqua length (cm)	0.4810	0.441**	0.164
10	Number of siliquae on main branch	15.5530	32.443**	6.488
11	Siliqua on primary branch	276.7220	1132.991**	87.172
12	Siliqua on secondary branch	446.8240	2130.567**	163.894
13	Biological yield (q/ha)	27.5240	323.733**	9.25
14	Harvest index (%)	6.3810	43.515**	2.899
15	Length of main shoot (cm)	0.4030	9.871*	4.078
16	Test weight (gm)	0.0240	0.961**	0.097
17	Seed yield (q/ha)	1.2950	19.822**	0.567

** significant at 1% level * significant at 5% level

Table 2: Genetic variability parameters for seed yield and yield attributing traits

S. No.	CHARACTERS	MEAN	RANGE		GCV (%)	PCV (%)	h ² (b) (%)	Genetic Advance 5%	GA as % of mean
			Max.	Min.					
1	Days to 50% flowering	49.01	55.01	46.00	4.77	7.28	42.951	3.16	6.44
2	Days to maturity	91.76	106.01	82.01	7.77	9.70	64.242	11.78	12.83
3	Plant height (cm)	151.68	184.60	135.41	6.68	9.45	49.99	14.77	9.74
4	Number of primary branches /plants	5.47	6.21	4.74	6.92	9.15	57.188	0.59	10.78
5	Number of secondary branches/ plants	14.05	16.94	9.34	14.72	15.88	85.899	3.95	28.10
6	Total number of branches per plant	17.89	23.20	15.41	10.45	12.07	75.003	3.34	18.64
7	Number of siliquae per plant	308.61	367.41	206.94	14.48	15.70	85.001	84.85	27.50
8	Number of seed per siliqua	13.71	16.87	11.87	8.92	11.47	60.486	1.96	14.29
9	Siliqua length (cm)	5.56	6.21	4.87	5.46	9.11	35.886	0.37	6.73
10	Number of siliquae on main branch	38.62	43.74	30.67	7.62	10.07	57.148	4.58	11.86
11	Siliqua on primary branch	134.63	165.60	90.87	13.87	15.51	79.996	34.40	25.55
12	Siliqua on secondary branch	173.70	213.40	112.67	14.74	16.48	80	47.18	27.16
13	Biological yield (q/ha)	35.18	61.24	18.03	29.11	30.36	91.891	20.22	57.48
14	Harvest index (%)	23.73	31.44	15.84	15.50	17.08	82.364	6.88	28.99
15	Length of main shoot (cm)	82.36	86.14	78.27	1.69	2.98	32.133	1.62	1.97
16	Test weight (gm)	4.33	5.51	3.39	12.39	14.33	74.777	0.96	22.07
17	Seed yield (q/ha)	8.04	15.07	4.21	31.51	32.87	91.884	5.00	62.22

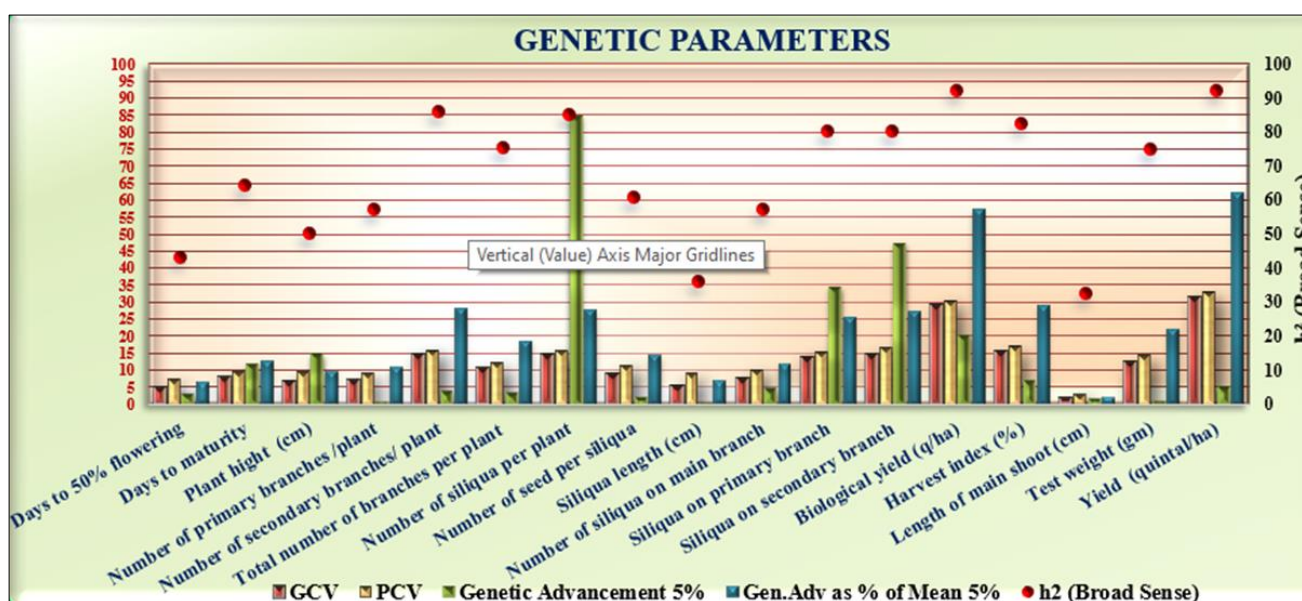


Fig: Genotypic and phenotypic coefficient of variation (GCV) and (PCV), heritability (h²), genetic advance (GA) and genetic advance as per cent of mean (GAM) for yield and related traits of rapeseed mustard genotypes

High Heritability in broad sense coupled with high genetic advance as percentage of mean was found for number of secondary branches per plant, siliqua on primary branch, siliqua on secondary branch, number of siliqua per plant, test weight (gm), biological yield (q/ha), seed yield (q/ha) and harvest index (%). The study suggests that these characters are influenced by additive gene effects, suggesting that phenotypic selection of these traits would be effective for further breeding purpose. Similar findings were reported by Pandey *et al.*, (2024) ^[5], Sreejaya Ghosh *et al.*, (2023) ^[2] Yadav *et al.*, (2021) ^[12], Rout *et al.*, (2019) ^[7].

Conclusion

Analysis of variance shows that variation among treatment is significant for all the characters and variation among replication is non-significant for all the character, with PCV greater than GCV for all the characters. This suggests that direct selection will be effective in improving these characters. The highest measure of GCV and PCV were seed yield and biological yield this trait can be used in the selection process to increase variability, which results in the production of new linkage groups and seed yield. High heritability

coupled with high genetic advance as a percentage of mean were observed in the current study for the biological yield, seed yield, number of secondary branches per plant, number of siliquae per plant, harvest index and siliqua on secondary branch. It indicates that heritability mainly due to the additive gene effect and hence selection may be effective. The other traits showed moderate to low genetic advance as a percentage of mean and high to medium heritability estimates, indicate that non additive genetic variance contributed to their expression.

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