



SHORT COMMUNICATION

Genetic constellation studies in stabilized advanced populations in okra (*Abelmoschus esculentus* L. Moench)

Shatakshi Sood*, Anil Bhushan, R.K. Samnotra and Vakul Sood¹

Division of Vegetable Science and Floriculture, SKUAST-Jammu

¹Department of Plant Pathology, CSKHPKV-Palampur

*Corresponding author; Email: soodshatakshi1997@gmail.com

Citation: Sood, S., Bhushan, A., Samnotra, R.K., & Sood, V. (2025). Genetic constellation studies in stabilized advanced populations in okra (*Abelmoschus esculentus* L. Moench). Vegetable Science 52 (1): 201-204.

Source of support: Nil

Conflict of interest: None.

Received: 15/05/2024 **Revised:** 11/09/2024 **Accepted:** 19/09/2024

Okra (*Abelmoschus esculentus* (L.) Moench) is an important vegetable crop widely grown in the tropical and subtropical regions of the world (Tindall, 1983). Though okra is native to tropical Africa, India is the leading producer in the world. The potential and worth of germplasm depend on the number of collections and their variability (Ren et al., 1995; Vinay et al., 2021). Information on the genetic divergence among the genotypes is important for pedigree as well as heterosis breeding programs. Mahalanobis D² statistics technique, which is based on the multivariate analysis of quantitative traits, is a powerful tool for measuring genetic divergence. The main objective is to measure the genetic divergence between and among different accessions and group them as clusters. Since successful plant breeding starts with variability between the crops, it has been extensively identified and used in the improvement of crop species. The degree of genetic diversity is worked out in a population based on the characters considered for the study. Genetically divergent population falls into different groups on clustering, thus enabling the selection of parents for hybridization and pedigree breeding programs for the development of superior okra varieties with diverse climatic adaptation.

The present study was carried out involving 100 stabilized advanced plant progenies and five checks at the Experimental Farm-I, Division of Vegetable Science and Floriculture, SKUAST- Jammu, during the spring season of 2022. The stabilized advanced individual plant progenies with replicated five checks were evaluated in an augmented block design with four blocks and in each block, 30 individual rows were maintained, including plant progenies along with checks. These plant progenies were grown in a single-row plot of 5 meters in length and 3 m in width with 45 cm (row to row) and 10 cm (plant to plant) spacing following all the agronomic practices. The observations were recorded on five randomly selected plants of each treatment for horticultural traits, viz., days to 50% flowering (DFF), days to first picking (DFP), plant height (cm) (PH), number of

primary branches (NPB), the node at which the first flower appears (NFFA), internodal distance (cm) (IND), number of nodes per plant (NNPP), fruit length (cm) (FL), fruit girth (cm) (FG), number of fruits per plant (NFPP), average fruit weight (g) (AFW), number of seeds per fruit, fruit yield per plant (g) (FYPP) and fruit yield per hectare (q) (FYPH).

The average mean for each trait in all individual lines in each block was computed for stabilized advanced plant progeny and analyzed statistically to determine the analysis of variance (ANOVA) for all the traits as recommended by Federer (1975). The genetic divergence in the germplasm was assessed following Mahalanobis D^2 statistics (Mahalanobis, 1936). The stabilized advanced plant progenies with checks were grouped on the basis of minimum generalized distance using Tocher's method as described by Rao (1952). The average intra and inter cluster distances and the character contribution towards genetic divergence were calculated and computed by the formula and method by Singh and Chaudhary (1977).

Genetic divergence among 100 stabilized advanced plant progenies with five checks for 14 traits was analyzed by using Mahalanobis D^2 and according to the analysis and, these were grouped into six clusters (Table 1). Among the six clusters, cluster I contains a maximum number of 52 stabilized plant progenies, followed by cluster IV, which contains 33 stabilized plant progenies, followed by cluster II and cluster III, containing 9 stabilized plant progenies each,

whereas cluster V and cluster VI were solitary clusters. Similar results were earlier reported by Nanthakumar *et al.* (2021).

Average intra and inter-cluster D^2 are values presented in (Table 2), indicating the nature of genetic divergence at intra and inter-cluster levels, respectively. In general, the inter-cluster distance was much more than the intra-cluster distance. This suggests that within cluster genotypes have the same genetic constitution, i.e., homogeneous are less divergent than those that occur in a different cluster. The information on the degree of genetic divergence would be helpful in the selection of parents for the hybridization programme. The highest intra-cluster distance was shown by IV (903.12), while cluster V and cluster VI showed zero intra-cluster distance. The maximum inter-cluster distance was found between cluster III and cluster VI (39308.62), followed by cluster II and cluster III (23608.33). The minimum inter-cluster distance was observed between cluster II and cluster V (2226.39). Based on inter-cluster distance, clusters III and VI were identified as more divergent clusters. Stabilized advanced lines of these diverse clusters should be used for further improvement in heterosis in yield-targeted traits with the creation of wider variability. These results are in accordance with the findings of Reddy *et al.* (2012). Cluster means to indicate the variation for the quantitative trait among the cluster (Table 3). Considering major yield attributing traits highest mean was in cluster VI followed by cluster II. Therefore, genotypes from these diverse clusters

Table 1: Clustering of 100 stabilized advanced plant progenies with five checks based on D^2 statistics

Cluster Group	Genotypes (No.)	Genotypes
Cluster I	52	Line 80, Line 87, Line 12, Line 83, Line 35, Line 4, Line 33, Line 17, Line 2, Line 39, Line 67, Kashi Pragati, Line 41, Line 43, Line 13, Line 55, Line 63, Line 56, Line 15, Line 19, Line 57, Line 22, Line 25, Line 44, Palam Komal, Line 14, Line 73, Line 64, Line 95, Line 89, Line 92, Line 68, Line 27, Line 9, Line 42, Line 81, Kashi Vibhuti, Line 48, Line 45, Line 84, Line 5, Line 85, Punjab Suhawani, Line 18, 91, Line 82, Line 90, Line 21, Line 37, Line 16, Line 34 and Line 59
Cluster II	9	Line 78, Line 86, Line 24, Line 20, Line 23, Line 62, Line 76, Line 38 and Line 75
Cluster III	9	Line 65, Line 77, Line 36, Line 58, Line 51, Line 54, Line 52, Line 53 and Line 79
Cluster IV	33	Line 69, Line 88, Line 71, Line 46, Line 7, Line 6, Line 72, Line 70, Line 40, Line 8, Line 94, Line 31, Line 10, Line 28, Line 60, Line 32, Line 3, Line 50, Line 29, Line 66, Line 47, Line 30, Line 11, Line 61, Line 96, Line 98, Line 93, Line 49, Line 1, Line 97, Line 99, Line 26 and Seli Special
Cluster V	1	Line 100
Cluster VI	1	Line 74

Table 2: Average intra (bold) and inter cluster D^2 values for 6 clusters in 100 stabilized advanced plant progenies in okra.

	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI
Cluster I	663.69					
Cluster II	2466.21	563.36				
Cluster III	12408.06	23608.33	842.81			
Cluster IV	3026.26	8913.55	4750.69	903.12		
Cluster V	2655.31	2226.39	20469.05	6809.60	0.00	
Cluster VI	8541.76	2851.47	39308.62	18594.90	3884.69	0.00

Table 3: Cluster mean values for different yield and yield contributing characters in okra

	DFF	DFP	PH (cm)	NPB	NFFA	IND (cm)	NNPP	FL (cm)	FG (cm)	NFPP	AFW (g)	NSPF	FYPP (g)	FYPH (q)
Cluster I	43.17	47.06	90.15	2.30	2.73	4.14	21.81	10.15	1.29	20.33	10.76	44.3	215.16	191.4
Cluster II	42.33	45.89	99.53	2.50	3.03	4.20	23.7	10.88	1.32	23.24	11.35	45.36	246.82	219.39
Cluster III	45.11	49.22	72.06	1.99	1.98	3.49	22.14	9.06	1.17	12.16	8.81	39.84	135.86	120.75
Cluster IV	43.35	47.45	72.48	1.94	2.31	4.02	19.36	9.26	1.24	17.23	10.03	40.30	182.51	162.22
Cluster V	41.00	45.00	56.40	2.20	3.00	3.28	17.20	10.7	1.31	23.00	11.46	44.50	240.6	213.86
Cluster VI	41.00	45.00	83.40	2.75	3.00	4.050	16.50	10.2	1.30	27.00	12.50	47.60	282.4	251.01

Where, DFF: days to 50% flowering; DFP: days to first picking; PH: plant height (cm); NPB: number of primary branches, NFFA: node at which first flower appear, IND: internodal distance (cm); NNPP: number of nodes per plant, FL: fruit length (cm); FG: fruit girth (cm); NFPP: number of fruits per plant; AFW: average fruit weight (g); NSPEF: number of seeds per fruit, FYPP: fruit yield per plant (g) and FYPH: fruit yield per hectare (q).

should be used for further breeding programme. The findings are in close proximate with Samiksha et al. (2020) and Narkhede et al. (2015).

Analysis of contribution of the characters to genetic diversity (Table 4) revealed that character fruit yield per plant (31.21%) contributed highest towards genetic divergence followed by fruit yield per hectare (18.54%), average fruit weight (8.80%), fruit girth (8.00%), internodal distance (7.25%), number of fruits per plant (5.80%), plant height (5.65%), node at which first flower appear (5.00%), fruit length (4.00%) and number of primary branches (3.00%). The lower percent contribution was found in the number of seeds per fruit (1.50%), the number of nodes per plant (0.70%), days to 50% flowering (0.31%) and days to first picking (0.24%) proposed that traits contributing maximum towards the D^2 values need to be given more emphasis for deciding the clusters to be taken for further selection and choice of parents for hybridization. Ramgiry and Singh (2017) also observed a similar level of contribution of fruit yield per plant.

Cluster I had the highest number of stabilized advanced plant progenies (52), followed by cluster IV (33) plant progenies, cluster II and III comprised (9) plant progenies each and cluster V and VI are solitary clusters. The maximum intra-cluster distance was exhibited by IV (903.12) followed by cluster III (842.81). The maximum inter-cluster distance was found between cluster III and cluster VI (39308.62), followed by cluster II and cluster III (23608.33). Analysis of the contribution of the characters to genetic diversity revealed that characters, viz., fruit yield per plant (31.21%), contribute highest to divergence, followed by fruit yield per hectare (18.54%). On the basis of an inter-cluster distance value, cluster III and cluster VI were identified as more divergent clusters and stabilized advanced plant progenies of these clusters could be selected as parents for future hybridization programmes in okra.

Table 4: Percentage contribution of different characters towards genetic divergence in okra

S. No.	Source	Contribution %
1	Days to 50% flowering	0.31
2	Days to first picking	0.24
3	Plant height (cm)	5.65
4	Number of primary branches	3.00
5	Node at which first flower appear	5.00
6	Internodal distance (cm)	7.25
7	Number of nodes per plant	0.70
8	Fruit length (cm)	4.00
9	Fruit girth (cm)	8.00
10	Number of fruits per plant	5.80
11	Average fruit weight (g)	8.80
12	Number of seeds per fruit	1.50
13	Fruit yield per plant (g)	31.21
14	Fruit yield per hectare (q)	18.54

References

- Federer, W.T., Nair, R.C. & Raghavarao, D. (1975). Some augmented row column designs. *Biometrics*, 31, 361-374.
- Mahalanobis, P.C. (1936). On the generalized distance in statistics. *Proceedings of the National Institute of Sciences of India*, 2, 49-55.
- Nanthakumar, S., Kuralarasu, C., & Gopikrishnan, A. (2021). D^2 analysis for assessing genetic diversity in okra (*Abelmoschus esculentus* (L) Moench). *Electronic Journal of Plant Breeding*, 12(4), 1249-1253.
- Narkhede, G.W., Gopal, G.R., & Deshmukh, S.B. (2015). Genetic divergence analysis in okra (*Abelmoschus esculentus* L. Moench). *Ecscan*, 7, 101-104.
- Ramgiry, M., & Singh, S. (2017). Genetic divergence analysis in okra (*Abelmoschus esculentus* (L.) Moench). *International Journal*

- of Pure and Applied Bioscience, 5(2), 981-986.
- Rao, C.R. (1952). Advanced statistical methods in biometrical research. John Wiley and Sons, New York, pp. 357-363.
- Reddy, M.T., Haribabu, K., Ganesh, M., Reddy K.C., & Begum, H. (2012). Genetic divergence analysis of indigenous and exotic collections of okra (*Abelmoschus esculentus* (L.) Moench). Journal of Agricultural Sciences and Technology 8(2), 611-623.
- Ren, J., Ferson, J., Kresovich, R.L., & Lamboy, W.F. (1995). Identities and relationships among chine vegetable brassicas as determined by Random Amplified Polymorphic DNA markers. Journal of American Society for Horticultural Science 12(3), 548-555.
- Samiksha, R.S., Patel, V.K., Prakash, S., Maurya, S.K., & Kumar, S. (2020). Genetic divergence in okra (*Abelmoschus esculents* (L.) Moench). Indian Journal of Pure and Applied Biosciences 8(4), 635-638.
- Singh, R.K., & Chaudhary, B.D. (1977). Biometrical Methods in Quantitative Genetic Analysis. Kalyani Publishers, New Delhi.
- Tindall, H.D. (1983) Vegetables in the tropics. Macmillan Press Ltd., London and Basingstoke, pp: 25-328.
- Vinay, N.D., Mahalik, M.K., Behera, T.K., Talukdar, A., Das, A., Yadav, R.K., & Lata, S. (2022). Estimation of genetic variability in diverse germplasm of okra (*Abelmoschus esculentus* (L.) Moench.). Vegetable Science, 48(2), 172-177.