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Genetic divergence studies among different *Brassica* species

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Abstract

The present investigation was undertaken to study the genetic divergence of different *Brassica* genotypes for white rust resistance in a group of 37 varieties/genotypes of *Brassica juncea, Brassica napus, Brassica rapa* (Toria) with respect to 11 different characters. The heritability value ranged from 99.3% for days to maturity to 23.2% for oil content under irrigated condition, whereas under rainfed condition it ranged from 99.3% for days to maturity to 32.6% for number of primary branches/plant. The maximum positive direct effect (genotypic level) on seed yield per plant(g) was exhibited by days to maturity and days to 50% flowering while as maximum negative indirect effect was exhibited by siliqua length (cm) under irrigated condition. Under rainfed condition maximum positive direct effect (genotypic level) on seed yield per plant (g) was exhibited by days to maturity and maximum negative indirect effect exhibited by days to 50% flowering. The genotypes NRCDR-2, Kranti, RSPR-01 and PT-2012-5, KBS-3, RMT-10-9 are more diverse genotypes under irrigated condition and from rainfed condition NRCHB-101, SKJM-5 and RSPT-6, RSPT-2 are more diverse genotypes. The cluster I and cluster VII from both environmental conditions contain maximum inter and intra cluster distances because of wide genetic diversity among its genotypes. Therefore it is possible to utilize that genetic variation in hybridization programme to develop new or productive varieties of *Brassica* species. This study further can be useful for selection of desirable genotypes of *Brassica* species to fulfil the various breeding objectives.

Keywords: Indian mustard, rainfed, genetic diversity & yield

Introduction

In India, rapeseed-mustard is the second most important oilseed crop after groundnut and shares about 28.6% of the Indian oilseed economy. India produced 10.1 million tons of rapeseed and mustard in year 2020-21. The area under rapeseed and mustard in India is 6.7 million hectares, with a productivity of 1511 kg/ha during 2020-21. In the state of Jammu & Kashmir the area under rapeseed - mustard is 51870 ha with production of 59600 MT and 1149 kg per productivity during 2018-19.

Genetic diversity serves as a way for populations to adapt to changing environments. With more variation, it is more likely that some individuals in a population will possess variations of alleles that are suited for the environment. Those individuals are more likely to survive to produce offspring bearing that allele. The population will continue for more generations because of the success of these individuals. In all populations, genetic drift occurs constantly-species gradually lose genetic variation. Genetic variation can be measured in a number of different ways. Various methods such as Euclidean distance, Manhattan distance, Pearson correlation, partial correlation, point correlation, linkage coefficients, Jaccard's coefficients etc. are used for studying genetic similarities or distances (Zhang *et al*., 2007) [10]. (Gupta *et al*., 1991) [2], (Vaishnava *et al*., 2006) [8], (Ray *et al*., 2014) [5] and (Singh *et al*., 2010) [6] using D2 analysis classified 48, 50, 30 and 33 genotypes, respectively, for seed yield and its important component traits in Indian mustard. Hu *et al*., 2007 assessed genetic diversity of *B. napus* germplasms from China and Europe by using agronomically important traits. Shannon Diversity index based on the k-means clustering and inertia score was used by (Yadava *et al*., 2009) [9] for the selection of diverse accession from 286 germplasm collections, ensuring higher evenness as well as richness in the sample. (Kumar *et al*., 2008) [3] evaluated 11 Indian mustard genotypes and found significant difference among them for different traits. He recorded high GCV and PCV for seed yield/ plant (GCV=42.5%, PCV=42.21%) and secondary branches/plant (GCV=41.53%, PCV=42.07%).

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Since plant breeding research and cultivar development are integral components of improving food production, therefore, availability of and access to diverse genetic sources will ensure that the global food production network becomes more sustainable.

Material and Methods
Thirty seven diverse strain/varieties of *B. juncea, B. napus,* and *B. rapa* (Toria) were grown during *rabi* season of 2019-2020 in a randomized block design with 3 replications. The field experiment was done in two locations (irrigated and rainfed) i.e. Division of Plant Breeding and Genetics, SKUAST-J, F.O.A. Chatha and Advanced centre for rainfed agriculture (ACRA), Dhiansar. Field observations are recorded for days to 50% flowering, number of primary branches/ plant, number of secondary branches/plant, number of siliqua/plant, siliqua length, number of seed/siliqua, plant height, test weight, oil content and seed yield/plant. Five competitive plants were randomly selected from each plot in each replication to record observations on the quantitative traits. The data recorded for each genotype at each environment were subjected to statistical analysis. An analysis of variance (ANOVA) was conducted in each environment to test significant differences among genotypes. Differences were considered to be significant at $p < 0.05$ and < 0.01. The data on the all characters were computed and agglomerative hierarchical clustering was done using Windostat version 9.2 software. The clustering was based on the squared Euclidean distance and the average linkage between groups was taken as the average of the distance between all pairs of cases with one member of each group.

Results and Discussion
Cluster analysis under Irrigated condition (E^1)
Distribution of genotypes into different clusters
By application of non-hierarchical clustering using covariance matrix, the 37 genotypes of *Brassica* species were grouped into 7 different clusters indicated in the table 1.In present study cluster I contained the genotypes i.e. NRCDR-2, Kranti, RSPR-01, Giriraj, RSPR-03, RH-0923, RSPR-69 and RB-50, cluster-II contained the genotypes i.e. DGS-1, RSPN-29, RSPN-25, CNH-11-2, JGS-12-3, GSH-1699, EC552608, GSC-6 and GSC-21, cluster III contained the genotypes i.e. RSPN-28, AKGS-1, HNS-1102 and GSC-101, cluster IV contained the genotypes of RH-1209, JM-12-6, NRCHB-101 and SKJM-5, and the cluster V contained the genotypes i.e. PTC-2010-2, RSPT-6 and RSPT-2 cluster VI contained the only one genotype i.e. JD-6 and cluster VII contained the genotypes of PT-2015-5, KBS-3, RMT-10-9, TH-1401, Tapeshwari, PT-303, BAUT-09 and Bhawani. The cluster II had highest number of genotypes (9) followed by cluster I (8) and cluster VII (8). While cluster III, IV and V had 4 or 3 genotypes and JD-6 could not be grouped together and formed separate clusters VI respectively. In present study the cluster I and cluster VII from both environmental conditions showed the maximum divergence between them, the similar findings were done by earlier workers D.A. Shathi *et al.* (2011) [7]. The cluster mean reflected appreciable variation for almost all characters, especially seed yield potential among different clusters. Grouping of 33 *B. juncea* genotypes, Singh *et al.,* (2010) [6] also found different clusters which were among the most divergent clusters having both seed yield and high oil content performance.

Table 1: Distribution of genotypes into different clusters under irrigated condition (E^1)

Cluster No.	No. of genotypes	Genotypes
I	8	NRCDR-2, Kranti, RSPR-01, Giriraj, RSPR-03, RH-0923, RSPR-69, RB-50
II	9	DGS-1, RSPN-29, RSPN-25, CNH-11-2, JGS-12-3, GSH-1699, EC552608, GSC-6, GSC-21
III	4	RSPN-28, HNS-1102, AKGS-1, GSC-101
IV	4	RH-1209, JM-12-6, NRCHB-101, SKJM-5
V	3	PTC-2010-2, RSPT-6, RSPT-2
VI	1	JD-6
VII	8	PT-2015-5, KBS-3, RMT-10-9, TH-1401, Tapeshwari, PT-303, BAUT-09, Bhawani

Average Inter and Intra cluster distance
Euclidean analysis was done to compute the inter and intra cluster distance (D^2) whose values are presented in table 2. Results indicated that the intercluster distance was larger than the intracluster distance in most of the cases suggesting wider genetic diversity among genotypes of different groups. The maximum intercluster distance was observed between cluster V (87.46) and cluster II (2758.919) followed by cluster V and cluster I (2235.773), cluster V and cluster III (2160.423), cluster VI and cluster II (1904.701). The minimum inter cluster distance was observed between cluster II and cluster I (177.403) followed by cluster III and cluster II (202.472)

indicating a close relationship among the genotypes of these clusters. The highest intra cluster distance was observed in cluster VII (121.349) followed by cluster II (99.99) and cluster IV (99.67). The lowest intra cluster distance was noticed for cluster VI (0.00). The results revealed that the genotypes in cluster VII were distantly related on the other hand the genotypes in cluster VI are closely related. These results confirmed the clustering pattern of the genotypes according to the principal component analysis. The genotypes of distant cluster could be used for further hybridization programme.

Table 2: Average (Diagonal) Intra and Inter cluster distances values for various clusters under irrigated condition (E^1)

	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	Cluster VII
Cluster I	97.84 (48.92)	177.40 (88.7)	221.99 (110.99)	263.48 (131.74)	2235.77 (1117.88)	1494.38 (747.19)	980.63 (490.31)
Cluster II		99.99 (49.99)	202.47 (101.23)	469.59 (234.79)	2758.91 (1379.45)	1904.70 (952.35)	1363.08 (681.54)
Cluster III			43.79 (21.89)	310.28 (155.14)	2160.42 (1080.21)	1274.86 (637.43)	1047.76 (523.88)

Cluster IV				99.67 (49.83)	1304.17 (652.08)	661.22 (330.61)	543.48 (271.74)
Cluster V					87.46 (43.73)	432.83 (216.41)	428.79 214.39)
Cluster VI						0.00 (0.00)	571.54 (285.77)
Cluster VII							121.34 (60.67)

Cluster means for the characters

The genotypes from Cluster I earned the highest mean value for number of siliqua/plant (469.667) followed by plant height (188.433) and days to maturity (146.667) while as lowest mean value was earned for the number of primary branches (3.542) followed by siliqua length (3.971) respectively in table 3. The genotypes from Cluster II earned the highest mean value for number of siliqua/plant (184.222) followed by plant height (179.074) and days to maturity (160.185) while as lowest mean value for the number of primary branches (3.889) followed by test weight (3.904). The Cluster III earned the highest mean value for the number of siliqua/plant (209.250) followed by plant height (169.250) and days to maturity (157.333) while as lowest mean value was earned for the number of primary branches (3.667) followed by test weight (3.658). The genotypes from Cluster IV earned the highest mean value for the number of siliqua/plant (556.583) followed by plant height (183.917) while as the lowest mean value was earned for the number of primary branches (3.667).

The genotypes from the Cluster V earned the highest mean value for the number of siliqua/plant (115.889) followed by plant height (104.111) while as lowest mean value was earned for the test weight (3.527) followed by siliqua length (3.989). The genotypes from the Cluster VI earned the highest mean value for the number of siliqua/plant (628.667) followed by plant height (177.667) while as lowest mean value was earned for the number of primary branches (3.667). The genotypes from Cluster VII earned the highest mean value for the plant height (114.708) followed by number of siliqua/plant (111.708) while as lowest mean values for test weight (3.727) followed by siliqua length (3.767). In present study, the mean performance of different clusters calculated for different traits revealed wide range of differences among clusters with respect to the 11 traits. The cluster VI containing one genotype under both conditions i.e. irrigated and rainfed. The similar condition found by Neeru, (2015) [4], D. A. Shathi (2011) [7].

Table 3: Cluster Means for 11 characteristics of 37 *Brassica* genotypes under irrigated condition (E[1])

Cluster	Days to 50% flowering	No. of Pri. Branch / plant	No. of sec. branch/ plant	No. of siliqua/ plant	Siliqua length (cm)	No. of seed/ siliqua	Test wt. (g)	Plant ht. (cm)	Days to maturity	Oil content (%)	Seed yield/ plant (g)
I	64.29	3.54	17.33	469.66	3.97	17.33	4.15	188.43	146.45	39.01	13.60
II	75.59	3.88	11.66	184.22	5.48	17.07	3.90	179.07	160.18	38.77	14.74
III	77.83	3.66	14.75	209.25	4.70	18.25	3.65	169.25	157.33	39.69	19.72
IV	67.91	3.66	18.41	556.58	4.02	18.75	4.42	183.91	139.50	40.14	13.65
V	41.00	4.66	13.11	115.88	3.98	13.44	3.52	104.11	95.44	41.90	8.06
VI	69.33	3.66	15.33	628.66	4.03	18.33	4.27	177.66	124.33	39.63	17.39
VII	38.41	4.45	15.25	111.70	3.76	13.37	3.72	114.70	106.50	42.33	8.96

Cluster analysis under rainfed condition (E[2])
Distribution of various genotypes into different clusters

Based on degree of divergence among 37 genotypes, these were grouped into 7 clusters. The computation from covariance matrix gave non-hierarchical clustering based on Mahalanobis-D[2] values of 37 genotypes and grouped into 7 clustering as shown in table 4. It explained the cluster IV contains the highest number of 10 genotypes i.e. RSPN25, RSPN-29, DGS-1, CNH-11-2, JGS-12-3, GSH-1699, NCN-13-4, NCN-13-6, EC552608 and RSPN-28 followed by

cluster V with 9 genotypes i.e. Bhawani, KBS-3, PT-2015-5, BAUT-09, PTC-2010-2, RMT-10-9, Tapeshwari, TH-1401 and PT-303. The cluster III contains 8 genotypes NRCDR-2, RB-50, RSPR-01, Kranti, Giriraj, RSPR-69, RSPR-03 and RH-0923. The cluster I has NRCHB-101, SKJM-5, RH-1209, JM-12-6 genotypes and cluster II has 3 genotypes which are GSC-101, GSC-21 and GSC-6. The cluster VII contains only 2 genotypes i.e. RSPT-2, RAPT-6 and cluster VI a single genotype JD-6.

Table 4: Distribution of genotypes into different clusters under rainfed condition (E[2])

Cluster no.	No. of genotypes	Genotypes
I	4	NRCHB-101, SKJM-5, RH-1209, JM-12-6
II	3	GSC-101, GSC-6, GSC-21
III	8	NRCDR-2, RB-50, RSPR-01, Kranti, Giriraj, RSPR-69, RSPR-03, RH-0923
IV	10	RSPN25, RSPN-29, DGS-1, CNH-11-2, JGS-12-3, GSH-1699, HNS-11-2, AKGS-1, EC552608, RSPN-28
V	9	Bhawani, KBS-3, PT-2015-5, BAUT-09, PTC-2010-2, RMT-10-9, Tapeshwari, TH-1401, PT-303
VI	1	JD-6
VII	2	RSPT-6, RSPT-2

Average inter and intra cluster distances
According to Mahalanobis D^2 statistics, the maximum inter cluster distance was observed between Cluster VII and cluster IV (2944.943) followed by cluster VII and cluster III (2185.733) and cluster V and cluster IV (1682.048) while as minimum inter cluster distance was observed between cluster III and cluster I (210.721) followed by cluster IV and cluster III (254.889) which indicates the close relationship between the genotypes of these clusters (Table 5). The highest intra cluster distance was found in cluster II (123.92) followed by cluster V (112.516) and cluster IV (110.052). The lowest intra cluster distance was observed in cluster VI (0.00) followed by cluster I (67.458). The genotypes of distant cluster could be used for further hybridization programmes.

Table 5: Average (Diagonal) Intra and Inter cluster distances values for various clusters under rainfed condition (E^2)

	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	Cluster VII
Cluster I	67.45 (33.72)	267.84 (133.92)	210.72 (105.36)	517.51 (258.75)	584.51 (292.25)	339.86 (169.93)	1301.14 (650.57)
Cluster II		123.25 (61.62)	288.97 (144.48)	307.43 (153.71)	1065.86 (532.93)	750.83 (375.41)	1936.88 (968.44)
Cluster III			82.54 (41.27)	254.88 (127.44)	1115.78 (557.89)	918.19 (459.09)	2185.73 (1092.86)
Cluster IV				110.05 (55.02)	1682.04 (841.02)	1428.76 (714.38)	2944.94 (1472.47)
Cluster V					112.51 (56.25)	306.28 (153.14)	326.34 (163.17)
Cluster VI						0.00 (0.00)	474.12 (237.06)
Cluster VII							103.15 (51.57)

Cluster means for the characters
The genotypes from cluster I earned the highest mean value for number of siliqua/plant (525.500) followed by plant height (164.417) and days to maturity (136.083) while as lowest mean value was earned for number of primary branches (3.083) as shown in table 6. The genotypes from cluster II obtained the highest mean value for days to maturity (152.778), number of siliqua/plant (148.333) while as the lowest mean value was earned for number of primary branches (3.333) followed by test weight (3.910). The cluster III genotypes earned having highest mean value for number of siliqua/plant (432.917) followed by plant height (167.125) while as lowest mean value was earned for number of primary branches (3.083). The genotypes from cluster IV earned highest mean value for number of siliqua/plant (177.967) followed by plant height (162.125) while as the lowest mean value was earned for number of primary branches (3.367). The genotypes from cluster V obtained the highest mean value for plant height (106.574) followed by days to maturity (102.296) while as lowest mean value was recorded for the number of primary branches (3.889). The genotypes from the cluster VI earned the highest mean value for number of siliqua/plant (590.00) while as the lowest mean value was earned for the number of primary branches (3.333) followed by test weight (4.213) and siliqua length (4.367). The genotypes from the cluster VII obtained the highest mean value for number of siliqua/plant (99.167) followed by plant height (92.167) while as the lowest mean value was earned for number of primary branches (3.167). The clustering of genotypes from three species of *Brassica* showed the divergence among them for the various traits under study. It is possible to utilize that genetic variation in selection and hybridization program to develop new or more productive *Brassica* varieties and to optimize donor parental lines. The similar findings were reported by Bibi *et al.* (2017) [1] showing that the genetic distances between the genotypes of one species can be increased through hybridization among suitable parents and manipulation of heterosis for developing better genotypes.

Table 6: Cluster Means for 11 characteristics of 37 *Brassica* genotypes in rainfed condition (E^2)

Cluster	Days to 50% flowering	No. of Pri. branch/ plant	No. of sec. branch/ plant	No. of siliqua/ plant	Siliqua length (cm)	No. of seed/ siliqua	Test wt. (g)	Plant ht. (cm)	Days to maturity	Oil content (%)	Seed yield /plant (g)
I	59.08	3.08	14.75	525.50	4.35	16.91	4.61	164.41	136.08	40.16	10.71
II	76.33	3.33	9.66	148.33	5.05	13.11	3.91	133.88	152.77	38.68	9.29
III	56.62	3.08	13.83	432.91	4.31	15.75	4.65	167.12	144.20	3907	0.81
IV	67.10	3.36	9.06	177.96	5.62	15.70	4.06	162.90	156.03	40.12	12.82
V	35.74	3.88	12.96	95.74	4.03	12.22	4.28	106.57	102.29	42.24	7.69
VI	59.33	3.33	13.00	590.0	4.36	17.00	4.21	156.66	120.66	40.01	10.58
VII	34.50	3.16	9.66	99.16	4.21	13.66	3.97	92.16	87.50	41.24	6.70

Conclusions
To exploit the hybridization programme postulated on the basis of genetic divergence may be successful in the genotypes found from both irrigated and rainfed environment conditions. The lines developed from experiment can be used as diverse varieties for further breeding programme. On the basis of genetic divergence, in case of *B. juncea* NRCDR-2 and JD-6, in case of *B. napus* DGS-1, GSC-101 and in case of *B. rapa* (Toria) PTC-2010-2 and Bhawani and Tapeshwari were found more diverse genotypes from both irrigated and

rainfed environment conditions.. The lines identified from experiment with diverse genotypes can be used for future breeding programme.

Reference

1. Bibi T, Riaz A, Mahmood T, Akhter M, Haider Z, Riaz M. Genetic divergence of quantitative traits in *Brassica juncea* L. genotypes based on multivariate analysis. Asian Research Journal of Agriculture. 2017;3(4):1-8.
2. Gupta VP, Sekhon MS, Satija DR. Studies on genetic diversity, heterosis and combining ability in Indian mustard [*Brassica juncea* L. (Czern and Coss)]. Indian Journal of Genetics. 1991;51:448-453.
3. Kumar G, Chakravarty NVK. A simple weather based forewarning model for white rust in *Brassica*. Journal of Agrometeorology. 2008;10(1):75-80.
4. Neeru, Thakral NK, Avtar R, Singh A. Evaluation and classification of Indian mustard (*Brassica juncea* L.) genotypes using principal component analysis. Journal of Oilseed Brassica. 2015;6(1):167-174.
5. Ray K, Pal AK, Banerjee H, Phonglosa A. Correlation and path analysis studies for growth and yield contributing traits in Indian mustard (*Brassica juncea* L.). International Journal of Bio-resource and Stress Management. 2014;5(2):200-206.
6. Singh D, Arya RK, Chandra N, Niwas R, Salisbury. Genetic diversity studies in relation to seed yield and its component traits in Indian mustard (*Brassica juncea* L. Czern & Coss.). Journal of Oilseed Brassica. 2010;1(1):19-22.
7. Shathi DA, Arifuzzaman M, Biswas BK, Hasanuzzaman M, Azad AK. Genetic divergence in mustard *(Brassica spp*. L). African Journal of Plant Science. 2011;6(8):239-243.
8. Vaishnava A, Sachan JN, Tewari SK. Genetic Divergence for Important quantitative traits in Indian mustard (*Brassica juncea* (L.) Czern and Coss). Agricultural Sciences Digest. 2006;26(4):269-272.
9. Yadava DK, Sapra RL, Sujata V, Dass B, Prabhu KV. Selection of high diversity with a minimal set of accessions from Indian Mustard [*Brassica juncea* (L.) Czern & Coss.] germplasm collection. Indian Journal of Agricultural Sciences. 2009;79(7):552-554.
10. Zhang W. Computer inference of network of ecological interactions from sampling data. Environmental Monitoring and Assessment. 2007;124(1-3):253.