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Genetic variability and genetic diversity studies in Indian mustard (*Brassica juncea* L.)

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Abstract
The present experimental research was carried out during *Rabi* season of 2021-2022. The experiment was carried out under Department of Genetics and Plant Breeding, Agriculture Research Farm, Lovely Professional University, Jalandhar, Punjab. The experimental material consists of 21 genotypes and observed 14 traits. The estimate of analysis of variance indicated that the mean sum of squares due to genotypes were highly significant for all the characters. The phenotypic coefficient of variation was greater than the genotypic coefficient of variation for all the characters suggesting that there is an influence of environment over the genotypes. Combination of heritability and genetic advance are high heritability and high genetic advance are combined for following characters 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, number of seeds per siliquae, biological yield per plant, 1000 seed weight, harvest index and seed yield per plant. 21 genotypes were grouped into six clusters. Maximum inter-cluster D^2 value was noted among the clusters II and V therefore it could be concluded that the genotypes present in these two clusters show maximum degree of diversification and could be utilized for successful breeding programme.

Keywords: Variability, heritability, genetic advance, genetic diversity

Introduction
Indian mustard is one of the finest and most important oilseed crops of the world and it has its own importance in the occupancy of land for cultivation in the Brassicaceae family. Brassica genus nearly have 150 species of annual and biannual herbs, most of them are cultivated as oil seed crops, vegetables or fodder crops. Mustard plants are tall (90-200 cm) which are erect and have more branches which exhibits tap root system. The leaves are clasping, stalked, broad and pinnatified. The siliquae of the plants are thin and long (2.0-6.5 cm) which are erect with short and stout beaks. The siliqua possesses two carpels covering a septum which bears seeds. The inflorescence is of corymbose raceme type. Flower of mustard species contains four sepals and four petals of yellow colour. Flower has six stamens; four long and 2 with short filaments. The pistil is compound which provides two chambers which are separated by a false septum. The total acreage of brown mustard in the world is 36.59 million hectares. In the world the highest producing country is Nepal which has a productivity of 214.1k metric tonnes. It is followed by Russia which has productivity of 103k metric tonnes occupying second place, the third place is occupied by Canada with 98.8k metric tonnes. According to the source of directorate of economics and statistics by the government of India in 2020 the all India mean production of rape seed and mustard is 1345, and according to state wise Gujarat tops in first place with production of 2100 kg/hectare, followed by Haryana with production of 1793 kg/hectare, followed by Telangana with production of 1631 kg/hectare, followed by Punjab in fourth place with production of 1497 kg/hectare, in fifth place stood Rajasthan with production of 1431 kg/hectare. Present study is conducted with twenty-one genotypes to estimate the genetic variability and genetic divergence among the genotypes. The pre-requisite for any breeding programme for improving yield 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. Seed yield being a complex character is controlled by non-additive gene actions, it is influenced highly by both i.e., morphological traits governed by a large number of genes as well as the environmental effects. Hence, partitioning of the overall variability into heritable and non-heritable components is important which enables the breeders to adopt suitable breeding procedure for further improvement of genotypes.

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For the selection of parents to obtain such ideal yield the genetic divergence helps by using mahalanobis D^2 analysis by forming the genotypes into clusters.

Materials and Methods
The present investigation was carried out with twenty-one diverse genotypes of Indian mustard for 14 characters in Rabi 2021-22 in a randomized block design with three replications at Agriculture farm, Department of Genetics and Plant breeding, School of Agriculture, Lovely Professional University, Jalandhar, Punjab. Geographically this place is located at latitude longitude range of 31.2554º and 75.7058º E and at an altitude of 235m above from mean sea level. Twenty-onegenotypes of Indian mustard with a spacing of row-to-row 45cm and15cm from plant-to-plant distancewere maintained. The characters observed were Days to 50% flowering, Days to maturity, Plant height (cm), 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, Length of siliqua (cm), Number of seeds per siliqua, Biological yield per plant (g), Harvest Index (%), Test weight (g), Seed yield per plant (g) on five randomly selected plants in each line and in each replication whereas, Days to 50% flowering and Days to maturity were recorded plot wise. The data of recorded characters subjected to analysis of variance on the basis of model described by (Panse and Sukhame 1985), estimation of coefficient of variation (Burton and de Vane, 1953) [3], heritability in broad sense (Hanson et. al., 1956) [5], genetic divergence analysis by Mahalanobis D2 statistic given by (Rao 1952) [10].

Results and Discussion
The estimate of analysis of variance indicated that the mean sum of squares due to genotypes were highly significant for all the characters as shown in table 1 at 5% and 1% level of significance. Similar results were also obtained by Tripathi, N, et al., (2020) [16] Rout, S., et al., (2018) [12] Yadav, S., et al., (2018) [17]. In their study analysis of variance, the characters showed highly significant difference among genotypes. The phenotypic coefficient of variation was greater than the genotypic coefficient of variation for all the characters suggesting that there is an influence of environment over the genotypes. The high magnitude of both coefficients was recorded for Number of siliqua per plant exhibited highest PCV (56.30) and GCV (55.88), followed by seed yield per plant (53.25) and (53.07), followed by number of secondary branches per plant (51.96) and (51.68), biological yield per plant (45.42) and (45.37), number of primary branches per plant (24.29) and (23.91), number of seeds per siliqua (20.87) and (20.71), harvest index (19.02) and (17.46), 1000 seed weight (17.28) and (16.94), length of main raceme (12.03) and (11.51), number of siliqua on main raceme (11.60) and (10.91), length of siliquae (9.42) and (9.22), plant height (8.06) and (7.45), days to 50% flowering (5.365) and (5.06), and days to maturity showed the least PCV and GCV are (3.827) and (3.611). Number of primary branches per plant, number of secondary branches per plant, number of siliquae per plant, number of seeds per siliquae, biological yield per plant and seed yield per plant showed high PCV and GCV values which shows substantial amount of variability and similar findings were found with S. Pal, et al., 2019 [7]. Number of siliquae on main raceme, 1000 seed weight and harvest index showed moderate PCV and GCV values similar findings were observed in Rout. S., et al., 2019 [11], length of main raceme is also moderate and similar findings were found in Tripathi A.M.et al., 2020 [14], these parameters showed considerable variability. Days to 50% flowering and days to maturity showed low PCV and GCV in our findings and similar findings were observed in B. Devi (2018) [4], Ganesh prasad and BR Patel (2018) [9], Yadav et. al., 2020 [18], Tripathi A, et al., 2020. Plant height and length of siliquae also showed low PCV and GCV and similar findings were observed in Rout. S., et al., 2019 [11]. Combination of heritability and genetic advance are high heritability and high genetic advance are combined for following characters 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, number of seeds per siliquae, biological yield per plant, 1000 seed weight, harvest index and seed yield per plant. This indicates that these traits are not much influenced by the environment but are mostly controlled by additive and / or additive x additive gene interaction and selection is effective for crop improvement, similar findings were found in S. Palet al., 2019; Tripati et al., 2019 [15]. High heritability is shown by biological yield per plant, followed by Seed yield per plant, number of secondary branches per plant, number of siliquae per plant, number of seeds per siliqua, number of primary branches plant per plant, 1000 seed weight, length of siliquae, length of main raceme, days to 50% flowering, Days to maturity, number of siliquae on main raceme, plant height, harvest index. Similar findings were observed in Tripathi A, et al., 2020; Rout. S et al., 2019 [11]; S. Palet al., 2019; Swetha and Janeja 2019; Akabari and Niranjan 2015 [2].

Table 1: Estimate of coefficient of variation, h2 (broad sense) and genetic advance in per cent of mean in Mustard

S. No.	Characters	Range		Mean	Coefficient of variation		Heritability in broad sense (%)	GA %	Genetic advance in per cent of mean
		min	max		PCV	GCV			
1	Days to 50% flowering	44.67	54.00	49.90	5.37	5.07	89.20	4.92	9.86
2	Days to maturity	134.00	150.33	141.19	3.83	3.61	89.00	9.91	7.02
3	Plant height (cm)	124.53	193.47	176.59	8.07	7.45	85.40	25.05	14.19
4	Primary branches	2.33	7.80	5.99	24.29	23.91	96.90	2.90	48.50
5	Secondary branches	0.93	18.67	9.36	51.97	51.69	98.90	9.91	105.90
6	Length of main raceme (cm)	41.53	70.70	60.43	12.04	11.52	91.50	13.71	22.69
7	No. of siliquae on main raceme	30.40	51.00	40.75	11.61	10.92	88.50	8.62	21.16
8	No. of siliquae per plant	136.00	1160.73	426.46	56.31	55.88	98.50	487.26	114.26
9	Length of siliquae	4.19	5.73	4.75	9.42	9.22	95.90	0.89	18.61
10	No. of seeds per siliquae	10.80	21.00	15.29	20.88	20.72	98.50	6.48	42.35
11	Biological yield	35.13	221.33	103.78	45.42	45.38	99.80	96.91	93.38
12	1000 seed weight	2.00	4.21	2.99	17.28	16.94	96.10	1.02	34.21
13	Harvesting index %	7.82	18.47	14.78	19.03	17.47	84.30	4.88	33.03
14	Seed yield per plant	5.45	36.44	15.31	53.25	53.08	99.30	16.68	108.98

Gentic Divergence

21 genotypes were grouped into six clusters as shown in table Mahalanobis D2 static is the best statistical method used for measuring the degree of genetic divergence between the genotypes and using related clustering patterns with the geographic origin. Distance between the clusters measures the degree of diversification, the greater the distance between two clusters the greater the divergence and vice versa. The little diversity with maximum cluster mean values is also useful for the hybridization program. Among six clusters, cluster I was the largest with 15 genotypes followed by cluster V with 2 genotypes and cluster II, III, IV, VI with 1 genotype each which were shown in table. Similar findings were observed by Tripati. A *et al.,* (2019) [15] with 6clusters and Mohan. S *et al.,* (2017) [6] with 6 clusters. In cluster I we have 15 genotypes including Aravali, Ashirwad, Basanti, Bhagirathi, BR-40, CS-52,DRMR-IJ-31, Durgamani, Gujarat mustard-2, Jawahar mustard-1, Jawahar mustar-2, kanti, Kranti, Laxmi, Maya, followed by cluster V having 2 genotypes they are Navgold (yrn-6) and Krishna. Cluster II with Jagannath, cluster III with Geeta, cluster IV Gujarat mustard-1, cluster VI with TL-17 which were shown in table 3. Diversity among the clusters varied from 30.98 to 108.73 inter-cluster distances (Table 2). Cluster II and V showed maximum inter cluster distance (108.73) followed by that between cluster V and I (91.14), cluster V and III (83.03), cluster IV and II (76.07), cluster VI and V (71.21), cluster VI and II (70.21), cluster IV and III (60.90), cluster V and IV (58.24), cluster VI and I (54.23), cluster VI and III (53.45), cluster IV and I (52.25), cluster VI and IV (43.70), cluster III and I (36.78), cluster II and I (35.38) and cluster III and II (30.98). The intra cluster distance ranged from 26.02 to 34.38 by cluster I and cluster V and the other four clusters ranged 0 values because they have single genotype in it. The cluster means and general mean values for 14 characters of 21 genotypes have been represented in table 4. Days to 50% flowering showing highest mean value in cluster V (51.33) and lowest mean value for cluster VI (44.67). Days to maturity showing highest mean value in cluster V (146.17) and lowest mean value for cluster IV (134).Plant height (cm) showing highest mean value in cluster III (188.03) and lowest mean value for cluster VI (124.53).No. of Primary Branches showing highest mean value cluster V (7.40) and lowest mean value for cluster VI (4.27).No. of secondary branches showing highest mean value in cluster III (18.67)and lowest mean value for cluster IV (1.93).Length of main raceme (cm) showing highest mean value in cluster IV (66.40) and lowest mean value for cluster II (58.90). No. of siliquae on main re showing highest mean value in cluster III (45.27) and lowest mean value for cluster VI (30.40).Number of siliquae per plant showing highest mean value in cluster V (998.33) and lowest mean value for cluster VI (195.53).Length of siliquae (cm) showing highest mean value in cluster VI (5.73) and lowest mean value for cluster I (4.62).No. of seeds per siliquae showing highest mean value in cluster VI (18.20) and lowest mean value for cluster II (10.87).Biological Yield showing highest mean value in cluster V (215.10)and lowest mean value for cluster I (84.21).Weight of 1000-grains (g) showing highest mean value in cluster VI (3.82) and lowest mean value for cluster III (2.70).HI% showing highest mean value in cluster IV (16.13) and lowest mean value for cluster VI (7.82).Seed yield per plant showing highest mean value in cluster V (35.82) and lowest mean value for cluster VI (8.53).

Table 2: Average inter cluster and intra cluster distances

	Cluster1	Cluster2	Cluster3	Cluster4	Cluster5	Cluster6
Cluster1	26.02	35.38	36.78	52.25	91.14	54.23
Cluster2		0	30.98	76.07	108.73	70.21
Cluster3			0	60.90	83.03	53.45
Cluster4				0	58.24	43.70
Cluster5					34.38	71.21
Cluster6						0

Table 3: Distribution of 21 genotypes into clusters

Cluster No.	No. of Genotypes	Genotypes
Cluster 1	15	Aravali, Ashirwad, Basanti, Bhagirathi, BR-40, CS-52, DRMR-IJ-31, Durgamani, Gujarat Mustard-2, Jawahar Mustard-1, Jawahar Mustard-2, Kanti, Kranti, Laxmi, Maya
Cluster 2	1	Jagannath
Cluster 3	1	Geeta
Cluster 4	1	Gujarat Mustard-1
Cluster 5	2	Navgold (YRN-6), Krishna
Cluster 6	1	TL-17

Table 4: cluster means for all the traits

	X1	X2	X3	X4	X5	X6	X7	X8	X9	X10	X11	X12	X13	X14
Cluster 1	50.69	141.80	177.73	5.73	8.60	60.03	41.04	371.60	4.62	15.52	84.21	2.93	15.09	12.78
Cluster 2	47.33	135.67	179.37	6.40	14.87	58.90	36.47	272.00	5.05	10.87	87.00	2.70	13.42	11.58
Cluster 3	47.00	141.00	188.03	7.13	18.67	58.93	45.27	506.33	5.18	14.60	142.40	2.70	14.58	20.98
Cluster 4	46.00	134.00	183.93	7.13	1.93	66.40	39.87	411.13	4.81	17.67	108.87	3.29	16.13	17.03
Cluster 5	51.33	146.17	183.27	7.40	12.47	62.73	44.07	998.33	4.89	13.50	215.10	3.14	16.05	35.82
Cluster 6	44.67	135.00	124.53	4.27	7.13	58.93	30.40	195.53	5.73	18.20	147.73	3.82	7.82	8.53

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 raceme, X8=Number of siliquae per plant, X9 = Siliquae length, X10 = Number of seeds per siliquae, X11 = Biological yield per plant, X12 = 1000 Seed weight, X13= harvesting index, X14 = Seed yield per plant.

Conclusion

From the analysis of variance (ANOVA), significant variations were observed for all the traits among the genotypes. Significant variation among genotypes showed existence of wide genetic diversity that would provide better

scope of selection. The PCV was greater than the GCV for all the characters studied, which indicated that there was less environmental influence on the expression of the characters. High Heritability with high genetic advance in percentage of mean was observed for plant height, number of primary branches per plant and number of secondary branches per plant. Future breeding program can be focused on these traits that would be a milestone for the improvement of Brassica. Twenty-one (21) genotypes were grouped into six clusters. Maximum inter-cluster D^2 value was noted among the clusters II and V which signifies that crossing would be obtained between the genotypes separated by considerable D^2 distance to supply superior hybrid within the F1 generation and to produce promising segregating generation. From the above research data observed from the cluster analysis was genotypes belonging to cluster I and cluster V can be utilized for the hybridization programme to obtain maximum heterosis in Indian mustard.

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