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Estimates of genetic components of variances for characters under study in mustard [*Brassica juncea* L. (Czern & Coss)]

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Abstract

The selection of superior characteristics in plants is an important phenomenon of natural selection. Genetic variation in plants is also regarded as one of the most essential reasons of natural selection, and it has the potential to offer up new possibilities for crop trait selection.

The present investigation was carried out on mustard [*Brassica juncea* L. (Czern & Coss)] crop during Rabi 2023-2024, with the aims of to estimate the genetic components of variances for characters under study. The experimental material comprising of 100 treatments (10 parents + 45 F₁'s and 45 F₂'s) was evaluated in RBD with three replications. Observation was based upon nineteen quantitative characteristics. For all characteristics, the phenotypic coefficients of variation (PCV) estimations were greater than the genotypic coefficients of variation (GCV). Oleic acid percentage exhibited the highest phenotypic coefficient of variation (PCV) at 26.83%, indicating substantial variability in this trait. Following closely were the Linoleic acid percentage and Palmitic acid percentage, with PCVs of 23.84% and 23.88%. Oleic acid (%) exhibited the highest genetic variability with a GCV of 26.65%, indicating significant potential for selection in breeding programs. The heritability estimates for various traits ranged from 34.19 (Oil content) to 99.19 (Linoleic acid). As a result of the above observations, it is possible to derive that there is ample opportunity for successful crop modification for improved yield and yield-attributing traits in existing mustard germplasm.

Keywords: Mustard [*Brassica juncea* L. (Czern & Coss)], variability, GCV, PCV, heritability, genetic advances

Introduction

Rapeseed-mustard (*Brassica* spp.), a member of the Brassicaceae family, constitutes a critical oilseed crop on a global scale. The genus *Brassica* is recognized for its economic importance, as it encompasses oilseeds, vegetables, and forage crops. Among these, (*Brassica juncea* L.)

Cytologically, *B. juncea* is an amphidiploid species (2n=36), derived from the natural hybridization between *Brassica campestris* L. (2n=20) and *Brassica nigra* L. (2n=16), (Kaur *et al.*, 2019) [5]. Mustard is the primary oilseed Brassica, accounting for around 85 to 90% of the total area under cultivation of all oilseed crops. (Rao *et al.*, 2017) [12]. It has a wide range of tastes, from sweet to spicy, and pungency levels range from mild to quite strong. Isothiocyanates, the most essential component in mustard oil, are responsible for its flavour and pungency. Rapeseed-mustard accounts for 22.7% of India's total oilseed production and occupies 19.2% of the nation's total cropped area. Globally, the crop represents 23.5% of the total oilseed hectareage and contributes 13.2% to global oilseed production. The cultivation and productivity of rapeseed-mustard in India have demonstrated significant growth, with production increasing from 2.68 million tons in 1985-86, with a productivity of 650 kg/ha, to 7.9 million tons in 2007-2008, with a productivity of over 1001 kg/ha (Gami *et al.*, 2014) [3]. As of 2015-16, Indian mustard occupied 5.74 million hectares, yielding 6.79 million tons with an average productivity of 1.18 t/ha (Anonymous, 2019) [2]. The degree of heritable variation in the variables evaluated is extremely important for determining the genotype's breeding potential. Variability for economic features must exist in the working germplasm for recombination breeding and selection to be successful.

Thus, phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability (h^2), and genetic advance (GA %) are all necessary for successful selection. Every breeder's primary goal is to increase productivity through a varietal development programme, which is entirely dependent on the genetic variability found in the available germplasm/breeding material of a certain crop.

The evaluation of numerous genetic factors such as genotypic coefficient of variation, phenotypic coefficient of variance, heritability, and genetic progress is a prerequisite for an effective selection procedure. Seed yield is a challenging trait that is usually controlled by non-additive gene activities. It is greatly impacted by a few morphological characters that are ruled by several genes, as well as the environment.

Materials and Methods

The current research work " To estimate the genetic components of variances for characters under study mustard [*Brassica juncea* L. (Czern & Coss)] has been conducted at the investigation was carried out at the Students' Instructional farm, Chandra Shekhar Azad University of Agriculture and Technology, Kanpur (U.P.). in a Randomised Block Design with three replications over the autumn-winter season of 2023-2024. The experimental basic material in the present investigation comprised of ten varieties/ strains of Indian mustard namely, Varuna, PR-20, Rohini, NRCDR-2, Basanti, KMR 18-2, Mathura Rai, KMR 15-5, Azad Mahak and Maya were taken from the germplasm maintained at Oilseed Section, Department of Genetics and Plant Breeding. C S Azad University of Agriculture and Technology, Kanpur. Comprising of 100 treatments (10 parents + 45 F₁'s and 45 F₂'s) for several variables to quantify the level of variability and scope of selection in mustard. Each parent and F₁'s planted in one row, and F₂'s in two rows of 5m long 45cm apart, Plant to plant distance was maintained 15 cm by thinning. All the recommended agronomic practices were adopted for raising a good crop. The observation included. Days to 50% flowering, days to maturity, plant height (cm), length of main raceme (cm), leaf area index (cm/m²), number of primary branches/plants, number of secondary branches/plants, number of siliqua on main raceme, number of seeds per siliqua, biological yield per plant (g), 1000-seed weight (g), harvest index (%), fatty acid profile, palmitic acid (%), oleic acid (%), linoleic acid (%), linolenic acid (%), erucic acid (%), oil content (%), seed yield per plant. The estimations of variability (GCV and PCV), heritability, and genetic progress were carried out by the methods proposed by Burton and de Vane (1953).

Results and Discussion

The combined analysis of variance (ANOVA) for parents and their forty-five each F₁'s and F₂'s for all the above nineteen characters (agronomic and biochemical) namely days to 50% flowering, days to reproductive maturity, plant height (cm), length of main raceme (cm), leaf area index, number of primary branches per plant, number of secondary branches per plant, number of siliqua on main raceme, number of siliquae per plant, number of seeds per siliqua, biological yield per plant (g), 1000-seed weight (g), harvest index, palmitic acid (%), oleic acid (%), linoleic acid (%), linolenic acid (%), erucic acid (%), oil content and seed yield per plant (g) and mean sum of squares are presented in (Table 1), respectively. Significant differences were

observed among the treatments (parents, F₁'s and F₂'s) for all the twenty attributes under study. Parents vs. F₁'s exhibited significant differences for all the characters except oil content, palmitic acid, erucic acid, biological yield, leaf area index and linoleic acid, parents vs. F₂'s significant differences for all the characters except days to biological yield, leaf area index (lai30, lai60), palmitic acid, linoleic acid and erucic acid. Further research into the specific traits contributing to these significant differences will enhance the understanding of genetic mechanisms at play and refine breeding strategies for future canola production Tripathi *et al.*, (2013) ^[16], Hasan *et al.*, (2015) ^[4], Akabari and Niranjana (2015) ^[1], Samahegn and Tesfaye (2016) ^[14], Maurya *et al.*, (2018) ^[10], Rout *et al.*, (2019) ^[13], Mahendra *et al.*, (2020) ^[8], Lakra *et al.*, (2020) ^[7], Kumar *et al.*, (2023) ^[6].

Table-2 shows the estimations of Phenotypic and genotypic coefficient of variation. In parents the analysis of phenotypic variation among the evaluated attributes revealed that the Oleic acid percentage exhibited the highest phenotypic coefficient of variation (PCV) at 26.83%, indicating substantial variability in this trait. Following closely were the Linoleic acid percentage and Palmitic acid percentage, with PCVs of 23.84% and 23.88%, respectively, demonstrating significant diversity as well. The Linolenic acid percentage also showed considerable variability at 20.41%. In terms of plant morphology, the number of secondary branches displayed a PCV of 20.16%, while the biological yield per plant and seed yield per plant recorded values of 19.89% and 15.38%, respectively. The Erucic acid percentage had a PCV of 16.26%, indicating variability in oil composition.

The number of primary branches had a PCV of 13.54%, and the leaf area index at 30 days (LAI 30) showed a PCV of 13.68%. The length of the main raceme recorded a PCV of 11.98%, while the 1000 seed weight demonstrated a PCV of 10.74%. The number of siliques on the main raceme and the harvest index had PCVs of 9.37% and 9.96%, respectively, highlighting variability in yield traits. The seed per siliqua attribute had a PCV of 9.49%, while plant height recorded a PCV of 8.19%. Finally, the days to 50% flowering and days to maturity exhibited lower variability with PCVs of 6.68% and 5.77%, respectively, alongside the oil content at 5.37%, and the leaf area indices at 60 days (5.46%) and 90 days (5.63%). This comprehensive overview underscored the varying degrees of phenotypic variation present among the different traits.

The phenotypic coefficient of variation (PCV) values for various fatty acid percentages reveals high variability in both F₁ and F₂ generations. Palmitic acid shows high PCV values of 26.06% in F₁ and 26.50% in F₂. Similarly, oleic acid displays values of 26.58% in F₁ and 26.70% in F₂, indicating significant variability in the population. Linoleic acid also follows this trend, with 26.03% in F₁ and 27.79% in F₂, suggesting even greater variation in the F₂ generation. Linolenic acid, while still high, has slightly lower PCV values of 19.85% in F₁ and 19.82% in F₂, implying a more consistent expression of this trait across both generations. Erucic acid exhibits moderate variability, with PCV values of 18.19% in F₁ and 18.05% in F₂.

In addition to the fatty acids, several other traits exhibit moderate PCV values, indicating balanced variability in the population. The number of primary branches shows PCV values of 12.19% in F₁ and 13.40% in F₂, while the number of secondary branches has values of 13.59% in F₁ and

13.22% in F2. The length of the main raceme has PCV values of 15.41% in F1 and 15.33% in F2, while the number of siliquae on the main raceme shows values of 7.93% in F1 and 8.69% in F2. Seed per siliqua displays PCV values of 7.89% in F1 and 8.45% in F2, and 1000 seed weight shows moderate variation with values of 14.48% in F1 and 14.88% in F2. Biological yield per plant has PCV values of 15.49% in F1 and 16.05% in F2, while the harvest index displays values of 12.01% in F1 and 12.76% in F2. Lastly, seed yield per plant exhibits moderate PCV values of 15.73% in F1 and 16.14% in F2, reflecting balanced genetic variability for these yield-related traits in the studied population.

In parents the genetic coefficient of variation (GCV) values for various attributes were analysed and organized from highest to lowest. Oleic acid (%) exhibited the highest genetic variability with a GCV of 26.65%, indicating significant potential for selection in breeding programs. Following closely was palmitic acid (%) and linoleic acid (%), both showing a GCV of 23.74%, suggesting that these traits also possessed substantial genetic diversity. Linolenic acid (%) followed with a GCV of 20.23%, and biological yield per plant (g) showed a GCV of 19.57%, emphasizing the variability present in these important agronomic traits.

On the other hand, the lowest GCV was found in oil content at 3.14%, indicating limited genetic variability in this trait, which may have constrained selection opportunities. Other attributes such as LAI 30 (13.02%), days to maturity (5.68%), and days to 50% flowering (6.44%) displayed moderate levels of genetic variation. Overall, the data

highlighted key traits with high genetic variability that could be targeted for improvement in breeding programs, while also identifying traits that might have required different strategies due to their lower variability.

The characters with high and moderate Genotypic Coefficient of Variation (GCV) values reveal significant variability in important traits. Notably, palmitic acid content shows high GCV values of 25.92% in F1 and 26.25% in F2, while oleic acid demonstrates even higher values at 26.41% in F1 and 26.44% in F2. Linoleic acid also exhibits high GCV, with values of 25.91% in F1 and 27.56% in F2. Linolenic acid shows moderate GCV values of 19.67% in F1 and 19.47% in F2, while erucic acid has values of 17.93% in F1 and 17.63% in F2. Additionally, traits such as biological yield per plant present moderate GCV values of 15.18% in F1 and 15.56% in F2, alongside seed yield per plant with 15.07% in F1 and 15.62% in F2. The length of the main raceme also reveals moderate GCV, measuring 15.03% in F1 and 14.81% in F2. These findings indicate a balanced level of genetic variability, particularly in the fatty acid compositions and yield-related traits, suggesting potential for effective selection in breeding programs. The study also highlights the importance of dominance effects and hybrid vigor in enhancing oil content and fatty acid composition, providing valuable insights for breeders focused on improving these traits through hybridization and selection. Shrimal *et al.*, (2016) [15], Mumtaz *et al.*, (2017) [11], Lal *et al.*, (2018) [10], Mandal *et al.*, (2022) [9], Kumar *et al.* (2023) [6].

Table 1: Combined analysis of variance for parent and hybrids F1 and F2 for 19 characters 10 x 10 diallel cross in Indian mustard (*Brassica juncea* L.) for various traits.

Sourced of variation	df	Days to 50% flowering	Days to maturity	Plant Height (cm.)	No. of primary branches	No. of secondary branches	Length of main raceme	No. of siliquae on main raceme	Seed per siliqua	1000 seed weight (g.)	Oil content	Palmitic acid (%)	Oleic acid (%)	Linoleic acid (%)	Linolenic acid (%)	Erucic acid (%)
Replication	2	4.27	9.02	31.41	0.228	0.85	60.84	9.80	0.955	0.043	3.50	0.03	0.20	0.03	0.26	5.76
Treatment	99	25.07**	44.27**	486.04**	2.05**	11.81**	465.04**	34.74**	2.20**	1.21**	8.94**	10.93**	34.98**	2.95**	11.64**	134.90**
PAR	9	38.15**	143.34**	503.02**	2.158**	24.02**	250.47**	41.04**	3.014**	0.577**	7.22**	9.13**	39.10**	2.28**	13.43**	107.18**
F1	44	20.82**	29.52**	338.14**	1.742**	8.58**	496.59**	29.17**	1.800**	1.226**	8.97**	11.05**	33.96**	2.76**	11.50**	140.68**
PVF1	1	61.11**	214.96**	6696.03**	0.427**	108.93**	289.69**	23.61**	4.980**	0.576**	0.65	0.50	17.94**	0.12	6.08**	3.06
F2	44	22.63**	32.25**	343.94**	2.387**	8.46**	485.05**	39.06**	2.341**	1.338**	9.64**	11.68**	36.19**	3.41**	11.73**	140.80**
PVF2	1	165.79**	159.80**	6883.38**	1.069**	94.58**	302.69**	44.59**	3.959**	1.293**	1.02	0.09	6.88**	0.09	2.88**	1.83
EROR	198	2.70	10.09	23.06	0.095	0.61	9.37	3.44	0.258	0.028	2.01	0.06	0.20	0.01	0.11	1.71

*, ** significant at 5% and 1% level, respectively

Table 2: Genetic variability, Mean, range and coefficient of variation for 19 characters derived from 10 parental diallel cross in Indian mustard (*Brassica juncea* L.) in parent

Genotypes	Mean	Min	Max	var (g)	var (p)	Heritability (%)	GA	GA% mean	GCV (%)	PCV (%)
Days to 50% flowering	54.67	49.00	59.33	12.40	13.34	92.98	7.00	12.80	6.44	6.68
Days to maturity	121.10	108.33	128.00	47.30	48.74	97.03	13.96	11.52	5.68	5.77
Plant Height(cm.)	159.62	145.63	181.20	166.01	171.01	97.07	26.15	16.38	8.07	8.19
No. of primary branches	6.62	5.40	8.17	0.68	0.80	84.28	1.56	23.51	12.43	13.54
No. of secondary branches	14.49	10.20	18.63	7.74	8.54	90.63	5.46	37.64	19.19	20.16
Length of main raceme	78.16	64.93	89.53	81.42	87.63	92.91	17.92	22.92	11.54	11.98
No. of silique on main raceme	44.28	39.53	51.83	11.91	17.22	69.18	5.91	13.35	7.79	9.37
Seed per siliqua	11.43	9.73	12.80	0.92	1.18	78.06	1.74	15.26	8.38	9.49
1000 seed weight (g.)	4.17	3.32	4.68	0.19	0.20	93.80	0.87	20.75	10.40	10.74
Oil content	38.56	35.93	41.20	1.47	4.29	34.19	1.46	3.78	3.14	5.37
Palmitic acid (%)	7.33	4.04	9.04	3.03	3.07	98.88	3.57	48.64	23.74	23.88
Oleic acid (%)	13.52	6.08	20.03	12.98	13.15	98.66	7.37	54.53	26.65	26.83
Linoleic acid (%)	3.67	2.02	4.52	0.76	0.76	99.19	1.79	48.71	23.74	23.84
Linolenic acid (%)	10.43	5.29	13.60	4.45	4.53	98.24	4.31	41.31	20.23	20.41
Erucic acid (%)	37.18	30.36	51.44	35.31	36.57	96.56	12.03	32.35	15.98	16.26
Biological yield plant (g)	89.64	65.84	113.90	307.59	317.95	96.74	35.53	39.64	19.57	19.89
Harvest index (%)	20.35	16.70	23.52	3.08	4.11	75.01	3.13	15.39	8.63	9.96
LAI 30	1.61	1.30	1.80	0.04	0.05	90.60	0.41	25.53	13.02	13.68
LAI 60	4.44	4.20	4.70	0.02	0.06	35.67	0.18	4.01	3.26	5.46
LAI 90	4.18	3.80	4.40	0.02	0.06	44.44	0.22	5.15	3.75	5.63
Seed yield /plant (g)	18.03	13.13	21.87	7.10	7.69	92.33	5.27	29.24	14.77	15.38

Conclusion

The all-yeild attributing characters showing high genetic advance provide a broad way for the improvement in genotypes for specific character. Highest phenotypic and genotypic value are found in oleic acid percentage exhibited the highest phenotypic coefficient of variation (PCV) at 26.83%, indicating substantial variability in this trait. Following closely were the Linoleic acid percentage and Palmitic acid percentage, with PCVs of 23.84% and 23.88%. The heritability estimates for various traits ranged from 34.19 (Oil content) to 99.19 (Linoleic acid).

Thus, there exist ample scope for improvement in available germplasm to develop new improved varieties of mustard in future.

Future scope

Information on the variability in terms of genotypic and phenotypic components was obtained from the current experiment. Genetic progress and heredity as a percentage of mean. In the future, it will be helpful to select genotypes based on these characteristics to create elite genotypes of mustard that produce more mustard. Mustard production may be directly increased by selecting for those specific qualities that have been found to have high heritability and strong genetic progress as a percentage of mean.

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Reference

1. Akabari VR, Niranjana M. Genetic variability and trait association studies in Indian mustard (*Brassica juncea* L.). International Journal of Agricultural Sciences. 2015;11(1):35-39.
2. Anonymous. 4th Advanced Estimates released by Ministry of Agriculture & Farmers Welfare, Government of India on 20/03/2020. 2019.
3. Gami RA, Chauhan RM. Genetic analysis for oil content and oil quality traits in Indian mustard [*Brassica juncea* (L.) Czern & Coss.]. International Journal of Agricultural Sciences. 2014;10(1):146-150.
4. Hasan EU, Bibi T, Mustafa HSB, Mahmood T, Kalyar MTA, Salim J. Genetic evaluation and characterization for yield and related traits in mustard (*Brassica juncea* L.). Research Journal of Agriculture and Environment Management. 2015;4(2):82-87.
5. Kaur S, Kumar R, Kaur R, Singh I, Singh H, Kumar V. Heterosis and combining ability analysis in Indian mustard [*Brassica juncea* (L.)]. Journal of Oilseed Brassica. 2019;10(1):1-9.
6. Kumar S, Bhardwaj R, Jhambhulkar SJ, Rai A. Assessment of genetic variability, heritability and genetic advance in Indian mustard (*Brassica juncea* L.). Journal of Oilseed Brassica. 2023;14(1):38-43.
7. Lakra A, Tantuway G, Tirkey AE, Srivastava K. Genetic variability and trait association studies in Indian mustard (*Brassica juncea* L.). International Journal of Agricultural Sciences. 2020;9(1):2556-2565.
8. Mahendra JL, Salam S, Kar RR, Saxena RR, Bhanwar T, Chandrakar S, *et al.* Genetic diversity estimation in Toria [*Brassica rapa* (L.)]. International Journal of Current Microbiology and Applied Sciences. 2020;9(3):2577-2584.
9. Mandal K, Subba V, Dasgupta D, Kundagrami S. Combining ability and heterosis for seed yield and yield components in Indian mustard [*Brassica juncea* (L.) Czern and Coss.]. Agricultural Reviews. 2022;44(1):100-106.
10. Maurya SK, Maurya KN, Lal K, Singh Y, Singh S, Dixit B, *et al.* Assessment of genetic variability, heritability and genetic advance in Indian mustard [*Brassica juncea* L. Czern & Coss.]. International Journal of Current Microbiology and Applied Sciences. 2018;7(11):13-18.
11. Mumtaz A, Sadaqat HA, Yousaf MI, Saeed M, Zaman RQ, Shehzad A, *et al.* Gene action studies in *Brassica rapa* for seed yield-related traits. Journal of Global Innovations in Agricultural and Social Sciences. 2017;4(4):160-166.
12. Rao P, Avtar R, Kumari N, Jattan M, Rani B, Manmohan, *et al.* Multivariate analysis in Indian mustard genotypes for morphological and quality traits. Electronic Journal of Plant Breeding. 2017;8:450-458.
13. Rout S, Kerkhi SA, Gupta A. Estimation of genetic variability, heritability and genetic advance in relation to seed yield and its attributing traits in Indian mustard [*Brassica juncea* (L.) Czern and Coss.]. Journal of Pharmacognosy and Phytochemistry. 2019;8(3):4119-4123.
14. Samahegn Y, Tesfaye M. Variability, heritability and genetic advance analysis for some morphological characters in oilseed *Brassica* breeding lines. Molecular Plant Breeding. 2016;7(20):1-8.
15. Shrimal TM, Chauhan RM, Gami RA, Patel PT. Diallel analysis in Indian mustard (*Brassica juncea* L. Czern & Coss.). Electronic Journal of Plant Breeding. 2016;7(4):919-924.
16. Tripathi N, Kumar K, Verma OP. Genetic variability, heritability and genetic advance in Indian mustard (*Brassica juncea* L. Czern and Coss.) for seed yield and its contributing attributes under normal and saline/alkaline conditions. International Journal of Science and Research. 2013;6(14):14-20.