The Pharma Innovation

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Genetic variability, character association and divergence analyses for seed yield and its contributing traits in Indian mustard [*Brassica juncea* (L.) Czern and Coss]

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Abstract
The present study was carried out with 21 different genotypes of Indian mustard including two checks. For the fourteen traits observed, analysis of variance was found highly significant for all characters excluding number of primary branches per plant, length of siliqua and test weight implying high inherent variation was present amongst the genotypes. PCV was greater than GCV for all the traits indicating that there is an influence of environment over the genotypes and thus selection based on these values could be misleading. High heritability coupled with high genetic advance was observed for all traits expect days to 50% flowering and days to maturity. For both genotypic and phenotypic correlation, seed yield per plant was found to be highly and significantly correlated with plant height, number of primary branches per plant, number of secondary branches per plant, number of siliquae per plant and biological yield per plant, positively and significantly correlated with number of siliquae on main raceme and harvest index suggesting that these characters should be given more importance while selection for improvement in seed yield. The path coefficient analysis showed nine direct effects on seed yield per plant *viz.,* biological yield per plant followed by harvest index, number of siliquae per plant, days to 50% flowering, number of primary branches per plant, length of main raceme, length of siliqua, number of siliquae on main raceme and number of seeds per siliquae revealing true relationship between them and that direct selection for these traits would be rewarding for yield improvement. Based on the MahalanobisD^2 statistics, the genotypes were grouped into 5 clusters. Most of the genotypes were grouped into cluster I (14 genotypes), while clusters IV and V were solitary. The intra-cluster divergence ranged from 0.0 to 39.01 while clusters IV and V showed maximum inter-cluster distance (111.45) and the lowest inter-cluster distance was noticed between cluster I and cluster II (47.96). This implies that clusters IV and V are highly divergent and hybridization between genotypes of these two clusters would show high heterosis.

Introduction
Brown Mustard (*Brassica juncea*) belongs to the family Brassicaceae (Cruciferae) is an allotetraploid species (AABB=2n=4x=36) and the place of origin is believed to be Middle East. The aroma and pungent flavor of mustard seeds is due to "*sinalbin*" which releases isothiocyanates on enzymatic reaction mediated by myrosinase enzyme which prevent the growth of stomach and colon cancer. The seeds also contain selenium, which reduces the severity of asthma and rheumatoid arthritis. The magnesium content helps in reducing high blood pressure and the frequency of migraines. Mustard seeds are used as mustard oil, mustard powder used in the manufacture of mayonnaise, dried or dehydrated mustard leaves, whole mustard seeds, smoothing leather in tanning industry. It is an annual herb which grows up to 2 m or more and has tap root system. The inflorescence is an elongated raceme, and the flowers open progressively upwards from the base of the raceme. Flower has all four whorls consisting of 4 oblong sepals, 4 cruciform petals of deep yellow to pale yellow colour, 6 stamens with tetradynamous condition. The pistil is compound, which is separated by a false septum, dividing it into two chambers. The seed pods known as siliqua are slightly appressed, slender and 2.0 to 6.5 cm in length. The mustard crop contributes around one-thirds of all the oil produced in India, making it the country's second most important edible oil crop after groundnut. It contributes about 28.6% to total oilseeds production in India. Mustard oil accounts for almost 40% of the total edible oil output in the country. The purpose of this study is to develop high yielding varieties by selecting elite genotypes and breeding them.

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The pre-requisite for initiating any breeding programme for higher yields is the availability of information on the nature and magnitude of variability present among the different genotypes along with the association among various morphological traits in the existing material. Since seed yield is a complex character which is controlled by non-additive gene actions, it is highly influenced by both *i.e.,* morphological traits governed by a large number of genes as well as environmental effects. Therefore, partitioning of the overall variability into heritable and non-heritable components is necessary. The heritability can be defined as the heritable portion of phenotypic variance while genetic advance is the improvement in the mean genotypic value of selected plants over parental population, these enable the breeders to select elite genotypes and adopt suitable breeding procedures for further improvement of genetic stocks. Mutual association of plant characters determined by correlation coefficient is useful for evaluation of relative influence of various components on yield. The path coefficient analysis is helpful in partitioning the correlation coefficient into direct and indirect effects. Estimation of degree of divergence between the genotypes and computation of relevant contribution of different components to the total divergence helps the breeder in identification and proper choice of parents for specific breeding objectives. Therefore, in this present study we analyzed 21 genotypes to find the genetic variability, correlation coefficient, path analysis and genetic divergence to recognize the traits contributing towards yield basing which we select the parents for the further work.

Materials and Methods
The experiment was carried out during *Rabi* season of 2021-2022 at Research Farm, under Genetics and Plant Breeding department, School of Agriculture, Lovely Professional University, Phagwara, Punjab. It is situated at latitude 31º 19'32'' N and longitude 75º 34'45''' E and at an altitude 243 meters above the mean sea level. The experimental material comprised 21 genotypes including two checks (All the commercial release varieties) given in Table-1, which were grown in randomized block design with three replications in three row plots of 3-meter length. The material was planted with a spacing of 45x15 cm. The observations taken were days to 50% flowering, days to maturity, plant height, number of primary branches per plant, number of secondary branches per plant, length of main raceme, 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, seed yield per plant and harvest index. The following statistical methods that were applied are
1. Analysis of variance of Randomized Block Design (Pans e and Sukhatme, 1967) [13]
2. Estimation of coefficients of variation (Burton and de Va ne, 1953) [3]
3. Heritability in broad sense (Hanson *et al.,* 1956) [8]
4. Genetic advance (Johnson *et al.,* 1955) [9]
5. Correlation coefficient analysis (Aljibouri *et al.,* 1958)
6. Path coefficient analysis (Dewey and Lu, 1959) [7]

Results and Discussion
The Anova indicated that the mean sum of squares for all genotypes were highly significant for all characters except number of primary branches per plant, length of siliqua and

1000 seed weight showing the presence of high variation among the genotypes. According to data presented in Table-2, phenotypic coefficient of variation is higher than genotypic coefficient of variation for all the traits implying that there is an influence of environment. Seed yield per plant showed the highest PCV (44.821) and GCV (44.634) followed by number of secondary branches per plant (43.065) and (42.895), number of siliquae per plant (41.478) and (41.101), biological yield (37.754) and (37.697), harvest index (31.14) and (31.026), number of seeds per siliqua (28.773) and (28.707), 1000 seed weight (22.435) and (22.359), number of primary branches per plant (19.016) and (18.174), number of siliqua on main raceme (18.86) and (18.466), plant height (16.825) and (16.308), siliqua length (14.604) and (14.393),length of main raceme (12.973) and (12.466), days to 50% flowering (8.052) and (7.768) and days to maturity has the lowest PCV(2.085) and GCV (1.147)and similar results were found by Tripathi, A. M., *et al*., 2019 [20], Rauf, M. A., & Rahim, M. A. 2018 [16], Ray, J., *et al.,* 2019 [17] and Devi, B. 2018. High heritability was coupled with high genetic advance for plant height, number of primary branches per plant, number of secondary branches per plant, length of main raceme, number of siliquae on main raceme, number of siliquae per plant, length of siliqua, number of seeds per siliqua, biological yield per plant, 1000 seed weight, harvest index, seed yield per plant. This implied that these traits were not much influenced by environment but are mostly controlled by additive and / or additive x additive gene action and selection is effective for crop improvement. These observations were in accordance with the results of Pal, S., *et al.,* 2019 and Tripathi, A., 2019 [20]. High heritability combined with moderate genetic advance was observed for days to 50% flowering. This implies that the character is governed by both additive and non-additive gene actions and phenotypic selection alone is not effective. This observation is in accordance with the results of Rout, S.,*et al.,* 2019 and Tripathi, A. M.*etal.,*2020 [21].

Perusal of the data from Table-3, genotypic correlation analysis showed highly significant and positive correlation of seed yield with number of siliquae per plant (0.8635) followed by biological yield per plant (0.8319), number of secondary branches per plant (0.7274), plant height (0.7003) and number of primary branches per plant (0.6354) while significant and positive with number of siliquae on main raceme (0.5122) and harvest index (0.4459).The phenotypic correlation analysis showed highly significant and positive correlation of seed yield with number of siliquae per plant (0.8623) followed by biological yield per plant (0.8309), number of secondary branches per plant (0.7281), plant height (0.6645) and number of primary branches per plant (0.6019) while significant and positive with number of siliquae on main raceme (0.5030) and harvest index (0.4492)similar findings were seen by Rout, S., (2018), Akabari, V. R., & Niranjana, M. 2015, Devi, B., 2018 [6] and Prasad, G., & Patil, B. R. (2018) [14].

From Table-4, out of the thirteen yield contributing traits, nine of them showed direct effect on seed yield per plant *viz.,* biological yield per plant (0.7328), harvest index (0.4837), number of siliquae per plant (0.1588), days to 50% flowering (0.1028), number of primary branches per plant (0.0902), length of main raceme(0.0829), length of siliqua (0.0795), and number of siliquae on main raceme (0.0071) and number of seeds per siliqua (-0.0985). Since maximum direct effects

were depicted by biological yield per plant and harvest index these traits should be considered as the most important yield contributing characters and emphasis should be given to these characters while breeding for higher yields. Number of secondary branches per plant (0.002), length of main raceme (0.0018), number of primary branches per plant (0.0008), biological yield (0.0005) showed an indirect effect on seed yield via days to maturity. Length of siliqua (0.0247) showed an indirect effect on seed yield via Plant height. Days to maturity (0.01), length of siliqua (0.0054), number of seeds per siliqua (0.0053) and days to 50% flowering showed an indirect effect on seed yield via number of secondary branches per plant. Harvest index (0.0060), number of seeds per siliqua (0.0036), number of primary branches per plant (0.0033), number of siliquae on main raceme (0.0032) showed an indirect effect on seed yield via 1000 seed weight and similar observations were found by Devi, B. (2018) [6] Chaturvedi, V. D., *et al*. (2021) [4] Ompal, S.A., *et al*. (2018) [11] and Tripathi, N., *et al*. (2020) [21].

The twenty-one genotypes were grouped into five clusters. Among five clusters, cluster I was the largest with 14 genotypes followed by cluster Ⅲ with 3 genotypes and cluster II with 2 genotypes and IV and V were solitary with 1 genotype each given in Table-5. Similar findings were observed by Singh, S. K. *et al*., 2020, Priyanka, N., & Pandey, M. K. 2021 [15] and Nandi, S., *et al*., 2021. The intra-cluster ranged from 0.00 (cluster IV and cluster V) to 39.01 (cluster III).Cluster III showed highest intra cluster distance which indicated that moderate to much diversity existed in this cluster. the clusters IV and V showed maximum inter-cluster distance (111.45) followed by cluster III and cluster IV (90.13) and cluster II and cluster IV (83.11) as presented in Table-6.Thus,it could be concluded that the genotypes present in combination of these two clusters could be utilized for successful breeding programme. Cluster I having 14 genotypes was characterized as having above average mean values for plant height (167.58), length of main raceme (58.57), number of siliquae per plant (472.54), 1000 seed weight (3.47), harvest index (15.92), seed yield per plant (18.01). Cluster II having 2 genotypes was characterized as having above average mean values for days to 50% flowering (49.17), days to maturity (118.83), plant height (173.9), number of primary branches per plant (7.83), number of secondary branches per plant (29.2), length of main raceme (63.47), number of siliqua on main raceme (42.47), number of siliqua per plant (669.17), biological yield per plant (214.49), 1000 seed weight(3.38), harvest index (15.29) and seed yield per plant (32.8).Cluster III having 3 genotypes was characterized as having above average mean values for days to 50% flowering (47.33), days to maturity (117.89) and length of siliqua (5.62).Cluster IV having 1 genotype was characterized as having above average mean values for plant height (154.53), number of siliquae on main raceme (53.33), length of siliqua (6.77), number of seeds per siliqua (25.87), harvest index (23.16) and seed yield per plant (19.23).Cluster V having 1 genotype was characterized as having above average mean values for days to 50% flowering (43), days to maturity (115.33), number of primary branches per plant (7.6) and number of secondary branches per plant (24.13).

Conclusion
The results acquired revealed anenormous genetic variability for hetraits under study, which could be potentially exploited to acquire further breeding gains. Biological yield and test weight traits were found to be more heritable; these were also positively correlated with yield and thus can be taken as important traits to be considered for selection of parent genotypes. The high positive direct effect was shown by biological yield per plant indicating the proper relationship between the trait and seed yield. Maximum inter-cluster D^2 value was noted among the clusters IV and V signifying that crossing could be obtained between the genotypes to supply superior hybrid within the F1generation along with subsequent promising segregating generation. Cluster an alysis revealed that he no types under study were more diverse, which could be employed for future hybridization programs, and can also release transgressive segregants for seed yield improvement.

Table 1: List of genotypes

Sr. No	Name of the Genotype	Pedigree/Source of the Genotype
1.	Pusa Bold	VARUNA X BIC1780 (IARI, New Delhi)
2.	Pusa Mustard 28	SEJ8 X PUSA JAGANNATH (IARI, New Delhi)
3.	Pusa Mustard 24	(PUSA BOLDXLEB) X LES-29 (IARI, New Delhi)
4.	Parwati Mustard	DRMR, Bharathpur
5.	KBS-3	Pusa Kalyani X Yukina (Oil seeds research station, Himachal Pradesh Krishi Vishwa Vidyalaya, Kangra.)
6.	DMH-1	5247 A X 2332 R (1-126 CMS system based)
7.	JD6	Pusa Bold X Glossy (IARI, New Delhi)
8.	Gujarath Mustard 1	MR71-3-2 X TM-4 (SDAU, S K Nagar)
9.	Vaibhav	Derived through biparental mating involving Varuna, Keshari, CSU 10 and B1775, B1786, B1866 (CSAUA&T , Uttar Pradesh)
10.	Rohini	Selection from natural population of Varuna. (CSAUA&T, Kanpur)
11.	TM4	Varuna X TM-1 (BARC, Mumbai, Maharashtra)
12.	GSL-2	Triton X GSL8851 hybridization (PAU, Ludhiana)
13.	BR-23	Selection from local germplasm of PURNEA (Government of Bihar)
14.	Gujarath Mustard 2	Selection from local germplasm (SDAU, S K Nagar)
15.	RH-701	DRMR, Bharathpur
16.	Ashirwad	CSAUA&T, Kanpur
17.	Basanthi	CSAUA&T, Kanpur
18.	Bhagirathi	Selection from Pusa Jai Kishan, (PORS, Berhampore, West Bengal)
19.	BR-40	Government of Bihar
20.	Pusa Jai Kishan (C1)	Somaclone of Varuna(IARI, New Delhi)
21.	TL-17 (C2)	-

Table 2: Estimate of coefficient of variation, h^2 (broad sense) and genetic advance in per cent of mean in mustard

S. No.	Characters	Range			Coefficient of variation		Heritability in broad sense (%)	Genetic advance in per cent of mean
		min	max	Mean	PCV	GCV		
1	X1	43	57.33	49.71	8.05	7.76	93	15.43
2	X2	115.33	124.66	119.57	2.08	1.14	30	1.29
3	X3	106.2	202.6	158.43	16.82	16.30	94	32.56
4	X4	3.86	8.96	6.17	19.01	18.17	91	35.78
5	X5	6.13	29.46	15.08	43.06	42.89	99	88.01
6	X6	43.91	71.46	58.40	12.97	12.46	92	24.67
7	X7	25.2	53.33	39.06	18.86	18.46	95	37.24
8	X8	89.93	770.2	426.33	41.47	41.10	98	83.89
9	X9	4.11	6.77	4.91	14.60	14.39	97	29.22
10	X10	9.53	25.86	13.86	28.77	28.70	99	59.00
11	X11	51.56	219.75	119.78	37.75	37.69	99.7	77.53
12	X12	2.39	5.4	3.310	22.43	22.35	99.3	45.90
13	X13	5.53	23.15	14.56	31.14	31.02	99.3	63.68
14	X14	4.16	32.83	17.27	44.82	44.63	99.2	91.56

Where, X1 = Days to 50% flowering, X2 = Days to maturity, X3 = Plant height, X4= Number of primary branches per plant, X5 = number of secondary branches per plant, X6 = length of main raceme, X7 = Number of siliquae on main, X8=Number of siliquae per plant, X9= length of siliqua, X10 = Number of seeds per siliqua, X11=Biological yield per plant, X12 = 1000 Seed weight, X13= harvesting index, X14 = Seed yield per plant.

Table 3: Estimates of Genotypic correlation (above diagonal) coefficient & Phenotypic correlation (below diagonal) coefficient for yield and yield contributing traits in mustard under study.

Traits	X1	X2	X3	X4	X5	X6	X7	X8	X9	X10	X11	X12	X13	X14
X1	1.00	1.1337**	0.22	-0.16	-0.10	-0.36	0.21	0.15	0.34	0.27	0.06	0.22	0.35	0.27
X2	0.60**	1.00	0.5362*	-0.25	-0.6044**	-0.5287*	0.47*	-0.01	0.5187*	0.32	-0.15	0.4646*	0.7273**	0.26
X3	0.19	0.23	1.00	0.5444*	0.38	0.5268*	0.76**	0.7719**	-0.36	0.10	0.5727**	0.30	0.34	0.70**
X4	-0.14	-0.17	0.51*	1.00	0.8084**	0.32	0.45*	0.6119**	-0.42	-0.17	0.6168**	-0.09	0.10	0.63**
X5	-0.10	-0.33	0.36	0.7686**	1.00	0.25	0.25	0.6756**	-0.32	-0.32	0.7293**	0.10	0.08	0.72**
X6	-0.34	-0.31	0.49*	0.28	0.24	1.00	0.4679*	0.36	-0.07	0.21	0.35	0.19	-0.01	0.31
X7	0.20	0.28	0.69**	0.43	0.25	0.4479*	1.00	0.4839*	-0.09	0.38	0.26	-0.09	0.48	0.5122*
X8	0.15	0.00	0.73**	0.5764**	0.6777**	0.35	0.47*	1.00	-0.4763*	-0.01	0.719**	0.32	0.39	0.86**
X9	0.32	0.25	-0.34	-0.42	-0.32	-0.04	-0.08	-0.4634*	1.00	0.4481*	-0.18	0.04	-0.20	-0.25
X10	0.26	0.19	0.09	-0.16	-0.31	0.20	0.37	-0.01	0.4394*	1.00	-0.22	-0.10	0.38	-0.01
X11	0.06	-0.08	0.55**	0.58**	0.729**	0.33	0.26	0.71**	-0.18	-0.22	1.00	0.47*	-0.10	0.83**
X12	0.21	0.26	0.29	-0.09	0.10	0.19	-0.09	0.32	0.04	-0.10	0.47*	1.00	-0.17	0.30
X13	0.34	0.41	0.31	0.09	0.09	-0.02	0.47*	0.39	-0.20	0.38	0.09	-0.17	1.00	0.44*

*, ** indicate significance at 5%-0.4329 and 1%-0.5487 probability level, respectively.

Where, X1 = Days to 50% flowering, X2 = Days to maturity, X3 = Plant height, X4= Number of primary branches per plant, X5 = number of secondary branches per plant, X6 = length of main raceme, X7 = Number of siliquae on main, X8=Number of siliquae per plant, X9= length of siliqua, X10 = Number of seeds per siliqua, X11=Biological yield per plant, X12 = 1000 Seed weight, X13= harvesting index, X14 = Seed yield per plant.

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

Traits	X1	X2	X3	X4	X5	X6	X7	X8	X9	X10	X11	X12	X13	X14
X1	0.10	0.12	0.02	-0.02	-0.01	-0.04	0.02	0.02	0.03	0.03	0.01	0.02	0.04	**0.10**
X2	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
X3	-0.02	-0.04	-0.07	-0.04	-0.03	-0.04	-0.05	-0.05	0.02	-0.01	-0.04	-0.02	-0.02	-0.02
X4	-0.01	-0.02	0.05	0.09	0.07	0.03	0.04	0.06	-0.04	-0.02	0.06	-0.01	0.01	-0.01
X5	0.00	0.01	-0.01	-0.01	-0.02	0.00	0.00	-0.01	0.01	0.01	-0.01	0.00	0.00	0.00
X6	-0.03	-0.04	0.04	0.03	0.02	0.08	0.04	0.03	-0.01	0.02	0.03	0.02	0.00	-0.03
X7	0.00	0.00	0.01	0.00	0.00	0.00	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00
X8	0.02	0.00	0.12	0.10	0.11	0.06	0.08	0.16	-0.08	0.00	0.11	0.05	0.06	0.02
X9	0.03	0.04	-0.03	-0.03	-0.03	-0.01	-0.01	-0.04	0.08	0.04	-0.01	0.00	-0.02	0.03
X10	-0.03	-0.03	-0.01	0.02	0.03	-0.02	-0.04	0.00	-0.04	-0.10	0.02	0.01	-0.04	-0.03
X11	0.04	-0.11	0.42	0.45	0.53	0.25	0.19	0.53	-0.13	-0.16	0.73	0.35	-0.07	0.04
X12	-0.01	-0.02	-0.01	0.00	0.00	-0.01	0.00	-0.01	0.00	0.00	-0.02	-0.04	0.01	-0.01
X13	0.17	0.35	0.16	0.05	0.04	-0.01	0.23	0.19	-0.10	0.19	-0.05	-0.08	0.48	0.17

R SQUARE = 0.9862 RESIDUAL EFFECT = 0.1174

Where, X1 = Days to 50% flowering, X2 = Days to maturity, X3 = Plant height, X4= Number of primary branches per plant, X5 = number of secondary branches per plant, X6 = length of main raceme, X7 = Number of siliquae on main, X8=Number of siliquae per plant, X9= length of siliqua, X10 = Number of seeds per siliqua, X11=Biological yield per plant, X12 = 1000 Seed weight, X13= harvesting index, X14 = Seed yield per plant.

Table 5: Distribution of 21 genotypes based on clusters in mustard

Cluster 1	14	DMH1, JD6, Gujarath Mustard 1, Vaibhav, Rohini, TM4, BR-23, Gujarath Mustard 2, RH-701, Ashirwad, Basanthi, Bhagirathi, BR-40, Pusa Jai Kishan (C1)
Cluster 2	2	Pusa Mustard 28, Pusa Mustard 24
Cluster 3	3	Pusa bold, KBS3, TL-17 (C2)
Cluster 4	1	GSL-2
Cluster 5	1	Parwati Mustard

Table 6: Cluster distances

	Cluster1	Cluster2	Cluster3	Cluster4	Cluster5
Cluster 1	29.45	47.96	57.02	54.46	79.2
Cluster 2		23.91	61.33	83.11	72.41
Cluster 3			39.01	90.13	51.96
Cluster 4				0	111.45
Cluster 5					0

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