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Genetic divergence analysis of indigenous and exotic collections in Okra (*Abelmoschus esculentus* (L.) Moench)

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Abstract

Using D^2 statistics, the 45 genotypes of okra were grouped into nine non-overlapping clusters. This indicated considerable diversity among the genotypes evaluated in the present study. The cluster I had 17 genotypes out of 45 entries. The cluster II contained 14 genotypes, while cluster IV had five genotypes of diverse origin. The cluster VI contained the genotypes having high mean performance for plant height, days to first fruit initiation, days to 50% flowering, number of branches/plant, days to first fruit harvest, cluster VIII having 4 genotypes having high mean for number of fruits/plant, fresh fruit weight, cluster IV had the genotypes with highest mean for 100 seed weight. The highest inter cluster distance was recorded between cluster VIII and IX followed by cluster I and VIII and cluster III and VIII. This showed that genotypes in different clusters are genetically variable which may provide basis for consideration in hybridization programme.

Keywords: Okra, Genetic divergence, D^2 statistics

Introduction

Okra [*Abelmoschus esculentus* (L.) Moench, $2x=2n=130$] is a fast growing, erect, herbaceous annual and belongs to the family Malvaceae. Okra is an economically important vegetable crop grown in tropical and subtropical parts of the world. This crop is suitable for cultivation as a garden crop as well as on large commercial farms. Okra is known by many local names like lady's finger in England, gumbo in United States of America, guino-gumbo in Spanish, guibeiro in Portuguese and bhindi in India. Its ripe seeds are roasted, ground and used as a substitute for coffee in Turkey. Tender edible fruits have high nutritive value containing proteins, calcium, phosphorus, iron, carotene, and vitamins A, B, C and iodine. Fruits are very useful against genito-urinary disorders, spermatorrhoea and chronic dysentery (Nandkarni, 1927) [7].

Genetic diversity plays an important role in plant breeding because hybrids between lines of diverse origin generally display a greater heterosis than those between closely related strains. The maximum heterosis generally occurs at an optimal or intermediate level of diversity. In addition to aiding the selection of divergent parents for hybridization, D^2 statistic measures the degree of diversification and determines the relative proportion of each component character to the total divergence.

Materials and Methods

Forty-five genotypes collected from different SAU's and Agricultural institutes of the country were evaluated using Completely Randomized Block Design with three replications at Nursery area, Department of Horticulture, College of Agriculture, Rajmata Vijayaraje Scindia Krishi Vishwa Vidyalaya, Gwalior, (M.P.) during *kharif* 2015. Each genotype was accommodated in a single row of 3 m length. The row to row spacing of 60 cm and plant to plant spacing of 30 cm was adopted. The recommended packages of practices were followed. Thirteen traits were recorded on five randomly selected plants of each genotype and yield contributing traits like Plant height (cm), Number of branches per plant, Days to first flowering, Days to 50 per cent flowering, Days to first fruit harvest, Number of fruits per plant, fruit length (cm), fruit width (cm), fresh fruit weight (g), dry fruit weight (g), Number of seeds per fruit, 100 seed weight and fruit yield per plant (g). The multivariate analysis (D^2 statistic) was carried out following to Mahalanobis. Grouping of genotypes into different

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clusters was carried out following Tocher's procedure 9 and the relative contribution of different characters towards total divergence was calculated as per Singh and Choudhary.

Results and Discussion

Distribution of genotypes into different clusters

The 45 genotypes of okra were grouped into nine distinct non-overlapping clusters (table 1). The highest numbers of genotypes were present in cluster I which contained 17 genotypes namely RVA-30, RVA-31, RVA-22, RVA-23,

RVA-11, RVA-29, RVA-27, RVA-32, RVA-34, RVA-19, RVA-16, RVA-35, RVA-8, RVA-5, RVA-21, RVA-18, and RVA-10. The cluster II contained, 14 genotypes namely RVA-38, RVA-39, RVA-37, RVA-33, RVA-36, RVA-14, RVA-15, RVA-20, RVA-12, RVA-13, RVA-9, RVA-7, RVA-6, and RVA-17. Cluster IV had five genotypes namely Arka Abhay, Pusa Sawni, Tox-52, VRO-6, and RVA-26. The cluster VIII contained four genotypes viz., RVA-25, RVA-28, RVA-24 and Arka Anamika, the rest of the clusters III, V, VI, VII, and IX contained single genotypes i.e. they were monogenotypic.

Table 1: Distribution of 45 genotypes into different clusters

Cluster No.	No. of Genotypes	Name of genotypes
1	17	RVA-30, RVA- 31, RVA- 22, RVA- 23, RVA- 11, RVA- 29, RVA- 27, RVA- 32, RVA- 34, RVA- 19, RVA- 16, RVA- 35, RVA- 8, RVA- 5, RVA- 21, RVA- 18, RVA- 10
2	14	RVA-38, RVA- 39, RVA- 37, RVA- 33, RVA- 36, RVA- 14, RVA- 15, RVA- 20, RVA- 12, RVA- 13, RVA- 9, RVA- 7, RVA- 6, RVA- 17
3	1	RVA-1
4	5	Arka Abhay, Pusa Sawni, Tox-52, VRO-6, RVA- 26
5	1	RVA-2
6	1	RVA-40
7	1	RVA-3
8	4	RVA-25, RVA- 28, RVA- 24, Arka Anamika
9	1	RVA-4

Average intra and inter- cluster distance

The estimates of intra and inter-cluster distances for the nine clusters have been presented in Table 2. The intra cluster distance ranged from 0.00 (cluster III, V, VI, VII, and IX) to 44.13 (cluster VIII). The maximum inter cluster distance (355.89) was observed in between cluster VIII and IX

followed by cluster I and VIII (253.13) and cluster III and VIII (251.74). The minimum inter cluster distance was observed in between clusters I and cluster VII (39.83) followed by cluster III and V (40.66), which indicated that these groups were less divergent.

Table 2: The average Intra and Inter cluster distances among the nine clusters

CLUSTER NO	1	2	3	4	5	6	7	8	9
1	28.52	52.90	44.50	67.34	68.66	120.43	39.83	253.13	70.07
2	52.90	31.47	62.53	57.92	48.36	57.96	61.69	153.65	121.61
3	44.50	62.53	0.00	66.49	40.66	103.50	44.32	251.74	45.56
4	67.34	57.92	66.49	42.59	67.94	78.04	77.92	186.07	145.70
5	68.66	48.36	40.66	67.94	0.00	42.21	60.21	109.75	91.50
6	120.43	57.96	103.50	78.04	42.21	0.00	86.81	72.62	193.72
7	39.83	61.69	44.32	77.92	60.21	86.81	0.00	237.28	84.23
8	253.13	153.65	251.74	186.07	109.75	72.62	237.28	44.13	355.89
9	70.07	121.61	45.56	145.70	91.50	193.72	84.23	355.89	0.00

Cluster means

The cluster means for thirteen characters are presented in Table 3. Cluster VI contained the genotypes having high mean performance for plant height (102.33cm), days to first fruit initiation (53.27), days to 50% flowering (58.50), number of branches/plant (2.43), days to first fruit harvest (58.73), while, cluster VIII had the genotypes with high mean for number of fruits/plant (14.08), fresh fruit weight (20.09), dry fruit weight (7.83), number of seeds/fruit (62.44), and

fruit yield (g)/ plant (279.27g). Cluster IV had the genotypes with highest mean for 100 seed weight (11.91g).

The lowest cluster mean was observed in cluster IX for plant height, days to first fruit initiation, days to 50% flowering, days to first fruit harvest, number of fruits/ plant, fruit length, fresh fruit weight, dry fruit weight, number of seeds/ fruit, 100 seed weight, and fruit yield/plant. Cluster V had the lowest mean for fruit diameter and cluster VII for number of branches/plant.

Table 3: Mean performances of different clusters for fruit yield and its component traits

Characters/Clusters	Plant height (cm)	Days to first flower initiation	Days to 50% flowering	No. of branches/plant	Days to first fruit harvest	Number of fruits/plant	Fruit length (cm)	Fruit diameter (cm)	Fresh fruit weight (g)	Dry fruit weight (g)	Number of seeds/ fruit	100 seed weight (g)	Fruit yield / plant(g)
Cluster 1	82.27	45.89	51.81	1.74	52.47	8.05	10.32	1.44	13.82	6.96	57.16	9.90	110.54
Cluster 2	96.88	46.09	52.33	2.10	52.69	10.00	10.93	1.57	15.48	6.70	62.11	9.43	150.69
Cluster 3	96.47	43.30	50.53	1.93	50.97	10.20	13.53	1.27	12.93	5.97	46.43	9.30	132.07
Cluster 4	89.37	45.53	51.25	2.05	52.33	12.04	13.80	2.07	13.39	7.13	58.25	11.91	157.94
Cluster 5	90.87	41.87	48.43	2.37	48.53	11.13	12.70	1.20	16.23	7.03	48.97	10.20	190.53
Cluster 6	102.33	53.27	58.50	2.43	58.73	11.73	13.03	1.80	18.23	6.20	55.47	10.93	208.47

Cluster 7	89.57	52.60	58.00	1.50	58.23	8.07	10.67	1.17	15.60	5.93	51.33	13.10	125.07
Cluster 8	90.08	45.59	51.00	2.32	51.44	14.08	13.25	1.51	20.09	7.83	62.44	10.23	279.27
Cluster 9	75.60	40.43	46.80	2.33	48.17	7.60	8.07	1.37	12.87	3.53	41.07	7.00	105.27

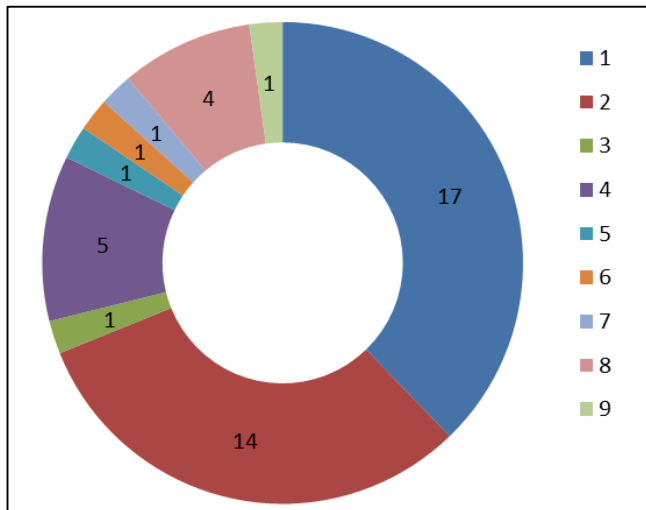


Fig 1: Number of germplasm contained in each cluster

Percent contribution to divergence

The maximum contribution to divergence was displayed by fruit yield/plant (30.11%) followed by number of seeds/fruit (21.03%), number of fruits/plant (10.3%), and plant height (6.46%). Rest of the characters showed less contribution to divergence (Table 4).

Using D² statistics, the 45 genotypes of okra were grouped into nine non-overlapping clusters. This indicated considerable diversity among the genotypes evaluated in the present study. The cluster I had 17 genotypes out of 45 entries. The cluster II contained 14 genotypes, while cluster IV had five genotypes of diverse origin. The cluster VI contained the genotypes having high mean performance for plant height, days to first fruit initiation, days to 50% flowering, number of branches/plant, days to first fruit harvest, cluster VIII having 4 genotypes having high mean for number of fruits/plant, fresh fruit weight, cluster IV had the genotypes with highest mean for 100 seed weight.

The cluster IX contained single genotype which had lowest mean for plant height, days to first flower initiation, days to 50% flowering, days to first fruit harvest, number of fruits/plant, fruit length, fresh fruit weight, dry fruit weight,

number of seeds/fruit, 100 seed weight, and fruit yield/plant. Cluster V had single genotype with lowest mean for fruit diameter and cluster VII containing single genotype having lowest mean for number of branches/plant. The nine clusters in aforesaid genetic divergence analysis contained frequently the genotypes of heterogenous origin. The genotypes originated in the same place or geographic region were also found to be grouped together in the same cluster. The instance of grouping of genotypes of different origin or geographic region in the same cluster were observed in case of all the nine clusters. This suggested lack of parallelism between genetic and geographic diversity. Therefore, the selection of parental materials for hybridization programme, simply based on geographic diversity may not be a successful exercise. The present findings is in agreement with the reports advocating lack of definite relationship between genetic and geographic diversity in okra (Singh and Singh, 1976; Ariyo, 1987) [8, 1].

An experimentation on the estimates of within and between cluster genetic diversity revealed that the genotypes of same cluster had little genetic distance from each other with respect to different characters. Therefore, the chance of obtaining good segregates by crossing the members of the same cluster are very low. It would be logical to attempt crosses between the genotypes belonging to clusters separated by large inter cluster distances. In this context the highest inter cluster distance was recorded between cluster VIII and IX followed by cluster I and VIII and cluster III and VIII. This showed that genotypes in different clusters are genetically variable which may provide basis for consideration in hybridization programme. Similar results reported by Gawande *et al.* (1972) [4]. The analysis of character contribution towards divergence among 45 genotypes of okra indicated that maximum contribution to divergence was displayed by fruit yield/plant followed by number of seeds/fruit, number of fruits/plant and plant height. Our findings are in accordance with that reported by Hazra *et al.* (2004) [5] who also observed maximum contribution of fruit yield/plant towards diversity. Akotkar *et al.* (2010) [2] in their studies on divergence in okra reported highest contribution of fruit yield/ plant followed by number of fruits/plant.

Table 4: Contribution of each of the thirteen characters to divergence in okra

Traits	Plant height (cm)	Days to first flower initiation	Days to 50% flowering	No. of branches/Plant	Days to first fruit harvest	Number of fruits/plant	Fruit length (cm)	Fruit diameter (cm)	Fresh fruit weight (g)	Dry fruit weight (g)	Number of seeds/ fruit	100 seed weight (g)	Fruit yield/plant (g)
Contribution in %	6.46	3.74	3.12	2.22	2.51	10.3	6.36	5.86	1.62	1.52	21.03	5.15	30.11

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