

Variability, heritability, genetic advance and genetic diversity studies on okra, *Abelmoschus esculentus* (L) Moench germplasm

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ABSTRACT

Field investigations were carried out with 52 okra accessions. High genotypic and phenotypic coefficients of variability (GCV and PCV= >20%) were observed for plant height at 90 DAS, number of nodes per plant, number of fruits per plant, rind thickness, seed yield per fruit and number of seeds per fruit. High heritability coupled with high genetic advance over mean was observed for plant height at 45 and 90 DAS, number of leaves at 90 DAS, first flowering node, number of nodes per plant, number of fruits per plant, fruit yield per plant, average fruit weight, fruit length, fruit diameter, rind thickness, number of ridges on fruit surface, seed yield per fruit and number of seeds per fruit. Thus most of the characters do have ample scope for improving through direct selection. Genetic divergence was studied with same genotypes and the maximum number of genotypes (37) was found in cluster I with intra-cluster distance of 9.85. The maximum inter-cluster distance was observed in between cluster IV and cluster VII. Hence genotypes belonging to these clusters may be utilized for involving in hybridization programme for crop improvement. The characters of number of ridges on fruit surface contributed maximum (32.5%) to the genetic diversity followed by rind thickness (16.67%) and seed yield per fruit (12.22%) contributed more to genetic divergence.

Keywords: Variability; heritability; genetic diversity; D² statistics, okra

INTRODUCTION

Okra, *Abelmoschus esculentus* (L) Moench also known as lady's finger and bhendi is an important spring-summer and rainy season vegetable crop cultivated in tropical and sub-tropical parts of the world. It has high nutritive value having 86.1 per cent water, 2.2 per cent protein, 0.2 per cent fat, 9.7 per cent carbohydrates, 1.0 per cent fibre and 0.8 per cent ash (Saifullah and Rabbani 2009) and is also rich in vitamin C (30 mg/100 g), calcium (90 mg/100 g) and iron (1.5 mg/100 g) content (Pal et al 1952). In addition to its usefulness as a vegetable crop it is also used medicinally in curing ulcer, suppressing the pains and haemorrhoid effects. The high iodine content of fruits is useful in curing goiter disease and also possesses export potential. The leaves and fruits produce mucilaginous substance. The mucilage has been used as a plasma replacement or blood volume expander (Grubben and Denton 2004).

The possibility of improvement in any crop is measured by variability available in the crop (Mohapatra et al 2007). The genetic variability in conjunction with total variability can be used in predicting the gain for a given selection intensity. The variation in the characters of any crop species is the raw material for a plant breeder and extent of variability present in the population with respect to various characters is the factor for the success of plant breeder in improvement of crop plant. Larger variability ensures better chances of producing desired crop variety. Hence it is very essential to screen out the available germplasm for higher production of okra.

Generally diverse germplasms are expected to give hybrid vigour and hence study of genetic divergence among the existing genetic stocks provides an opportunity for selecting the diverse parents for hybridization. Such parents are expected to produce superior segregants in combination with others and thus

are most valuable for breeders. The D^2 statistics developed by Mahalanobis (1930) provides a measure of magnitude of divergence between two genotypes under comparison. Grouping of genotypes based on D^2 analysis is useful in choosing suitable parental lines for heterosis breeding which in turn can help farmers by making available the elite varieties.

MATERIAL and METHODS

The present investigations were conducted during the year 2014 in Kharif season at experimental site of Department of Vegetable Science, College of Horticulture, Bagalkot, Karnataka. The experimental material comprised fifty two genotypes of okra. The experiment was laid out in randomized block design with two replications. 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. For recording observations five plants in each experimental plot were chosen at random as per NBPGR minimal descriptors from five competitive plants from each replication on twenty one parameters viz plant height (cm) at 45 and 90 DAS, number of leaves at 45 and 90 DAS, number of branches at 45 and 90 DAS, inter-nodal length (cm) at 45 and 90 DAS, days to first flowering, days to first harvest, first flowering node, number of nodes per plant, number of fruits per plant, fruit yield per plant (g), average fruit weight (g), fruit length (cm), fruit diameter (cm), rind thickness (mm), number of ridges on fruit surface, seed yield per fruit (g) and number of seeds per fruit. The analysis of variance for each character was followed according to Panse and Sukhatme (1967). The genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were calculated as per Burton and DeVane (1953). Heritability (broad sense) and genetic advance as per cent of mean were computed by following the methods of Johnson et al (1955) and Allard (1960) respectively.

Genetic diversity was studied following Mahalanobis (1936) generalized distance D^2 extended by Rao (1952). Based on the D^2 values the genotypes were grouped into clusters following the Tocher's method (Rao 1952). Intra- and inter-cluster distances were calculated by the methods of Singh and Chaudhary (1979). Statistical analysis was carried out using WINDOSTAT software.

RESULTS and DISCUSSION

Genetic variability studies

The estimates of genotypic and phenotypic coefficients of variation, heritability and genetic advance as per cent of mean are presented in Table 1. The phenotypic coefficient of variation was higher than genotypic coefficient of variation for all the traits. High GCV and PCV (>20%) were observed for plant height at 90 days after sowing (24.03 and 25.85% respectively) (Kandasamy 2015, Sibsankar et al 2012), number of fruits per plant (25.00 and 27.64% respectively) (Kandasamy 2015, Khajuria et al 2015), rind thickness (25.43 and 26.45% respectively), seed yield per fruit (27.20 and 31.07% respectively) and number of seeds per fruit (24.64 and 29.48% respectively) indicating maximum amount of variability present in the genotypes for these characters which would be amenable for further selection. Characters like days to first flowering (7.05 and 8.80% respectively) (Kandasamy 2015, Sibsankar et al 2012) and days to first harvest (6.78 and 8.81% respectively) (Kandasamy 2015) indicated the existence of limited variability in the genotypes evaluated for the traits showing low genetic variability in the genotypes stock studied. This necessitates the need for generation of new variability for these characters.

Higher (>20%) values of genetic advance over mean (GAM) coupled with high estimates of heritability (>60%) were observed for the characters viz plant height both at 45 (71.29 and 34.00% respectively) (Kumar et al 2016a, Chandra et al 2014) and 90 (86.44 and 46.03% respectively) (Kandasamy 2015, Sibsankar et al 2012) days after sowing, number of leaves per plant at 90 days after sowing (72.56 and 31.61% respectively) (Sibsankar et al 2012), first flowering node (91.51 and 41.19% respectively) (Kandasamy 2015, Sibsankar et al 2012), number of nodes per plant (66.35 and 37.16% respectively) (Sibsankar et al 2012, Chandra et al 2014), number of fruits per plant (81.84 and 46.60% respectively) (Kumar et al 2016a, Kandasamy 2015, Khajuria et al 2015), fruit yield per plant (74.03 and 30.86% respectively) (Kumar et al 2016a, Kandasamy 2015, Sibsankar et al 2012, Chandra et al 2014), average fruit weight (72.49 and 28.44% respectively) (Kumar et al 2016a, Kandasamy 2015, Sibsankar et al 2012, Khajuria et al 2015, Chandra et al 2014), fruit length (91.61 and 33.75% respectively) (Kumar et al 2016a, Sibsankar et al 2012, Khajuria et al 2015, Chandra et al 2014), fruit diameter (88.30 and

Table 1. Estimates of mean, range, component of variance, heritability and genetic advance for growth earliness yield, quality and seed parameters in okra genotypes

Character	GV	PV	GCV (%)	PCV (%)	h ² (%)	GAM (%)
Plant height (cm) (45 DAS)	63.65	89.29	19.54	23.15	71.29	34.00
Plant height (cm) (90 DAS)	1057.26	1223.12	24.03	25.85	86.44	46.03
Number of leaves/plant (45DAS)	8.03	15.93	16.27	22.92	50.42	23.80
Number of leaves/plant (90 DAS)	18.49	25.48	11.07	18.01	72.56	31.61
Number of branches/plant (45 DAS)	0.38	0.68	16.86	22.43	56.54	26.13
Number of branches/plant (90 DAS)	0.16	0.44	9.95	16.12	38.07	12.64
Internodal length (cm) (45 DAS)	0.16	0.39	14.76	22.97	41.28	19.54
Internodal length (cm) (90DAS)	0.17	0.33	11.69	15.92	53.89	17.68
Days to first flowering	8.78	13.69	7.05	8.80	64.16	11.63
Days to first harvest	10.37	17.51	6.78	8.81	59.21	10.75
First flowering node	1.709	2.11	19.81	22.07	91.51	41.19
Number of nodes/plant	129.49	195.14	22.14	27.19	66.35	37.16
Number of fruits/plant	24.92	30.45	25.00	27.64	81.84	46.60
Fruit yield/plant (g)	3609.89	4876.02	17.41	20.23	74.03	30.86
Average fruit weight (g)	8.40	11.59	16.21	19.04	72.49	28.44
Fruit length (cm)	4.78	5.22	17.11	17.88	91.61	33.75
Fruit diameter (cm)	0.10	0.11	15.93	16.95	88.30	30.83
Rind thickness (mm)	0.14	0.15	25.43	26.45	92.46	50.37
Number of ridges on fruit surface	0.99	1.02	17.70	17.98	96.98	35.95
Seed yield/fruit (g)	1.46	1.90	27.20	31.07	76.63	49.05
Number of seeds/fruit	250.91	359.48	24.62	29.48	69.80	42.38

DAS= Days after sowing, PCV= Phenotypic coefficient of variation, GV= Genotypic variance, h²= Heritability (broad sense), PV= Phenotypic variance, GA= Genetic advance, GCV= Genotypic coefficient of variation, GAM= Genetic advance as per cent of means

30.83% respectively) (Kumar et al 2016a, Sibsankar et al 2012), rind thickness (92.46 and 50.37% respectively), number of ridges on fruit surface (96.98 and 35.95% respectively), number of seeds per fruit (69.80 and 42.38% respectively) (Sibsankar et al 2012, Khajuria et al 2015) and seed yield per fruit (76.63 and 49.05% respectively) (Khajuria et al 2015). These results indicate the predominant role of additive genetic component in governing these traits and improvement of these traits through direct selection would be rewarding. Moderate (10-20%) values of genetic advance over mean (GAM) coupled with moderate estimates of heritability (30-60%) were observed in internodal length both at 45 (41.28 and 19.54% respectively) and 90 (53.89 and 17.68% respectively) days after sowing and days to first harvest (59.21 and 10.75% respectively). This indicates the importance of additive effects for this trait and selection may be rewarding.

High heritability coupled with moderate genetic advance over mean was observed for days to first flowering (64.16 and 11.63% respectively) (Sibsankar et al 2012, Khajuria et al 2015) indicating non-additive gene action. The high heritability was being exhibited

due to favorable influence on environment and genotype and selection for such traits may not be rewarding.

Genetic divergence

Clustering pattern: The classification of okra genotypes into different clusters based on D² value is given in Table 2. The material for present study included 52 genotypes grouped into nine clusters using Tocher's method. Of the nine clusters studied the cluster I was the largest having 37 genotypes. Genotypes usually did not cluster according to geographical distribution. There is no any direct relationship between geographical distribution and genetic distance.

Intra- and Inter-cluster distances: The average D² values of intra- and inter-cluster distances are given in Table 3. Intra-cluster distances revealed that cluster II with eight genotypes showed maximum intra-cluster diversity (D²= 159.65) followed by cluster I (D²= 99.85) with thirty seven genotypes. The clusters IV, V, VI, VII, VIII and IX had no intra-cluster distance (D²= 0.00) as they possessed single genotype. Maximum intra-cluster distance was observed in cluster III indicating existence of wide genetic divergence among

Table 2. Cluster composition based on D² statistics in okra

Cluster	Number of genotypes	Genotypes included in the cluster
I	37	BGKB-39, BGKB-44, BGKB-40, BGKB-41, BGKB-37, BGKB-31, BGKB-38, BGKB-34, BGKB-10, BGKB-24, BGKB-11, BGKB-15, BGKB-51, BGKB-18, BGKB-8, BGKB-19, BGKB-35, BGKB-33, BGKB-36, BGKB-52, BGKB-6, BGKB-9, BGKB-2, BGKB-13, BGKB-12, BGKB-42, BGKB-16, BGKB-47, BGKB-43, BGKB-5, BGKB-49, BGKB-17, BGKB-1, BGKB-46, BGKB-14, BGKB-3, BGKB-4
II	8	BGKB-21, BGKB-30, BGKB-25, BGKB-22, BGKB-20, BGKB-29, BGKB-27, BGKB-32
III	1	BGKB-45
IV	1	BGKB-7
V	1	BGKB-50
VI	1	BGKB-28
VII	1	BGKB-26
VIII	1	BGKB-23
IX	1	BGKB- 48

Table 3. Intra- and inter-cluster D² and D values in okra genotypes

Cluster	I	II	III	IV	V	VI	VII	VIII	IX
I	99.85	432.56	178.48	246.29	186.54	203.34	516.19	347.97	329.65
II		159.65	469.05	407.70	299.58	489.49	680.51	237.36	302.54
III			0.00	280.88	192.07	115.29	300.52	507.35	298.01
IV				0.00	295.13	415.12	713.87	597.74	326.74
V					0.00	95.34	265.90	249.77	254.05
VI						0.00	138.30	381.24	307.74
VII							0.00	687.68	396.91
VIII								0.00	413.72
IX									0.00

Diagonal values indicate intra-cluster distances

the constituent genotypes in it as compared to other clusters. 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. Maximum inter-cluster D² values were observed between the clusters IV and VII (D²= 713.87) followed by cluster VII and VIII (D²= 687.68), cluster II and VII (D²= 680.51), cluster IV and VIII (D²= 597.74), cluster I and VII (D²= 516.19) and cluster II and VI (D²= 489.49) indicating that the genotypes in these clusters can be used as parents in hybridization programme to get higher heterotic hybrids and segregating population contribution of characters. The cluster V had the least inter-cluster distance (D²= 95.34) with the cluster VI indicating that close relationship and less divergence between the genotypes were included in these clusters.

Contribution of characters to genetic divergence

Relative contribution of different characters to divergence is given in Table 4. Among these characters the number of ridges on fruit surface (32.5%) contributed to the genetic diversity followed by rind thickness (16.67%), seed yield per fruit (12.22%), fruit length (9.88%), number of fruits per plant (7.32%), fruit diameter (6.64%), plant height 45 DAS (6%), first flowering node (6%), average fruit weight (3.32%), plant height 90 DAS (3.09%), number of seeds per fruit (2.71%) and fruit yield per plant (2.11%).

Characters like number of nodes per plant (0.75%), internodal length 90 DAS (0.68%), number of leaves 90 DAS (0.38%), number of leaves 45 DAS (0.3%), number of branches per plant 45 DAS (0.15%) and internodal length 45 DAS (0.08%) contributed

Table 4. The mean values and per cent contribution of 21 characters for 52 genotypes of okra

Cluster	Character																				
	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21
I	41.01	141.83	17.05	23.83	3.47	3.94	2.71	3.60	40.69	45.53	6.14	48.17	20.16	350.12	17.61	13.69	1.89	1.42	5.16	4.27	58.07
II	39.58	113.41	18.89	22.63	4.40	4.69	2.83	3.83	44.75	50.69	7.69	60.34	20.47	355.35	18.33	10.22	2.27	1.49	7.78	5.49	85.34
III	37.35	124.05	13.40	17.50	4.50	4.50	2.15	2.84	40.50	44.50	5.30	39.80	22.84	435.10	19.05	12.07	1.95	2.40	5.15	5.12	74.72
IV	44.50	120.30	25.60	41.00	3.70	4.30	1.99	2.94	42.00	46.00	6.80	48.45	35.21	395.61	11.32	12.06	1.72	1.08	5.00	4.25	55.75
V	47.65	145.80	14.50	23.35	4.80	4.90	2.80	3.56	51.50	57.50	8.40	69.80	21.68	265.17	12.50	8.59	2.50	1.65	6.10	5.17	86.25
VI	37.60	152.50	18.40	28.90	4.40	4.80	2.80	3.37	46.00	51.50	8.40	60.90	15.43	287.05	18.59	10.11	2.57	2.55	5.05	3.19	72.09
VII	40.35	120.60	20.10	22.60	4.60	4.90	2.80	3.40	56.00	62.50	11.90	92.90	14.18	376.92	26.57	10.08	2.18	3.15	5.65	3.59	79.48
VIII	35.80	96.50	18.40	21.15	3.60	4.30	3.95	4.19	45.00	50.50	6.50	46.95	11.55	177.74	15.37	10.36	3.16	1.23	7.15	3.94	82.20
IX	45.10	120.35	13.40	23.85	2.50	3.25	2.64	3.64	41.00	46.00	6.60	47.60	7.42	208.65	28.22	13.19	1.76	1.63	5.50	4.05	62.65
#	6	3.09	0.3	0.38	0.15	*	0.08	0.68	*	*	6	0.75	7.32	2.11	3.32	9.88	6.64	16.67	32.5	12.22	2.71

#Contribution of individual character towards total genetic divergence (%), *Not contributed to total genetic divergence

1. Plant height (45 DAS) (cm), 2. Plant height (90 DAS) (cm), 3. Number of leaves (45 DAS), 4. Number of leaves (90 DAS),

5. Number of branches/plant (45 DAS), 6. Number of branches/plant (90 DAS), 7. Internodal length (45 DAS) (cm),

8. Internodal length (90 DAS) (cm), 9. Days to first flowering, 10. Days to first harvest, 11. First flowering node, 12. Number of nodes/plant,

13. Number of fruits/plant, 14. Fruit yield/plant (g), 15. Average fruit weight (g), 16. Fruit length (g), 17. Fruit diameter (cm),

18. Rind thickness (mm), 19. Number of ridges on fruit surface, 20. Seed yield/fruit (g), 21. Number of seeds/fruit

meagerly to the total divergence. Some of the characters like number of branches at 90 DAS, days to first flowering and days to first harvest did not contribute to genetic divergence. Similar observations were also made by Balai et al (2015), Ramya and Senthilkumar (2009), Reddy et al (2012), Kumar et al (2016b), Ramgiry and Singh (2017), Narkhede et al (2015) and Prabhat and Pathak (2012) for different characters in okra.

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