Journal of Pharmacognosy and Phytochemistry

Available online at www.phytojournal.com

E-ISSN: 2278-4136
P-ISSN: 2349-8234
JPP 2018; SP1: 2093-2096

Veena Kumari Tudu
Department of Genetics & Plant Breeding, Birsa Agricultural University, Ranchi, Jharkhand, India

Arun Kumar
Department of Genetics & Plant Breeding, Birsa Agricultural University, Ranchi, Jharkhand, India

Varsha Rani
Department of Crop Physiology, Birsa Agricultural University, Ranchi, Jharkhand, India

Correspondence
Veena Kumari Tudu
Department of Genetics & Plant Breeding, Birsa Agricultural University, Ranchi, Jharkhand, India

Assessment of genetic divergence in Indian mustard (*Brassica juncea* L. Czern & Coss.) based on yield attributing traits

Veena Kumari Tudu, Arun Kumar and Varsha Rani

Abstract
Genetic divergence was assessed in thirty genotypes of Indian mustard [*Brassica juncea* (L.) Czern & Coss.] using D^2 statistics based on quantitative characters. Genotypes were grouped into seven clusters. Cluster I was the largest group accommodating twelve (12) genotypes followed by cluster III and cluster IV with seven genotypes in each, while clusters II, V, VI and VII accommodated only one genotype in each cluster. Cluster group means of characters revealed that genotypes accommodated under cluster IV have most of the desirable characters *viz.*, number of primary branches per plant and secondary branches per plant, plant height, number of siliqua per plant, 1000 seed weight and average seed yield per plant. Days to 50% flowering contributed maximum towards divergence followed by number of secondary branches per plant, siliqua length, number of seeds per siliqua and 1000 seed weight.

Keywords: Indian mustard, Genetic diversity, Phenotypic trait, Distance, Clusters, D^2 statistic

Introduction
Indian mustard [Brassica juncea (L) Czern & Coss.], the crop considered for present study is one of the most important oilseed crops of the country occupying considerably larger acreage among the *Brassica* crops. These crops are being cultivated mostly in Rajasthan, Uttar Pradesh, Madhya Pradesh, Haryana, Punjab and West Bengal on an area of 6.51 million ha with a total production of 7.67 million tonnes, and with an average yield of 1179 kg/ha (Anonymous, 2011). In Jharkhand, Indian Mustard ranks first among the different oilseeds with an acreage of 2.5lakh ha, but the average productivity ranged only between7-8q/ha. (Rabi Karmshala Report, Dte of Agriculture, GOJ, 2013). It is cultivated in *rabi* season mainly in Northwest India, and contributes nearly 27 per cent to edible oil pool of the country (Singh *et al*., 2010). To meet the projected demand of 13.4mt of rapeseed-mustard by the end of 2020 in our country, there is a need to increase the productivity through varietal improvement (DRMR vision -2050) which is primarily dependent on the genetic diversity present in the available germplasms of any crop.

Genetic divergence study is essential to develop cultivars with increased yields, wider adaptation, desirable qualities, and pest and disease resistance. Hence, it is essential for a plant breeder to have the knowledge of genetic divergence and the information of characters used for discrimination among the population for successful breeding programme. Morphological characterization is the easiest way for the assessment of genetic diversity. Estimation of degree of divergence between biological population and computation of relevant contribution of different components to the total divergence is done by D^2 statistic (Mahalanobis, 1936). It is being widely utilized to assemblage and assessment of divergence to know the spectrum of diversity in any crop (Lodhi *et al.* 2013). Inclusion of more diverse parents in hybridization programme increases the chances of obtaining maximum heterosis and gives a broad spectrum of variability in segregating generations. Keeping this back ground in view, the present study was undertaken to analyse genetic diversity among 30 elite genotypes of Indian mustard and to identify divergent parents for program, which would provide superior segregates on hybridization.

Materials and Methods
Present study was carried out with 30 genotypes of Indian mustard grown in Randomized Block Design with three replications during *Rabi* 2012-13 at the experimental area of Department of Genetics & Plant Breeding, Birsa Agricultural University, Ranchi, Jharkhand. Each genotype was sown in three rows per plot per replication in a plot size of 0.9m x 4m with spacing of 30cm maintained between rows and 10cm between plant. Recommended agronomic

practices were followed to raise the crop.

Data were recorded on five representative plants selected randomly from each genotype from each of the three replications for 10 quantitative traits *viz*., days to 50% flowering, days to maturity, plant height, number of primary branches, number of secondary branches, number of siliqua, siliquae length, number of seeds per siliquae, 1000 seed weight and seed yield on per plant basis. However, data on days to 50% flowering and days to maturity were recorded on plot basis. Data were subjected to multivariate analysis of genetic divergence using Mahalanobis D^2 statistic (Mahalanobis, 1936). Grouping of entries was done by following Tocher's method (Rao, 1952).

Results and discussion

The analysis of variance revealed highly significant differences among genotypes for most of the yield attributing traits. All the thirty genotypes including three checks were grouped into seven clusters based on Mahalanobis D^2 value as shown in table 1 and figure 1 as per Tocher's method. Out of seven clusters, cluster I was the largest one in size which accommodated twelve (12) genotypes followed by cluster III and cluster IV with seven genotypes in each cluster. Clusters II, V, VI and VII had accommodated only one genotype in each cluster. The clustering pattern revealed that the distribution of the genotypes was random and independent. This could be due to genetic drift, selection pressure and environmental effect which create morphological diversity rather than actual genetic distances. Genotypes developed at same place have been grouped into different clusters while the genotypes originated at different regions got accommodated into same cluster. The grouping of genotypes indicated that geographical distribution need not necessarily be the indicator of genetic divergence as reported by Verma and Sachan (2000), Jeena and Sheikh (2003). This indicated that genotypes originated from same place exhibits maximum diversity which may be due to the use of diverse parent in their pedigree. On the other hand, some genotypes of quite different pedigree though originated from same place have minimum diversity, which may be due to unidirectional selection pressure, which were genetically closer to their parents. It was also observed that genetic diversity is not associated with the geographical diversity but with the inherent genetic variability. The study of Pandey *et al*. (2013), Singh *et al*. (2013), Mahto (2012) and Lodhi *et al*. (2013) also indicated no relationship between genetic divergence and geographical diversity.

Table 1: Composition of genotypes in different clusters based on yield components

Sl. No.	Cluster	No. of Genotype	Name of genotypes
1.	I	12	BAUM-08-17, BAUM-08-56, BAUM-08-45, Pusa Agarni, LAXMI, Vardan, Pusa Bold, BAUM-08-34, BAUM-08-15, BAUM-08-16, BIO 902, RH-30
2.	II	1	PBR 91
3.	III	7	BAUM- 08-24, BAUM- 08-26, BAUM- 08-48, BAUM- 08-47, BAUM- 08- 57, BAUM- 08-35, BAUM- 08- 46,
4.	IV	7	BAUM- 08-67, RL 1359, BAUM- 08-37, BAUM- 08- 25, BAUM- 08-23, BAUM- 08-14, BAUM- 08-12
5.	V	1	Shivani
6.	VI	1	BAU-M-08-36
7.	VII	1	BAUM- 08-27

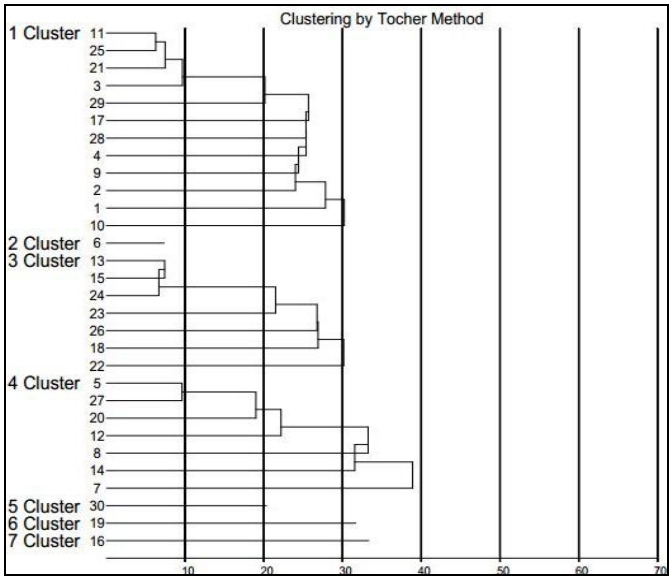

Fig 1: Dendrogram showing clustering of genotypes based on yield attributing traits.

Intra and Inter-Cluster distance have been presented in Table 2. Maximum differences among the genotypes within the same cluster was registered by cluster IV (6.11) followed by cluster III (5.43) and cluster I (5.27). Rest of the clusters had zero intra cluster distance as they consist of only one genotype. The inter cluster distance which measure the diversity of genotypes accommodated in different clusters varied from 4.78 to 16.08. The magnitude of inter- cluster distances was greater than intra-cluster distances which suggests the presence of considerable diversity among the clusters. The cluster IV and VI recorded highest inter cluster distance (16.08) followed by cluster III and VI (13.40) and cluster IV and VII (12.30). Considerable amount of inter cluster distances were also registered between cluster II and VI (12.20); cluster IV and V (10.95); cluster I and VI (10.06); cluster V and VI (9.07); cluster III and VII (8.70) and cluster I and IV (8.39). The crosses involving genotypes belonging to maximum divergent clusters *i.e*., cluster IV and VI would be expected to manifest maximum heterosis and also wide genetic variability. Ghaderi *et al.*, (1984) also had suggested higher heterosis from the crosses between genetically distant parents. The minimum inter cluster distance was found between cluster II and III (4.78). Large inter- cluster distance signifies that genotypes grouped in these clusters were different from the genotypes of other clusters for one or more characters, which made them so divergent from other.

Table 2: Average Intra and Inter-Cluster Distance based on yield and yield components

Sl. No	Cluster	I	II	III	IV	V	VI	VII
1.	**I**	5.27	6.04	6.87	8.39	7.04	10.06	7.39
2.	**II**		0.00	4.78	8.08	8.07	12.20	7.31
3.	**III**			5.43	7.43	8.27	13.40	8.70
4.	**IV**				6.11	10.95	16.08	12.30
5.	**V**					0	9.07	8.10
6.	**VI**						0	7.34
7.	**VII**							0

The mean performances of 10 characters in seven clusters are shown in Table 3. Genotypes accommodated under cluster IV have most of the desirable characters *viz.*, number of primary branches per plant and secondary branches per plant, plant height, number of siliqua per plant, 1000 seed weight and average seed yield per plant. The genotypes accommodated under cluster VI were found early to flower as well as early in maturity. Siliqua length and seeds per siliquae was maximum in cluster V. Thus, crosses between the genotypes of cluster IV with that of cluster V would exhibit high heterosis and is also likely to produce new recombinants with desired traits in Indian mustard. This shows that cluster comprising only one cultivar with specific traits could also be used in hybridization programme for exploiting hybrid vigour as reported by Saini and Kaicker (1987).

Table 3: Intra -Cluster group means of different yield contributing characters

Sl. No.	Cluster	Days to 50% flowering	Days to maturity	Plant height (cm)	No. of primary branches/ plant	No. of secondary branches/ plant	No. of siliqua /plant	Siliquae length (cm)	No. of seeds/ siliquae	1000 seed weight (g)	Yield/ plant (g)
1.	I	49.50	110.47	132.32	4.31	6.29	159.56	3.72	12.62	4.28	6.33
2.	II	54.33	113.67	130.93	3.87	5.33	151.20	4.07	13.07	4.40	6.27
3.	III	53.24	113.05	138.80	4.36	6.41	165.74	4.10	13.84	4.13	6.65
4.	IV	52.76	112.62	142.75	5.37	8.05	179.56	3.88	13.69	4.51	7.17
5.	V	46.67	108.00	140.77	4.60	5.97	151.27	4.15	14.40	4.34	6.12
6.	VI	43.00	106.33	123.53	3.67	4.77	135.90	3.71	10.67	3.59	4.79
7.	VII	50.33	109.00	146.00	3.73	4.53	148.33	3.78	11.33	3.45	5.51

The relative contribution of each character towards total diversity has been presented in Table 4. Days to 50% flowering (28.28%) contributed maximum towards divergence followed by number of secondary branches per plant (19.77%), siliquae length (13.79%), number of seeds per siliqua and 1000 seed weight. While the contribution from days to maturity (5.06%), yield per plant (3.68%), number of primary branches per plant (2.99%) and number of siliqua per plant (1.84%) were low in magnitude. The plant height contributed least (0.46%) to the total divergence. Similarly Gangapur *et al*. (2010) also indicated that number of secondary branches per plant attributed maximum per cent towards divergence. In contrast Shathi *et al*. (2012) indicated that days to 50% flowering, 1000 seed weight and yield per plant contributed lowest to the total divergence. The characters having great contribution to total divergence were responsible for genetic diversity in the present experimental materials. This indicated that the parents selected for hybridization on the basis of these characters would result into development of transgressive recombinants with high Heterosis. Similar results were obtained by Verma and Sachan (2000); Goswami and Sheikh (2003); Patel *et al*. (2006).

Table 4: Contribution of different yield components to total divergence

Sl No.	Characters	Contribution %
1.	Days to 50% flowering	28.28
2.	Days to maturity	5.06
3.	Plant height (cm)	0.46
4.	No. of primary branches/plant	2.99
5.	No. of secondary branches/plant	19.77
6.	No. of siliqua /plant	1.84
7.	Siliquae length (cm)	13.79
8.	No. of seeds/siliqua	13.56
9.	1000 seed weight (g)	10.57
10.	Yield/ plant (g)	3.68

Conclusion

In the present study, days to 50% flowering, days to maturity, secondary branches per plant, number of siliqua per plant, siliqua length, number of seeds per siliqua, 1000 seed weight are among the phenotypic traits contributing towards seed yield and can be used as indices for future breeding programme.

References

1. Anonymous. Directorate of Economics and Statistics, Department of Agriculture and Cooperation. 4th Advance Estimates released as on 19.07.2011.
2. Anonymous. Rabi Karmshala Report, Dte of Agriculture, Govt. of Jharkhand, 2013.
3. Anonymous. In: DRMR Vision. Directorate of Rapeseed-Mustard Research, Bharatpur, 2015. http://www.drmr.res.in/publication/DRMR%20Rajasthan-(Vision2050)-Final.pdf
4. Gangapur DR, Prakash BG, Hiremath CP. Genetic Diversity Analysis of Indian Mustard (*Brassica juncea* L.). Electronic Journal of Plant Breeding. 2010; 1(4):407-413. http://citeseerx.ist.psu.edu/viewdoc/download?doi=10.1.1.177.6930&rep=rep1&type=pdf
5. Ghaderi A, Shishegar M, Regai A, Ehdaie B. Multivariate analysis of genetic diversity for yield and its components in mungbean. J American Soc. Hort. Sci. 1984; 104:728-732.
6. Goswami PK, Sheikh FA. Genetic divergence analysis in Indian mustard. Ann. Agril. Res 2003; 27:187-190.
7. Jeena AS, Sheikh FA. Genetic divergence analysis in gobhi sarson (*Brassica napus* L.). Oilseed Res. 2003; 20:210-212.
8. Lodhi B, Thakral NK, Singh D, Avtar R, Bahadur R. Genetic diversity analysis in Indian mustard (*Brassica juncea*). J Oilseed Brassica. 2013; 4(2):57-60. http://srmr.org.in/upload/journal/full/13965171061.pdf
9. Mahalanobis PC. On the generalized distance in statistics. Proc. Natl. Sc. India. 1936; 2:49-55.
10. Mahto JL. Genetic divergence in Indian mustard (*Brassica juncea* L. Czernj & Cosson). In: Cruciferae Newsletter. 2012; 31:10-12. http://www.brassica.info/info/publications/cn/CruciferaeNewsletter_vol31_2012.pdf
11. Pandey R, Kumar B, Kumar M. Genetic Divergence for Quantitative Traits in Indian mustard (*Brassica juncea* L. Czern & Coss). American-Eurasian J Agric. & Environ. Sci. 2013; 13(3):348-351.
12. Patel JM, Patel KM, Patel CJ, Prajapati KP. Genetic variability of divergence in Indian mustard. Indian J

Genet 2006; 66:49-50.
13. Rao CR. In: Advanced Statistical methods in Biometrical Research. John wiley and sons, New York, 1952.
14. Saini HC, Kaicker US. Genetic diversity in Opium Poppy. Indian J Genet. 1987; 47:291-296.
15. Shathi DA, Arifuzzaman M, Biswas BK, Hasanuzzaman M, Azad AK. Genetic divergence in mustard (*Brassica* spp. L). African J Plant Sc. 2012; 6(8):239-243. http://www.academicjournals.org/journal/AJPS/article-full-text-pdf/12ED9D311921
16. Singh A, Avtar R, Singh D, Sangwan O, Balyan P. Genetic variability, character association and path analysis for seed yield and component traits under two environments in Indian mustard. J Oilseed Brassica. 2013; 4(1):43-48 http://srmr.org.in/upload/journal/full/139651686707.pdf
17. 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.) Czern & Coss.]. J Oilseeds Brassica. 2010; 1:19-22.
18. Verma SK, Sachan JN. Genetic divergence in Indian mustard (*Brassica juncea* (L.) Czern & Coss.). Crop Research Hisar. 2000; 19(2):271-276 https://www.cabdirect.org/cabdirect/abstract/20001612148