

Analysis of Genetic Variability, Heritability and Genetic Advance for Growth and Yield Attributes in Inidan Mustard [Brassica Juncea L. Czeru & Coss.]

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Abstract

This study, conducted during the Rabi season of 2022-23 at the AICRP-R&M field of plant breeding and genetics at Sher-e-Kashmir University of Agricultural Sciences and Technology-Jammu (SKUAST-Jammu), aimed to discriminate mustard genotypes based on seed and plant characters and assess genetic diversity among Brassica genotypes. Estimates of genetic parameters revealed significant variability across 12 traits namely, Days to 50% flowering, Days to maturity, Plant height (cm), Length of Main Shoot (cm), Number of primary branches, Number of secondary branches, Siliqua length (cm), Number of seeds per siliqua, Seed diameter (mm), test weight (g), numbers of siliquae per plant, Seed yield per plant (g), with the highest genetic coefficient of variation (GCV) 36.38 noted for the number of siliquae per plant, followed by primary and secondary branches 23.66, 22.67 respectively. Conversely, the lowest GCV values 4.17, 4.76 were recorded for plant height and days to 50% flowering. Moderate phenotypic coefficient of variation (PCV) was observed in traits such as main shoot length 16.73 and seed metrics. High heritability was identified in several traits, particularly the 95.81 for number of siliquae per plant, indicating strong genetic control and selection potential. The mean values of the trait's, days to 50% flowering 50.01, Days to maturity 143.64, Plant height 211.84 cm, Length of main shoot 58.64 cm, Numbers of primary branches 7.11, Numbers of secondary branches 16.44, Siliqua length 4.04 cm, Numbers of seeds per siliqua 10.24, Seed diameter 1.61, Test weight 4.6 g, Numbers of siliquae per plant 192.72, Seed yield per plant 11.18 g. The genetic advance as a percentage of the mean was highest for traits like the number of siliquae and 3.98 for seed yield, suggesting favorable outcomes for breeding programs. Overall, this research highlights the genetic diversity and potential for trait enhancement in the studied mustard genotypes.

Keywords

Diversity, GCV, PCV, Heritability, Genetic Control, Genetic Advance

Introduction

Mustard (*Brassica spp.*) is one of the most important oil crops in the world. The genus *Brassica* belongs to the family Brassicaceae, previously the Cruciferae. Rapeseed (*Brassica campestris* L.) is more often known in Bangladesh as mustard. In addition to being photosensitive, it is also a thermosensitive crop (Ghosh and Chatterjee, 1988). Mustard is one of the first known spices and was one of the first crops to be produced, according to Sanskrit writings from circa 3000 BC (Mehra *et al.*, 1968). The Latin term “mustum,” from which the English word “mustard” is derived, originally denoted a condiment. Mustum ardens, sometimes referred to as hot or fiery must, was a common Roman speciality condiment created by combining crushed mustard seeds with the juice taken from grapes or other fruits. The Europeans adopted the Romans’ fondness of mustard and used it extensively to season meat and fish.

Since ancient times, many species of mustard plants have been widely farmed and used as food, medicine, and spices (Ildiko *et al.*, 2006). The protein content of mustard seeds is high. The protein is of outstanding nutritional quality, being rich in lysine with acceptable levels of sulphur-containing amino acids-limiting amino acids in the majority of cereals and oilseed proteins (Sadeghi *et al.*, 2009). The use of protein-rich full-fat or defatted flour holds promise for increasing the nutritional value of the finished product and ensuring optimal flour use (Mir *et al.*, 2021) because consumers are becoming more conscious of their health and the quality of their food, fortifying food with protein is a topic of interest right now (Tyagi *et al.*, 2007). India experiences a huge economic effect from rapeseed-mustard, which is used to make culinary oils, vegetables, sauces and animal feed. In India, nine oilseeds serve as the primary sources of vegetable oil. India produced 10210 tonnes of rapeseed and mustard in the 2020–21 growing season. Rapeseed and mustard are grown on 6700 hectares of land in India, with an estimated productivity of 1542/kg/ha (Anonymous 2021-22). Jammu and Kashmir’s state planted rapeseed and mustard on 43.02 hectares, with production output of 33.77 tonnes and 785 kg/ha of productivity (Anonymous 2021-22).

With chromosome number $2n = 36$, Indian mustard is an amphidiploid plant. It is an annual herbaceous plant that grows to a height of several feet. There may be a 12 to 20% inclination for outcrossing even when the crop is primarily self-pollinated. How successfully a crop can be genetically improved depends on how much genetic variety and variability there is within a given crop type. Any hybridization effort must include genetic variety in order to yield desirable genotypes, including unique land races, local selection, elite cultivars, and foreign agricultural plant germplasm. To accomplish the numerous

goals of plant breeding, including those of developing cultivars with improved yield (Chauhan *et al.*, 2011), broader acceptance, desirable quality, and pest resistance. Planning a breeding program to create superior cultivars or hybrids depends heavily on the genetic diversity present in the breeding material. In order to produce the desired recombinants in segregating generations, the genetically diverse parents are often used.

The information on the pattern of variation across farmed varieties of different regions is scanty due to the restricted number of genotypes used in earlier research on diversity analysis in Indian mustard based on a small number of morphological parameters. The objective of the current study was to evaluate the pattern of variation in Indian mustard varieties for morphological attributes, the degree of variability, the relationship between various variables for the purpose of establishing future breeding strategies.

Materials and Methods

Present study was carried out at the AICRP-R&M in the field of plant breeding and genetics, Chatha of Sher-e-Kashmir University of Agricultural Sciences and Technology-Jammu (J&K) during *Rabi* season 2022-23 SKUAST-Jammu. The investigation was carried out with an aim to discriminate the mustard genotypes using seed and plant characters and to determine the genetic diversity among *Brassica* genotypes. The experiment was sown on plot size of 7.2m² using Randomised Complete Block Design (RCBD) with 3 replications. Each treatment was sown in rows with length of 4m.

The material was evaluated and data recorded for each line for traits *viz.* days to 50% flowering, days to maturity, plant height, length of main shoot, number of primary branches, number of secondary branches, siliqua length, number of seeds per siliquae, seed diameter, test weight, number of siliquae per plant and seed yield per plant.

Table 3.1: List of Indian mustard genotypes along with their source and origin.

S.No.	Genotype	Source	Origin
1	DRMRDR 2155	AICRP - RM, JAMMU	DRMR, Bharatpur
2	DRMRDR 2203	AICRP - RM, JAMMU	DRMR, Bharatpur
3	DRMRCI 169	AICRP - RM, JAMMU	DRMR, Bharatpur
4	DRMRDR 2133	AICRP - RM, JAMMU	DRMR, Bharatpur
5	DRMRSJ 9	AICRP - RM, JAMMU	DRMR, Bharatpur
6	DRMRDR 2201	AICRP - RM, JAMMU	DRMR, Bharatpur
7	DRMRDR 2152	AICRP - RM, JAMMU	DRMR, Bharatpur
8	ROHINI (SC)	AICRP - RM, JAMMU	CSAUAT, Kanpur
9	DRMR 2018-26	AICRP - RM, JAMMU	DRMR, Bharatpur
10	DRMRDR 2156	AICRP - RM, JAMMU	DRMR, Bharatpur

11	NRCHB 101 (SC)	AICRP - RM, JAMMU	DRMR, Bharatpur
12	DRMR 2020-15	AICRP - RM, JAMMU	DRMR, Bharatpur
13	DRMRDR-2141	AICRP - RM, JAMMU	DRMR, Bharatpur
14	DRMRCI (Q) 57	AICRP - RM, JAMMU	DRMR, Bharatpur
15	DRMR 2019-20	AICRP - RM, JAMMU	DRMR, Bharatpur
16	DRMRSJ 22	AICRP - RM, JAMMU	DRMR, Bharatpur
17	DRMRDR 2236	AICRP - RM, JAMMU	DRMR, Bharatpur
18	DRMRCI 170	AICRP - RM, JAMMU	DRMR, Bharatpur
19	DRMRDR-2195	AICRP - RM, JAMMU	DRMR, Bharatpur
20	DRMRDR-2241	AICRP - RM, JAMMU	DRMR, Bharatpur
21	RH-1700-3	AICRP - RM, JAMMU	CCSHAU, Hissar
22	PHR-2	AICRP - RM, JAMMU	PAU, Ludhiana
23	DRMRCI 171	AICRP - RM, JAMMU	DRMR, Bharatpur
24	DRMRDR-2135	AICRP - RM, JAMMU	DRMR, Bharatpur
25	DRMRDR 2242	AICRP - RM, JAMMU	DRMR, Bharatpur

Result and Discussion

Analysis of Variance:

The first and most crucial step in starting any breeding program for plant development is to hunt for enough genetic variation for different traits with economic value. Every breeding program relies on selection, which only works on genetically based variation (Johansen, 1909). Any crop has a greater probability of producing the desired kinds when it has a wide range of variability (Vavilov, 1951).

The analysis of variance are found to be significant for all the traits viz. days to 50% flowering, days to maturity, plant height, length of main shoot, number of primary branches, number of secondary branches, siliqua length, number of seeds per siliqua, seed diameter, test weight, number of siliqua per plant and seed yield per plant. The significant data recorded for all the traits show that there is sufficient variability among the genotypes. These results and finding are similar to other researchers Yadava *et al.* (2011), Verma *et al.* (2021), Devi *et al.* (2018), Sutariya *et al.* (2011) and Rout *et al.* (2019)

The Analysis of variance for all the different characters is given in table number 4.1. The results showed that all the genotypes shows significant differences at 5% level of significance for all the 12 traits. This suggests that all the genotypes are genetically variant and can be used further for breeding programme.

Table 4.1: Analysis of Variance for twelve characters of Indian mustard

S.no.	Source	Mean Sum of Squares (MSS)		
		Replication	Treatment	Error
	Degrees of freedom	2	24	48
1	Days to 50% flowering	8.17	73.65**	2.56
2	Days to maturity	3.88	145.41**	5.03
3	Plant height (cm)	121.12	277.22**	42.8
4	Length of Main Shoot(cm)	51.84	253.22**	17.67
5	Number of primary branches	0.37	8.82**	0.34
6	Number of secondary branches	1.92	43.02**	1.33
7	Silique length(cm)	0.176	0.84**	0.11
8	Number of seeds per silique	2.68	5.45**	1.15
9	Seed diameter(mm)	0.026	0.10**	0.01
10	Test weight(g)	0.342	0.78**	0.15
11	Number of siliques per plant	442.36	14962.96**	214.69
12	Seed yield per plant(g)	0.914	15.09**	1.12

****Significant at 1 percent level of significance**

Estimation of qualitative parameters:

The results based on the seed colours are shown in table 4.2. Out of 25 genotypes maximum frequency is gained by black colour having 12 genotypes [DRMRDR 2241, DRMRDR 2152, DRMRDR 9, DRMRJ 22, DRMR 2019-20, DRMRCI 171, DRMRDR 2236, DRMRDR 2201, RH 1700-3, DRMRDR 2242, DRMRDR 2203, ROHINI(SC)] followed by reddish brown colour having 6 genotypes (DRMR 2020-15, DRMRDR 2156, DRMRCI 170, DRMRDR 2155, DRMRDR 2152, DRMRCI-169), brown colour having 5 genotypes (DRNRSJ 2133, NRCHB 101(SC), DRMRDR 2018-26, DRMRDR 2195, DRMRDR 2141) and yellow colour having 2 genotypes[PHR-2, DRMRCI (Q)], respectively.

This attribute is investigated to establish distinctness between the newly produced genotypes together with the old ones and to characterize the genotypes of Indian mustard based on qualitative morphological characteristics. Qualitative character seed colour shows 4 different colours for twenty five genotypes viz., yellow, reddish brown, brown and black maximum genotypes were found under black genotypes followed by reddish brown, brown and yellow. Yadav *et al.* (2013), Avtar *et al.* (2014) and Neeru *et al.* (2017) supports our findings and results.

Table 4.2: Qualitative parameters of Indian mustard are as under:

Traits	Classified as	Varieties	Frequency	Percentage %
Seed Colour	Yellow	PHR-2, DRMRCI (Q)	2	8
	Reddish Brown	DRMR 2020-15,DRMRDR 2156, RMRCI 170,DRMRDR 2155,DRMRDR 2152,DRMRCI-169, DRNRSJ 2133, NRCHB	6	24
	Brown	101(SC),DRMRDR 2018-26,DRMRDR 2195,DRMRDR 2141, DRMRDR 2241,DRMRDR, 2152,DRMRDR 9,DRMRJ 22,DRMR	5	20
	Black	2019-20,DRMRCI 171,DRMDR, 2236,DRMRDR 2201,RH 1700-3, DRMRDR 2242,DRMRDR 2203, ROHINI(SC)	12	48

Estimation of mean range performance

In order to evaluate phenotypic variability and as a starting point for removing unsuitable germplasm, plant breeders employ the comparatively straight forward metric of mean performance. It assesses the genetic potential of various germplasm. Because yield and yield-attributing characteristics are the selection criteria for direct development of the plant population, they are of utmost importance in every breeding effort. The mean performance of 12 characters is given in table number 4.4.

5.1 Estimation of mean range performance

The twenty five genotypes depicted wide range in their means. It is also possible to employ the genotypes listed below to enhance the traits for which they have high mean performance. These genotypes have extremely high mean performance in desired directions for a variety of qualities. The highest mean for day to 50% flowering is noticed by DRMR 2019-20(59.00) followed by days to maturity with maximum mean in DMRDR 2141(158.67), plant height with highest mean in DRMRDR 2241(224.33), length of main shoot with maximum mean in genotype DRMRDR 2242(75.00), number of primary branches having highest mean in DRMR 2155(12.67), Number of secondary branches showing maximum mean in DRMRCI 171(24.33), siliqua length with greatest mean in DRMR 2019- 20(5.10), number of seeds per siliqua showing high mean in DRMRDR 2242(13.00), Seed diameter with maximum mean in DRMR 2019-20(1.87) genotype, test weight with greatest mean in DRMRDR 2242(5.45) genotype, number of siliquae per plant showing greatest mean in DRMRDR 2203(362.67), Seed yield per plant with

maximum mean of DRMRCI 169 (15.09) genotype and seed oil content (%) with highest mean of [Rohini (SC)] this work view in accordance to Kumar *et al.* (2013), Singh *et al.* (2010) and Chaturvedi *et al.* (2021) suggesting mean ranges referred to above parameters.

Table 4.3: Estimation of oil content % of Indian mustard

S.No.	Genotype	Mean data
1	DRMRDR 2155	39.5
2	DRMRDR 2203	38.3
3	DRMRCI 169	39.1
4	DRMRDR 2133	38.2
5	DRMRSJ 9	37.8
6	DRMRDR 2201	38.1
7	DRMRDR 2152	37.9
8	ROHINI (SC)	39.1
9	DRMR 2018-26	38.1
10	DRMRDR 2156	37.7
11	NRCHB 101 (SC)	39.2
12	DRMR 2020-15	40.1
13	DRMRDR-2141	39.8
14	DRMRCI (Q) 57	37.1
15	DRMR 2019-20	38.6
16	DRMRSJ 22	38.7
17	DRMRDR 2236	39.5
18	DRMRCI 170	37.8
19	DRMRDR-2195	38.4
20	DRMRDR-2241	38.4
21	RH-1700-3	39.2
22	PHR-2	38.7
23	DRMRCI 171	39.8
24	DRMRDR-2135	38.1
25	DRMRDR 2242	37.9

Estimation of coefficient of variability

Any initiative to enhance crops must start with genetic diversity. The amount of variety present in the foundation material for a characteristic determines how much that trait may be improved. Characters with a wide range and a high coefficient of variation (CV) would provide selection of superior genotypes additional possibilities. Estimates of

the genotypic and phenotypic coefficients of variation (PCV and GCV), respectively were calculated and are shown in Table 4.4.

In this the highest GCV and PCV data was recorded for all the 12 traits. Basically the PCV is higher than GCV. This shows the amount of variability present in the traits. The highest PCV was noticed in number of siliquae per plant (37.17) followed by number of primary branches (25.06), number of secondary branches (23.74) and seed yield per plant (21.51), respectively whereas the lowest PCV was observed in plant height (5.19) and days to maturity (5.01). The moderate PCV values were attained by length of main shoot (16.73) followed by number of seeds per siliqua (15.70), siliqua length (14.81), seed diameter (13.14), test weight (13.13) and days to 50% flowering (10.25).

The highest GCV value noticed in number of siliqua per plant (36.38) followed by number of primary branches (23.66) and number of secondary branches (22.67) while the lowest GCV values were noticed by days to 50% flowering (9.73) followed by days to maturity (4.76) and plant height (4.17). The moderate GCV values obtained by traits are seed yield per plant (19.3) followed by length of main shoot (15.11), siliqua length (12.16), number of seeds per siliquae (11.70), seed diameter (10.58) and test weight (10.00).

4.4 Estimation of Heritability (Broad sense) and Genetic advance

Character transferability from parents to children is shown by heritability. All of the characters heritability estimates were calculated and are shown in Table 4.4. The high heritability was observed in number of siliquae per plant (95.81%), followed by number of secondary branches (91.22%), days to maturity (90.29%), days to days to 50% flowering (90.24%), number of primary branches (89.10%), length of main shoot (81.62%), seed yield per plant (80.50%), siliqua length (67.43%), seed diameter (64.88%) and plant height (64.61) while the moderate heritability was noticed in test weight (58.01%) and number of seeds per siliqua (55.48%).

The genetic advancement provides a preview of the projected improvement brought about by selection in the following generation. The prospect of improvement through selection is clearly shown by the greater heritability estimate and higher estimated genetic progress. Significant variances were seen for many features in the genetic progress in % of mean.

The high genetic advance as percent of means was depicted higher in no of siliqua per plant (73.36%) followed by number of primary branches (46%), number of secondary branches (44.61%), seed yield per plant (35.67%), length of main shoot (28.12%) and siliqua length (20.57%). The moderate GA was observed in days to 50% flowering (19.04%)

followed by number of seeds per siliqua (17.95), seed diameter (17.56%) and test weight (15.69%). The lowest GA is observed in days to maturity (9.32%) and plant height (6.9%).

5.2 Estimation of coefficient of variability

The genetic diversity present in crops has a significant impact on the success of any plant breeding operation. The genotypic coefficient of variation quantifies the variety of variability present in the crop and also makes it possible to compare the degree of variability existing among various traits. The relationship between the genotype and environment, as well as the genotype itself, determines how a characteristic is expressed genetically. So that the real breeding nature of that specific trait can be evaluated, the overall variation has to be divided into heritable and non-heritable components

The PCV values show higher range than GCV values in general terms which indicates that the environment has a significant impact on how these traits are expressed. In these twenty five genotypes the high (more than 20%) PCV and GCV were recorded for number of siliqua per plant followed by number of primary branches and number of secondary branches, whereas the lowest (less than 10%) PCV and GCV were recorded for plant height and days to maturity. Moderate PCV and GCV (between 10 to 20%) were noticed in length of main shoot followed by number of seeds per siliqua, siliqua length, seed diameter and test weight Jat et al., (2019), Mandal *et al.* (2022), Kumar *et al.* (2020), Maurya *et al.* 2018, Evangelin et al. (2023) and Patel *et al.* (2021) found out the similar findings for these traits indicating impact of environment.

5.3 Estimation of heritability (Broad sense) and genetic advance

The success of choosing any character is dependent not only on the level of variability available, but also on the degree to which it is passed on from parents to their children. It is an effective measure of the character passing down from parents to children. Outstanding genetic advancement under selection is possible when the characters under choices are very stable and heritable. In light of this, characters plant breeders place more attention on traits with high heritability than those whose heritability is poor.

High heritability coupled with high genetic advance for twenty genotypes are number of siliquae per plant followed by number of primary branches, number of secondary branches, seed yield per plant, length of main shoot and siliqua length while with low heritability and genetic advance are test weight and number of seeds per siliqua. High heritability when relate to high genetic advance shows that these traits were having environment effect and caused by additive gene action Similar findings and results agreed with Swetha *et al.*, (2019), Evangelin *et al.* (2023), Khulbe *et al.* (2000) and Ali *et al.* (2003).

Table 4.4: General mean, range, genotypic variance, phenotypic variance, heritability, genetic advance and genetic advance as % means given as under

Characters	General Mean	Range		GCV	PCV	(h ² b)	Genetic Advance	GAM 5%
Days to 50% flowering	50.01	59.00	41.67	9.73	10.25	90.24	9.52	19.04
Days to maturity	143.64	158.67	132	4.76	5.01	90.29	13.39	9.32
Plant height(cm)	211.84	224.33	189.67	4.17	5.19	64.61	14.63	6.91
Length of main shoot(cm)	58.64	75.00	42.0	15.11	16.73	81.62	16.49	28.12
Number of primary branches	7.11	12.67	4.67	23.66	25.06	89.10	3.26	46.00
Number of secondary branches	16.44	24.33	11.67	22.67	23.74	91.22	7.33	44.61
Silique length(cm)	4.04	5.10	2.83	12.16	14.81	67.43	0.83	20.57
Number of seeds per silique	10.24	13.0	8.00	11.70	15.70	55.48	1.83	17.95
Seed diameter	1.61	1.87	1.23	10.58	13.14	64.88	0.28	17.56
Test weight(g)	4.6	5.45	3.60	10.00	13.13	58.01	0.72	15.69
Number of siliquae per plant	192.72	362.7	95.0	36.38	37.17	95.81	141.38	73.36
Seed yield per plant(g)	11.18	15.09	7.00	19.3	21.51	80.50	3.98	35.67

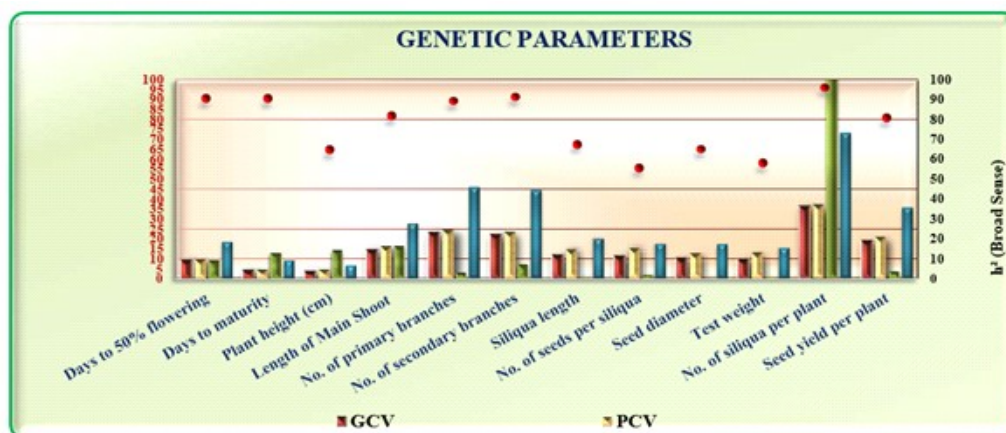


Figure 4.1: Graphical representation of genetic parameter

Conclusion

The present investigation revealed the existence of substantial genetic variability among the twenty-five Indian mustard (*Brassica juncea* L. Czern. & Coss.) genotypes

evaluated for twelve growth and yield-related traits under the agro-climatic conditions of Jammu. Analysis of variance indicated highly significant differences among genotypes for all the characters studied, confirming the presence of adequate genetic diversity for effective selection and crop improvement. The phenotypic coefficient of variation (PCV) was consistently higher than the genotypic coefficient of variation (GCV), indicating the influence of environmental factors on trait expression, although the differences between PCV and GCV were relatively small for several traits, suggesting a strong genetic basis. High heritability coupled with high genetic advance as percent of mean was observed for the number of siliquae per plant, number of primary branches, number of secondary branches, seed yield per plant, length of main shoot, and siliqua length, indicating the predominance of additive gene action and the effectiveness of direct phenotypic selection for these traits. Among all the characters, the number of siliquae per plant exhibited the highest GCV, PCV, heritability, and genetic advance, identifying it as the most reliable selection criterion for enhancing seed yield in Indian mustard. The study also identified several promising genotypes exhibiting superior mean performance for specific agronomic traits, which can serve as valuable parental lines in future hybridization and breeding programmes. Overall, the findings demonstrate that considerable scope exists for genetic improvement of Indian mustard through selection based on highly heritable yield-contributing traits. The identified superior genotypes and traits may be effectively utilized in developing high-yielding cultivars with improved productivity, thereby contributing to sustainable mustard production and oilseed breeding programmes.

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