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Genetic diversity studies in Indian mustard [*Brassica juncea* (L.) Czern & Coss.] For yield and its component traits

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Abstract
Thirty-eight genotypes of Indian mustard [*Brassica juncea* (L.) Czern & Coss.] were evaluated to estimate the genetic diversity with respect to seed yield and yield components traits during *rabi* season, 2019. Mahalanobis D^2 statistics grouped 38 genotypes into seven different clusters with uneven distribution of the genotypes with 22 genotypes grouped in cluster I. Cluster II, cluster IV, cluster V, cluster VI and cluster VII had the null value for intra-cluster distance because of single genotype. D^2 analysis revealed that test weight followed by days to 50% flowering and days to physiological maturity contributed maximum towards total diversity. Inter-cluster distance was found maximum between cluster V and cluster VII which signifies that genotypes are highly divergent. Similarly, intra-cluster distance was also found maximum in cluster I followed by cluster III. Principal component analysis revealed four major components possessed more than one eigen-value indicated that the components containing the observable traits are the major cause for the genetic diversity. The PC scores revealed that number of siliquae per plant contributed maximum to the variation for PC 1, days to 50% flowering for PC 2, Plant height for PC 3 and test weight for PC 4. The above results indicated that these genotypes have maximum genetic diversity and useful for developing many segregants through crossing programme by using maximum diverse genotypes.

Keywords: Indian mustard, *brassica juncea*, diversity, principle component analysis, divergence

1. Introduction
Brassica juncea (AABB) (n=18) is an amphidiploid species which evolved from the cross between *Brassica rapa* (AA) (n=10) and *Brassica nigra* (BB) (n=8) and belongs to *Cruciferae* family, which is composed of 338 genera and 3700 species. The crop *Brassica juncea* has been identified by variety of its name *viz*., Brown mustard, Chinese mustard, Indian mustard, Leaf mustard, Oriental mustard and Vegetable mustard. Some other *Brassica* species belonging to this family are being cultivated in many parts of the world. They are Yellow sarson (*Brassica campestris* L. *var*. *yellow sarson*), Gobhi sarson (*Brassica napus*), brown mustard (*Brassica campestris* L. *var. brown sarson*), Toria (*Brassica campestris* L. *var*. *toria*), Tara mira or sonha (*Eruca sativa*) and Banarasi rai (*Brassica nigra*).
Indian mustard [*Brassica juncea* (L.) Czern & Coss.] is one of the most important oilseed crops of the country and stands second in both acreage and production of rapeseed and mustard in Asia. In India, among the oilseed crops, rapeseed and mustard stands second position in production after soybean. Among the various crops, oilseed crops are grown in 25.5 million hectares in India occupying 13.33 per cent area. Total production of oilseeds crop during 2018-19 was 32.26 million tons. Rapeseed and mustard occupied second position among the oilseed crops with an area and production of 6.23 million hectares and 9.34 million tons, respectively during 2018-19 (Anon, 2019) [1]. Prominent states growing mustard in India are Rajasthan, Uttar Pradesh, Haryana, Madhya Pradesh and Gujarat which contribute more than 80 per cent in area and production.
Oil and fats which constitute the principal content of this crop are not only used as food purposes but also serve as important material for the industries. In general, it consists of 35 to 45% oil, 17 to 25% protein, 8-10% fiber, 6-10% moisture and 10 to 12% extractable substances. Oil is predominantly triglyceride composed of fatty acid and consists of un-saponiable hydrocarbons like terpenes, sterols, tocopherols, glycolipids and phospholipids. Erucic acid and glucosinolate are the anti-nutritional components present in the oil.

The extent of diversity available in the crop decides the success of any crop improvement programme with manifested objectives. The genetic diversity among the parents is of paramount importance in selecting parental genotypes for crossing programmes. More diverse the parents, greater are the chances of developing heterotic hybrids and broad spectrum of variability in segregating generation. The prime concern of the breeders is to minimize the gap between potential yield and realized yield. This can be done by developing the lines which are well-adapted to diverse agro climatic condition. Mahalanobis statistics and Principal Component Analysis (PCA) helps to estimate the genetic distances for identifying dissimilar parents.

2. Materials and Methods

2.1 Experimental material, location and statistical analysis

Thirty-eight Indian mustard genotypes including two checks were evaluated following randomized block design with three replications during *rabi* 2019 at the experimental block, College of Agriculture, Bheemarayanagudi, University of Agricultural Sciences, Raichur. Each genotype was sown in three rows of 3 m length with row to row spacing of 0.45 m and plant to plant spacing of 0.10 m. All the recommended packages of practices were followed to raise a healthy crop. Observations on 10 quantity traits were recorded on five competitive plants randomly selected from each genotype in each replication.

The statistical data of sampled plants were averaged to get mean values. The character means for each replication were used for analysis. The Genetic divergence among the genotypes of Indian mustard was estimated by the multivariate technique as follow: Tocher's cluster analysis as described by Rao (1952) [17], using Mahalanobis D^2 statistics (1936) to measure the genetic distance. Principal component analysis (PCA) was performed for better understanding of correlation between seed yield and its contributing characters.

3. Result and Discussion

Genetic diversity can be estimated through biometrical procedures such as Mahalanobis D^2 statistic and is possible to choose genetically diverse parents. Therefore, the present study was undertaken to collect information on genetic divergence in the genot ypes and selection of suitable diverse parents for the utilization in future hybridization programme.

3.1 Clustering pattern of genotypes using D^2 statistics

The clustering using Tocher's method (Rao, 1952) [17] grouped all the 38 genotypes of Indian mustard into seven clusters and the results were confirmatory with the cluster pattern of the genotypes obtained through Dendrogram (Table 1 and Fig 1). The grouping of genotypes into different clusters indicated that the number of genotypes per cluster ranged from 1 to 22. Cluster I had the largest number of genotypes (22) followed by cluster III (11 genotypes). Remaining 5 clusters *i.e.*, cluster II, cluster IV, cluster V, cluster VI and cluster VII had only one genotype each. The clustering pattern revealed that presence of enough divergence to enable the formation of individual clusters. Earlier, different workers reported different numbers of clusters in their investigation. Naznin *et al*. (2015) [14] reported five clusters; (Kumar and Pandey, 2013) [16] reported seven clusters; Trivedi Shyam Dilip (2013) [22] and Sumit and Singh (2015) [21] reported 6 clusters.

3.2 Intra and inter-cluster distances

The inter-cluster D^2 values were maximum (160.25) between cluster V and VII, followed by cluster I and VII (148.61), cluster IV and VII (139.06), and cluster II and VII (104.55) whereas, the minimum inter-cluster distance was recorded between cluster IV and V (3.57) (Table 2). It is also known that higher the inter-cluster distance, more is the diversity among the genotypes included in those clusters. The average inter-cluster D^2 values were almost higher than the average intra-cluster D^2 values which showed considerable amount of diversity among the genotypes studied. In the present study inter cluster distance was more compared intra cluster distance indicating presence of considerable amount of genetic diversity among the genotypes studied. Genotypes belonging to clusters with maximum intra-cluster distance (Cluster I) are genetically more divergent and hybridization between divergent clusters is likely to produce wide variability with desirable sergeants. The results are in proximity with the findings of Trivedi Shyam Dilip (2013) [22], Lodhi *et al*. (2013) [11], Sumit and Singh (2015) [21] and Ravi *et al.* (2018) [18].

3.3 Cluster means

The cluster VII registered highest cluster mean values for siliquae per plant (1089.00) and seed yield per plant (12.32 g) indicating that the genotypes present in this cluster are high yielding. The cluster VI had the highest number of seeds per siliqua (13.00) and siliqua length (5.32). The cluster V had the highest number of primary branches per plant (5.00) and number of secondary branches per plant (17.00). Cluster II had the genotypes which were earliest in days to 50% flowering (44 days) and days to physiological maturity (82 days) indicating that the genotypes present in this cluster were early maturing and short duration. Cluster III and Cluster I had the genotypes with highest plant height (146.47 cm) and highest 1000-seed weight (4.21cm), respectively. Cluster IV had lower cluster mean values for all characters (Table 3). If the parents from cluster II and VII were involved in hybridization programme then the highest heterosis in respect of yield, earliness and siliquae per plant might be obtained. The results revealed the existence of differences in cluster means. Cluster I comprised of 22 genotypes which were characterized as having above average values for plant height, seeds per siliqua, siliqua length,1000-seed weight, seed yield per plant. Cluster II had only one genotype that indicated above average values for 1000-seed weight. Cluster III comprised of 11 genotypes which had above average values for plant height, seeds per siliqua, siliqua length and seed yield per plant. Cluster IV and V comprised of one genotype each which were characterized as having above average values for days to 50% flowering, days to physiological maturity, primary branches per plant, secondary branches per plant, seeds per siliqua, siliqua length and 1000-seed weight Cluster VI consisting of one genotype recorded above average values for days to 50% flowering, days to physiological maturity, primary branches per plant, secondary branches per plant, siliquae per plant, seeds per siliqua and siliqua length. Cluster VI comprised of one genotype and characterized by having above average values for days to 50% flowering, siliquae per plant and seed yield per plant. Similar findings were reported by Ravi *et al.* (2018) [18]. The average /mean of cluster mean (Table 3.) for all characters indicated that maximum variation was accounted by siliquae per plant (486.00) followed by plant height (122.06), days to

physiological maturity (91.00). The average/mean was lowest for 1000-seed weight (3.38). Similarly, Baviskar *et al.* (2015) [2] reported minimum and maximum average cluster mean values for different characters.

3.4 Contribution of individual characters towards genetic divergence: The contribution of various characters towards genetic divergence (Table 4) indicated that seven characters contributed maximum towards genetic divergence. The maximum per cent contribution was recorded by 1000-seed weight (58.46%) followed by days to 50% flowering (16.93%), days to physiological maturity (7.97%), siliquae per plant (3.70%), seeds per siliqua (3.56%), plant height (3.27%) and siliqua length (2.42%). Remaining traits *i.e.*, number of primary branches per plant, number of secondary branches per plant, seed yield per plant contributed very little or nearly no contribution towards genetic divergence. The present investigation revealed that the characters contributing more towards divergence were offering greater scope for selection or choice of superior genotype/parents for hybridization to exploit heterosis to maximum extent for that character. Choudhary and Joshi (2001) [4], Singh *et al.* (2007), Singh *et al.* (2010), Lodhi *et al.* (2013) [11], Pandey *et al.* (2013) [16], Dilip *et al.* (2016) [7] and Devi *et al.* (2017) [6] reported higher contribution of 1000-seed weight; Choudhary and Joshi (2001) [4], Zaman *et al.* (2010) [26], Chaurasia *et al.* (2014) [5] and Jahan *et al.* (2013) [8] reported maximum contribution of days to 50% flowering; Monalisa *et al.* (2005) [13], Zaman *et al.* (2010) [26], Chaurasia *et al.* (2014) [5], Verma *et al.*, (2016) [23] and Kumar *et al.* (2017) [9] reported maximum contribution of days to physiological maturity towards genetic divergence.

3.5 Principal component analysis

Principal Component Analysis (PCA) is the statistical procedure which is used for compression reduction and transformation of the data. Principal component analysis helps in identifying most relevant characters by explaining the total variation in the original set of variables with few of the components as possible and reduces the complexity or dimension of the problem. Evaluation of germplasm is useful not only in selection of core collection, but also its utilization in breeding programmes. The analysis of the results of present investigation revealed the cumulative variability of 81.58% (Table 5) by the first four major axis (possessing eigen-value >1). The eigen-value of the first principal component equalled 3.05 and represented 30.53% of total variability. The Principal component scores revealed that siliquae per plant contributed maximum (0.45) to the variation followed by days to 50% flowering (0.05) for PC 1. The second PC had eigen value 2.58 giving 25.77% variability. The maximum variability was contributed by days to 50% flowering (0.56) and days to physiological maturity (0.46). The PC 3 with the eigen-value 1.77 contributed 17.71% to total variability. The traits plant height (0.56) had the maximum contribution towards total variability followed by primary branches per plant (0.47). The PC 4 with the eigen- value 0.76 represented 7.57% total variability. The maximum contribution to the total variability was contributed by test weight (0.45) followed by seed yield per plant (0.22). Similarly, Yousuf *et al.* (2011) [24] in rape seed, Zada *et al.* (2013) [25] in Ethiopian mustard, Neeru *et al.* (2014) [15] and Bhattarai (2019) [3] reported contribution of different principal components towards variation in Indian mustard.

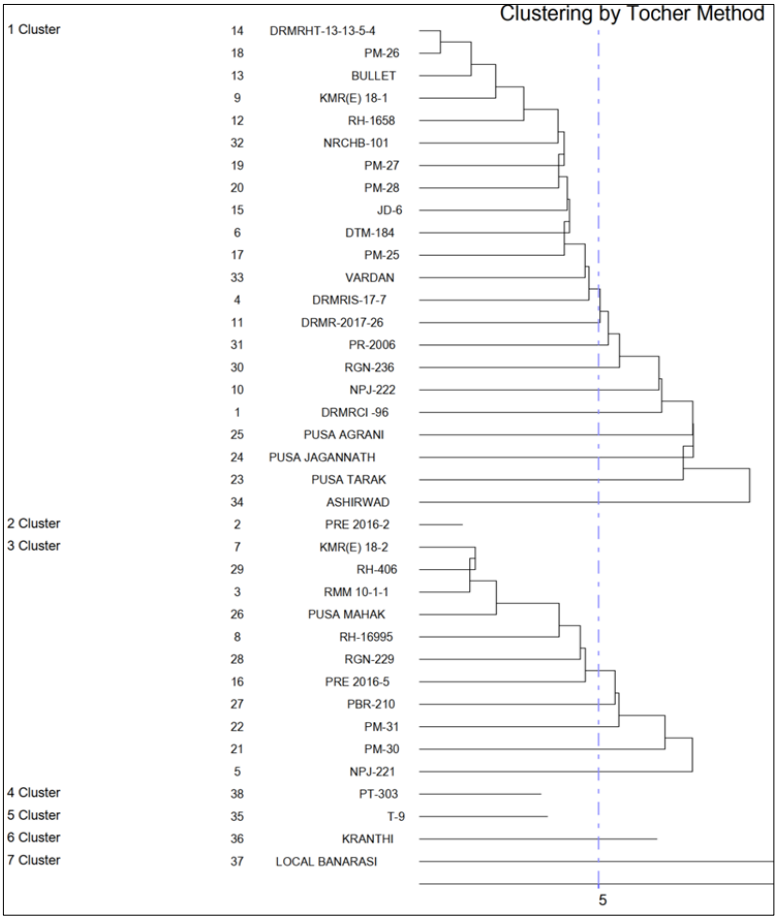

Fig 1: Dendrogram showing clustering of Indian mustard genotypes by Tocher's method

Table 1: Distribution of Indian mustard genotypes in the various clusters

Cluster	Number of genotypes	Name of genotypes
Cluster I	22	DRMRHT-13-13-5-4, PM-26, Bullet, KMR(E) 18-1, RH-1658, NRCHB-101, PM-27, PM-28, JD-6, DTM-184, PM-25, Vardan, DRMRIS-17-7, PR-2006, DRMR-2017-26, RGN-236, NPJ-222, DRMRCI-96, Pusa Agrani, Pusa Tarak, Pusa Jagannath, Ashirwad.
Cluster II	1	PRE 2016-2
Cluster III	11	KMR(E) 18-2, RH-406, RMM 10-1-1, Pusa s, RH-16995, RGN-229, PRE 2016-5, PBR-210, PM-31, PM-30, NPJ-221.
Cluster IV	1	PT-303
Cluster V	1	T-9
Cluster VI	1	Kranti
Cluster VII	1	Local Banarasi

Table 2: Average inter-cluster and intra-cluster distances in Indian mustard genotypes

Cluster distance							
Cluster	**Cluster I**	**Cluster II**	**Cluster III**	**Cluster IV**	**Cluster V**	**Cluster VI**	**Cluster VII**
Cluster I	6.41	11.41	15.65	10.49	10.68	27.86	148.61
Cluster II		0	7.24	16.07	21.06	24.07	104.55
Cluster III			6.17	17.19	21.94	16.45	95.47
Cluster IV				0	3.57	13.27	139.06
Cluster V					0	19.68	160.25
Cluster VI						0	89.8
Cluster VII							0

Table 3: Cluster mean performance for the different characters in Indian mustard genotypes

Cluster Mean										
Character Cluster	**Days to 50% flowering**	**Days to physiological maturity**	**Plant height**	**Primary branches per plant**	**Secondary branches per plant**	**Siliquae per plant**	**Seeds per siliqua**	**Siliqua length**	**1000-seed weight**	**Seed yield per plant**
Cluster I	50.00	90.00	134.98	04.00	09.00	342.00	11.00	4.74	4.21	11.64
Cluster II	44.00	82.00	121.67	03.00	08.00	300.00	11.00	4.28	3.51	08.68
Cluster III	48.00	89.00	146.47	03.00	09.00	379.00	12.00	4.60	3.25	12.1
Cluster IV	59.00	92.50	110.62	04.00	16.00	376.00	11.00	5.14	3.95	08.58
Cluster V	56.00	98.00	117.67	05.00	17.00	247.00	12.00	5.22	4.11	07.42
Cluster VI	60.00	95.00	114.67	05.00	15.00	672.00	13.00	5.32	3.20	05.61
Cluster VII	53.00	89.00	108.33	03.00	08.00	1089.00	07.00	1.40	1.40	12.32
Average	53.00	91.00	122.06	04.00	12.00	486.00	11.00	4.39	3.38	09.48

Table 4: Contribution of different characters towards total diversity in Indian mustard genotypes

Sl. No.	Source	Contribution (%)
1	Days to 50% flowering	16.93
2	Days to physiological maturity	7.97
3	Plant height	3.27
4	Primary branches per plant	1.71
5	Secondary branches per plant	1.14
6	Siliquae per plant	3.70
7	Seeds per siliqua	3.56
8	Siliqua length	2.42
9	1000-seed weight	58.46
10	Seed yield per plant	0.85

Table 5: Principal component analysis (PCA) for seed yield and its component traits in Indian mustard genotypes

Principal component	PC1	PC2	PC3	PC4
Eigen value (Root)	3.05	2.58	1.77	0.76
Per cent variability	30.53	25.77	17.71	7.57
Cumulative variability	30.53	56.30	74.01	81.58
PCA SCORES				
Days to 50% flowering	0.05	0.56	0.03	0.12
Days to physiological maturity	-0.08	0.46	0.41	0.07
Plant height	-0.07	-0.29	0.56	-0.13
Primary branches per plant	-0.06	0.36	0.47	0.16
Secondary branches per plant	-0.05	0.37	-0.51	0.10
Siliquae per plant	0.45	0.04	0.15	-0.05
Seeds per siliqua	-0.33	0.20	-0.02	-0.81
Siliqua length	-0.52	0.05	-0.03	-0.12
1000-seed weight	-0.48	0.01	-0.05	0.45
Seed yield per plant	-0.40	-0.28	0.10	0.22

4. References

1. Anonymous. Agriculture statistics at a glance, Ministry of Agriculture, New Delhi, India, 2019.
2. Baviskar S, Patil S, Patil S, Charjan S. Diversity Analysis in *Brassica* Species for Selection of genotypes for drought tolerance breeding based on biometrical traits. Special Issue 2015, 17-23.
3. Bhattarai M. "Studies on Genetic Components of Variation, Correlation, Path Coefficient and Divergence in Indian Mustard [*Brassica juncea* (L.) Czern and Coss]" M. Sc. (Agri.) Thesis, Banaras Hindu University, Varanasi, 2019.
4. Chaudhary BR, Joshi P. Genetic diversity in advanced derivatives of *Brassica* interspecific hybrid. Euphytica 2001;121(1):1-7.
5. Chaurasia RK, Bhajan R, Chougule GR. Genetic divergence for seed yield and component traits in Indian mustard [*Brassica juncea* (L.) Czern & Coss.]. AGRES – An International e-Journal 2014;3(3):260-269.
6. Devi TR, Devi ND, Vivekananda Y, Sharma PR. Genetic diversity analysis in Indian mustard [*Brassica juncea* (L.) Czern & Coss.] genotypes using agro-morphological parameters. Electron. J Pl. Breed 2017;8(3):749-753.
7. Dilip TS, Singh SK, Kumar R. Genetic divergence in Indian mustard. Techno fame 2016;5(2):7-10.
8. Jahan N, Bhuiyan SR, Talukder MZA, Alam MA, Parvin M. Genetic diversity analysis in *Brassica rapa* using morphological characters. Bangladesh J Agril. Res 2013;38(1):11-18.
9. Kumar BSR, Nair B. Assessment of genetic diversity and genetic potential of recombinant inbred lines of *Brassica juncea* (L.). J Soils Crops 2017;27(1):106-109.
10. Kumar B, Pandey A, Singh SK. Genetic diversity for agro-morphological and oil quality traits in Indian mustard [*Brassica juncea* (L.) Czern & Coss.] *Bioscan*, 2013;8(3):771-775.
11. Lodhi B, Thakral NK, Singh D, Avtar R, Bahadur R. Genetic diversity analysis in Indian mustard (*Brassica juncea*). J Oilseed Bra 2013;1(2):57-60.
12. Mahalanobis PC. Mahalanobis distance. Pro. Nat. Ins. Sci. Ind 1936;49(2):234-256.
13. Monalisa P, Singh NB, Singh NG, Laishram JM., Genetic divergence and combining ability in relation to heterosis in Indian mustard [*Brassica juncea* (L.) Czern & Coss.] for seed yield, its attributes and oil yield. Indian J Genet 2005;65(4):302-304.
14. Naznin LS, Kawochar MA, Sultana S, Zeba N, Bhuiyan SR. Genetic divergence in *Brassica rapa.* Bangladesh J. Agril Res 2015;40(3):421-433.
15. Neeru NK, Avtar R, Singh A. Evaluation and classification of Indian mustard (*Brassica juncea* L.) genotypes using principal component analysis. J Oilseed Bra 2014;6:167-174.
16. Pandey R, Kumar B, Kumar M. Genetic divergence for quantitative traits in Indian mustard (*Brassica juncea* L.). Am-Eurasian J Agric. Environ. Sci 2013;13(3):348-351.
17. Rao CR. Advanced statistical methods in biometric research. J. Wiley Sons Inc. New York 1952, 390.
18. Ravi N, Dubey N, Avinashe H, Tamatam D. Assessment of genetic diversity in mustard genotypes. Pl. Arch 2018;18(2):2091-2096.
19. Singh D, Arya RK, Chandra N, Niwas R, Salisbury P. Genetic diversity studies in relation to seed yield and its component traits in Indian mustard (*Brassica juncea* L.). J Oilseed Bra 2010;1(1):19-22.
20. Singh V, Bhajan R, Kumar K. Genetic diversity in Indian mustard (*Brassica juncea* L. Czern & Coss.). Progress. Agric 2007;7(1):105-109.
21. Sumit Singh K. D^2 analysis in Indian mustard (*Brassica juncea*) M. Sc. (Agri.) Thesis, Sardar Vallabhbhai Patel University of Agriculture and Technology, Meerut, 2015.
22. Trivedi SD. D^2 analysis in Indian Mustard (*Brassica juncea*) *M. Sc.* (*Agri.) Thesis*, Sardar Vallabhbhai Patel University of Agriculture and Technology, Meerut, 2013.
23. Verma S, Singh VV, Meena ML, Rathore SS, Ram B, Singh S et al., Genetic analysis of morphological and physiological traits in Indian mustard (*Brassica juncea* L.). SABRAO J. Breed. Genet 2016, 48(4).
24. Yousuf M, Ajmal SU, Munir M, Ghafoor A. Genetic diversity analysis for agro-morphological and seed quality traits in rapeseed (*Brassica campestris* L.). Pakistan J Bot 2011;43:1195-1203.
25. Zada M, Zakir N, Rabbani M, Ashiq, Shinwari KZ. Assessment of genetic diversity in Ethiopian mustard (*Brassica carinata* A. Braun) germplasm using multivariate techniques. Pakistan J Bot 2013;45:583-59.
26. Zaman MA, Khatun MT, Ullah MZ, Moniruzzamn M, Rahman MZ. Multivariate analysis of divergence in advanced lines of mustard (*Brassica spp*.). Bangladesh J Pl. Breed. Genet 2010;23(2):29-34.