Variability, Correlation, Path Coefficient and Genetic Diversity Analysis in Indian Mustard

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Authors' contributions

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

Original Research Article

ABSTRACT

Phenotypic and genotypic coefficient of variation (PCV & GCV), heritability, genetic advance (GA), correlation, path and diversity analysis for fourteen characters in twenty-five genotypes of Indian mustard (*Brassica juncea* L.) were evaluated for seed yield and thirteen other yield contributing traits. Genetic variability indicated that, the PCV was greater than GCV for all the traits studied was majorly due to the influence of environment. High heritability along with high genetic advance as percent of mean were recorded for plant height, number of primary branches per plant, number of secondary branches per plant, length of main raceme, number of siliqua on main raceme, number of siliqua per plant, 1000 seed weight, biological yield per plant, seed yield per plant and harvest index, Indicating the breeding improvement through direct selection. In correlation analysis, seed yield per plant had significant and positive correlation with number of primary branches per plant, number of secondary branches, number of siliqua on main raceme, number of siliqua per plant, length of siliqua, number of seeds per siliqua, 1000 seed weight, biological yield per plant and harvest index at both genotypic and phenotypic levels. Path coefficient analysis indicated that, the highest positive direct effects was noted for days to 50% flowering, plant height, number of siliqua per plant, number of seeds per siliqua, length of main raceme, number of primary branches per plant, 1000 seed weight, biological yield per plant, harvest index. Therefore, these traits should be given more priority for selection in breeding programme. Genetic divergence assessed using D^2 statistics for characters enabled grouping of all the genotypes in six clusters. Diversity among the

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clusters varied from 9.67 to 24.03 inter-cluster distances, cluster II and V showed maximum inter cluster distance followed by that between cluster V and VI. The genotypes falling in these clusters could be utilized for hybridization programme in Indian mustard.

1. INTRODUCTION

Oilseed Brassicas, often 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" derives from the European practice 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 therapeutic purposes. However, the crop is mostly grown for the manufacture of edible vegetable oil. Despite belonging to the same family and genus, rapeseed and mustard exhibit unique 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 pinnated. 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 [3]. 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 [4]. 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 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 25 different genotypes of Mustard (Table 1) were grown in a RBD with three replications during *rabi* 2021-22. Each plot consists of four rows of 5.0 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. The standard method of analysis of variance was given [5], phenotypic and genotypic coefficient of variation, heritability (Broad Sense) and genetic advance as percent of mean were estimated by the formula al suggested by [6] and [7]. The formula of genotypic correlation coefficients was estimated by [8]. Path analysis along with genotypic correlation coefficient is applied to know the direct and indirect effects of the components on yield as suggested by [9] and illustrated by [4].

The replicated data were subjected to genetic divergence analysis using Mahalanobis's D2 - statistic [10].

3. RESULTS AND DISCUSSION

The analysis of variance indicated that the mean sum of squares due to genotypes were highly significant at 1% and 5% levels for all the traits except for four traits number of primary branches, number of secondary branches, length of siliqua and 1000 seeds weight (g) (Table2). Similar results were also obtained by [11-14] 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. The high magnitude of both coefficients was recorded for traits; number of siliqua per plant recorded the highest PCV and GCV followed by seed yield per plant, number of siliqua on main raceme, harvest index, biological yield per plant and plant height (Table 2). The estimates of phenotypic and genotypic coefficient of variability for the characters under study are in accordance with earlier reports, [15-21] and [12].

High heritability with high genetic advance was recorded for plant height, number of primary branches per plant, number of secondary branches per plant, length of main raceme, number of siliqua on main raceme, number of siliqua per plant, 1000 seed weight, biological yield per plant, seed yield per plant and harvest index (Table 2). 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, [22] for number of Siliqua per plant, [23] for 50% flowering, [24,25] for 50% flowering, plant height, seeds per Siliqua, 1000 seed weight, [26] for seed yield per plant, number of secondary branches, 1000 seed weight, number of seeds per Siliqua, primary branches per plant and Siliqua length, [27-30].

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 siliqua on main raceme, number of siliqua per plant, length of siliqua, number of seeds per siliqua, 1000 seed weight, biological yield per plant and harvest index (Table 3). 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 phenotypic correlation coefficient were greater than corresponding genotypic correlation coefficient (in general also) similar findings by [12,31,21,14] and [20].

The path coefficient analysis of different characters revealed that positive direct effect on seed yield per plant was observed for days to 50% flowering, plant height, number of siliqua per plant, number of seeds per siliqua, length of main raceme, number of primary branches per plant, 1000 seed weight, biological yield per plant and harvest index (Table 4). We can conclude based on present finding that those all character which had positive direct effect on seed yield per plant. So, these traits may be useful in overall improvement of seed yield per plant. 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 [31- 33,20,21] viz seed yield per plant.

Genetic divergence analysis based on Mahalanobis D2 statistics, twenty-five genotypes were grouped into six clusters in mustard (Table 5). The maximum differences among the genotypes within the same cluster (intra-cluster) were shown by cluster I followed by cluster II. Clusters III, IV &V showed zero intra-cluster distances (Table 6). Diversity among the clusters varied from 9.67 to 24.03 inter-cluster distances, cluster II and V showed maximum inter cluster distance followed by that between cluster V and VI. The lower intercluster distance was noticed between cluster III and IV followed by that between cluster I and III. 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 [34-38].

It was observed that biological yield per plant was the highest contributor towards divergence followed by all except Length of main raceme (Table7) don't contribute significantly to the total divergence. Similarly, [17] 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 25 genotypes have been represented in (Table 7). The data revealed that differences in cluster means had existed. The maximum cluster mean for days to 50% flowering in cluster V&VI, days to maturity in cluster VI, plant height in cluster VI, No. of primary branches per plant VI, No. of secondary branches per plant in cluster VI, Length of main raceme in cluster VI , Number of siliqua on main raceme cluster in cluster VI, number of siliqua per plant in cluster III, Length of siliqua in cluster V, 1000 grain weight in cluster II, biological yield

per plant cluster II, harvest index in cluster VI, Number of seeds per siliqua in cluster II, and seed yield per plant in cluster II. The cluster mean range was presented in (Table 7). For yield improvement cluster II which contains 6 genotypes exhibited highest mean value for 1000 seed weight biological yield and seed yield per plant and cluster VI which contains 1 genotype also exhibited highest mean value for harvest index also would be promising if taken for hybridization programmes. Hence, crossing between genotypes belonging to these clusters may result in high heterosis, which could be exploited in crop improvement. In conformity to the present investigation, similar findings were found by [34-36] and [39].

Table 1. Details of the Genotypes is given below

Sr. No.	Entries	Pedigree / Source (DRMR)
1	BHAGIRATHI	SELECTION FROM PUSA JAI KISHAN
2	NRCHB 101	BL-4 X PUSA BOLD
3	VAIBHAV	DRIVED THOUGHT BIPARENTALMATTING INVOLVING VARUNA,KESHARI, CSU10 AND B1775, B1786, B1866
4	TM 4	VARUNA X TM-1
5	KRANTHI	SELECTION FOR VARUNA
6	RH 30	SELECTION FROM P26/3-1
7	DMH 1	DEVLOPED BY CMS
8	RH 119	PUSA BOLD X RAJAT(PCR-7)
9	KBS 3	PUSA KALYANI X YUKINA
10	ROHINI	SELECTION FROM NATURAL POPULATIONOF VARUNA
11	URVASHI-18	VARUNA X KRANTI
12	PUSA MUSTARD 24	PUSA BOLDXLEB) X LES-29
13	PUSA JAI KISHAN	SOMACLONE OF VARUNA
14	GUJARATH MUSTARD 2	SELECTION FROM MATERIAL COLLECTED FROM VENDACHU, GUJRAT
15	GUJARATH MUSTARD 1	MR 71-3-2 X TM-4
16	PUSA BOLD	VARUNA X BIC1780
17	SMR 9	-
18	RH 749	DRMR
19	BR 23	SELECTION FROM LOCAL GERMPLASM OF PURNEA, BHIHAR
20	TL 17	-
21	JD 6	PUSA BOLD X GLOSSY
22	PUSA MUSTARD 28	SEJ8 X PUSA JAGANNATH
23	RH 701	-
24	PARWATHI MUSTARD	SELECTION FROM GAMMA IRRIGATED BT4
25	PUSA MUSTARD 27	DIVYA/PUSABOLD/PR666EPS/PR704EPS2

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

Sr. No.	Characters	Source of variation			Range	Mean	Coefficient ofvariation		Heritabilityin broad sense (%)	Genetic advancein % of mean
		Replication	genotypes	Error			PCV	GCV		
	DF	2	24	48						
1	DFF	1.33	27.18**	3.20	43.33-52.00	48.23	6.24 %	5.86 %	88.20	11.34 %
2	DM	10.09	20.72**	3.88	116.00-128	119.33	2.20 %	1.98 %	81.25	3.68 %
3	PH	59.43	1597.16**	180.49	103.33-202.67	144.08	16.01 %	15.08 %	88.70	29.26 %
4	NPBP	0.23	0.72	0.15	3.06-5.46	3.73	13.19 %	11.67 %	78.19	21.25 %
5	NSBP	0.06	2.92	0.32	5.20-9.60	6.85	14.43 %	13.50 %	87.64	26.05 %
6	LMR	72.74	178.52**	26.10	51.47-84.40	62.25	12.39 %	11.44 %	85.38	21.79 %
7	NSMR	28.40	96.77**	9.30	23.47-54.13	30.98	18.33 %	17.42 %	90.39	34.13 %
8	NSPP	36.30	11410.59**	846.89	193.27-414.27	277.40	22.23 %	21.39 %	92.58	42.39 %
9	LS	0.01	0.68	0.03	4.60-6.40	5.73	8.35 %	8.13 %	94.77	16.31 %
10	NSPS	1.01	4.40**	0.59	16.60-21.40	19.33	6.26 %	5.82 %	86.55	11.17 %
11	BYPP	0.03	2.71	0.07	3.27-5.03	4.13	13.87 %	13.77 %	98.56	28.17 %
12	TSW	271.31	2105.68**	92.50	120.30-213.60	162.50	16.29 %	15.93 %	95.61	32.09 %
13	SYPP	20.20	387.61**	16.91	23.10-68.70	51.20	22.21 %	21.7253%	95.64	43.76 %
14	HI	21.04	80.52**	13.94	18.90-41.90	31.60	16.39 %	14.9109%	82.68	27.92 %

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

S.N.	Characters	DFF	DM	PH	NPBP	NSBP	LMR	NSMR	NSPP	LS	NSPS	BYPP	TSW	HI	SYPP
1	DFF	1.0000	+	+**	+*	+**	+*	+	-**	+**	+	-	-	-	-
2	DM	+	1.0000	+*	+	+	+*	+*	+	+	+	-	-	+	_
3	PH	+**	+**	1.0000	+**	+**	+**	+*	-*	+**	-	-	-	+	-
4	NPBP	+*	+*	+**	1.0000	+**	+	+**	-	+	-	-	-	+*	+
5	NSBP	+**	+	+**	+**	1.0000	+*	+*	-*	+	+	-	-	+	+
6	LMR	+**	+*	+**	+*	+**	1.0000	+**	-	+	+	+	+	+	+
7	NSMR	+	+**	+*	+**	+*	+**	1.0000	+	-	-	-	-	+*	+
8	NSPP	-**	+	-*	-	-*	-*	+	1.0000	-**	+	+	+	-	+
9	LS	+*	+	+*	+	+*	+*	-	-**	1.0000	+	-	-	+	+
10	NSPS	+	+	-	-	+	+	-	+*	+	1.0000	+**	+*	-	+
11	BYPP	-	-	-	-	-	+	-	+	-	+*	1.0000	+	+**	+**
12	TSW	-	-	-	-	-	+	-	+	-	+	+**	1.0000	-	+**
13	HI	+	+	+	+*	+*	+	+*	-	+	-	+	+	1.0000	+**
14	SYPP	-	-	-	+	+	+	+	+	+	+	+**	+**	+**	1.0000

*** indicate significant at 5% and 1% probability level, respectively. DFF = 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

S.N.	Characters	DFF	DM	PH	NPBP	NSBP	LMR	NSMR	NSPP	LS	NSPS	BYPP	TSW	HI
1	**DFF**	**0.0142**	0.0042	0.0108	0.0069	0.0105	0.0079	0.0021	-0.0085	0.0101	0.0022	-0.0015	-0.0028	0.0024
2	**DM**	-0.0303	**-0.1025**	-0.0520	-0.0486	-0.0250	-0.0504	-0.0677	-0.0051	-0.0107	-0.0059	0.0078	0.0205	-0.0217
3	**PH**	0.1887	0.1263	**0.2489**	0.1396	0.1807	0.1817	0.1124	-0.1100	0.1443	-0.0423	-0.0608	-0.0483	0.0283
4	**NPBP**	0.0241	0.0235	0.0278	**0.0496**	0.0402	0.0217	0.0407	-0.0136	0.0055	-0.0127	-0.0024	-0.0178	0.0296
5	**NSBP**	-0.0312	-0.0102	-0.0305	-0.0340	**-0.0421**	-0.0238	-0.0183	0.0203	-0.0171	-0.0018	0.0018	0.0050	-0.0179
6	**LMR**	0.0622	0.0549	0.0815	0.0489	0.0633	**0.1117**	0.0652	-0.0483	0.0462	0.0069	0.0071	0.0055	0.0418
7	**NSMR**	-0.0400	-0.1761	-0.1205	-0.2187	-0.1162	-0.1558	**-0.2669**	-0.0483	0.0369	0.0273	0.0207	0.0585	-0.1331
8	**NSPP**	-0.1202	0.0100	-0.0886	-0.0551	-0.0969	-0.0866	0.0363	**0.2005**	-0.1132	0.0802	0.0173	0.0484	-0.0028
9	**LS**	-0.0802	-0.0119	-0.0656	-0.0126	-0.0461	-0.0469	0.0156	0.0639	**-0.1132**	-0.0161	0.0009	0.0095	-0.0097
10	**NSPS**	0.0009	0.0003	-0.0010	-0.0015	0.0002	0.0004	-0.0006	0.0023	0.0008	**0.0058**	0.0027	0.0032	-0.0004
11	**BYPP**	-0.0294	-0.0214	-0.0685	-0.0137	-0.0122	0.0177	-0.0218	0.0242	-0.0023	0.1316	**0.2805**	0.2247	0.1057
12	**TSW**	-0.0783	-0.0806	-0.0780	-0.1445	-0.0477	0.0198	-0.0881	0.0971	-0.0336	0.2223	0.3221	**0.4020**	0.0176
13	**HI**	0.1115	0.1393	0.0747	0.3915	0.2804	0.2457	0.3279	-0.0092	0.0562	-0.0459	0.2477	0.0287	**0.6573**
14	**SYPP**	-0.0081	-0.0442	-0.0610	0.1076	0.1892	0.2430	0.1368	0.1653	0.0098	0.3517	0.8441	0.7372	0.6969
15	**Partial R2**	-0.0001	0.0045	-0.0152	0.0053	-0.0080	0.0271	-0.0365	0.0331	-0.0011	0.0020	0.2367	0.2964	0.4581

R SQUARE = 1.0025 RESIDUAL EFFECT =SQRT (1- 1.0025), Bold figures indicate direct effect. DFF = 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 D^2 statistic

Cluster No.	No. of Genotypes	Genotypes
Cluster 1	15	URVASHI-18, KBS-03, TL-17, TM-04, PUSA JAI KISHAN, RH-749, ROHINI, NRCHB-101, VAIBHAV, GUJRAT MUSTARD 1, PUSA MUSTARD 28, PUSA MUSTARD 24, RH 119, JD-06, PUSA MUSTARD 27.
Cluster 2	6	RH-30, KRANTHI, RH-701, BR-23, PARWATHI MUSTARD, BHAGIRADHI
Cluster 3	1	PUSA BOLD
Cluster 4	1	SMR-09
Cluster 5	1	GUJARAT MUSTARD 2
Cluster 6	1	DMH-01

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 6
Cluster 1	9.71	14.20	12.72	13.35	15.25	13.96
Cluster 2		10.58	19.09	18.92	24.03	16.40
Cluster 3			0.00	9.67	14.37	17.03
Cluster 4				0.00	15.08	17.22
Cluster 5					0.00	20.64
Cluster 6						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	48.36	118.87	142.64	3.70	6.83	62.10	29.43	251.09	5.80	18.83	4.03	154.38	32.52	49.96
Cluster 2	47.89	118.78	134.30	3.64	6.66	60.71	31.11	321.97	5.66	20.53	4.81	194.77	32.40	62.74
Cluster 3	45.67	120.67	136.53	3.87	6.33	51.47	32.73	319.00	4.59	18.40	3.49	138.13	27.55	38.03
Cluster 4	43.33	119.33	142.13	3.27	6.20	60.99	30.27	394.53	5.27	20.00	3.29	185.67	18.92	34.93
Cluster 5	52.00	119.00	175.40	3.47	6.73	63.73	29.33	252.33	6.42	19.53	3.27	120.27	19.20	23.08
Cluster6	52.00	128.00	202.67	5.47	9.60	84.40	54.13	270.93	6.09	19.67	3.98	136.53	41.86	57.30
MEAN	48.2	120.7	155.6	3.9	7.1	63.9	34.5	301.7	5.7	19.5	3.8	154.9	28.7	44.3
CV%	3.71	1.65	9.32	10.68	8.79	8.21	9.85	10.49	3.31	3.98	5.92	2.88	11.82	8.04
Time ranked 1st	8	2	2	2	2	0	5	20	38	6	144	10	55	6
% Contribution	2.67%	0.67%	0.67%	0.67%	0.67%	0.00%	1.67%	6.67%	12.67%	2.00%	48%	3.33%	18.33%	2.00%

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

4. CONCLUSION

Plant height, number of primary branches, number of secondary branches, number of siliqua on main raceme, 1000 seeds weight, biological yield per plant, seed yield per plant and harvesting index found the most important yield component characters to keep in mind while working with mustard improvement. 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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