

Original Research Article

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Genetic Diversity Analysis in Okra (*Abelmoschus esculentum* (L.) Moench) Genotypes for Productivity and Quality Traits

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ABSTRACT

Keywords

Okra, Genetic diversity, D^2 statistics, Intra and inter cluster distance.

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Genetic diversity among sixty three okra genotypes was estimated using Mahalanobis D^2 statistic. The genotypes were grouped into nine clusters. The maximum number of genotypes was found in cluster I (36) followed by cluster III (15) and Cluster II (6). Remaining all were solitary clusters with single genotype. The characters *viz* total phenols (21.35 %), number of leaves at 90 DAS (12.08 %), fruit length (11.73 %) and plant height at 90 DAS (10.60%) contributed more towards genetic divergence. Cluster III with fifteen genotypes showed maximum intra cluster distance ($D^2= 130.13$) followed by cluster II ($D^2= 82.57$) with six genotypes and Cluster I ($D^2= 66.10$) with thirty six genotypes. Maximum inter-cluster distance was observed between cluster VI and cluster VI. Hence, genotypes belonging to these clusters may be utilized for hybridization programme to get better recombinants

Introduction

Okra [*Abelmoschus esculentus* (L.) Moench] commonly known as lady's finger is a perennial flowering plant belonging to family Malvaceae. It is extensively grown in temperate, subtropical and tropical regions of the world, including Indian sub-continent and East Asia (Rashid, 1990). Nutritious okra fruit plays an important role to meet the demand of vegetables in the country. India is the largest producer of okra in the world with an annual production of 63.46 lakh tonnes from an area of 6.59 lakh hectares with a productivity of 11.9 tonnes per hectare (Anon., 2015a). Uttar Pradesh, Bihar, Orissa, West Bengal, Andhra

Pradesh, Karnataka and Assam are the major okra growing states. In Karnataka, okra occupies an area of 8,286 hectares with an annual production of 68,252 tonnes and an average productivity of 8.23 tonnes per hectare (Anon., 2015b). Okra has a tremendous export potential as fresh vegetable, which accounts for 60 per cent of the fresh vegetables exported from India.

Okra breeding in India is hampered because of the non-availability of high yielding, improved and locally adapted cultivars. Improvement of okra requires a broad

spectrum of genetic variability, from where useful characters can be selected. Genetic diversity plays an important role in plant breeding either to exploit heterosis or to generate productive recombinants. The present investigation was therefore, undertaken to evaluate the extent of genetic diversity for different characters in sixty three okra genotypes to select suitable parents for improved breeding programme.

Materials and Methods

Material under study consists of 63 diverse genotypes of okra including both indigenous and exotic collections. Details of the genotypes used in present study were presented in table 1. These 63 genotypes were evaluated in a randomized block design with two replications during *Kharif* 2015 at College of Horticulture, Bagalkot. Ridges and furrows were opened at a distance of 60 cm apart. Two to three seeds per hill were dibbled at a distance of 30 cm in a row. The plants were thinned to one seedling per hill after germination. Irrigation, weed control and other cultural practices were followed as per the package of practices of University of Horticultural Sciences, Bagalkot (Anon, 2014). Ten plants were accommodated in a row, out of which, data was recorded from five randomly selected plants for fifteen productivity and quality traits, viz., plant height (90 DAT), number of branches (90 DAT), inter nodal length (90 DAS) number of leaves (90 DAS), fruit length, fruit diameter, average fruit weight, fruit yield per plant (g), flesh thickness (mm), number of fruits per plant, total yield per plant, yield per hectare, trichome density and phenol content. Genetic diversity was estimated with the help of Mahalanobis (1936) generalized distance D^2 extended by Rao (1952). Based on the D^2 values, genotypes were grouped into different clusters following the method suggested by Tocher's (Rao, 1952). Statistical analysis was carried out using WINDOSTAT software.

Results and Discussion

Quantification of genetic diversity existing within and between groups of germplasm is important and particularly useful in proper choice of parents for realizing higher heterosis and obtaining useful recombinants. Among the several methods available, Mahalanobis generalized distance estimated by D^2 statistic is a unique tool for discriminating populations considering a set of parameters together rather than inferring from indices based up on morphological similarities, eco-geographical diversity and phylogenetic relationships. In the present study, based on D^2 values, 63 okra genotypes were grouped into nine different clusters (Table 2). Among the nine clusters, cluster I was the largest having 36 genotypes followed by cluster III with 15 genotypes, cluster II with 6 genotypes and remaining all cluster IV, V, VI, VII, VIII, IX are solitary with single genotype. The clustering pattern of genotypes was observed to be random indicating that geographical diversity and genetic divergence were independent.

Intra-cluster distance revealed that, cluster III with fifteen genotypes showed maximum intra-cluster distance ($D^2= 130.13$) followed by cluster II ($D^2= 82.57$) with six genotypes and cluster I ($D^2= 66.10$) with thirty six genotypes (Table 3). Maximum intra-cluster distance was observed in cluster III, indicating existence of wide genetic divergence among the constituent genotypes in it as compared to other cluster.

High degree of divergence among the genotypes within a cluster would produce more segregating breeding material and selection within such cluster might be executed based on maximum mean value for the desirable characters. High intra cluster distance was also observed by Prakash and Pitchaimuthu (2010), Akotkar *et al.*, (2010) and Nwangburuka *et al.*, (2011).

Table.1 Details of okra genotypes used for diversity study

Genotype code	Genotype	Genotype code	Genotype	Genotype code	Genotype
L ₁	MHO-1	L ₂₂	MHO -22	L ₄₃	KRCO -13
L ₂	MHO-2	L ₂₃	MHO -23	L ₄₄	KRCO -14
L ₃	MHO-3	L ₂₄	MHO -24	L ₄₅	KRCO -15
L ₄	MHO-4	L ₂₅	MHO -25	L ₄₆	KRCO -16
L ₅	MHO -5	L ₂₆	MHO -26	L ₄₇	KRCO -17
L ₆	MHO -6	L ₂₇	MHO -27	L ₄₈	KRCO -18
L ₇	MHO -7	L ₂₈	MHO -28	L ₄₉	KRCO -19
L ₈	MHO -8	L ₂₉	MHO -29	L ₅₀	KRCO -20
L ₉	MHO -9	L ₃₀	MHO -30	L ₅₁	KRCO-21
L ₁₀	MHO -10	L ₃₁	KRCO-1	L ₅₂	KRCO-22
L ₁₁	MHO -11	L ₃₂	KRCO -2	L ₅₃	KRCO-23
L ₁₂	MHO -12	L ₃₃	KRCO -3	L ₅₄	KRCO-24
L ₁₃	MHO -13	L ₃₄	KRCO -4	L ₅₅	KRCO-25
L ₁₄	MHO -14	L ₃₅	KRCO -5	L ₅₆	KRCO-26
L ₁₅	MHO -15	L ₃₆	KRCO -6	L ₅₇	KRCO-27
L ₁₆	MHO -16	L ₃₇	KRCO -7	L ₅₈	KRCO-28
L ₁₇	MHO -17	L ₃₈	KRCO -8	L ₅₉	KRCO-29
L ₁₈	MHO -18	L ₃₉	KRCO -9	L ₆₀	KRCO-30
L ₁₉	MHO -19	L ₄₀	KRCO -10	L ₆₁	GKL-1
L ₂₀	MHO -20	L ₄₁	KRCO -11	L ₆₂	BGK-1
L ₂₁	MHO -21	L ₄₂	KRCO -12	L ₆₃	KLL-1

Table.2 Clustering pattern of 63 okra genotypes

Clusters	Number of genotypes	Genotypes included in the cluster
I	36	L26, L47, L33, L48, L51, L32, L45, L46, L34, L44, L60, L42, L38, L35, L21, L43, L59, L58, L62, L36, L41, L50, L23, L14, L61, L20, L24, L13, L5, L11, L10, L27, L22, L28, L25 and L8
II	6	L4, L17, L8, L6, L63 and L9
III	15	L1, L49, L19, L54, L3, L12, L30, L1, L29, L37, L39, L57, L31, L55 and L40
IV	1	L52
V	1	L56
VI	1	L15
VII	1	L16
VIII	1	L53
IX	1	L7

Table.3 Average intra and inter cluster distances in okra genotypes

Clusters	I	II	III	IV	V	VI	VII	VIII	IX
I	66.10	122.77	120.11	114.65	120.07	194.05	181.86	141.66	158.27
II		82.57	184.65	260.19	197.27	191.78	126.83	279.44	137.91
III			130.13	163.51	182.20	182.75	202.09	166.90	232.89
IV				0.00	110.71	303.69	337.57	103.36	266.91
V					0.00	259.21	187.04	155.39	79.47
VI						0.00	77.64	263.74	198.27
VII							0.00	278.63	115.17
VIII								0.00	259.64
IX									0.00

Diagonal values indicate intra cluster distance
Above diagonal valves indicate inter cluster distance

Table.4 Per cent contribution of different characters to the total diversity in okra genotypes

Sl. No.	Characters/Source	Number of times ranked first	% Contribution to total divergence
1.	Total phenols (mg/g)	417.00	21.35
2.	Number of leaves (90 DAS)	236.00	12.08
3	Fruit length (cm)	137.00	11.73
4.	Plant height (cm) (90 DAS)	207.00	10.6
5.	Total fruit yield per (ha)	158.00	8.09
6.	Seed yield per fruit (g)	137.00	7.01
7.	Average fruit weight (g)	126.00	6.45
8.	Fruit yield per plant (g)	124.00	6.35
9.	Trichome density (no/cm ²)	99.00	5.05
10.	Number of fruits per plant	93.00	4.76
11.	Flesh thickness (mm)	66.00	3.38
12.	Number of seeds per fruit	60.00	3.07
13.	Fruit diameter (mm)	1.00	0.5
14.	Number of branches (90 DAS)	0.00	0.00
15.	Inter nodal length (cm) (90 DAS)	0.00	0.00

Table.5 Cluster mean for 15 productivity and quality characters in okra genotypes

Clusters	X ₁	X ₂	X ₃	X ₄	X ₅	X ₆	X ₇	X ₈	X ₉	X ₁₀	X ₁₁	X ₁₂	X ₁₃	X ₁₄	X ₁₅
I	88.43	3.49	4.38	22.06	20.63	282.46	15.75	13.41	15.64	12.10	10.98	79.97	6.30	40.26	19.97
II	103.31	4.25	4.36	22.97	20.47	265.49	14.62	13.26	14.17	10.56	10.52	82.83	6.39	48.34	16.42
III	90.26	3.54	4.38	24.12	20.69	336.61	18.76	15.85	15.21	11.65	11.35	77.89	6.08	41.00	21.17
IV	74.00	3.84	4.12	21.34	23.17	301.11	18.10	13.00	20.36	11.35	14.94	54.00	4.77	30.87	19.00
V	86.84	4.67	4.60	30.67	21.17	256.20	14.25	10.91	18.58	12.99	12.83	94.17	6.95	37.22	18.00
VI	92.68	3.83	4.00	28.83	15.50	261.81	14.24	16.92	12.65	10.78	8.25	48.33	4.97	46.47	24.00
VII	95.00	4.00	4.45	30.67	17.33	234.72	13.61	13.60	11.72	9.35	7.60	78.34	7.17	52.25	15.50
VIII	72.33	3.84	3.97	23.17	23.83	320.09	16.98	13.25	13.51	9.37	1177	76.34	8.99	26.91	24.50
IX	102.72	3.84	4.64	30.67	16.83	199.70	10.87	11.87	16.81	12.01	12.26	92.83	8.67	38.44	15.00

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|----------------|---------------------------------------|-----------------|--|
| X ₁ | Plant height (90 DAS) (cm) | X ₉ | Fruit diameter (mm) |
| X ₂ | Number of branches per plant (90 DAS) | X ₁₀ | Fruit length (cm) |
| X ₃ | Internodal length (90 DAS) (cm) | X ₁₁ | Flesh thickness (mm) |
| X ₄ | Number of leaves (90 DAS) | X ₁₂ | Number of seeds per fruit |
| X ₅ | Number of fruits per plant | X ₁₃ | Seed yield per fruit (g) |
| X ₆ | Fruit yield per plant (g) | X ₁₄ | Total Phenols (mg/g) |
| X ₇ | Average fruit weight (g) | X ₁₅ | Trichome density (no/cm ²) |
| X ₈ | Fruit yield per (t/ ha) | | |

Maximum inter cluster distance was observed between cluster IV and VII ($D^2=337.57$) followed by cluster IV and VI ($D^2=303.69$) followed by cluster II and VIII ($D^2=279.44$), cluster VII and VIII ($D^2=278.63$). Maximum inter-cluster D^2 values was observed between the clusters IV and VII indicating that the genotypes in these clusters can be used as a parents in hybridization programme to get higher heterotic hybrids and better segregating population. Similar results were reported by Pachiyappan and Saravanan (2012) and Prakash and Pitchaimuthu (2010). The cluster VI had the least inter-cluster distance ($D^2=77.64$) with the cluster VII indicating that close relationship and less divergence between the genotypes included in these clusters.

Relative per cent contribution of different characters to divergence was presented in table 4 and mean values of 15 productivity and quality characters across the nine clusters was presented in table 5. Among fifteen characters studied, the total phenols (mg/g) contributed maximum (21.35%) to the genetic diversity with its average range from 26.91(mg/g) in cluster VIII to 48.34(mg/g) in cluster VII followed by number of leaves at 90 DAS (12.08%) ranged from 21.34 in cluster II to 30.67 (cluster V, VII and IX), fruit length (11.73%) with an average ranged from 9.35cm for Cluster VII to 12.99cm for cluster V, plant height at 90 DAS (10.60%) with average value ranged from 72.35cm (cluster VIII) to 103.31cm (cluster II), which suggest that the planning of breeding programme by crossing between clusters containing maximum average values for improvement of particular character will yield fruitful results. The characters like total phenols (mg/g) followed by number of leaves at 90 DAS and fruit length were contributed maximum to the total genetic divergence so, these characters may be used in selecting genetically diverse parents for hybridization

programme to exploit either maximum heterosis or to execute efficient selection in the segregating generation. The observed results are in confirmative with the results obtained by Prakash and Pitchaimuthu (2010) and Reddy *et al.*, (2012). Characters like number of branches at 90 DAS and internodal length at 90 DAS did not contribute to total genetic divergence. Hence these traits may given less importance while selection.

References

- Akotkar, P. K., De, D. K. and Pal, A. K., 2010. Genetic variability and diversity in okra [*Abelmoschus esculentus* (L.) Moench]. *Electronic J. Plant Breed.*, 1 (4): 393-398.
- Anonymous, 2014. Integrated Horticultural crops management (Kannada). *Univ. Hort. Sci., Bagalkot*, p. 58-62.
- Anonymous, 2015a. *Indian Horticultural Database*. National Horticulture Board, Haryana.
- Anonymous, 2015b. Crop wise area and production of horticulture crops in Karnataka. <http://www.horticulture.kar.nic.in>.
- Jasol, F.S., 1989, Export prospectus of horticultural produce from India. *Indian Hort.*, 34: 79-85.
- Mahalanobis, P. C., 1936. On the generalized distance in statistics. *Proceed. Nat. Acad. Sci.*, 19: 201-208.
- Nwangburuka, C. C., Kehinde, O. B., Ojo, D. K., Denton, O. A. and Popoola, A. R., 2011. Morphological classification of genetic diversity in cultivated okra [*Abelmoschus esculentus* (L.) Moench] using principal component analysis (PCA) and single linkage cluster analysis (SLCA). *African J. Biotech.*, 10 (54): 1165 - 1172.
- Pachiyappan, R., and Saravanan, K., 2012. Genetic divergence analysis in okra [*Abelmoschus esculentus* (L.) Moench].

- Plant Archives*, 12 (1): 331-334.
- Prakash, K., and Pitchaimuthu, M., 2010. Nature and magnitude of genetic variability and diversity studies in okra [*Abelmoschus esculentus* (L.) Moench]. *Electron. J. Plant Breed*, 1 (6): 1426-1430.
- Rao, C. R., 1952. Advanced statistical methods in biometrical research. *John Wiley and sons.Inc*, 390.
- 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. Tech.*, 8 (2): 611-623.

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