Journal of Pharmacognosy and Phytochemistry
Available online at www.phytojournal.com

E-ISSN: 2278-4136
P-ISSN: 2349-8234
www.phytojournal.com
JPP 2020; 9(2): 2398-2401
Received: 06-01-2020
Accepted: 10-02-2020

Tabassum
Department of Genetics and Plant Breeding, College of Agriculture, Govind Ballabh Pant University of Agriculture and Technology, Pantnagar, Uttarakhand, India

AS Jeena
Department of Genetics and Plant Breeding, College of Agriculture, Govind Ballabh Pant University of Agriculture and Technology, Pantnagar, Uttarakhand, India

Arvind Singh Negi
School of Agriculture, Graphic Era Hill University, Dehradun, Uttarakhand, India

Deepak Kaujalagi
Department of Agriculture, Karnataka, India

Corresponding Author:
Tabassum
Department of Genetics and Plant Breeding, College of Agriculture, Govind Ballabh Pant University of Agriculture and Technology, Pantnagar, Uttarakhand, India

Genetic diversity analysis of *Brassica rapa* germplasm collected from Uttarakhand hills

Tabassum, AS Jeena, Arvind Singh Negi and Deepak Kaujalagi

Abstract
Diversity among thirty *Brassica rapa* germplasm accessions was analysed through Mahalanobis's D^2 statistic. The accessions were evaluated in RBD with two replications along with three checks to identify genetically diverse accessions for the improvement of yield and other traits in *Brassica rapa.* Data was recorded on 8 characters *viz.*, plant height, shoot length, siliqua length, beak length, number of siliqua, number of seeds per siliqua, siliqua density and grain yield per plant. All the germplasm accessions were grouped into nine clusters using Tocher's method. Cluster I was largest containing 20 accessions followed by cluster II and III each with three germplasm accessions and cluster IV having two accessions. Highest intra-cluster distance was recorded for cluster IV followed by cluster III, cluster II and cluster I. Maximum inter cluster distance was observed between cluster VI and IV followed by cluster VII and V and cluster VIII and IX. Therefore, probability of obtaining useful segregants and promising recombinants is expected to be more by selecting genotypes from these clusters.

Keywords: *Brassica rapa*, diversity, Mahalanobis's D^2 statistic, clustering

Introduction
The genus *Brassica* belongs to the family cruciferae and consists of some economically important species useful for various purposes. The genus contains over 3200 species having highly diverse morphology. Among them rapeseed-mustard is one of the most important oilseed crop of India. Many species are used as a source of oil and some are grown as forage crop. Out of the total rapeseed-mustard production of India, Indian mustard accounts for 75-80% and contributes 24.2% of the total edible oil pool of the country (Devi *et al.*, 2017) [4]. Many species are used as a source of oil and some are grown as forage crop. The oil is primarily used as edible oil and also as solvent of vitamin A, D, E and K. The oil cake contains proteins of high biological value with appreciable quantities of calcium and phosphorus and used as a very good animal feed as well as fertilizer for various crops (Khatun *et al.*, 2010) [9]. The primary centre of origin for *Brassica campestris* (now *Brassica rapa*) is near Himalayan region and the secondary centre of origin is the European-Mediterranean area and Asia (Downey and Robbelen, 1989) [6]. *Brassica rapa* L. commonly known as field or turnip mustard. The seeds of *Brassica rapa* L. contain 42% oil and 25% protein (Khaleque, 1985) [8] and also provides raw material for different industrial purposes such as hair oils, soaps, textile auxiliaries, wall paints, and different kinds of pharmaceutical products. For increasing the production of *Brassica rapa*, there is a need to expand the area under cultivation and per unit area production. But the scope of area increase under cultivation is limited therefore one way to increase production is to enhance production per unit area. Moreover the crop should fit in the cropping pattern. Therefore, high yielding and short duration *Brassica rapa* varieties should be developed to fit into the existing cropping pattern (Naznin *et al.*, 2015) [12]. According to a report of National Mission on Oilseeds and Oil Palm (NMOOP), the production of all oilseeds has increased from 24.35 million tonnes in 2004-05 to 26.68 million tonnes in2014-15. The oilseeds yield which was 885 kg per hectare in 2004-05 increased to 1037kg per hectare in 2014-15 (Annual report 2015-16). Globally, India is third largest producer of edible oils and among them *Brassica* accounts for almost 5% gross national product and 10% of the value of agricultural products. India is the third largest producer of repeseed and mustard after China and Canada. In India the production of all *Brassica* species was 6.31 million tonnes from an area of 5.79 million hectares with average productivity of 1089 kg/ha (Anonymous, 2015) [2]. Major rapeseed and mustard growing states are Rajasthan, Uttar Pradesh, Madhya Pradesh, Haryana, Assam, Gujarat, Punjab and West Bengal.

In any breeding programme, the existence of genetic variability is of great value. For the development of superior improved cultivar, utilization of existing germplasm, the sum total of existing variability in a crop species and its related species is important to fulfil different kinds

of needs of the present day and future. Existing genetic variability for important characters plays an important role in plant breeding as selection will be effective. Diverse lines when used in hybridization programme generally display a great heterosis and throws transgressive segregants in future generations. Genetic diversity can be estimated through biometrical procedures such as Mahalanobis's D^2which helps the breeder in identification of parents for specific breeding objectives. Multivariate analysis is a useful tool in quantifying the degree of divergence between biological population at genotypic level and to assess relative contributions of different components to the total divergence both at intra- and inter-cluster levels (Zahan *et al.*, 2008). Therefore the present study was carried out to revealgenetic divergence in the collected germplasm accessions and for the identification of suitable divergent parents for future hybridization program.

Materials and methods

Thirty *Brassica* germplasm accessions collected from different districts of Uttarakhand hills were used in this experiment. These thirty germplasm along with three check varieties *viz.*, Kranti, PPS-1 and PT-303 were grown in Randomized Block Design (RBD) with two replications during *Rabi* 2017-18 at the experimental field of Pantnagar Centre of Plant Genetic Resources, Govind Ballabh Pant University of Agriculture and Technology, Pantnagar. Each accession was sown in a single row of 3m in each replication with row to row spacing of 30 cm. Data were recorded on 5 plants from each line for eight quantitative characters *viz.*, plant height (cm), shoot length (cm), siliqua length (cm), beak length (cm), number of siliqua, number of seeds per siliqua, siliqua density and seed yield per plant (g). Genetic distance among the test entries was measured by using Mahalanobis's (1936) D^2 statistic. The clusters of genotypes was formed by using Tocher's method as described by Rao (1952) [13] while the intra and inter cluster distance was calculated using formula given by Singh and Choudhary (1985) [14].

Results and Discussion

Thirty-three *Brassica rapa* genotypes were classified into nine clusters (Table 1) after comparing D^2 values in such a way that within cluster genotypes had smaller genetic distance as compare to genotypes in other clusters. Clustering pattern reflected that considerable amount of genetic variability was present among the germplasm accessions under study. Cluster I waslargest containing 20accessions followed by cluster II and III each with three germplasm accessions and cluster IV having two accessions. All remaining cluster contained one accession each. Similarly, Doddabhimappa *et al.*, (2010) [5] got seven clusters while assessing 46 Indian mustard germplasm accessions and Naznin *et al.*, (2015) [12] obtained five clusters by using thirty-three genotypes in their experiment. Cluster I contained germplasm accessions GP-2017-775, GP-2017-769, PT-303, GP-2016-1, GP-2016-4, GP-2016-3, GP-2016-2, GP-2016-7, GP-2016-115, GP-2016-46, GP-2016-5, GP-2016-6,GP-2016-14, GP-2017-404, GP-2017-422, GP-2016-254, GP-2017-52, GP-2016-253 and GP-2016-252 while cluster II and III had GP-2017-806, GP-2017-773, GP-2017-776 and GP-2017-771, GP-2017-772, GP-2016-15 germplasm accessions, respectively. Cluster IV composed of GP-2017-392 and GP-2017-774 whereas cluster V had GP-2017-770, cluster VI GP-2016-47, cluster VII PPS-1, cluster VIII and IX had Kranti and GP-2016-52, respectively. The clustering pattern of theses germplasm accessions revealed that the germplasm collected from the same region can also be grouped into different clusters indicated that geographic diversity was not related to genetic diversity of the materials.

Cluster mean values for different characters are represented in Table 2. Results showed that Cluster II had the highest mean values for shoot length (74.41) while cluster IV had highest mean for number of siliqua (34.65) and siliqua density (1.61). Similarly, cluster V possessed highest cluster mean value for siliqua length (5.99) and beak length (1.60). Cluster VI had highest mean value for number of seeds per siliqua (37.00) and cluster VIII exhibited highest mean value for plant height (166.00 cm) andseed yield per plant (70.60 g). If parents from cluster IV and V are involved in hybridization program then the highest heterosis with respect tonumber of siliqua, siliqua density and siliqua length might be obtained. Similarly if crossing involves parents from cluster VIII and IV then there is a good chance of obtaining higher heterosis for seed yield per plant. Jahan *et al.*, 2013 [7] reported that cluster III had highest value of cluster mean for plant height, number of siliqua per plant and seed yield per plant while for number of seeds per siliqua cluster II had highest cluster mean. Devi *et al.*, 2017 [4] obtained highest cluster mean values for plant height, shoot length, siliqua length, number of seeds per siliqua and seed yield per plant. Percent contribution of all the traits to total divergence presented in Table 3. It was found that maximum contribution towards divergence was attributed by seed yield per plant (19.13) followed by number of siliqua (14.77), siliqua length (13.64), plant height (13.26), shoots length (11.94), number of seeds per siliqua (11.74), beak length (11.18) and siliqua density (4.36).

The intra and inter cluster distances among the different clusters of *Brassica* accessions are presented in Table 4. The intra cluster distance was ranged from 2.69 (cluster I) to 3.59 (cluster IV). Highest intra cluster distance was observed for cluster IV (3.59) followed by cluster III (3.22), cluster II (2.96) and cluster I (2.69). Similar results are also obtained by Bind *et al.*, 2015 [3]. Maximum inter cluster distance was observed between cluster VI and IV (6.00), followed by between cluster VII and V (5.54), cluster VIII and IX (5.52), cluster IV and V (5.49), Cluster II and Cluster IV (5.45) and between cluster IV and IX (5.28).Cluster IV showed highest within cluster distance i.e., diversity within the cluster leave the scope of inter crossing among genotypes of this cluster. Earlier, similar confirmatory results had also been obtained by Khatun *et al.*, 2010 [9] and Jahan *et al.*, 2013 [7] in *Brassica rapa* and also by Lodhi *et al.*, 2013 [10] in *Brassica juncea*. It was observed that the inter-cluster distances were higher as compare to intra cluster distances. These results indicated that greater amount of genetic diversity was present among germplasm accessions of different clusters and therefore can serve as a selection criteria for the selection of genetically diverse parents from the germplasm accessions. Maximum diversity between clusters based on inter-cluster distance was recorded for cluster VI and IV followed by cluster VII and V and cluster VIII and IX. Therefore, genotypes from these clusters could be used in hybridization programme by crossing genotypes of one cluster with genotypes of others. This could lead to maximum heterosis and useful transgressive segregants in future generations.

Conclusion

All the accessions were classified into nine clusters based on eight quantitative traits. Present results revealed that cluster IV, VI and VIII exhibit larger mean values for yield and yield contributing traits.The highest intra cluster distance was

observed for cluster IV and maximum inter-cluster distance was recorded for cluster VI and IV. Presence of greater amount of genetic diversity was revealed from present investigation among germplasm accessions of different clusters. Therefore these results can serve as selection criteria for the selection of genetically diverse germplasm accessions for further hybridization programme. The results of the present study will also help to improve the understanding of diversity within a germplasm collectionso that these germplasm could be usedto fulfil various requirements of present day and future breeding programmes.

Table 1: Clustering pattern of 33 *Brassica rapa* genotypes on the basis of D^2 values

Cluster No.	No. of genotypes	Name of germplasm lines
I	20	GP-2017-775, GP-2017-769, PT-303, GP-2016-1, GP-2016-4, GP-2016-3, GP-2016-2, GP-2016-7, GP-2016-115, GP-2016-46, GP-2016-5, GP-2016-6,GP-2016-14, GP-2017-404, GP-2017-422,GP-2016-254,GP-2017-52,GP-2016-253,GP-2016-252
II	3	GP-2017-806, GP-2017-773, GP-2017-776
III	3	GP-2017-771, GP-2017-772, GP-2016-15
IV	2	GP-2017-392, GP-2017-774
V	1	GP-2017-770
VI	1	GP-2016-47
VII	1	PPS-1
VIII	1	Kranti
IX	1	GP-2016-52

Table 2: Cluster means for different characters in *Brassica rapa*

Cluster	Plant height (cm)	Shoot Length (cm)	Siliqua length (cm)	Beak length (cm)	No of siliqua	No of seeds/ siliqua	Siliqua density (cm)	Seed yield/plant (g)
I	129.15	47.94	5.60	1.57	29.95	16.63	0.63	37.29
II	131.44	74.41	4.74	1.36	33.30	14.33	0.45	53.92
III	120.13	50.18	3.82	0.61	32.37	17.17	0.65	25.40
IV	155.45	21.60	2.96	0.93	34.65	12.25	1.61	17.80
V	141.90	52.88	5.99	1.60	17.00	21.50	0.32	37.45
VI	104.80	48.00	5.25	1.42	32.90	37.00	0.69	51.25
VII	98.50	37.00	5.66	1.27	33.40	18.00	0.91	61.95
VIII	166.00	62.50	4.16	0.61	32.00	17.50	0.51	70.60
IX	79.30	42.50	5.34	1.44	17.50	21.50	0.64	24.00

Table 3: Relative contribution of different characters towards genetic divergence in *Brassica rapa*

S. No.	Character	Contribution %
1	Plant height	13.26
2	Shoot length	11.94
3	Siliqua length	13.64
4	Beak length	11.18
5	No of siliqua	14.77
6	No of seeds/siliqua	11.74
7	Siliqua density	4.36
8	Seed yield per plant	19.13

Table 4: Intra and Inter cluster distance between clusters of *Brassica rapa* based on D values as revealed by Mahalanobis D^2 statistic

	I	II	III	IV	V	VI	VII	VIII	IX
I	2.69	3.97	3.83	4.76	3.56	4.56	3.77	3.86	4.20
II		2.96	4.62	5.45	4.65	5.17	5.06	4.00	4.83
III			3.22	5.22	4.70	5.07	4.63	3.79	4.69
IV				3.59	5.49	6.00	5.21	5.16	5.28
V					0	4.53	5.54	4.06	3.73
VI						0	4.85	4.62	4.79
VII							0	4.53	4.55
VIII								0	5.52
IX									0

Acknowledgement
Authors are very much thankful to the National Mission on Himalayan Studies (NMHS), who provided financial support to conduct the research programme and to obtain its significant findings.

References

1. Annual Report. Department of Agriculture, Cooperation and Farmer's Welfare, Ministry of Agriculture and Farmer's Welfare, Government of India, Krishi Bhawan, New Delhi, 110001, 2015-16, 41-42.
2. Anonymous. Agricultural statistics at a glance. Government of India Ministry of Agriculture & Farmers welfare Department of Agriculture, Cooperation and farmers welfare Directorate of Economics and Statistics, 2015, 120-122.
3. Bind D, Singh SK, Dwivedi VK. Assessment of genetic diversity and other genetic parameters in Indian mustard

[Brassica Juncea (L.) Czern & Coss.]. Indian J Agric. Res. 2015; 49(6):554-557.
4. Devi R, Devi ND, Vivekananda Y, Sharma R. Genetic diversity analysis in Indian mustard (*Brassica juncea* L. Czern and Coss) genotypes using agro-morphological parameters. Electronic Journal of Plant Breeding. 2017; 8(3):749-753.
5. Doddabhimappa R, Gangapur B, Prakash G, Channayya PH. Genetic Diversity Analysis of Indian Mustard (*Brassica juncea* L.). Electronic Journal of Plant Breeding. 2010; 1(4):407-413.
6. Downey RK, Roebbelen G. Brassica species, In: G. Rocbbelen, R. K. Downey, A. Ashri (eds). Oil crops of the world. Mc Graw Hill Pub. Co, 1989, 339-362.
7. 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.
8. Khaleque MA. A Guide Book on Production of Oilcrops in Bangladesh. DAE and FAO/UNDP project BGD/79/034, strengthening the Agricultural Extension service Khamarbari, Framgate, Dhaka, 1985, 3.
9. Khatun H, Rasul MG, Saikat MMH, Haque MM. Genetic Diversity In Brassica rapa L. Bangladesh J Pl. Breed. Genet. 2010; 23(1):31-37.
10. Lodhi B, Thakral NK, Singh D, Avtar R, Bahadur R. Genetic diversity analysis in Indian mustard (*Brassica juncea*). Journal of Oilseed Brassica. 2013; 4(2):57-60.
11. Mahalonobis PC. A statistical study at Chinese head measurement. J Asiat. Soc. Bengal. 1936; 25:301-377.
12. Naznin LS, Kawochar MA, Sultana S, Zeba N, Bhuiyan SR. Genetic Divergence In *Brassica rapa*. Bangladesh J Agril. Res. 2015; 40(3):421-433.
13. Rao CR. Advanced statistical methods in biometrics research. John Willey and Sons, Inc., New York, 1952.
14. Singh RK, Chaudhary BD. Biometrical methods in quantative genetic analysis. Kalayni Publishers. New Delhi, India, 1985.