Electronic Journal of Plant Breeding, 6(2): 619-624 (June 2015)
ISSN 0975-928X

Research Note

Genetic divergence studies in okra [Abelmoschus esculentus (L.) Moench.] genotypes

Tara Chand Balai, I. B. Maurya, Shankar Verma[1] and Narendra Kumar[2]*
Department of Horticulture, Rajasthan College of Agriculture,
Maharana Pratap University of Agriculture and Technology, Udaipur - 313 001, Rajasthan, India.
[1]Department of Horticulture, College of Agriculture, Junagadh Agricultural University, Junagadh-362 001, Gujarat, India.
[2]Directorate of Groundnut Research, Ivnagar road, P.B.No. 5, Junagadh- 362 001, Gujarat, India.
Email: narendrapb09@gmail.com

(Received:22 Dec 2014; Accepted:06 Feb 2015)

Abstract
Genetic divergence of 27 okra genotypes was studied using Mahalanobis D^2 statistics revealed that considerable genetic diversity among genotypes in okra. Twenty seven diverse genotypes were grouped into four clusters with the highest of 20 genotypes in the cluster I, 5 in the cluster II and one each genotype in the cluster III and IV. Intra and inter cluster D^2 values ranged from 32.27 to 38.64 and 45.17 to 120.09 respectively. It showed that inter cluster distance was higher than the intra cluster distance indicating wide genetic diversity among the genotypes of different groups. The cluster means of 15 characters among four clusters indicated that high genetic variability range present for yield per plant (155.2-334.1), average weight of edible pod (19.6-38.8), number of seeds per pod (58.7-93.6) and plant height (109.3-133.3). The relative contribution of studied characters indicated that weight of 100-seeds (1082), followed by number of epicalyx per pod (1950), average weight of edible pods (2272), number of seeds per pods (2278) and plant height (2465) contributed highest towards the genetic divergence. Genotype having these characters in different cluster could be used in breeding programme to develop high yielding cultivars in okra.

Keywords
Okra, genetic diversity, Mahalanobis D^2 statistics, cluster

Okra [*Abelmoschus esculentus* (L) Moench.] is an important vegetable crop widely grown in the tropical and subtropical regions of the world (Tindall, 1983). Cultivated okra has significant variations in the chromosome numbers but most frequent observed chromosome number is 2n = 130 (Joshi and Hardas, 1956) and it belongs to the family Malvaceae. The centre of origin of okra remains unclear, but their centre of genetic diversity includes West Africa, India and Southern Asia (Hamon and Van Sloten, 1998). Okra is an annual and day neutral plant cultivated in all seasons for its delicious tender pods in one and other different parts of the country. Fresh okra fruit contains 35 calories, 89.6 g water, 6.4 g carbohydrate, 1.9 g protein, 0.2 g fat, 1.2 g fiber and minerals per 100 g of edible portion (Gopalan *et al*., 2007). Okra is said to be very useful against genito-urinary disorders, spermatorrhoea and chronic dysentery (Nadkarni, 1927). Okra is an often cross pollinated crop, heterosis is being exploited in form of development of hybrids. Hence, genetic divergence is an important tool while selecting the parents for hybrid breeding. Divergence analysis is more authentic and powerful tool for systematic identification of the diverse genotypes for hybridization purposes (Mahalanobis, 1936).

To develop high yielding varieties, genetic diversity is an important tool to select genetically diverse parents with high yield and wider adaptability in breeding programme. Progress of any breeding programmes depends to a great extent on the availability of genetic variability for desirable traits in genotypes (Kumar *et al*., 2013, Balai *et al*., 2014). Genetic diversity helps the breeders in deciding the most appropriate breeding method to increase the genetic potentialities as well as to surpass the yield barrier (Langade *et al*., 2013). Use of genetically diverse parents in recombination breeding supposed to give maximum heterosis in F_1's and also getting broad spectrum of variability for quantitative traits in segregating generations to select desirable recombinant. Therefore, genetic diversity is prerequisites for any successful breeding programme.

Now considerable efforts are being made to improve yield and other attributes like pod yield, number of pods per plant, pod weight, pod length and pod width. The weight of the pod and the number of pods per plant and pod length has been consistently identified as very important components of pod yield (Akinyele and Osekita 2006, Dakahe *et al*., 2007, Adeniji, and Aremu 2007, Nasit *et al*., 2009, Adiger *et al*., 2011). Number of internodes, days to flowering, days to maturity and plant height are also most important quantitative characters influencing yield of okra (Dakahe *et al*., 2007, Nasit *et al*., 2009, Kumar *et*

al., 2012). Several workers have emphasized the importance of genetic divergence for the selection of desirable parents for breeding programme in okra (Ariyo 1990, Bindu *et al*., 1994, Bisht *et al*., 1995, Hazra *et al*., 2002, Dhaduk *et al*., 2004, Akotkar *et al*., 2010, Reddy *et al*., 2012, Ab. Mazid *et al*., 2013). Balai *et al*. (2014) also reported that plant height, length of pod, average weight of edible pod and number of seeds per pod are very important characters in okra and these should be used as selection criteria for improvement in fruit yield.

To improve yield and its component traits in okra, the information on genetic divergence of different genotypes for various quantitative traits is necessary. Therefore keeping this in view, the present study was undertaken to investigate genetic divergence in 27 genotypes of okra to identify the diverse genotypes to be used in breeding programme.

The experimental material comprised of 27 genotypes of okra. These genotypes were grown in randomized block design with three replications at the Horticulture Farm, Rajasthan College of Agriculture, Udaipur. Each genotype was grown in two row of 4.5 m length with spacing of 60 × 45 cm. The recommended agronomic package of practices and plant protection measures were followed to raise a healthy crop. The observations were recorded on five randomly selected plants in each replication for each genotype on 15 characters *viz*., plant height (cm), number of branches per plant, number of leaves per plant, length of internode (cm), number of pods per plant, length of pod (cm) average weight of edible pod (g), number of seeds per pod, weight of 100-seed (g), days to first flower , days to first harvest, yield per plant (g), number of ridges, dry matter content (%) and number of epicalyx per pod. The data were statistical analyzed as per Mahalanobis D2 analysis (Mahalanobis, 1936) to measure of genetic divergence among 27 genotypes. The grouping of 27 genotypes into different clusters was done by following K.D. Tocher's methods (Rao, 1952).

Wilk's criteria were used to test the aggregate effects of all the characters. It showed that significant differences among the genotypes for all the characters. Genetic divergence among 27 genotypes for 15 characters was made by using Mahalanobis D^2 analysis as per Rao (1952). Based on Mahalanobis D^2 analysis, 27 genotypes were grouped into four clusters on the basis of observed smaller D^2 values among genotypes within a cluster than those belonging to different cluster following Tocher's methods (Table 1). Out of the four clusters, Cluster I contains maximum number of 20 genotypes followed by cluster II with five genotypes and cluster III and cluster IV with one genotype in each. It is indicating that Cluster III and cluster IV are more diverse from resting other clusters. The genotypes in these clusters are more genetically diverse and may be used as potential parents for breeding programmes to develop high yielding cultivars. It was also observed that geographical distance between the genotypes had no relation with the genetic divergence as the genotypes from same source had fallen into different clusters as well as the same cluster contained genotypes from different sources. It indicats that clustering pattern of okra genotypes did not follow their geographic distribution. These findings are in agreement to earlier reports of Bindu *et al*. (1994), Bisht *et al.* (1995), Mishra *et al.* (1996), Dhaduk *et al.* (2004), Akotkar *et al*. (2010), Reddy *et al*. (2012), Ab.Mazid *et al*. (2013) in okra.

Average intra and inter cluster D^2 values presented in Table 2, indicating nature of genetic divergence at intra and inter cluster levels, respectively. In general, inter cluster distance was much more than intra cluster distances. This suggesting that within cluster genotypes have same genetic constitution *ie*., homogeneous are less divergent than those occurred in a different cluster. The information on the degree of genetic divergence would be helpful in selecting parents for hybridization programme.

The D^2 values of intra cluster and inter cluster ranged from 32.27 to 38.64 and 45.17 to 120.09 respectively. Maximum intra cluster distance was observed in cluster I (38.64) followed by cluster II (32.27) while inter cluster distance was maximum in between cluster II and cluster IV (120.09) followed by cluster III and cluster IV (109.82) and cluster I and cluster IV (103.95). Higher intra and inter cluster distance indicating that high degree of genetic divergence within cluster and between clusters respectively. Therefore, genotypes belonging to these inter clusters may be used in hybridization programme to obtain transgressive segregants with broad spectrum of genetic variability for yield and other component traits to isolate high yielding genotypes in okra. These results are in accordance with the finding of Vahab *et al*. (1994), Bisht *et al.* (1995), Mishra *et al.* (1996), Dhaduk *et al.* (2004), Akotkar *et al*. (2010), Reddy *et al*. (2012), Ab. Mazid *et al*. (2013).

Since high yield and earliness is a prime objective in any breeding programme, cluster those having high means for fruit yield per plant, earliness and its components traits need to be considered for selection of genotypes for breeding programme. The cluster means for 15 characters (Table 3) indicated that considerable variability present in characters among the four clusters. The data

showed that maximum cluster mean variation was observed for edible pod yield per plant (155.2 g in cluster II to 334.1 g in cluster IV), average weight of edible pod (19.6 g in cluster II to 38.8 g in cluster IV), number of seeds per pod (58.7 in cluster II to 93.6 in cluster IV) and plant height (109.3 cm in cluster II to 141.6 cm in cluster III).

It was observed that cluster IV genotype has highest desirable cluster mean for seven characters followed by cluster III for four characters, two characters in each cluster II and cluster III and cluster I and cluster II. Cluster IV recorded highest mean for number of leaves per plant (17), number of pods per plant (8.6), length of pod (19.6 cm), average weight of edible pod (38.8 g), number of seeds per pod (93.6), edible pod yield per plant (334.1 g) and number of ridges (9.2). Cluster III recorded highest desirable cluster mean for plant height (141.6 cm), length of internode (9.9 cm), dry matter content (10%) and number of epicalyx per pod (10). Cluster I and cluster II has lowest desirable cluster mean for days to first flower (49.4) and days to first harvest (54.5).

Cluster II and cluster III has highest desirable cluster mean for number of branches per plant (1.6) and weight of 100-seed (6.1 g). It indicates cluster IV followed by cluster III genotype has high mean than other cluster genotypes for different characters. Therefore, divergent genotypes should be selected from these clusters for different characters while selecting parents for hybridization programme.

The results on relative contribution of different character presented in Table 4 showed that weight of 100-seeds (1082) followed by number of epicalyx per pod (1950), average weight of edible pods (2272), number of seeds per pods (2278) and plant height (2465) contributed maximum towards the genetic divergence. It suggested that these characters are highly genetic variable and these characters should be considered while selecting parents for hybridization programmes under studied genotypes. John *et al*. (1992), Abdul *et al*. (1994), Kumari and Chaudhury (2006), Akotkar *et al*. (2010) and Ab. Mazid *et al*. (2013) also observed contribution of plant height, fruit length and weight of fruits towards the genetic divergence.

In the present study, it is concluded that genotypes for hybridization programme should be selected between cluster II and cluster IV followed by cluster III and cluster IV and cluster I and cluster IV. These clusters contain wide genetic diversity among the genotypes for different traits under studied. Therefore, selection of these divergent genotypes and use in crossing programme would give greater chances of obtaining high heterosis and high genetic variability for quantitative and other desirable traits in segregating generations to develop high yielding cultivars in okra.

References

Ab. Mazid, S. M. S. A. M., Mohrir, M. N and Jadhav, R. S. 2013. Genetic divergence in okra (*Abelmoschus esculentus* L. Moench.). *Electron. J. Plant Breed.*, **4** (3): 1258-1260.

Abdul, M. V., Nirmala Devi, S., Mathew, S. K. and Prabhakaran, P. V. 1994. Genetic divergence in okra. *Hort. J*. **7**: 117-120.

Adeniji, O. T. and Aremu, C. O. 2007. Interrelationship among characters and path analysis for pod yield components in West African Okra [*Abelmoschus caillei* (A. Chev) Stevels]. *Journal of Agronomy*. **6** (1): 162-166.

Adiger, S., Shanthkumar, G., Gangashetty, P. I. and Salimath, P. M. 2011. Association studies in okra [*Abelmoschus esculentus* (L.) Moench]. *Electron. J. Plant Breed.*, **2** (4): 568-573.

Akinyele, B. O. and Osekita, O. S. 2006. Correlation and path coefficient analyses of seed yield attributes in okra [*Abelmoschus esculentus* (L.) Moench]. *Afr. J. Biotechnol*. **5** (14): 1330-1336.

Akotkar, P. K., De, D. K. and Pal, A. K. 2010. Genetic Variability and Diversity in Okra [*Abelmoschus esculentus* (L.) Moench]. *Electron. J. Plant Breed.*, **1** (4): 393-398.

Ariyo, O. J. 1990. Measurement and classification of genetic diversity in okra [*Abelmoschus esculentus* (L.) Moench]. *Annals of Appl. Biol.*, **116** (2): 335-341.

Balai, T. C., Maurya, I. B., Verma, S. and Kumar, N. 2014. Correlation and path analysis in genotypes of okra [*Abelmoschus esculentus* (L.) Moench]. *The Bioscan*, (Supplement on Genetics and Plant Breeding). **9** (2): 799-802.

Bindu, K. K., Manju, P. and Sarashwathy, P. 1994. Genetic divergence in bhindi [*Abelmoschus esculentus* (L.) Moench]. *J. Trop. Agric*., **32** (2): 115-117.

Bisht, I. S., Mahajan, R. K. and Rana, R. S. 1995. Genetic diversity in South Asian okra [*Abelmoschus esculentus* (L.) Moench] germplasm collection. *Annals of Appl. Biol*., **126** (3): 539-550.

Dakahe, K., Patil, H. E. and Patil S. D. 2007. Genetic variability and correlation studies in Okra [*Abelmoschus esculentus* (L) Moench]. *The Asian J. Horti.*, 2(1): 201-203.

Dhaduk, L. K., Mehta, D. R. and Patel, K. D. 2004. Genetic diversity in okra. *The Orissa J. Horti.*, **32** (1): 70-72.

Gopalan, C., Rama Sastri, B. V. and Balasubramanian, S. 2007. Nutritive Value of Indian Foods, published by National Institute of Nutrition (NIN), ICMR.

Hazra, P., Basu, D. and Sahu, F. K. 2002. Genetic divergence in okra. *Indian J. Horti*., **59** (4): 406-410.

John, M. S., George, W. and Mc Collum, J. P. 1992. Producing Vegetable Crops. (4th edn.) International Book Distribution Co. Lucknow.

Joshi, A. B. and Hardas, M. W. 1956. Alloploid Nature of Okra, *Abelmoschus esculentus* (L.) Monech. *Nature*. **178**: 1190.

Kumar, N., Joshi, V. N. and Dagla, M. C. 2013. Estimation of components of genetic variance in maize (*Zea mays* L.). *The Bioscan*. **8** (2): 503-507.

Kumar, P., Singh, K. V., Singh, B., Kumar, S. and Singh, O. 2012. Correlation and path analysis studies in okra [*Abelmoschus escutentus* (L) Moench]. *Prog. Agric.* **12** (2): 354 -359.

Kumari, M. and Chaudhury, D. N. 2006. Genetic divergence in okra [*Abelmoschus esculentus* (L.) Moench]. *Veg. Sci*., **33** (1): 71-72.

Langade, D. M., Ram, C. N., Vishwakarma, D. N. and Sharma, A. 2013. Evaluation of genetic divergence in berseem (*Trifolium alexandrinum* L.) germplasms. *The Bioscan*. **8** (3): 767-770, 2013.

Mahalanobis, P.C. 1936. On the generalized distance in statistics. *Proc. Nat. Inst. Sci*., India, **2**: 49-55.

Mishra, S. N., Dash, S. N. and Mishra, D. 1996. Multivariate analysis of genetic divergence in okra (*Hibiscus esculentus*). *Indian J. Agric. Sci.*, **66** (8): 502-503.

Nandkarni, K. M. 1927. Indian Meteria Medica. Nadkarni and Co Bombay.

Nasit, M. B., Dhaduk L. K., Vachhani J. H. and Savaliya, J. J. 2009. Correlation and path analysis studies in okra [*Abelmoschus esculentus* (L.) Moench]. *The Asian J. Horti*., **4** (2): 394-397.

Rao, C. R. 1952. Advanced statistical methods in Biometric Research. John Wiley and Sons Inc. New York.

Reddy, M. T., Haribabu, K., Ganesh, M., Reddy, K. C. and Begum H. 2012. Genetic divergence analysis of indigenous and exotic collections of okra (*Abelmoschus esculentus* (L.) Moench). *J. Agric. Technol.*, **8** (2): 611-623.

Tindall, H. D. 1983. Vegetables in the tropics. Macmillan Press Ltd., London and Basingstoke. pp: 25-328.

Vahab, M. A., Devi, S.N., Mathew, S. K. and Prabhakaran, P. V. 1994. Genetic divergence in okra [*Abelmoschus esculentus* (L.) Moench]. *Hort. J.*, **7** (2): 117-120.

Table 1. Grouping of 27 genotypes of okra into different clusters

SN	Cluster	Number of genotypes	Genotypes
1	I	20	Parbhani Kranti, Punjab Padmani, BO-2, NB-55, Arka Abhay, Arka Anamika, Varsha Uphar, Nirmal-303, HRB-52, Ankur-40, PF-11, VRO-5, Pusa Sawani. Heritage Green, Swati-10, AOL-95-32, Selection-2, Nirmal-101, Swati-25 and CO-3
2	II	5	Sagun, Selection-51, Harbhajan, JO(2000k)-l and HRB-9-2
3	III	1	VRO-6
4	IV	1	IIVR-10

Table 2. Average intra (diagonal and bold) and inter (above diagonal) cluster distance (D^2 values) in 27 genotypes of okra

Cluster	I	II	III	IV
I	**1493.66 (38.64)**	3197.97 (56.55)	3359.93 (57.96)	10805.68 (103.95)
II		**1041.91 (32.27)**	2041.21 (45.17)	14422.86 (120.09)
III			**0.00**	12062.04 (109.82)
IV				**0.00**

Data in parenthesis are $\sqrt{D^2}$ values.

Table 3. Cluster mean of 27 genotypes for 15 characters in okra

Character	Clusters with their number of genotypes			
	I	II	III	IV
	20	5	1	1
Plant height (cm)	119.0	109.3	141.6	133.3
Number of branches/plant	1.3	1.6	1.6	1.5
Number of leaves/plant	15.3	15.4	14.2	17.0
Length of internode (cm)	7.7	7.1	9.9	7.8
Number of pods per plant	8.5	8.0	8.2	8.6
Length of pod (cm)	14.8	13.3	14.5	19.6
Average weight of edible pod (g)	22.4	19.6	23.4	38.8
Number of seeds per pod	60.5	58.7	64.1	93.6
Weight of 100-seed (g)	5.5	6.1	6.1	5.7
Days to first flower	49.4	49.4	49.7	50.5
Days to first harvest	54.5	54.5	54.8	54.6
Edible pod yield per plant (g)	189.9	155.2	191.4	334.1
Number of ridges	5.0	5.0	5.0	9.2
Dry matter content (%)	9.4	9.2	10.0	9.4
Number of epicalyx per pod	9.3	8.8	10.0	9.0

Table 4. Relative contribution of 15 different characters to divergence in 27 genotypes of okra

Character	Rank total	Rank
Plant height (cm)	2465	5
Number of branches/plant	3028	11
Number of leaves/plant	2521	6
Length of internode (cm)	4467	15
Number of pods per plant	3703	13
Length of pod (cm)	2523	7
Average weight of edible pod (g)	2272	3
Number of seeds per pod	2278	4
Weight of 100-seed (g)	1082	1
Days to first flower	3344	12
Days to first harvest	2750	8
Edible pod yield per plant (g)	4226	14
Number of ridges	2754	10
Dry matter content (%)	2754	9
Number of epicalyx per pod	1950	2