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Genetic diversity analysis in Indian mustard (*Brassica juncea*)

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Abstract
Genetic divergence determine in thirty six genotypes of Indian mustard [*Brassica juncea* (L.) Czern & Coss.] by applying D^2 statistics for ten characters facilitate grouping of all the genotypes into eleven clusters. Days to 50% flowering, plant height, days to maturity, siliqua on main shoot, total no of siliqua per plant, no of seed per siliqua, seed yield, biological yield per plant, test weight, harvest index were the main contributors for genetic diversity among the genotypes. Out of 11 clusters, cluster I is used to be the most important comprising 11 genotypes pursuing by cluster IV consisting of seven genotypes, cluster II and V have 5 genotypes, cluster VIII has 2 genotype whereas, rest have single genotypes each. The cluster V presented maximum intra-cluster distance (8.20), while maximum inter-cluster distance was detected between cluster XI and VI (41.82).

Keywords: Oilseed, mustard, genetic diversity, d^2

Introduction
Indian mustard [*Brassica juncea* (L.), 2n=36] is one among the foremost valuable oilseed crops of the country occupying considerably larger acreage among the Brassica crops. European Union (27) is that the leading producer of mustard seed within the world accounting for 35% of the planet production - followed by Canada (21%), China (22%) and India (11%) (Mustard crop Survey Report 2014-15). Indian mustard (*Brassica juncea* L.czern & cross, 2n=2x=36) commonly called rai (raya or laha). On the Indian subcontinent *B. juncea* is that the dominant species grown right along with *B.rapa* (sync. *B.campestris*) and *B. napus*. As these species are considered as of Asian origin besides, Taramira believed to be a south Europe and North African species is grown within the a part of the north west India. In India the main rapeseed-mustard growing states are Rajasthan, Uttar Pradesh, Madhya Pradesh, Gujarat, Haryana, Odisha, West Bengal, Assam and Punjab. The concept of D^2 was originally developed by P.C Mahalanobis (1928) to review the Anthropometry and Psychometry. Now this system is extensively utilized in plant breeding and genetics for the study of genetic divergence. Assemblage and assessment of divergence is vital to understand the spectrum of diversity in any crop. Genetic divergence study is important to develop cultivars with increased yields, wider adaptation, desirable qualities, and pest and disease resistance. Genetic divergence arise thanks to geographical separation or thanks to genetic barriers in crossability. Thus keeping this information in sight, this study was undertaken to analyze genetic diversity among 36 recognized genotypes of Indian mustard

Materials and Methods
The present study was administered at the Agricultural research Farm Santiniketan, Department of Genetics and Plant Breeding (Palli Siksha Bhavana), Visva bharati University, Birbhum during rabi, 2017-18 and 2018-2019. Thirty -six diverse genotypes of Indian mustard (B. *juncea*) were planted in randomized block design with three replications in plot size of 1.5 × 3 m. The row to row and plant to plant distance was maintained at 30 × 30 cm. All recommended package of practices was applied to boost an honest crop. the info were recorded on ten characters, viz. days to maturity, plant height (cm), days to 50% flowering, total number of siliqua per plant, number of seeds per siliqua, number of siliqua on main shoot, arrangement of siliqua based upon angle from main shoot, seed yield per plant (g), 1000- seed weight (g), Harvest index (%) and Biological weight (g).

Estimation of genetic divergence using D^2 statistic
Mahalanobis's D^2 statistic (Rao, 1952) was applied for assessment of genetic divergence among twenty eight genotypes with reference to 10 selected traits. Genetic divergence (D^2) between two genotypes is given by the formula:

$$D^2 x = \sum_{i=1}^{p} \sum_{j=1}^{p} (\lambda_{ij})\ d_i d_j$$

Where, x is that the number of metric trait during a point, λij is that the inverse of the common dispersion matrix λij, p is that the number of populations / genotypes while di and dj are the difference within the means of two populations for ith and jth characters. The computation of D^2 using this formula gets complicated and laborious when more number of mutually correlated characters is involved in divergence analysis. Therefore the character means were altered into sets of uncorrelated variables with the help of pivotal condensation of common dispersion matrix following (Rao, 1952). After this transformation the formula for genetic divergence is:

$$D^2 = \sum_{i=1} di^2$$

Where, d_i is the difference between the transformed values of any two-population means for the i^{th} character. The relative contribution of individual character towards genetic divergence was assessed from rank average.

Grouping of genotypes into different clusters

Grouping of genotypes into different clusters was done following Tocher's method. Usually a cluster is defined as a gaggle of populations per clusters such any two populations belonging to an equivalent cluster should on the average, show a smaller D^2 than those belonging to 2 different clusters. an easy device suggested by Tocher (Rao, 1952) for construction of clusters is to start out with two most closely related populations (having the littlest D^2) then find a 3rd one which has small average D^2 from the primary two and so on. At certain stage when it's felt that after adding a specific population there's an abrupt increase within the average D^2, then that population isn't added to the cluster. Similarly construction of 2nd, 3rd and other clusters are formed till all the populations are included in one or the opposite cluster.

Average intra- and inter-cluster distance

For the measure of intra-cluster distances the formula ΣDi^2 / n was used, where ΣDi^2 is that the sum of distances between all possible combinations (n) of populations (genotypes) included during a cluster. For calculating inter-cluster distance the formula Di^2 / ninj was used; where Di^2 is that the sum of all possible pair wise D^2 values between the individuals of 1 cluster there upon of others, ni is that the number of population in cluster 'i' and nj is that the number of population in cluster 'j'. The info were analyzed within the computer using the Windostat version 8.6 from Indostat service Hyderabad, India.

Result and Discussion

The analysis of variance were highly significant among all the genotypes for all ten characters evaluated which shows the presence of considerable genetic variability among the genotypes. On the basis of relative magnitude of D^2 Values, all the thirty-six genotypes are grouped into 11 clusters (Table- 1). Out of the 11 clusters, Cluster I compromises of maximum number of 11 genotypes representing (Swarna jyoti, Pusa bold, PM-30, Durgamani, Pusa jaikisan, Geeta, Gujarat Mustard-02, PM-26, PM-25, Pusa Mahak, Shivani) genotypes, Cluster II had 5 genotypes, cluster III had 1 genotypes, Cluster IV had 7 genotypes, Cluster V had 5 genotypes, Cluster VI had 1 genotypes, Cluster VII has 1 genotypes, Cluster VII had 2 genotypes, Cluster IX had, 1 genotypes, Cluster X had 1 genotypes and Cluster XI comprises 1 genotypes supported present investigation. It had been concluded that generally, there was parallelism between genetic and geographic diversity. This view point has been supported by the work of Monalisa *et al*., (2005) [11]; Goswami and Behl, (2006) [6]; Kumar *et al*., (2007) [3]; Doddabhimappa *et al.*, (2010) [4] and Goyat *et al*., (2012) [7]. The clustering pattern shows that there was a substantial diversity among the genotypes, and no relationship between the genetic and geographical diversity of the genotypes, but the distribution of the genotypes was quite random and mostly independent. Similar results have also been reported earlier by Singh *et al.* (2010) in Indian mustard. Relative contribution to the entire divergence was higher for days to maturity (32.50%) followed by days to 50% flowering (30.76%), Test weight (26.30%), plant height (1.48%), number of seed per siliqua (1.27%), Total number of siliqua per plant (0.63%), seed yield (5.32%), Number of siliqua of main shoot (1.27%), Harvest Index, (0.50%), and biological weight (0.23%) as per shown in (Table- 2). These results are somewhat in accordance with the findings of (Thul *et al*., 2004 [12]; Monalisa *et al*., 2005 [11]; Goswami and Behl, 2006 [6]; Kumar *et al.*, 2007 [3]. The cluster means for various characters are presented in (Table 3). Cluster VII was characterized by the highest mean values for days to 50% flowering (51.50), plant height (170.42) and number of siliqua on main shoot (39.13), cluster IX for Day to maturity (146.27), Cluster X height for seed yield (5.38), Cluster XI for biological weight (27.32) and Cluster III for harvest Index (17.10), Cluster IV had highest mean for Test weight (5.65), Cluster VI for Total number of siliqua per plant (91.69), Cluster V number of seed per siliqua (13.12). The intra cluster distance among various clusters exhibited maximum intra cluster distance for cluster V (8.20) and lowest intra cluster distance was recorded for cluster VIII (2.75). Within the present study, the utmost inter cluster distance was revealed between cluster VI and XI (41.82) followed by cluster VI and IX (37.68) cluster V and VII (36.58), cluster VII and IX (36.37), cluster V and II (31.94) and cluster VII and cluster X (31.89) cluster V and IX (29.9) (Table. 4). The clearly indicates that the genotypes included during this clusters are having broad spectrum of genetic diversity and will proficiently be utilized in hybridization programme of Indian mustard for improving seed yield. The smallest amount inter cluster distance was between clusters IX and XI (4.10) followed by cluster III and that I (5.34) and cluster I and VI (6.06). This indicated that clusters were homogenous within themselves and heterogeneous between themselves. Considering genetic divergence, relative importance of characters in determining the yield especially population and performance of the genotypes as intrinsically also as cluster means, crossing between the intra-cluster genotypes Durgamani × Pusa Mahak, Shivani × PM 30 (Cluster 1); PM 22 × Jawahar Mustard 01 (Cluster IV); Pusa Agrani × T2 (Cluster V) and inter-cluster genotypes Jagannath × Varuna (T 59) (Cluster II × Cluster X); Pusa Jaikisan × Vaibhav (Cluster I x Cluster VI) are presumably to yield a substantial amount of heterosis in F_1 generation and to supply a good spectrum of recombinants in segregating generations. Selection of diverse parents having most of the desirable characters from such clusters and using them in breeding programs is probably going to supply more trangressive segregants and heterotic F_1's when crossed.

Table 1: Contribution of different characters in creating diversity in Indian mustard based on Mahalanobis's D^2 analysis.

Cluster	No of genotype	Name of genotype
I	11	Swarna Jyoti,, Pusa Bold, PM-30, Durgamani, Pusa Jaikisan, Geeta, Gujarat Mustard-02, PM-26, PM-25, Pusa Mahak, Shivani
II	5	Jagannath, PV, Vasundhara, PM-21,Saurabh(RH-8113)
III	1	PM-28
IV	7	Laxmi, Gujarat Mustard-01, Jawahar Mustard-02, PM-22, Gujarat Mustard-03, NRCHB-101, Jawahar Mustard-01
V	5	,Pusa Agrani, Kanti, PM-27, TPM, T2
VI	1	Vaibhav
VII	1	Patan Mustard 67
VIII	2	Rohini, PM-29
IX	1	NRCDR-02
X	1	Varuna(T-59)
XI	1	RH-30

Table 2: Contribution of different characters in creating diversity in Indian mustard based on Mahalanobis's D^2 analysis.

S. No.	Characters	Contribution %
1	Days to 50% flowering	30.76
2	Plant height	1.48
3	Days to maturity	32.50
4	No of siliqua main shoot	1.23
5	Total no siliqua per plant	0.62
6	No of seed pe siliqua	1.27
7	Biological weight	0.23
8	Test weight	26.83
9	Harvest Index	0.50
10	Seed Yield	5.32

Table 3: Average intra and inter-cluster $\sqrt{D^2}$ value

Cluster	I	II	III	IV	V	VI	VII	VIII	IX	X	XI
I	3.93	13.54	5.34	12.74	6.53	6.06	8.70	9.06	20.63	13.62	23.79
II		3.96	15.52	14.39	31.94	22.75	23.68	10.39	13.05	6.94	7.70
III			0.00	17.41	8.87	9.58	17.93	15.13	17.85	9.26	21.54
IV				6.35	23.70	23.50	10.89	21.14	11.65	21.98	16.87
V					8.20	25.33	26.13	36.58	19.13	23.44	29.9
VI						0.00	10.23	7.45	37.68	23.20	41.82
VII							0.00	15.33	28.27	31.89	36.37
VIII								2.75	30.20	14.29	26.73
IX									0.00	13.44	4.10
X										0.00	8.38
XI											0.00

Table 4: Clusters mean of ten quantitative characters in mustard germplasm

	Days to 50% flowering	Plant height (cm)	Days to maturity	No of siliqua on main shoot	Total no of siliqua per plant	No of seed per siliqua	Biological weight (g)	Test weight (g)	Harvest Index (%)	Seed yield (g)
Cluster 1	45.89	160.85	116.23	31.38	73.96	12.95	21.87	4.09	15.40	3.71
Cluster II	44.50	154.21	141.42	30.97	77.79	12.77	22.68	4.33	15.90	4.14
Cluster III	40.83	147.23	114.23	31.53	83.71	13.77	20.94	3.60	17.10	4.13
Cluster IV	45.14	163.89	126.63	33.96	66.92	12.91	23.67	5.65	16.99	4.62
Cluster V	36.43	143.12	106.13	30.84	71.83	13.12	20.91	4.36	16.40	3.86
Cluster VI	49.33	151.98	109.17	31.83	91.69	11.93	21.30	3.44	14.79	3.68
Cluster VII	51.00	170.42	112.10	39.13	58.38	12.67	21.55	5.17	14.65	3.49
Cluster VIII	50.33	154.80	128.85	31.88	80.59	11.59	21.36	3.59	14.98	3.51
Cluster IX	38.17	146.43	146.27	29.53	59.79	12.57	19.63	4.90	16.12	3.60
Cluster X	37.00	132.77	135.50	32.77	64.08	11.80	21.83	3.95	16.90	5.38
Cluster XI	39.67	166.50	134.93	34.10	81.66	12.57	27.32	3.51	14.01	3.81

Conclusion

Among the thirty-six genotypes Cluster I consists of maximum number of genotypes (11), which ensures that the genotypes grouped within a specific cluster were more or less genetically almost like one another and apparent wide diversity was mainly thanks to the remaining genotypes distributed over remainder of the opposite clusters The intra cluster distance among various clusters exhibited maximum intra cluster distance for cluster V (8.20) and, the utmostinter cluster distance was revealed between cluster VI and XI (41.82). Therefore it are often concluded that the effect of crossing would be more between genotypes separated by the considerable statistical distance to supply superior hybrid within the F1 generation and promising segregating generation in next generations.

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