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Diversity Analysis in Indian Mustard *(Brassica juncea* L. Czern & Coss)

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The present investigation was conducted with forty-six Indian mustard genotypes involving *B. juncea x B. juncea* and related species i.e. *B. juncea x B. carinata, B. juncea x B. napus* and somaclone background. These were evaluated to identify the genetically diverse genotypes for exploitation in a breeding programme aimed at improving yield potential of Indian mustard. Amongst seven clusters formed (Mahalanobis D_2, 1936), each of the cluster I and IV had the largest genotypes (nine) and cluster II with smallest (two genotypes). Maximum divergence was observed between cluster V and VI followed by cluster V and VII and cluster II and VI. The genotypes RAURD-166, RAURD-205, RAURD-241, RAURD-32, JD-6, RAURD-168, RAURD-78, RAURD-195, RAURD-246, RAURD-172, RAURD-25 and RAURD-34 were observed as more divergent. Cluster V recorded minimum for plant height with early flowering and maturity, cluster VI, had more for primary branches per plant, secondary branches per plant, number of siliqua per plant, number of seeds per siliqua, biological yield per plant and seed yield per plant. The cluster VII had high mean for length of main raceme, siliqua on main raceme and seed yield per plant and cluster II, had high mean value for siliqua density. The clusters VI, VII, V and II were observed as more divergent clusters with high seed yield. The probability of getting better segregants and promising recombinants is expected to be more, from selecting genotypes of these clusters.

Key words*: Brassica juncea* L.*,* genetic divergence, D_2 analysis, cluster analysis.

Mustard has been grown in the Indian sub continent for hundreds of years as an oil seed crop (Labana and Gupta, 1993). The genus *Brassica* is an important member of the cruciferae family. It comprises of several economically important species which yield edible root, stems, leaves, buds, flowers and seed condiment. Indian mustard (*Brassica juncea* L. Czern & Coss) popularly known as Rai, Raya or Laha is one of the most important oilseed crop of the country and it contributes around 7% in the global production. It is the second largest cultivated oilseed crop in India after soybean and cultivated in *rabi* season mainly in north-west India and contributes nearly 27 % to edible oil pool of the country. Genetic diversity is the pre-requisite for hybridization programme to obtain desirable genotypes and it comprises new land races, local selection, elite cultivars and exotic germplasm of crop plants. Genetic diversity is very much essential to meet the diverse goals in plant breeding such as for producing cultivars with increased yield (Joshi and Dhawan, 1966), wider adoption, desirable quality and pest resistance (Nevo *et al* ., 1982). Obtaining the high heterotic F_1 and broader spectrum of variability in succeeding segregating generations depends upon the using of more diverse parents (Arunachalm, 1981). According to Tomooka (1991), the evaluation of diversity is important to know the source of genes for particular trait within the available germplasm. So, to know the genetic diversity of the existing genotypes. Diversity analysis was done in the lines derived from Indian mustard background.

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Materials and Methods

The experimental material comprised forty-six genotypes of Indian mustard derived from different genetic background *viz., B. juncea (j), B.carinata (c)* and *B. napus (n)* were grown in Randomized Block Design with three replications at the research farm of Tirhut College of Agriculture, Dholi, Muzaffarpur (Rajendra Agricultural University-Pusa) Bihar during *rabi* season of 2010-11. Each genotype was sown in a plot consisting of three rows of 5m length in three replications with a spacing of 30cm x 10cm. Recommended package of practices were followed to raise a healthy crop. Data were recorded on five randomly selected competitive plants of each genotype in all the replications for Sixteen characters *viz.,* days to 50% flowering, days to maturity, plant height (cm), primary branches per plant, secondary branches per plant, number of siliqua per plant, siliqua length (cm), beak length (cm), number of seeds per siliqua, length of main raceme (cm), number of siliqua on main raceme, density of siliqua

on main raceme, 1000 seed weight (g), biological yield per plant (g), harvest index (%) and seed yield per plant (g) and their mean values were subjected to various statistical and biometrical analyses. Test of significance for each character were analyzed as per methodology advocated by (Panse and Sukhatme 1967). The genetic divergence was estimated by Mahalanobis (1936) D_2 statistics and elaborated by Murty and Arunachalam (1966). The grouping of the genotypes into clusters were done using Tochers method (Rao, 1952).

Results and Discussion

The analysis of variance was highly significant among the divergent genotypes for all the 16 traits under study, which revealed the presence of considerable variability among the genotypes. This suggested that adequate scope is available for selection of superior genotypes aimed at enhancing genetic yield potential of *Brassica juncea*. The forty-six genotypes were grouped into seven clusters using the closer genetic distance in such a way that the genotypes within the cluster had smaller D_2 values among themselves than those belonging to different clusters (Table 1). Pattern of distribution of genotypes among various clusters reflected the considerable genetic variability present in the genotypes under study. The maximum number of genotypes (nine) were comprised into cluster I and IV respectively, followed by eight in cluster III, seven in cluster VI, six in cluster VII and five genotypes in cluster V respectively. The minimum genotypes (two) comprised into cluster II. The grouping of genotypes indicated that geographical distribution need not necessarily be the indicator of genetic divergence reported by Verma and Sachan (2000) and Jeena and Sheikh (2003). Bansal *et al.* (1990) reported that clustering pattern was influenced by the pedigree of breeding lines. Similar results were found in case of *Brassica juncea* (Singh *et al*., 2010). The D_2 analysis showed intra and inter-cluster distance (Table 2). The inter-cluster distances in all cases were larger than the intra-cluster distance which indicated that wider diversity existed among the genotypes belonging to distantly spaced groupes. The maximum inter -cluster distance (41.55) existed between cluster V and VI followed between cluster V and VII (37.08) and between cluster II and VI (34.99), suggesting wide diversity between them and the genotypes in these cluster could be used as parents in hybridization programme for isolating transgressive segregates. The highest intra-cluster distance was observed in cluster I (17.45) and the lowest in cluster II (8.93) (Fig: 1).

Table 1. Grouping of *Brassica juncea* genotypes in different clusters

CLUSTER	No.of genotypes	Genotypes
I	9	RAURD-35, RAURD-7, RAURD-171, RAURD-273, RAURD-200, RAURD-170, RAURD-89, Pusa Bold, Rajendra Anukool
I	2	EC-401574, EC-399788
III	8	RAURD-153, RAURD-212, RAURD-156, RAURD-214, Rajendra Suflam, Kranti, Laxmi, RH-30
IV	9	RAURD-154, RAURD-242, RAURD-164, RAURD-185, RAURD-245, RAURD-221, RAURD-220, Varuna, Vardan
V	5	RAURD-166, RAURD-205, RAURD-241, RAURD-32, JD-6
VI	7	RAURD-168, RAURD-78, RAURD-195, RAURD-246, RAURD-172, RAURD-25, RAURD-34
VII	6	RAURD-190, RAURD-23, RAURD-63, RAURD-69, RAURD-193, Ragendra Rai Piccheti

Table 2. Average intra and inter-cluster distance D_2 and (D) values in *Brassica juncea.*

CLUSTER	1 Cluster	2 Cluster	3 Cluster	4 Cluster	5 Cluster	6 Cluster	7 Cluster
I	304.27	586.12	411.09	351.46	605.07	873.50	490.27
	(17.45)	(24.21)	(20.28)	(18.74)	(24.59)	(29.55)	(22.14)
II		79.71	583.48	625.40	667.85	1224.80	958.44
		(8.93)	(24.16)	(25.01)	(25.84)	(34.99)	(30.96)
III			257.91	281.07	535.53	749.27	576.33
			(16.06)	(16.76)	(23.14)	(27.37)	(24.01)
IV				144.78	691.84	512.26	355.42
				(12.03)	(26.30)	(22.63)	(18.85)
V					218.59	1726.18	1374.70
					(14.78)	(41.55)	(37.08)
VI						286.81	329.18
						(16.94)	(18.14)
VII							115.86
							(10.76)

The genotypes grouped into same cluster displayed the lowest degree of divergence from one another, and when crosses are made among the genotypes of the same cluster, no transgressive segregant is expected from such combinations. Therefore, hybridization programmes should always be formulated in such a way that the parents belonging to different clusters with maximum divergence could be utilized to get desirable transgressive segregants. The genotypes for

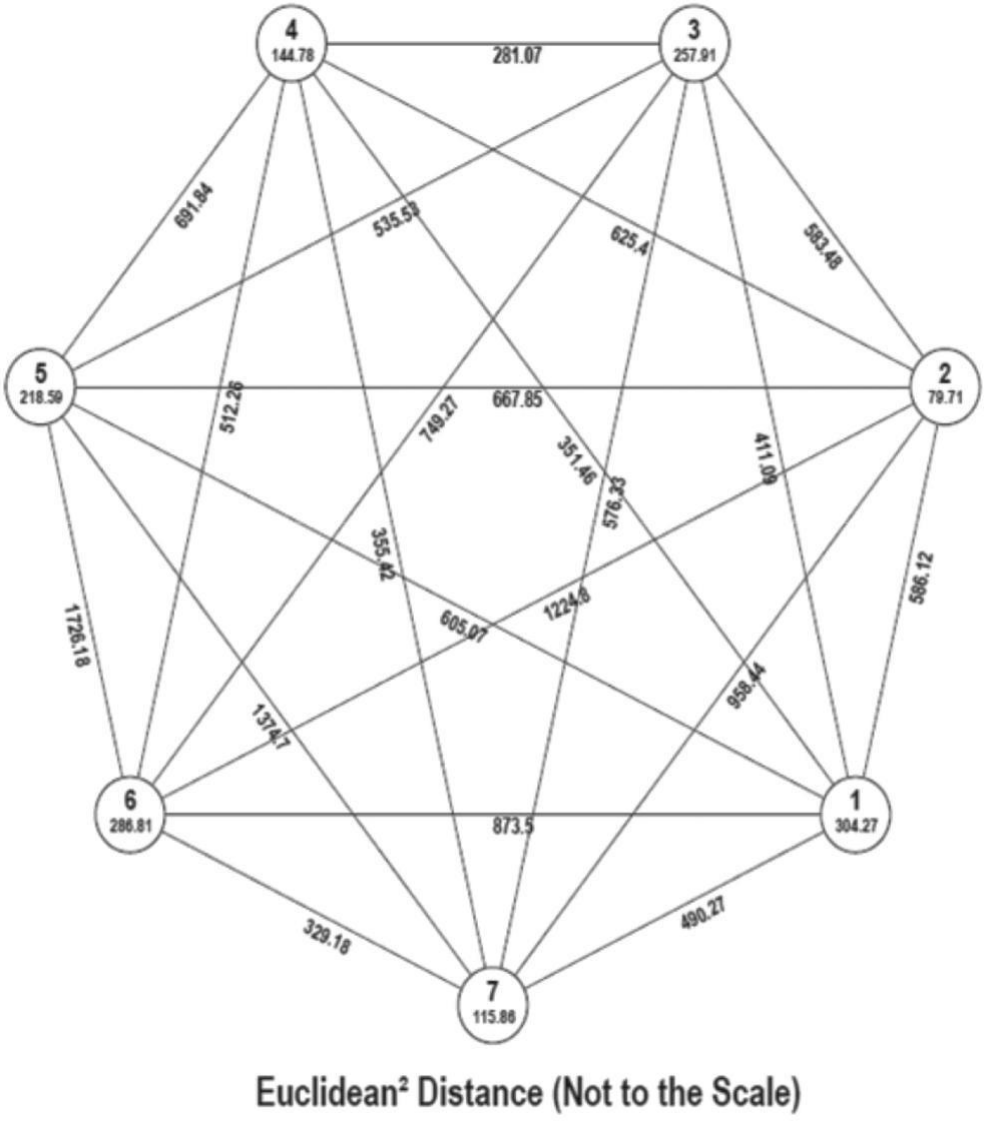

Fig. 1. Euclidean cluster distance diagram

hybridization may be chosen from widely separated clusters (fig. 2), as it is observed that there are several genotypes included in the crossing programme from widely separated clusters. (e.g. RAURD-166 *(j x j)*, RAURD-205 *(j x n)*, RAURD-241 *(j x j)*, RAURD-32 *(j x c)*, JD-6, RAURD-168 *(j x j)*, RAURD-78 *(j x j)*, RAURD-195 *(j x j)*, RAURD-246 *(j x j),* RAURD-172 *(j x j),* RAURD-25 *(j x c)* and RAURD-34 *(j x n).* Although, for final selection of the parents for breeding programme, the genotypes to be used may be selected almost without exception or its proven performance in the areas of intended use including quantitative characters and include in crossing with the existing varieties for their further improvement (Allard, 1960).

The variance for the cluster means were calculated for sixteen quantitative characters of mustard. Maximum variance for cluster mean was observed for number of siliqua per plant, length of main raceme, number of siliqua on main raceme, biological yield per plant, seed yield per plant, plant height, days to maturity and secondary branches per plant, which suggested that these characters were highly responsible for genetic divergence in the present materials. This indicated that the parents selected for hybridization on the basis of these characters were represented to be genetically diverse. Similar results were obtained by Verma and Sachan (2000), Goswami and Behal (2006), Kumar *et al*. (2007) and Yu-cheng *et al*. (2007).

The mean values (Table 3) of cluster V had the shortest plant height (187.40) along with earliness in days to 50% flowering (54.07) and maturity (114.87), cluster VI, had the highest mean values for primary branches per plant (5.27), secondary branches per plant (9.12), number of siliqua per plant (452.91), number of seeds per siliqua (13.21), biological yield per plant (60.05) and seed yield per plant (10.46), cluster VII had highest mean for length of main raceme (67.62), siliqua on main raceme (50.24) and seed yield per plant (11.10) and cluster II, had highest mean value for siliqua density(1.41).

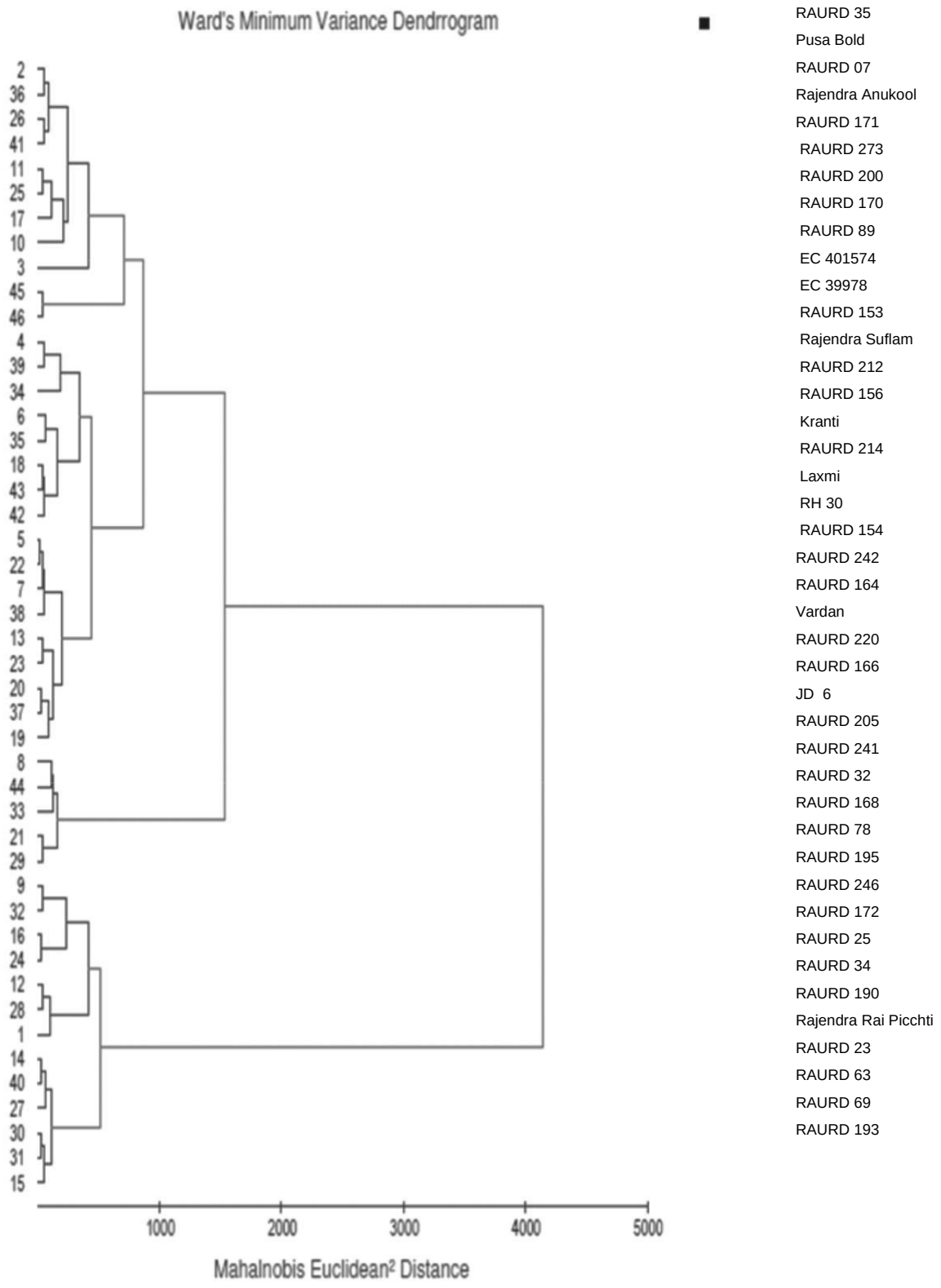

Fig. 2. Euclidean average linkage dendrogram

It is assumed that maximum amount of heterosis will be manifested in cross combinations involving the parents belonging to most divergent clusters. But for a plant breeder, the objective is not only high heterosis but also reduction of duration. The greater distance between two clusters, the wider genetic diversity between genotypes. Keeping this in view, the cluster VI, VII, V and II were among the most divergent clusters having high seed yield performance along with its contributing traits could

Table 3. Cluster mean of different characters of *Brassica juncea* genotypes.

Cluster	DF	DM	PH	PBP	SBP	SPP	SL	BL	SPS	LMR	SMR	SD	TW	BYP	SYP	HI
I	59.44	117.63	199.69	5.08	8.36	309.37	4.74	0.81	12.42	63.64	48.62	1.29	2.94	48.33	10.23	22.85
II	55.17	131.67	209.10	5.23	5.80	289.83	4.71	0.82	10.23	52.43	45.20	1.41	2.80	52.67	7.90	15.13
III	53.21	116.38	190.45	4.98	9.07	312.28	5.41	0.96	13.01	51.15	39.40	1.29	3.20	54.83	13.17	23.74
IV	58.93	117.26	190.34	4.57	8.06	342.42	5.46	1.02	13.66	51.57	38.98	1.33	3.16	48.26	9.28	19.32
V	54.07	114.87	187.40	5.16	7.97	204.59	4.96	0.85	12.84	49.90	36.18	1.39	2.77	45.93	9.89	21.72
VI	57.14	117.05	196.76	5.27	9.12	452.91	5.02	0.85	13.21	50.80	40.88	1.25	2.83	60.05	10.46	17.67
VII	59.06	117.61	200.70	4.74	9.12	417.88	5.14	0.70	13.03	67.62	50.24	1.35	3.12	58.22	11.10	19.79

DF= Days to flowering, DM =Days to maturity, PH= Plant height, PBP= Primary branches/ Plant, SBP= Secondary branches/ Plant, SPP= No. of Siliquas/ Plant, SL= Siliqua length, BL= Beak length, SPS= No. of seeds/ Siliqua, LMR=Length of main raceme, SMR= siliquas on main raceme, SD= Siliqua density, TW=test weight, BYP= Biological yield/ Plant, SYP= Seed yield/ plant, HI =Harvest index

be utilized in hybridization programme for getting desirable transgressive segregants and high heterotic response.

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