

## Variability, Heritability and Genetic advance Studies of Mustard [*Brassica juncea* (L.)] Genotypes at Satna District of Madhya Pradesh.

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### Abstract:

Twenty diverse cultivars of mustard in a Completely Randomized block design (CRBD) at AKS University, Satna, during *Rabi* season on November 2022. The twelve quantitative characters studied viz., days to 50% flowering, plant height (cm), primary branches per plant, secondary branches per plant, length of main raceme (cm), siliquae on main raceme, days to maturity, length of siliqua, seeds per siliqua, test seed weight (g), biological yield per plant (g) and seed yield per plant. Data were collected for twelve quantitative traits and estimated for variance, genetic variability, heritability and genetic advance. The design of the experiment indicated highly significant differences for all the characters due to treatments. The analysis of variance indicated the existence of sufficient amount of variability among genotypes for all the studied characters. PCV was higher than GCV for all the studied characters. The maximum GCV and PCV was observed for secondary branches per plant followed by seed yield /per plant, primary branches per plant, biological yield /plant, length of main raceme and siliquae on main raceme. High heritability ( $h^2b$ ) >80% were observed for all the studied characters except siliquae on main raceme and seeds per siliqua. High estimate of expected genetic advance at 5% were found for secondary branches per plant followed by seed yield per plant, biological yield per plant and primary branches per plant. High heritability coupled with high genetic advance indicated the predominance of additive gene action in the expression of these traits.

**Keywords:** Mustard, Variance, variability, heritability and genetic advance

### I. Introduction:

Oilseed crops are the strong backbone of agricultural economy of India. Most of edible oils are obtained from rapeseed and mustard. The oil content of seeds of different forms ranges from 30 to 46 percent. Canola and mustard belong to the *cruciferous* (*Brassicaceae*) family. In the regional Indian languages rapeseed-mustard is called as Rai, Banarasi rai Kalee sarson, in sanskrit it is called as Asuri, Bimbata. Indian subcontinent, accounting for more than 80% of the total area of rapeseed mustard in the country. *Brassica juncea* ( $2n=36$ ) is an allopolyploid species obtained from natural interspecific cross between *Brassica nigra* ( $2n=18$ ) and *B. campestris/rapa* ( $2n=20$ ) (Nagaharu, U. 1935).

The origin of *B. juncea* is controversial. The Middle East seems to be the origin of the parent species; *B. nigra* and *B. campestris* are crossed (Olson 1960). Biochemical and molecular studies support this finding and provide further evidence for the existence of two races, Chinese and Indian (Vaughan *et al.* 1963, Vaughan and Gordon 1973). It is expected that, 19<sup>th</sup> century Indian mustard [*B. juncea* (L.) Czern & Coss] originated in China and may have traveled to India.

Among different oilseeds crops, rapeseed and mustard are important both for human consumption and for industrial purposes. In human diet, they provide not only essential fatty acids as a good source of energy, but also help in metabolism of fat-soluble vitamins A, D, E and K. In each gram of oil supplies 5 kilo calories. The leaves of young plants are used as green vegetables locally known as (Sarson ka saag) and plants are used as green fodder for cattle. Oil of rapeseed and mustard are used for cooking and for the preparation of various food products and pickles.

Worldwide, *Brassica species* are mainly grown in the temperate and subtropical zones of Europe, Asia and North America. India, China, Pakistan, Europe, Canada and Russia are the principal oilseeds growing countries. India contributes 6.30 million hectares area and 7.20 million tones of production of rapeseed and mustard in 2018-19 The chief oilseeds producing states are Rajasthan, Madhya Pradesh, Uttar Pradesh, Punjab, Haryana, Assam, Bihar, West Bengal and Orissa. (Anonymous, 2021-2022).

Genetic variability is a basic feature of a crop improvement programme. The assessment of genetic variability for yield and its components is a pre-requisite for improvement of the crop to the desired level and the effectiveness of selection depends upon its nature and magnitude in genetic material. The concept of heritability explains whether differences observed between individuals due to the differences in genetic constitution or because of environmental forces. Genetic advance gives the impression or idea of possible improvement of new individuals through selection as compared to the original populations. The genetic gain depends upon the quantity of genetic variability and magnitude of masking effect of the environment. Therefore, the analysis of variability, heritability, and genetic advance are of exquisite significance for creating a success breeding programme in mustard crop. This may assist in selecting proper line for hybridization which may also give better segregants in Indian mustard.

## II. Material And Method

The present investigation was conducted during *Rabi*, 2022-23 at Research farm, Genetics and Plant Breeding, AKS University, Sherganj, Satna, Madhya Pradesh. The material consists 20 varieties/strains of Mustard (*Brassica juncea* L.) germplasm comprising indigenous genotypes, evaluated in Completely Randomized Block Design. The entire experimental field divided in 3 blocks of equal size and each block had 20 plots. Each plot was consisted of three rows 2 meters length, following row to row spacing of 45 cm. and plant to plant spacing of 15 cm. These genotypes exhibiting wide spectrum of variability for various agronomic and morphological characters were obtained from the, eleven from Bundelkhand University Jhansi, U.P. eight from local market Satna, M.P. one from Farmers field, Satna, M.P.

Twelve observations on yield and yield contributing characters were recorded. In each plot, five competitive plants were randomly selected for

recording observations for all the twelve quantitative characters, which were recorded on the plot basis.

The analysis of variance for the design of the experiment was carried out according to the procedure outlined by Panse and Sukhatme, (1967). The genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV) and environmental coefficient of variation (ECV) was estimated by the formula suggested by Burton and de Vane, (1953). Heritability in broad sense ( $h^2b$ ) was estimated using the formula suggested by Burton and de Vane, (1953). Genetic advance was calculated by the method suggested by Johnson *et al.*, (1955).

## III. Result And Discussion

The analysis of variance for the design of the experiment involving 20 strains/varieties of mustard was evaluated in Randomized Block Design with three replications for the twelve quantitative characters. The design of the experiment indicated highly significant differences for all the characters presented in **Table: 1**, indicating thereby the presence of sufficient genetic variability in the genotypes. All the twelve characters selected for study showed highly significant inter-varietal variation and hence these characters can be used for selection in formulating breeding programmes. The similar results were found by **Raliya *et al.*, (2018), Gadi *et al.*, (2020), Priyanka and Pandey, (2021), Gupta *et al.*, (2022), Nishad *et al.*, (2022), Vanukuri and Pandey, (2022), Yadav *et al.*, (2022).**

The mean performance, grand means, range, GCV, and PCV of 20 genotypes of mustard for 12 quantitative characters are presented in **Table: 2** and **Table: 3**. The magnitude of phenotypic coefficients of variation (PCV) was slightly higher than corresponding genotypic coefficients of variation for all the seed quality parameters due to the environmental influence. The magnitude of GCV ranged from secondary branches per plant (35.668) to days to maturity (4.673). The magnitude of PCV ranged from seed yield /per plant (38.569) to days to maturity (5.213). The high GCV and PCV were recorded for secondary branches per plant (35.668) followed by seed yield /per plant (35.219), primary branches per plant (28.858), biological yield /plant (28.159), length of main raceme (15.541) and siliquae on main raceme (14.595). This is an indicative of less amenability of these characters to environmental fluctuations and hence, greater emphasis should be given to these

traits. The traits with high environmental coefficient of variation (ECV) indicated more influence of environmental factors. Therefore, caution has to be exercised during the selection programme because the environmental variations are unpredictable in nature and may mislead the results. Earlier researchers also observed high amount of PCV and GCV values for plant height **Akkenapally and Chetariya, (2022)**, for primary branches per plant **Chakraborty et al. (2021)**, **Akkenapally and Chetariya (2022)**, **Gupta et al. (2022)**, **Reddy and Shrivastav, (2022)**, **Vanukuri and Pandey, (2022)**, for secondary branches per plant **Chakraborty et al. (2021)**, **Priyanka and Pandey, (2022)**, **Akkenapally and Chetariya (2022)**, **Gupta et al. (2022)**, **Reddy and Shrivastav, (2022)**, **Yadav et al., (2022)**, for length of main raceme **Akkenapally and Chetariya, (2022)**, **Gupta et al., (2022)**, for biological yield per plant **Akkenapally and Chetariya, (2022)**, **Gupta et al., (2022)**, **Yadav et al., (2022)** and for seed yield per plant **Chakraborty et al. (2021)**, **Akkenapally and Chetariya (2022)**, **Gupta et al. (2022)**, **Nishad et al., (2022)**, **Reddy and Shrivastav, (2022)**, **Vanukuri and Pandey, (2022)**, **Yadav et al. (2022)**.

Heritability estimates are used to predict expected advance under selection so that breeders are able to anticipate improvement from different of selection intensity. The major function of heritability estimates is to provide information on transmission of characters from parents to the progeny. Such estimates facilitate evaluation of hereditary and environmental effect in phenotypic variation and thus aid in selection. **Burton and De Vane (1953)** suggested that the GCV along with heritability estimate could provide better picture of the genetic advance to be expected by phenotypic selection. Heritability  $h^2$  (Broad Sense),  $h^2$  (Broad Sense)%, Genetic Advancement @ 5%, Genetic Advancement @1%, Genetic Advance as % of Mean 5%, Genetic Advance as % of Mean 1%, and Variation was estimated for all the characters and has been presented in **Table: 4**.

The heritability value ranged from lowest seeds per siliqua (77.00%) to highest plant height (97.7%). plant height (97.7%) followed by days to 50% flowering (95.9%), biological yield /plant (93.4%), length of siliqua (90.6%), length of main raceme (88.7%), seed yield /per plant (83.4%), primary branches per plant (82.2%), test seed weight (81.7%) and days to maturity (80.4%) suggested that the characters are least influenced by the environmental factors and also indicates the

dependency of phenotypic expression which reflect the genotypic ability of strains to transfer the gene to their offspring.

Genetic advance is a measure of genetic gain under selection which depends upon main factors viz., genetic variability, heritability, and selection index **Allard RW, (1960)**. The expected genetic advance as percent of mean at 5% ranged from days to maturity (8.63%) to secondary branches per plant (69.788%). High estimate of expected genetic advance as percent of mean at 5% were found for secondary branches per plant (69.788%) followed by seed yield /per plant (66.249%), biological yield /plant (56.075%) and primary branches per plant (53.915%). High heritability coupled with high genetic advance observed for biological yield per plant, seed yield per plant, primary branches per plant and secondary branches per plant indicating that these characters could be prominently governed by additive gene action. So the selection of these traits could be more effective for desired genetic improvement. Similar results were reported earlier by **Chakraborty et al., (2021)**, **Gadi et al., (2020)** reported high heritability for days to flowering. High heritability for days to maturity was also reported by few workers like **Gadi et al., (2020)**. High heritability for plant height was also reported by **Akkenapally and Chetariya, (2022)**, **Gupta et al., (2022)**. High heritability along with high genetic advance was also recorded for primary branches per plant by **Gupta et al., (2022)**, **Reddy and Shrivastav, (2022)**, **Chakraborty et al., (2021)**. High heritability along with high genetic advance was also recorded for secondary branches per plant by **Akkenapally and Chetariya, (2022)**, **Gupta et al., (2022)**, **Reddy and Shrivastav, (2022)**, **Chakraborty et al., (2021)** **Kumar, (2008)**. **Akkenapally and Chetariya, (2022)**, **Reddy and Shrivastav, (2022)**, reported high heritability along with high genetic advance for length of main raceme in this crop. High heritability along with high genetic advance was also recorded for 1000- grain weight by **Akkenapally and Chetariya, (2022)**, **Reddy and Shrivastav, (2022)**. High heritability coupled with high genetic advance was also reported for biological yield per plant by **Akkenapally and Chetariya, (2022)**, **Gupta et al., (2022)**, **Reddy and Shrivastav, (2022)**. High heritability coupled with high genetic advance was also reported by a number of workers such as **Akkenapally and Chetariya, (2022)**, **Chakraborty et al., (2021)** for seed yield.

#### IV. Conclusion

In the light of above findings it may be concluded that wide spectrum of exploitable variability in the material studied with respect to seed yield per plant and its component characters. As per mean performance the maximum yield was recorded by varieties/genotypes viz., Gold star, Varuna, Vasundhra, NRDR-2 and Mahiko gold-plus. The maximum GCV and PCV was observed for secondary branches per plant followed by seed yield /per plant, primary branches per plant, biological yield /plant, length of main raceme, and siliquae on main raceme. Higher estimates ( $h^2b$ ) >80% were observed for all the characters except number of seed per siliqua, harvest index (%) and seed yield per plant (g). High heritability coupled with high genetic advance observed for biological

yield per plant, seed yield per plant, primary branches per plant and secondary branches per plant indicating that these characters could be prominently governed by additive gene action. So the selection of these traits could be more effective for desired genetic improvement and will help in improving the seed yield in mustard.

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**Table 1 Analysis of variance for 12 quantitative characters in Mustard.**

S.No.	Traits	Replications (df = 2)	Treatments (df = 19)	Error (df = 38)
1	Days to 50% flowering	75.37	208.46**	8.63
2	Plant height	2.97	889.64**	25.21
3	Primary branches per plant	2.66	12.19**	2.16
4	Secondary branches per plant	82.22	103.37**	10.11
5	Length of main raceme	53.6	231.93**	26.19
6	Siliquae on main raceme	219.06	167.61**	34.81
7	Days to maturity	331.69	119.55**	23.47
8	Length of siliqua	1.01	1.42**	0.13
9	Seeds per siliqua	1.29	3.32**	0.76
10	Test seed weight	2.02	1.49**	0.27
11	Biological yield /plant	185.55	1258.83**	82.49
12	Seed yield /per plant	308.28	340.97**	56.66

\*Significant at 5% probability level.

\*\*Significant at 1% probability level.

**Table 2 Mean performance of 12 characters of mustard genotypes.**

S.N.	Genotypes	Days to 50% flowering	Plant height (cm)	Primary branches per plant	Secondary branches per plant	Length of main raceme (cm)	Siliquae on main raceme	Days to maturity	Length of siliqua (cm)	Seeds per siliqua	Test seed weight (g)	Biological yield /plant (g)	Seed yield /per plant (g)
1	NRDR-2	61.29	159.81	6.08	18.74	66.05	53.59	117.52	5.23	12.81	5.33	53.48	38.72
2	RVM-3	64.05	178.59	5.63	15.56	57.76	42.69	123.75	4.12	13.35	4.15	78.67	33.69
3	JM-3	67.03	176.57	5.68	12.06	55.08	42.61	126.40	6.50	14.25	5.25	70.12	22.12
4	PM-26	55.75	165.56	6.06	13.40	44.01	46.51	124.56	5.35	13.21	4.01	54.00	22.94
5	Sej-2	64.58	165.26	6.29	14.84	56.44	47.10	121.11	4.78	13.70	5.55	54.31	16.43
6	Vasundhra	59.75	183.33	9.55	24.88	62.38	44.63	116.11	4.96	13.27	5.18	90.42	41.44
7	Maya	50.64	163.09	6.01	16.86	46.04	49.83	126.66	5.38	13.24	4.68	60.44	26.79
8	Varuna	66.00	191.49	11.49	24.00	58.91	63.45	125.42	6.26	15.26	5.14	113.53	42.01
9	Rohini	49.24	177.99	6.07	12.46	36.58	42.23	104.36	5.28	12.64	4.58	50.65	23.14
10	Pusa vijay	69.18	181.30	8.46	19.24	64.95	45.44	108.89	5.93	13.87	5.12	83.81	30.74
11	MS-2	67.58	171.03	6.11	11.17	57.48	61.73	125.68	5.79	13.64	3.99	80.74	21.61
12	Kaliya-92	63.31	171.81	4.59	11.74	51.94	45.57	125.25	4.82	12.93	4.43	62.22	16.58
13	Krishna Gold	48.21	166.08	5.85	11.57	58.15	43.40	123.56	4.85	13.19	5.53	61.79	25.23
14	Basanti	65.08	152.74	5.98	12.25	45.81	30.95	122.71	4.53	12.20	4.47	66.54	17.31
15	Kalawati	67.60	150.77	5.37	12.93	55.91	39.30	122.34	4.89	12.46	3.46	64.13	17.39
16	Gold star	71.54	209.78	9.80	33.31	53.73	38.72	123.58	5.83	14.01	4.54	126.18	55.99
17	Mahiko gold-plus	57.11	137.99	3.65	10.69	35.29	37.79	118.25	4.83	13.01	4.65	48.61	35.52
18	Chutki sarson	73.08	176.87	6.06	14.28	50.19	45.48	128.77	3.85	10.58	3.32	66.82	21.34
19	Karuna	70.70	142.31	4.03	11.90	45.51	45.96	124.01	4.79	12.28	3.96	55.45	26.77
20	Local variety(L1)	44.59	149.38	3.97	10.77	63.53	44.74	113.13	4.36	11.03	3.33	64.49	17.07

**Table 3 Mean, Range, Genotypic, Phenotypic and environmental variances, and coefficient of variation for 12 quantitative characters in mustard.**

S.N.	Characters	Grand mean	Range		GCV	PCV	ECV	C.D. @ 5%
			Max	Min.				
1	Days to 50% flowering	61.82	73.08	44.59	13.203	13.485	4.754	4.86
2	Plant height	168.59	209.78	137.99	10.069	10.215	2.978	8.30
3	Primary branches per plant	6.34	11.49	3.65	28.858	31.82	23.22	2.43
4	Secondary branches per plant	15.63	33.31	10.69	35.668	37.552	20.345	5.26
5	Length of main raceme	53.29	66.05	35.29	15.541	16.501	9.604	8.46
6	Siliquae on main raceme	45.59	63.45	30.95	14.595	16.396	12.942	9.75
7	Days to maturity	121.10	128.77	104.36	4.673	5.213	4.001	8.01
8	Length of siliqua	5.12	6.50	3.85	12.819	13.465	7.137	0.60
9	Seeds per siliqua	13.05	15.26	10.58	7.075	8.064	6.702	1.45
10	Test seed weight	4.53	5.55	3.32	14.085	15.58	11.534	0.86
11	Biological yield /plant	70.32	126.18	48.61	28.159	29.13	12.916	15.01
12	Seed yield /per plant	27.64	55.99	16.43	35.219	38.569	27.233	12.44



**Table 4 Heritability (%) in broad sense, Genetic advance and genetic advance as percent of mean for 12 quantitative characters in mustard.**

S.N.	Characters	Heritability (h <sup>2</sup> b)	Heritability (h <sup>2</sup> b %)	Genetic Advancement 5%	Genetic Advancement 1%	Gen. Adv. as % of Mean 5%	Gen. Adv as % of Mean 1%
1	Days to 50% flowering	0.959	95.90	16.461	21.095	26.629	34.126
2	Plant height	0.972	97.70	34.469	44.174	20.446	26.203
3	Primary branches per plant	0.822	82.20	3.416	4.378	53.915	69.095
4	Secondary branches per plant	0.902	90.20	10.909	13.981	69.788	89.438
5	Length of main raceme	0.887	88.70	16.068	20.591	30.153	38.643
6	Siliquae on main raceme	0.792	79.20	12.2	15.635	26.762	34.296
7	Days to maturity	0.804	80.40	10.451	13.394	8.63	11.060
8	Length of siliqua	0.906	90.60	1.286	1.649	25.139	32.217
9	Seeds per siliqua	0.77	77.0	1.668	2.138	12.788	16.388
10	Test seed weight	0.817	81.70	1.189	1.524	26.232	33.618
11	Biological yield /plant	0.934	93.40	39.433	50.535	56.075	71.863
12	Seed yield /per plant	0.834	83.40	18.312	23.468	66.249	84.901

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