

Variability Studies of Mustard Genotypes [*Brassica juncea* (L.) Czern and Coss] for Quantitative Traits and Yield Components at Satna District of Madhya Pradesh (India)

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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 2021. 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 in no. of silique/plant followed by primary branches/plant, test weight (1000 seed) (g), seed yield/plant (g) and biological yield per plant (g). Higher estimates (h^2b) >80% were observed for all the characters except number of seed/silique, harvest index (%) and seed yield/plant (g). High estimate of expected genetic advance at 5% were found for number of silique/plant followed by primary branches/plant, test weight (1000 seed)(g), biological yield/plant (g), and seed yield/plant (g). 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

Introduction:

The oilseed crop has long been an important part and backbone of Indian agricultural economy. 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. It is mentioned in many scriptures and ancient documents/literatures and may have been commercially cultivated as early as 5000 BC. It was discovered by Channhudo of the Indus Valley Civilization between 2300-1750 BC. The Aryans used the Brassica plant as food and fuel. *Brassicaceae* has about 3500 species and 350 genera. Indian subcontinent, accounting for more than 80% of the total area of rapeseed mustard in the country.

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). From there it quickly spread to Europe, Africa, Asia, India and the Far East. It occurs more than once in ancestry and in many places such as China, eastern India, and the Caucasus, which are now two centers of diversity. Biochemical and molecular studies support this finding and provide further evidence

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for the existence of two races, Chinese and Indian (Vaughan *et al.* 1963, Vaughan and Gordon 1973). It is expected that, 19th 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. For industrial purposes, their oil serves as important raw material for manufacturing paints, varnishes, lubricants, soaps, hair oil and other type of cosmetics. The oilseed cake is largely used for feeding cattle and also as manure.

Botanically, the genus Brassica, belonging to the family cruciferae now it is known as Brassicaceae has six species (*B. nigra* (BB, 2n=16), *B. oleracea* (CC, 2n=18), *B. campestris* (AA, 2n=20), *B. carinata* (BBCC, 2n= 34), *B. juncea* (AABB, 2n=36) and *B. napus* (AACC, 2n=38). Among them first three species *B. nigra*, *B. oleracea* and *B. campestris* are elementary and diploid with 2n=16, 18 and 20 chromosomes, respectively. The other three *B. carinata*, *B. juncea* and *B. napus* are tetraploids with chromosome numbers 2n=34, 36 and 38, respectively. All these crops are grown under wide range of agro-climatic conditions. *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).

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 (ICAR –Directorate of Rapeseed and Mustard research bharatpur developed and maintain by ICAR-DRMR). Rajasthan ranks first in both area (2.74 mha) and production (3.46 mt) in the country. The chief oilseeds producing states are Rajasthan, Madhya Pradesh, Uttar Pradesh, Punjab, Haryana, Assam, Bihar, West Bengal and Orissa.

Oilseed production assumes exquisite significance in India because of gap in demand and supply of edible oils, which compelled our country to import vegetable oils to the tune of crores of rupees, causing a heavy drain of the foreign exchange in past years. Though, this crop has witnessed few improvement during the last two decades but the progress has been rather slow, perhaps due to the narrow genetic base, inherent susceptibility to biotic and abiotic stresses, and inconsistent information relating to the genetic parameters underlying characters under improvement, However, information on these aspects has come to stay as backbone for a rational breeding program.

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.

Material and method

The present investigation was conducted during *Rabi*, 2020-21 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 data were recorded for days to 50 % flowering, primary branches per plant, plant height (cm), days to maturity, length of main raceme, no. of siliqua per plant, siliqua length (cm), no. of seed per siliqua, test weight (1000 seed), biological yield per plant (g), harvest index (%) and seed yield per plant (g).

Analysis of variances:

The analysis of variance for the design of experiment was done for partitioning the variance into treatments and replications, which was carried out according to the procedure outlined by **Panse and Sukhatme, (1967)**. The significance of difference among treatment means was tested by “F” test. To test the Hypothesis $H_0: t_1 = t_2 \dots t_v$. The fixed effect modal for analysis of variance for Randomized Block Design is given below:

$$Y_{ij} = \mu + t_i + b_j + e_{ij}$$

Where,

Y_{ij} = Yield of i^{th} entry in the j^{th} replication

μ = General mean

t_i = Effect of the i^{th} entry ($i = 1, 2, \dots, V$)

b_j = Effect of the j^{th} replication ($j = 1, 2, \dots, V$)

e_{ij} = Environmental effect

Estimation of variability:

- **Mean**

The mean of i^{th} trait was measured by dividing the total of all observations ($\sum X_{ij}$) by their number and was denoted by $\bar{X}_i$

$$\bar{X}_i = \frac{1}{N} \left(\sum_{j=1}^n X_{ij} \right)$$

$$J = 1$$

Where,

$\bar{X}_i$ = Mean of the i^{th} trait

X_{ij} = The value of j^{th} observations of i^{th} trait

n = Number of observations

- **Range:**

This was estimated as the differences between the least and the greatest value of a series of observations of accessions.

- **Estimation of coefficient of variation:**

The coefficient of variation for i^{th} trait was estimated by using following formula;

$$C.V. = \frac{\sqrt{MSE}}{\bar{X}_i} \times 100$$

Where,

MSE = The sample estimate of the experimental error

$\bar{X}_i$ = Mean of the i^{th} trait

The genotypic coefficient variation (GCV), phenotypic coefficient of variation (PCV) and environmental coefficient of variation (ECV) was computed following Burton and de Vane, (1953)

$$GCV = \frac{\text{Genotypic standard deviation } (\sigma_g)}{\text{Mean } \bar{X}}$$

$$PCV = \frac{\text{Phenotypic standard deviation } (\sigma_p)}{\text{Mean } \bar{X}}$$

$$ECV = \frac{\text{Environmental standard deviation } (\sigma_e)}{\text{Mean } \bar{X}}$$

Heritability:

Heritability in broad sense (h^2) was calculated using the formula suggested by Burton and de Vane, (1953).

$$h^2 = \frac{\sigma^2 g}{\sigma^2 g + \sigma^2 e}$$

Or

$$H^2 b (\%) = \frac{\sigma^2 g}{\sigma^2 p} \times 100$$

Expected genetic advance:

Genetic advance was calculated by the method suggested by **Johnson *et al.*, (1955)**.

$$\begin{aligned} G.A. &= \frac{\sigma^2 g}{\sigma^2 p} K \cdot \sigma^2 p \\ &= h^2 \cdot K \cdot \sigma^2 p \end{aligned}$$

Where,

K = Selection differential at 5% selection intensity (2.06).

Genetic advance as percent of mean (G.A.) %:

It was calculated by following formula;

$$G.A. \% = \frac{\text{Genetic advance}}{\bar{X}} \times 100$$

Where,

$\bar{X}$ = Grand mean of the character

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. The maximum variances due to replication were found for number of siliqua per plant (9631.064453) and highest variances due to treatment for number of siliqua per plant (208568.278478**). 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)**.

The maximum genotypic coefficient variation was observed in number of siliqua per plant (57.459) followed by primary branches per plant (31.816), test weight (1000 seed) (g) (25.156), seed yield per plant (g) (23.771) and biological yield per plant (g) (23.586). This is an

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indicative of less amenability of these characters to environmental fluctuations and hence, greater emphasis should be given to these traits. The magnitude of GCV ranged from highest number of siliqua per plant (57.459) to lowest days to maturity (4.182).

The mean performance, grand means, range, GCV, and PCV of 20 genotypes of mustard for 12 quantitative characters are presented in **Table: 2, Table: 3, Fig. 1 and Fig. 2**. The high PCV were recorded for number of siliqua per plant (58.792) followed by primary branches per plant (33.998), seed yield per plant (g) (28.962), test weight (1000 seed) (g) (25.374), biological yield per plant (g) (25.204) and harvest index (%) (21.331). The magnitude of PCV ranged from highest number of siliqua per plant (58.792) to days to maturity (4.463). The traits with high genotypic and phenotypic coefficient of variation 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. 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.

High degree of PCV and GCV were recorded for the traits like Number of Siliqua per plant followed by Primary branches per plant, Test weight (1000 seed)(g), Biological yield per plant (g), Seed yield per plant (g) and Length of main raceme (cm) indicating simple selection for these traits will be useful for the planning of a breeding programme. 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)**, for secondary branches per plant **Chakraborty et al. (2021)**, for biological yield per plant and for seed yield per plant **Chakraborty et al. (2021)**,

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 and Fig. 3**.

The heritability value ranged from lowest harvest index (%) (55.8%) to highest test weight (1000 seed) (g) (98.3%). High heritability estimates (h^2b) >80% were found for test weight (1000 seed) (g) (98.3%) followed by plant height (cm) (95.9%), number of siliqua per plant (95.5%), days to 50 % flowering (94.2%), length of main raceme (cm) (93.9%), siliqua length (cm) (90.6%), days to maturity (87.8%), primary branches per plant (87.6%) and

biological yield per plant (g) (87.6%) 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 transmit the gene to their progenies.

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 lowest, days to maturity (8.073%) to highest, number of siliqua per plant (115.684%). High estimate of expected genetic advance as percent of mean at 5% were found for number of siliqua per plant (115.684%) followed by primary branches per plant (61.337%), test weight (1000 seed)(g) (51.374%), biological yield per plant (g) (45.466%), seed yield per plant (g) (40.19%), length of main raceme (cm) (39.074%) and plant height (cm) (30.284%). High heritability coupled with high genetic advance observed for length of main raceme (cm), number of siliqua per plant, test weight (1000 seed)(g), biological yield per plant (g), primary branches per plant and plant height (cm) 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 in mustard breeding programme. 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. High heritability along with high genetic advance was also recorded for primary branches per plant by **Chakraborty et al., (2021)**. High heritability along with high genetic advance was also recorded for secondary branches per plant by **Chakraborty et al., (2021)** **Kumar, (2008)**. 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 .High heritability coupled with high genetic advance was also reported for biological yield per plant. High heritability coupled with high genetic advance was also reported by a number of workers such as **Chakraborty et al., (2021)** for seed yield.

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., Pusa Musterd 28, NRCHB 101, Pusa M 21, Radhika, NRC DR 02 and Super Mahagold G 9. The maximum GCV and PCV was observed in number of siliqua per plant followed by primary branches per plant, test weight (1000 seed) (g), seed yield per plant (g) and biological yield per plant (g). 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 length of main raceme (cm), number of siliqua per plant, test weight (1000 seed)(g), biological yield per plant (g), primary branches per plant and plant height (cm) 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. As per the study the characters like plant height (cm.), number of primary branches per plants, biological yield per plant and 1000 seed weight 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	26.919212	199.709479**	11.492168
2	Primary branches per plant	4.452182	18.673307**	2.319422
3	Plant height (cm)	313.288635	1682.083715**	68.998097
4	Days to maturity	15.017055	85.658052**	10.446553
5	Length of main raceme (cm)	33.74332	440.230857**	26.832792
6	No. of Siliqua per plant	9631.064453	208568.278478**	9347.16203
7	Siliqua length (cm)	1.004712	1.424276**	0.133392
8	No. of Seed per Siliqua	1.297655	3.320378**	0.764388
9	Test weight (1000 seed)(g)	0.079982	4.013461**	0.068861
10	Biological yield per plant (g)	85.790924	411.840502**	51.203162
11	Harvest index (%)	79.984306	79.032319**	34.90932
12	Seed yield per plant (g)	38.219013	30.457118**	9.93992

*Significant at 5% probability level.

**Significant at 1% probability level.

Table: 2 Mean performance of 12 characters of twenty mustard genotypes.

S.N.	Genotypes	Days to 50 % flowering	Primary branches per plant	Plant height (cm)	Days to maturity	Length of main raceme (cm)	No. of Siliqua per plant	Siliqua length (cm)	No. of Seed per Siliqua	Test weight (1000 seed) (g)	Biological yield per plant (g)	Harvest index (%)	Seed yield per plant (g)
1	Pitambari	45.39	4.11	114.61	106.32	33.53	195.57	4.79	12.28	3.63	23.75	29.02	6.74

2	PBR 210	65.19	5.27	134.62	120.48	67.42	382.72	4.36	11.03	5.85	33.54	23.71	7.90
3	Radhika	44.17	13.11	189.58	118.05	63.53	929.00	5.23	12.81	5.56	63.72	22.78	14.51
4	Pusa Musterd 25	67.00	5.65	144.49	124.48	65.86	193.25	4.12	13.35	5.46	41.98	26.83	11.36
5	Pusa Musterd 28	68.11	6.88	159.48	124.69	75.50	263.43	4.83	13.01	5.73	47.50	33.24	16.17
6	DRMR IJ 31	67.45	11.13	179.30	118.86	61.08	901.56	3.85	10.58	4.63	60.74	20.00	12.01
7	DRMR 150 35	59.33	6.80	146.65	116.49	71.33	388.13	6.50	14.25	4.61	53.70	22.24	12.07
8	RH 0119	45.66	6.25	124.87	109.25	64.66	297.62	5.35	13.21	3.48	36.77	29.86	11.22
9	PUSA M 21	67.42	6.54	171.55	121.95	58.66	359.82	4.89	12.46	6.23	49.96	29.07	14.55
10	NRCHB 101	57.57	6.78	171.18	119.11	61.46	311.76	5.83	14.01	5.65	48.38	31.58	15.26
11	Divya 203	68.02	9.39	173.60	126.69	43.03	649.11	4.78	13.70	3.60	59.76	14.31	8.50
12	NRCDR 02	64.41	7.62	175.75	122.03	63.83	363.82	4.96	13.27	3.87	59.49	22.99	13.48
13	RGN 73	64.43	5.37	150.84	119.58	67.31	199.97	4.85	13.19	3.76	34.68	23.32	7.98
14	Farm Sona	64.68	10.82	182.27	115.36	51.50	809.52	4.53	12.20	5.76	47.07	25.62	11.94
15	Ganga	56.14	5.60	155.05	118.06	67.67	266.33	5.38	13.24	4.29	45.15	29.03	13.37
16	MUSTERD 2541	54.19	5.93	141.43	121.10	78.33	438.02	6.26	15.26	2.70	40.41	20.97	8.47
17	Super Mahagold G 9	64.80	11.37	178.72	122.32	43.22	988.55	5.79	13.64	5.67	62.48	21.35	13.42
18	PM 0031	65.91	6.06	124.94	120.14	60.59	235.68	4.82	12.93	4.98	36.46	20.93	7.09
19	US 126	64.47	7.40	159.73	119.60	62.78	554.79	5.28	12.64	3.26	54.77	16.13	8.67
20	Local Check	70.77	4.67	110.59	129.80	38.15	241.01	5.93	13.87	2.45	29.42	18.26	5.35

Table: 3 Mean, Range, Genotypic, Phenotypic and environmental variances, and coefficient of variation for 12 quantitative characters in Indian 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	Length of main raceme	53.29	66.05	35.29	15.541	16.501	9.604	8.46
5	Siliquae on main raceme	45.59	63.45	30.95	14.595	16.396	12.942	9.75
6	Days to maturity	121.10	128.77	104.36	4.673	5.213	4.001	8.01
7	Length of siliqua	5.12	6.50	3.85	12.819	13.465	7.137	0.60
8	Seeds per siliqua	13.05	15.26	10.58	7.075	8.064	6.702	1.45
9	Test seed weight	4.53	5.55	3.32	14.085	15.58	11.534	0.86
10	Biological yield /plant	70.32	126.18	48.61	28.159	29.13	12.916	15.01
11	Harvest index (%)	24.06	33.24	14.31	15.938	21.331	24.555	9.77
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	Traits	h^2 (Broad Sense)	h^2 (Broad Sense)%	Genetic Advancemen t 5%	Genetic Advancem ent 1%	Gen.Adv as % of Mean 5%	Gen.Adv as % of Mean 1%	Var Genotypica l	Var Phenotypical	Var Environment al
1	Days to 50 % flowering	0.942	94.2	15.84	20.3	25.86	33.141	62.739	66.57	3.831
2	Primary branches per plant	0.876	87.6	4.501	5.768	61.337	78.606	5.451	6.224	0.773
3	Plant height (cm)	0.959	95.9	46.778	59.948	30.284	38.811	537.695	560.695	22.999
4	Days to maturity	0.878	87.8	9.665	12.386	8.073	10.346	25.07	28.553	3.482
5	Length of main raceme (cm)	0.939	93.9	23.433	30.031	39.074	50.075	137.799	146.744	8.944
6	No. of Siliqua per plant	0.955	95.5	518.821	664.897	115.684	148.255	66407.0 4	69522.76	3115.721
7	Siliqua length (cm)	0.906	90.6	1.286	1.649	25.139	32.217	0.43	0.475	0.044
8	No. of Seed per Siliqua	0.77	77	1.668	2.138	12.788	16.388	0.852	1.107	0.255
9	Test weight (1000 seed)(g)	0.983	98.3	2.342	3.001	51.374	65.839	1.315	1.338	0.023
10	Biological yield per plant (g)	0.876	87.6	21.136	27.086	45.466	58.267	120.212	137.28	17.068
11	Harvest index (%)	0.558	55.8	5.903	7.565	24.533	31.44	14.708	26.344	11.636
12	Seed yield per plant (g)	0.674	67.4	4.422	5.667	40.19	51.506	6.839	10.152	3.313

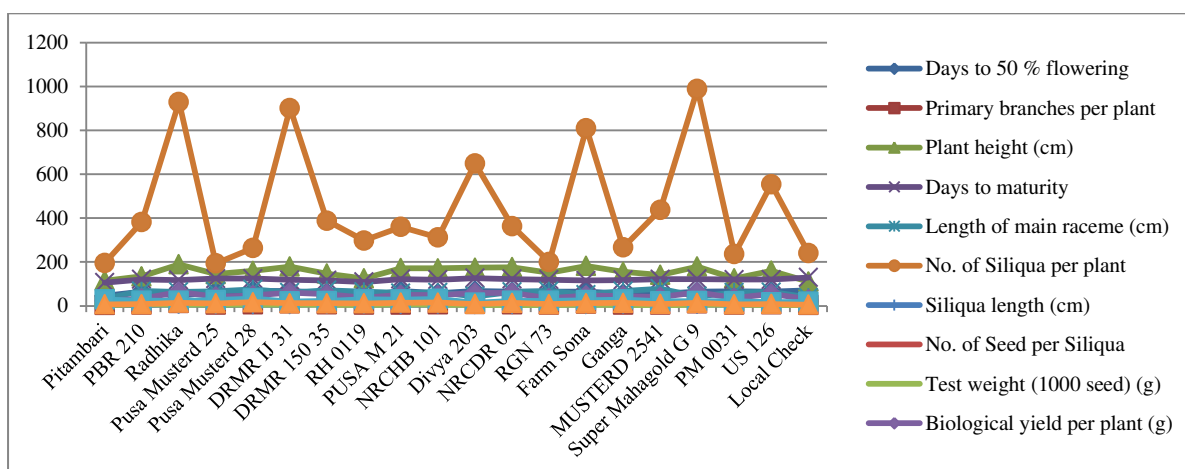


Fig. 1 Mean performance of mustard genotypes

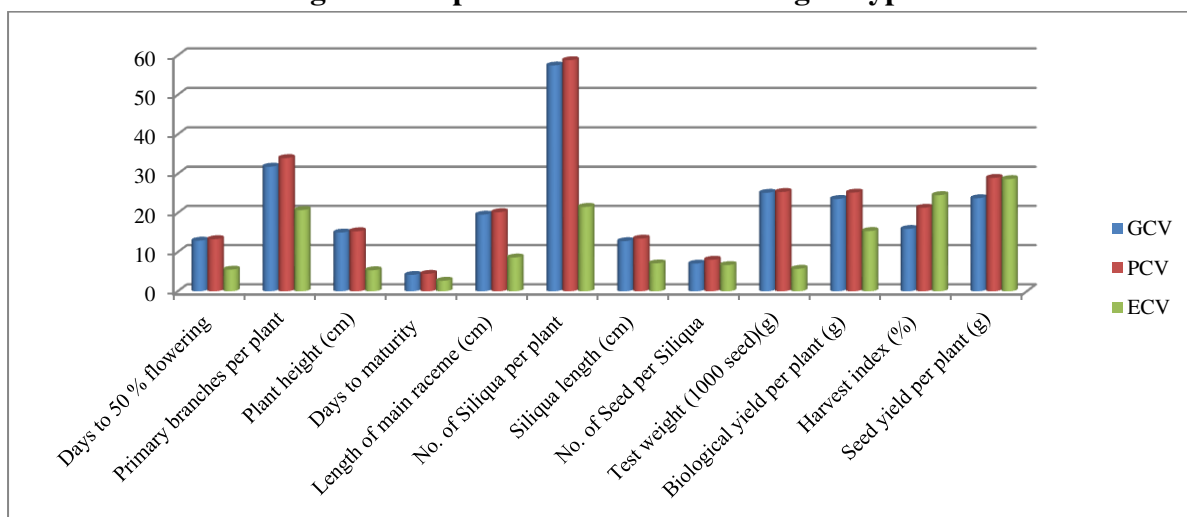
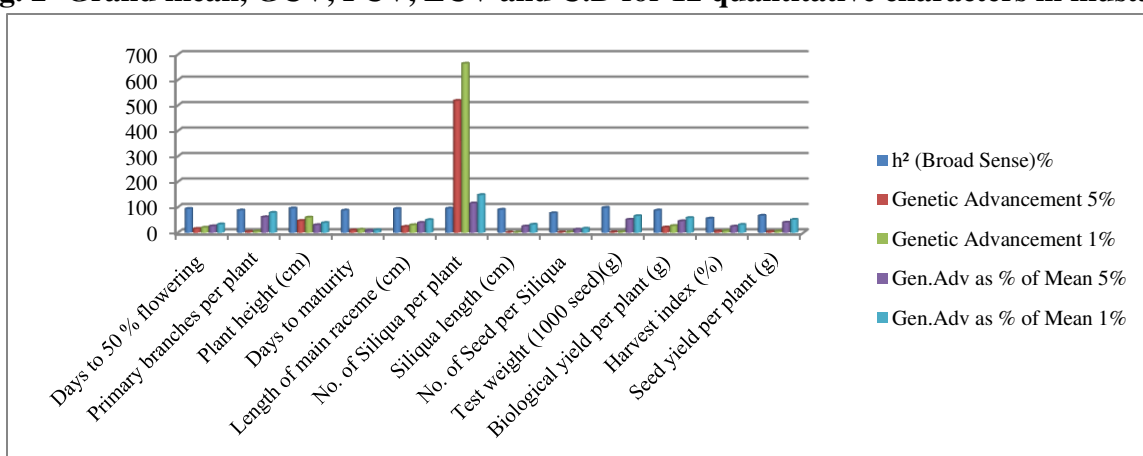


Fig. 2- Grand mean, GCV, PCV, ECV and C.D for 12 quantitative characters in mustard.

Fig. 3- h^2_b , GA @5% and 1%, and GA as % of mean 5% and 1%

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