



Studies on Genetic Variability and Divergence in Mustard (*Brassica Juncea* L.).

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Authors' contributions

This work was carried out in collaboration between both authors. Author SNKR carried out the research work. Author SPS planned the research and analyzed and wrote the manuscript. Both authors read and approved the final manuscript.

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ABSTRACT

The purpose of the research is to study Genetic Variability, Divergence and correlation studies on 20 genotypes of mustard. The phenotypic coefficient of variation was greater than genotypic coefficient of variation for all the traits. The high magnitude of both coefficients was recorded in case of number of primary number, secondary, number of siliquae per plant, seed yield per plant and harvesting index. High heritability with high genetic advance was recorded for number of primary branches, number of secondary branches, length of main raceme, number of siliquae in main raceme, number of siliqua per plant, number of seeds per siliquae, biological yield, 1000 seed weight, seed yield per plant and harvesting index. In the present findings the significant phenotypic correlation of seed yield per plant were found positive for the characters Days to 50% flowering, plant height, number of primary branches, number of secondary branches, length of main raceme, number of siliqua per plant, length of siliqua, number of seeds per siliqua, harvesting index and seed yield per plant showed positive significant correlation with seed yield per plant. The path coefficient analysis of different characters revealed that highest positive direct effect on seed yield per plant per plant was exerted by harvest index per plant followed by biological yield and negative direct effect on seed yield / plant was exhibited by number of siliqua per plant followed by length of siliqua, days to 50% flowering, number of secondary and number of primary branches. Diversity among clusters varied from 11.87 to 33.28. The highest intra-cluster distance was recorded in cluster II. The genotypes falling in these clusters could be utilized for hybridization programme in Indian mustard.

Keywords: Indian mustard; variability; genetic advance; heritability; correlation; path analysis; diversity.

1. INTRODUCTION

Oilseed Brassicas, also known as rapeseed-mustard, are a significant category of oilseed crops worldwide, consisting of eight cultivated crops from the Brassiceae tribe of the Brassicaceae family (Cruciferae). The term "mustard" comes from the European practise of preparing a heated paste by combining the sweet "must" of old wine with crushed seeds of black mustard (*Brassica nigra*) [1]. In India, Indian mustard (*Brassica juncea* (L.) 2n=36) is a major oilseed crop. It is grown for oil, condiments, and medicinal purposes. However, the crop is primarily grown to produce edible vegetable oil. Despite sharing the same family and genus, rapeseed and mustard have distinct botanical characteristics. Rapeseed is an annual herb that grows to a height of 45 to 150 cm. In most situations, a waxy covering covers the stems. Plant leaves are easily distinguished from mustard (rai) plants. Rapeseed leaves are sessile, glabrous, and hairy. The stalk is partially or completely grasped by the lowest segment of the blade (lamina). The fruits are thicker than mustard (rai) and feature a beak that is one-third to half the fruit's length. The seeds are golden or brown in colour, with a smooth seed coat. Mustard plants are tall (90-200 cm), erect, and highly branched. Instead of being dilated at the base and clasping like rapeseed, the leaves are stalked, broad, and pinnatifid. The fruits are narrow, ranging in length from 2 to 6.5 cm, with strong ascending or erect stems and short, thick beaks. The seed has a rough seed coat and is brown to dark brown in colour. Mustard is the world's third most significant oilseed crop, behind soybeans and palm oil. Among the several oilseed crops produced globally, the estimated area, production, and yield of mustard were 34.88 mha, 69.22 mt, and 1.98 Mt/ha, respectively [2]. Rapeseed production, area, and yield in India are 8.30 million hectares, 1.3 million tonnes, and 1.1 million tonnes per acre, respectively. Where rapeseed yield is lower than that of other crops.

Genetic variety and diversity are crucial requirements for crop development because they allow for more selective breeding. Because seed yield is a polygenic characteristic that frequently leads to changes in other characters, the link between seed yield and other traits is useful for selecting the proper selection in breeding

programmes. During the selection process, correlation analysis measures the degree, direction, and strength of the association between two or more variables. Path coefficient analysis quantifies the direct and indirect impacts of numerous independent variables on a dependent variable [3]. As a result, the current study is being carried out to estimate the heritability and diversity of genotypes for yield and yield contributing variables, as well as to assess the amount of direct and indirect reasons of linkage among various characters through path analysis in mustard.

2. MATERIALS AND METHODS

The present investigation entitled was carried out under, Department of Plant Breeding & Genetics at Agriculture Farm, School of Agriculture, Lovely Professional University, Jalandhar (Punjab) during the *rabi* 2021-22. The experimental design comprised 20 different genotypes of Mustard (Table 1) were grown in a RBD with three replications during *rabi* 2021-22. Each plot consists of two rows of 1.8 m length. Five competitive plants were selected from each replication for 14 quantitative traits *viz*: days to 50% flowering, days to maturity, plant height, number of primary branches per plant, number of secondary branches per plant, number of siliqua per plant, number of seed per siliqua, siliqua length of siliqua, number of siliqua on main raceme, 1000- seed weight, biological yield per plant, harvest index, seed yield per plant. The mean values of each genotype were computed for statistical analysis by using INDOSTAT software. The standard method of analysis of variance was given [4], phenotypic and genotypic coefficient of variation, heritability (Broad Sense) and genetic advance as percent of mean were estimated by the formula al suggested by [5] and [6]. The formula of genotypic correlation coefficients was estimated by [7]. Path analysis along with genotypic correlation coefficient is applied to know the direct and indirect effects of the components on yield as suggested by [8] and illustrated by [3]. The replicated data were subjected to genetic divergence analysis using Mahalanobis's D² - statistic [9].

3. RESULTS AND DISCUSSION

Analysis of variance revealed that the treatments were highly significant for all the traits except

length of siliquae and 1000 seed weight under study viz. days to 50% flowering, days to maturity, plant height, length main raceme, number of siliquae on main raceme, number of siliquae per plant, number of seeds per siliqua, biological yield per plant, seed yield per plant and harvest index which signified that genotype is highly variable for the observed traits. Similar results were also obtained by [10,11,12] and [13] in which analysis of variance showed significant differences for all the characters under their study.

In the present study, the phenotypic coefficient of variation (PCV) was greater than genotypic coefficient of variation (GCV) for all the traits number of primary numbers, secondary, number of siliquae per plant, seed yield per plant and harvesting index. The high magnitude of both coefficients was recorded for traits; (Table 3). The estimates of phenotypic and genotypic coefficient of variability for of the characters under study are in accordance with earlier reports, [14,15,16,17,18,19,11] and [20].

High heritability with high genetic advance was recorded for number of primary branches, number of secondary branches, length of main raceme, number of siliquae in main raceme, number of siliquae per plant, number of seeds per siliquae, biological yield, 1000 seed weight, seed yield per plant and harvesting index (Table

3). This might be attributed to additive gene action responsible for their expression and hence, phenotypic selection for their amenability, can be brought about. Similar result found, [19] for 1000 seed weight, [21] for number of Siliqua per plant, [22] for 50% flowering, [23,24] for 50% flowering, plant height, seeds per Siliqua, 1000 seed weight, [25] for seed yield per plant, number of secondary branches, 1000 seed weight, number of seeds per Siliqua, primary branches per plant and Siliqua length, [26,27,28] and [29].

The significant phenotypic correlation of seed yield per plant was found positive for the characters namely, number of primary branches per plant, number of secondary branches, number of siliquae on main raceme, number of siliquae per plant, length of siliqua, number of seeds per siliqua, 1000 seed weight, biological yield per plant and harvest index (Table 4). This suggests that these characters should be considered while selecting for improvement in seed yield per plant provided the character should show high variability, which is the basis for selection. However, days to maturity and plant height showed negative correlation with seed yield per plant. In the present findings, the magnitudes of genotypic correlation coefficient were greater than corresponding phenotypic correlation coefficient (in general also) similar findings by [11,30,20,13] and [19].

Table 1. Details of the genotypes is given below

S. No	Entries	Pedigree / source (DRMR)
1	Laxmi	DRMR
2	Geeta	DRMR
3	Gujarat Mustard-1	DRMR
4	Aravali	DRMR
5	Maya	DRMR
6	Kranthi	SELECTION FOR VARUNA
7	RNG-73	DRMR
8	Pusa Bold	VARUNA X BIC1780
9	Bhagirathi	SELECTION FROM PUSA JAI KISHAN
10	Durgamahi	DRMR
11	RH-119	DRMR
12	NRCHB-101	BL-4 X PUSA BOLD
13	DRMR-IJ-31	DRMR
14	Pusa Mustard-27	DIVYA/PUSABOLD//PR666EPS///PR704EPS2
15	Pusa Saag-1	DRMR
16	SMR-1	DRMR
17	Urvashi	VARUNA X KRANTI
18	RH-30	SELECTION FROM P26/3-1
19	RH-749	DRMR
20	RB-50	DRMR

Table 2. Estimate of Analysis of variance coefficient of variation, h² (broad sense) and genetic advance in per cent of mean in Mustard

S. No.	Characters	Mean Sum of Squares			CV	Range		Mean	Coefficient of variation		Heritability in broad sense (%)	Genetic advance in per cent of mean
		Replication	Genotypes	Error		Min	Max		PCV	GCV		
1	Days to 50% flowering	3.516	25.132**	2.885	3.29	44	55	49.6167	5.8335%	5.4885 %	88.52	10.6375 %
2	Days to maturity	45.033	166.583**	416.966	2.75	115	126	118.0833	1.4477 %	0.7261 %	25.15	-0.7501 %
3	Plant height	43.015	328.024**	177.078	7.83	144	180	165.1100	6.3331 %	4.2961 %	46.02	6.0035 %
4	Number of primary branches	0.024	4.052**	0.259	7.88	2	7	4.2800	27.1564 %	26.2741 %	93.61	52.3662 %
5	Number of secondary branches	0.020	8.649**	0.324	6.67	4	11	6.7267	25.2429 %	24.7649 %	96.25	50.0494 %
6	Length of main raceme	6.640	239.879**	22.809	7.32	41	78	60.5567	14.7664 %	14.0468 %	90.49	27.5263 %
7	Number of siliquae in main raceme	2.498	65.230**	6.904	6.17	24	48	38.3200	12.1685 %	11.5065 %	89.42	22.4140 %
8	Number of siliquae per plant	2325.190	26420.137**	1804.069	10.64	222	555	393.8217	23.8291 %	23.0011 %	93.17	45.7360 %
9	Length of siliquae	0.512	0.965	0.534	9.04	4.3	6.4	5.1352	11.0482 %	7.3813 %	44.64	10.1586 %
10	Number of seeds per siliquae	3.555	16.175**	0.659	5.24	11.9	20.4	13.9950	16.5919 %	16.2504 %	95.93	32.7868 %
11	Biological Yield	0.009	0.976	0.043	4.68	112	182	140.9333	13.4671 %	13.1747 %	95.71	26.5507 %
12	1000 seed weight	5.820	10180.672**	46.409	6.49	3.2	5.2	3.8358	14.8700 %	14.5317 %	95.50	29.2544 %

S. No.	Characters	Mean Sum of Squares			CV	Range		Mean	Coefficient of variation		Heritability in broad sense (%)	Genetic advance in per cent of mean
		Replication	Genotypes	Error		Min	Max		PCV	GCV		
13	Seed yield per plant	2.791	274.841**	13.461	7.20	23	61	46.3007	20.672 %	20.1599 %	95.10	40.4996 %
14	Harvesting index	0.695	143.820**	7.751	7.39	20.5	49.5	33.0847	20.927 %	20.3560 %	94.61	40.7 %

Table 3. Summary of phenotypic correlation (above diagonal) coefficient & genotypic correlation (below diagonal) coefficient for yield and yield contributing traits in mustard under study

S. N.	Characters	D 50% F	DM	PH	NPB	NSP	LMR	NSMR	NSP	LS	NSPS	TW	BW	HI	SYP
1	DFF	1	+	+	—	—	—	—	+	—	—	—	+	+	+
2	DM	—	1	—	—	—	+	—	—	+	—	—	—	+	+
3	PH	+	+	1	—	—	+	+	—	—	—	—	+	—	—
4	NPB	+	+	—	1	+	+	+	+	—	+	—	+	—	+
5	NSB	—	+	—	+	1	+	+	+	+	+	+	+	+	+
6	LMR	—	—	+	+	+	1	—	—	+	—	—	+	—	—
7	NSMR	—	+	+	+	+	+	1	+	+	+	+	—	+	+
8	NSP	—	+	—	+	+	—	+	1	+	+	+	+	+	+
9	LS	—	—	—	—	+	+	+	+	1	+	—	+	+	+
10	NSPS	—	+	—	+	+	—	+	+	+	1	+	+	+	+
11	TW	—	—	—	+	+	—	+	+	—	+	1	+	—	+
12	BY	+	+	+	+	+	+	—	+	+	+	+	1	+	+
13	HI	+	—	—	—	+	—	+	+	+	+	—	+	1	+
14	SYPP	+	—	—	+	+	—	+	+	+	+	+	+	+	1

** indicate significant at 5% and 1% probability level, respectively. DF = Days to 50% flowering, DM = Days to maturity, PH = Plant height, NPB = Number of primary branches, NSB = Number of secondary branches, LMR = Length of main raceme, NSMR = Number of siliqua on main raceme, NSP = Number of siliqua/plants, LS = Length of siliqua, NSS = Number of seeds/siliqua, TSW = 1000 seed weight, BY = Biological yield/plant, SY = Seed yield/plant and HI = Harvest index

Table 4. Genotypic direct and indirect effect of different characters on seed yield per plant in Mustard

Characters	D F50%	DM	PH	NPB	NSP	LMR	NSMR	NSP	LS	NSPS	BW	TW	HI
D F50%	-5.5376	-5.0432	-1.0980	-0.3159	0.8396	1.9156	-0.0096	1.0554	1.6396	1.7352	1.0235	-1.3527	-1.9079
DM	0.0498	0.0547	-0.0337	-0.0040	-0.0336	0.0279	-0.0425	-0.0001	0.0325	-0.0228	-0.0018	-0.0175	0.0171
PH	-0.2612	0.8113	-1.3172	0.0076	0.2743	-0.1510	-1.0578	0.0497	0.1204	0.6553	0.2358	-0.0884	0.1768
NPB	-0.2102	0.2674	0.0214	-3.6853	-2.0007	-1.4378	-0.7215	-0.1178	1.5255	-0.4861	-1.4641	-1.2270	0.4990
NSP	0.7439	3.0166	1.0217	-2.6635	-4.9063	-1.9809	-2.1179	-1.2422	-0.0687	-1.6949	-1.3715	-1.2673	-0.9123
LMR	-2.2629	3.3342	0.7499	2.5521	2.6411	6.5415	-0.0956	-0.4678	1.8452	-1.1543	-0.6549	1.1041	-1.1457
NSMR	0.0053	-2.3942	2.4726	0.6028	1.3290	-0.0450	3.0788	1.1274	0.3270	1.2386	0.3596	-0.2355	0.9256
NSP	1.5908	0.0175	0.3151	-0.2669	-2.1133	0.5969	-3.0563	-8.3468	-3.4078	-5.5741	-2.9369	-0.1599	-5.4377
LS	2.3512	-4.7182	0.7258	3.2871	-0.1112	-2.2400	-0.8433	-3.2421	-7.9409	-3.3027	1.2711	-0.7290	-4.2408
NSPS	0.1954	0.2596	0.3103	-0.0823	-0.2154	0.1100	-0.2509	-0.4165	-0.2594	-0.6236	-0.2957	-0.0454	-0.2678
BY	-1.4092	-0.2482	-1.3649	3.0289	2.1314	-0.7632	0.8906	2.6827	-1.2204	3.6158	7.6243	1.3338	-1.6263
TW	-0.2306	0.3024	-0.0634	-0.3143	-0.2438	-0.1593	0.0722	-0.0181	-0.0867	-0.0688	-0.1651	-0.9440	-0.2512
HI	5.1506	4.6634	-2.0068	-2.0242	2.7798	-2.6185	4.4942	9.7393	7.9837	6.4196	-3.1889	3.9776	14.9497
SY	0.1753	0.3235	-0.2672	0.1222	0.3708	-0.2038	0.3403	0.8030	0.4901	0.7374	0.4355	0.3487	0.7786

R SQUARE = 1.0025 RESIDUAL EFFECT = SQRT (1- 1.0025), Bold figures indicate direct effect. DF = Days to 50% flowering, DM = Days to maturity, PH = Plant height, NPB = Number of primary branches, NSB = Number of secondary branches, LMR = Length of main raceme, NSMR = Number of siliqua on main raceme, NSP = Number of siliqua/plants, LS = Length of siliqua, NSS = Number of seeds/siliqua, TSW = 1000 seed weight, BY = Biological yield/plant, SY = Seed yield/plant and HI = Harvest index

Table 5. Clustering pattern of 25 Mustard genotypes & based on Mahalanobis's D² statistic

Cluster No.	No. of Genotypes	Genotypes
Cluster 1	12	Maya, RH 30, Pusa Bold, Laxmi, Geeta, Gujarat Mustard 1, Aravali, Urvashi, SMR 1, DRMRIJ31, Durgamani, RH 749
Cluster 2	5	Kranti, Pusa Mustard 27, RNG73, NRCHB101, RH 119
Cluster 3	1	Pusa saas 1
Cluster 4	1	RB 50
Cluster 5	1	Bhagirathi

Table 6. Estimates of average intra and inter-cluster distances for the fiveclusters in Mustard

Clusters	Cluster 1	Cluster 2	Cluster 3	Cluster 4	Cluster 5
Cluster 1	11.87	18.71	16.37	18.19	24.02
Cluster 2		12.02	26.71	28.08	16.19
Cluster 3			0.00	23.43	33.97
Cluster 4				0.00	33.28
Cluster 5					0.00

Table 7. Cluster means and percentage contribution for different characters in mustard

Characters	DFF	DM	PH	NPBP	NSBP	LMR	NSMR	NSPP	LS	NSPS	BYPP	TSW	HI	SYP
Cluster 1	50.25	117.83	167.87	3.89	6.07	58.21	38.43	384.08	5.02	13.39	138.10	3.63	32.88	45.05
Cluster 2	48.87	118.47	162.40	5.50	8.89	67.73	38.27	398.46	5.20	14.59	150.17	4.41	33.19	49.85
Cluster 3	47.00	118.33	165.00	3.10	4.60	61.40	32.80	222.97	5.63	11.93	115.60	3.36	20.57	23.78
Cluster 4	51.00	118.67	163.13	3.27	5.27	55.20	38.87	520.63	5.79	13.80	112.40	4.47	49.53	55.60
Cluster 5	47.00	118.33	147.60	5.10	7.33	57.33	42.27	531.53	5.01	20.47	182.60	3.30	31.08	56.74

DF = Days to 50% flowering, DM = Days to maturity, PH = Plant height, NPBP = Number of primary branches, NSBP = Number of secondary branches, LMR = Length of main raceme, NSMR = Number of siliqua on main raceme, NSP = Number of siliqua/plants, LS = Length of siliqua, NSS = Number of seeds/siliqua, TSW = 1000 seed weight, BY = Biological yield/plant, SY = Seed yield/plant and HI = Harvest index

The path coefficient analysis of different characters revealed that positive direct effect on seed yield per plant per plant was observed by harvest index per plant followed by biological yield and negative direct effect on seed yield / plant was exhibited by number of siliquae per plant followed by length of siliquae, days to 50% flowering, number of secondary and number of primary branches (Table 5). We can conclude based on present finding that those all character which had positive direct effect on seed yield per plant that universal traits for overall improvement. Negative direct effect on seed yield per plant was exerted by days to 2 maturity, number of secondary branches per plant, number of siliqua on main raceme and length of siliqua. In the present findings, the similar results are also reported by Direct and positive effect by [30,31,13,19,20,32] and [31] viz seed yield per plant.

Genetic divergence analysis based on Mahalanobis D2 statistics, twenty genotypes were grouped into five clusters in mustard (Table 6). The highest intra-cluster distance was recorded in cluster II followed by cluster I, while the lowest value was recorded in case of cluster III, IV and V (Table 7). The genotypes showing maximum diversity from clusters I & II could be utilized directly for future hybridization programs. In conformity to the present investigation, similar findings were found by [33,34] and [35].

It was observed that biological yield per plant was the highest contributor towards divergence followed by all except Length of main raceme (Table 7) don't contribute significantly to the total divergence. Similarly, Devi et al., (2017) was observed, biological yield, Harvest index 1000 seed weight and seed yield per plant were the major contributors for genetic diversity among the genotypes. The cluster mean values for 14 characters of 20 genotypes have been represented in (Table 7).

4. CONCLUSION

The conclusion that can be reached from variability, correlations, path coefficient analysis and genetic divergence is that plant height, number of primary branches, number of secondary branches, length of siliqua, number of seeds per siliqua, biological yield per plant, seed yield per plant and harvesting index found the most important component characters. Hence, these traits should be considered as selection criteria for yield improvement in mustard.

COMPETING INTERESTS

Authors have declared that no competing interests exist.

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