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Research Article

Nature and magnitude of genetic variability and diversity studies in okra (*Abelmoschus* esculentus L. Moench)

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Abstract:
In the present investigation, an attempt has been made to evaluate the genetic variability of yield contributing characters, and the genetic diversity in forty-four genotypes of okra collected from the IIHR, Bangalore, India. Analysis of variance indicated significant differences among the genotypes for different morphological characters. High GCV and PCV were observed for plant height, inter-nodal length, first flowering node, first fruit producing node, height of first flowering node, average fruit weight and number of seeds per fruit. On the basis of D^2 analysis, the 44 genotypes were grouped into twelve clusters. The cluster III was the largest with eight genotypes followed by cluster I and VIII with seven, cluster II with five, cluster XII with three while, clusters IV, V, VI, IX, X and XI included only two genotype in each. The intra-cluster distance was maximum in cluster XII (28.14), while inter-cluster distance was maximum between cluster VI and VIII (35.57) followed by I and IX (35.31), thus being a good source for attempting hybridization. Among the 44 genotypes, IIHR-238, IIHR-241 showed maximum number of fruits per plant and total yield per plant (g). The characters namely days to 50% flowering (35.62%), 100 seed weight (28.44%), number of seeds per fruit (17.23%) and average fruit weight (8.14%) directly contributed towards maximum divergence and, therefore, selection of divergent parents based on these characters is recommended for getting good hybrids or segregants in okra.

Keywords: Okra, genetic variability, heritability, genetic divergence, D^2 statistics.

Introduction

Okra (*Abelmoschus esculentus* L. Moench) is one of the important spring-summer and rainy season vegetable crops grown chiefly for its tender green fruits for consumption. It has high nutritive value, particularly 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). The high iodine content of fruits is useful in curing goiter disease and also possesses export potential. The high yielding varieties in okra has been developed by exploiting the genetic diversity available in the crop. The importance of genetic diversity for selecting parents in combination breeding of different autogamous crops to obtain transgressive segregants has been very well emphasized by Khanna and Mishra (1977), Singh and Ramanujam (1981) and Cox and Murphy (1990). Knowledge, nature and magnitude of variation existing in available breeding material are prerequisite to choose desirable genotypes to undertake planned breeding programme. Further, to improve the productivity, information about the nature and magnitude of genetic divergence would help selection of diverse parents, which upon hybridization might lead to effective gene recombinations. The available literature reveals that breeding programme on the basis of variability on the one hand and diversity on the other is scanty. The present investigation was, therefore, undertaken to evaluate the genetic variability for different characters to estimate the scope of advance for selection and diversity of genotypes for identification of suitable parents for hybridization to improve yield and yield attributing characters.

Material and methods

The experimental material for the present study consisted of 44 genotypes collected from Indian Institute of Horticultural Sciences (IIHR), Bangalore. The genotypes were evaluated through a field experiment conducted in randomized block design with three replication at the Vegetable Breeding Block, Indian Institute of Horticultural Research (IIHR), Bangalore, Karnataka. Each entry was sown at 30 cm between rows and 15 cm between plant, accommodating 30 plants in each row per replication. All the recommended package of practices was followed for raising a healthy crop. The observations were recorded as per NBPGR minimal descriptors from five competitive plants from each replication on twelve parameters *viz*., plant height (cm), inter-nodal length (cm), days to 50 % flowering, days to 80 % maturity, stem girth (mm), fruit length (cm), fruit width (mm), number of fruits per plant, average fruit weight (g), number of seeds per fruit, hundred seed weight (g) and total fruit yield per plant (g) computed in each genotype by adding the fruit weight of all the pickings and divided by number of plants. The mean

values were subjected to statistical analysis (ANOVA) as suggested by Panse and Sukatme, 1967. Phenotypic and genotypic co-efficient of variation (Burton and De-Vane, 1953), heritability and genetic advance as per cent mean (Johnson *et al*., 1955) were calculated. Genetic diversity between groups was estimated by using D^2 statistics given by Mahalanobis (1936) following the procedure given by Rao (1952). The mean values were computed to calculate D^2 values between all possible pairs of genotypes. The grouping of genotypes was done using Tocher's method as described by Rao (1952) and the relative contribution of different characters towards total divergence was calculated as per Singh and Choudhury (1985).

Results and discussion

The analysis of variance showed that the genotypes under study differed significantly among themselves for all the fifteen characters. The mean, range, genotypic variance (GV), phenotypic variance (PV), genotypic co-efficient of variance (GCV), phenotypic co-efficient of variance (PCV), heritability (h^2), genetic advance (GA) and genetic advance over mean (GAM) for different characters are presented in Table 1. Among 15 traits studied, the phenotypic variance ranged from as low 0.73 for hundred seed weight (g) to 8972.84 in total yield per plant. Plant height at full maturity stage exhibited a high phenotypic variance (1475.15) but next only to fruit yield (Indurani and Veeraragavathatham, 2005). The phenotypic co-efficient of variation ranged from 3.52% for days to 80% maturity to 33.84% for first fruit producing node. The genotypic variance was also high in respect of yield per plant (8400.00) followed by plant height (1333.24) similar to results found by Vijay and Manohar, (1990) and Rao (1996). The magnitude of PCV was higher than that of GCV for all the traits. The estimate of heritability was highest for hundred seed weight (98.93%), while it was least for stem girth (56.98). High magnitude of broad sense heritability (above 90 %) was noticed for average fruit weight, number of seeds per fruit, days to 50% flowering, first fruit producing node, yield per plant, plant height and hundred seed weight. Jeyapandi and Balakrishnan, (1992), Mahajan and Sharma, (1979) recorded maximum heritability for yield per plant, where as Gandhi *et al*. (2001) observed higher heritability estimates for plant height.

High heritability coupled with high GAM were observed for almost all the characters studied, except for days to 50% flowering and days to 80% maturity which showed high heritability with low GAM and confirming the preponderance of additive genes in controlling the expression of these characters and thus providing better opportunity for effective and reliable selection for these characters. These results are in agreement with the earlier workers Sarkar *et al*. (2004) and Panda and Singh, (1997). Moderate heritability with moderate to low genetic advance as per cent of mean was recorded for inter-nodal length and height of first flowering node. This might be attributed to the fact that the parental genotypes might have possessed both additive and/or non-additive genes for these traits in different magnitudes and as a result of more pronounced expression of non-additive genes moderate heritability with low genetic advance was noticed. These findings were also corroborated with the findings of Panda and Singh (1997) and Gandhi *et al*. (2001). Hence, selection for inter-nodal length and height of first flowering node may not be that much effective, as these traits are more influenced by environment.

After compiling D^2 values for all the possible pairs, the 44 genotypes were grouped into twelve clusters (Table 2). Number of genotypes per cluster ranged from two to eight. The cluster III was the largest with eight genotypes followed by cluster I and VIII with seven, cluster II with five, cluster XII with three genotypes while, clusters IV, V, VI, IX, X and XI had two genotypes each. The genotypes got distributed randomly among the different clusters irrespective of their geographical origin. Present results are similar to findings of Martin *et al.* (1981) and Mandal and Dana, (1993). The intra and inter-cluster distance D represent the index of genetic diversity among clusters as given in Table 3. The cluster XII (28.14) recorded the maximum intra cluster distance followed by cluster VIII (24.71). Maximum inter-cluster distance was observed between cluster VI and VIII (35.57) followed by that between cluster I and IX (35.31) suggesting thereby that the genotypes belonging to cluster I and IX and VI and VIII are more divergent than the rest of the clusters, can be undertaken in a hybridization programme for evolving good hybrids or segregants. The inter-cluster distance was least between cluster IV and V indicating close relationship among the genotypes included in these clusters.

Comparison of cluster means for different characters indicated considerable differences between clusters for all the characters (Table 4). Cluster VI had genotypes (IIHR-247, IIHR-249) with maximum plant height, days to 50% flowering, days to 80% maturity and stem girth. Cluster V had genotypes (IIHR-238, IIHR-241) recorded maximum number of fruits per plant and total yield per plant (g). Genotypes (IIHR-224, IIHR-225, IIHR-226, IIHR-227, IIHR-229, IIHR-230 and IIHR-231) in cluster

VIII recorded maximum mean values for fruit length and average fruit weight. Cluster X had (genotype IIHR-232, IIHR-244) maximum mean value for inter-nodal length; cluster XI had maximum number of seeds per fruit and cluster IV had maximum mean value for hundred seed weight. Per cent character contribution towards genetic divergence among the okra genotypes was maximum for days to 50% flowering (35.62%) followed by 100 seed weight (28.44%), number of seeds per fruit (17.23%) and average fruit weight (8.14%), showing selection of these characters (Table 4). Hence, the importance of selection for divergent parents based on these characters will be useful for heterosis breeding in okra.

Apart from the above findings it can be concluded that, selection and hybridization of genotypes from high divergent clusters VI (IIHR-247, IIHR-249) and clusters VIII (IIHR-224, IIHR-225, IIHR-226, IIHR-227, IIHR-229, IIH-230, IIHR-231) are expected to yield potential F1s and transgressive for further exploitation.

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Table 1. Estimates of mean, range, genotypic variance (GV), phenotypic variance (PV), genotypic coefficient of variance (GCV), phenotypic coefficient of variance (PCV), heritability (h^2), genetic advance (GA) and genetic advance over mean (GAM) for different characters

Characters	Mean ± S.Em	Range		GV	PV	GCV (%)	PCV (%)	h^2 (%)	GA	GAM (%)
		Min	Max							
Plant height (cm)	153.15 ± 6.88	63.33	214.33	1333.24	1475.15	23.84	25.08	90.38	71.51	46.69
Inter-nodal length (cm)	10.61 ± 0.80	6.33	15.80	5.27	7.21	21.62	25.29	73.06	4.04	38.08
Days to 50% flowering	45.80 ± 0.29	44.33	55.33	8.52	8.77	6.37	6.46	97.12	5.92	12.93
First flowering node	7.44 ± 0.51	5.00	13.33	4.81	5.60	29.49	31.83	85.89	4.19	56.32
First fruit producing node	7.20 ± 0.16	5.00	13.33	5.87	5.94	33.62	33.84	98.68	4.95	68.75
Height of first flowering node (cm)	23.79 ± 2.19	15.93	38.33	30.18	44.61	23.08	28.07	67.65	9.31	39.13
Days to 80% maturity	61.04 ± 0.47	59.33	66.00	3.96	4.62	3.26	3.52	85.59	3.79	6.21
Stem girth (mm)	16.28 ± 1.04	11.26	23.13	4.34	7.61	12.79	16.94	56.98	3.24	19.90
Fruit length (cm)	19.58 ± 0.86	9.90	30.56	15.32	17.56	19.98	21.39	87.23	7.53	38.46
Fruit girth (mm)	22.86 ± 0.86	16.14	36.86	9.88	12.11	13.75	15.22	81.57	5.85	25.59
Number of fruits per plant	10.51 ± 0.46	8.00	15.00	2.79	3.43	15.88	17.62	81.23	3.09	29.40
Average fruit weight (g)	42.08 ± 0.65	30.33	71.00	97.20	98.46	23.43	23.58	98.73	20.18	47.96
Number of seeds per fruit	62.14 ± 1.59	31.66	103.33	425.89	433.48	33.21	33.51	98.25	42.14	67.81
Hundred seed weight (g)	6.42 ± 0.05	4.63	8.27	0.72	0.73	13.26	13.33	98.93	1.74	27.10
Yield per plant (g)	514.61 ± 13.82	308.3	691.6	8400	8972.84	17.81	18.41	93.61	182.6	35.49

Table 2: Clustering patterns of 44 okra genotypes based on D^2 analysis

Cluster Number	No. of accessions in each cluster	Accessions Names
I	7	IIHR-15, IIHR-18, IIHR-20, IIHR-31, IIHR-55, IIHR-134, IIHR-181
II	5	IIHR-72, IIHR-81, IIHR-91, IIHR-10 (Arka Anamika), IIHR-04 (Arka Abhay)
III	8	IIHR-101, IIHR-108, IIHR-116, IIHR-133, IIHR-182, IIHR-213, IIHR-219, IIHR-239
IV	2	IIHR-237, IIHR-251A
V	2	IIHR-238, IIHR-241
VI	2	IIHR-247, IIHR-249
VII	2	IIHR-242, IIHR-252
VIII	7	IIHR-224, IIHR-225, IIHR-226, IIHR-227, IIHR-229, IIH-230, IIHR-231
IX	2	IIHR-243, IIHR-246
X	2	IIHR-232, IIHR-244
XI	2	IIHR-233, IIHR-240
XII	3	IIHR-245, IIHR-248, IIHR-250A

Table 3: Inter and intra-cluster (bold) distance (D) values in 44 genotypes of okra

Clusters	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII
I	21.28	28.19	19.44	21.83	27.88	34.51	21.04	33.77	35.31	17.76	33.28	30.91
II		18.99	22.54	27.54	24.68	28.04	20.32	28.71	20.79	26.29	24.76	25.56
III			17.28	19.63	23.73	30.51	15.74	29.51	29.46	16.56	28.08	27.38
IV				7.7	14.22	33.05	20.66	24.26	32.01	19.33	24.63	29.18
V					8.72	30.81	24.90	23.75	26.62	26.11	23.39	27.17
VI						9.3	29.16	35.57	19.74	31.97	32.72	21.21
VII							10.03	26.39	26.48	17.00	23.52	27.80
VIII								24.71	28.69	30.92	22.15	33.09
IX									14.21	32.77	24.96	22.76
X										17.97	30.66	29.00
XI											20.70	31.45
XII												28.14

Table 4: Cluster means for 12 quantitative parameters in okra based on D^2 analysis

Cluster Number	PH	INL	50% FLG	80% MAT	SG	Fr.L	Fr.G	No.FrPP	AFr.W	No.SPFr	100 SW	Yl.PP
I	157.09	8.71	44.95	60.61	15.24	17.26	19.77	10.66	33.95	51.57	7.15	456.66
II	122.73	9.30	44.66	59.93	16.29	15.67	25.06	10.80	39.13	64.00	5.69	530.00
III	163.29	10.22	44.66	60.12	15.98	19.16	23.13	10.95	35.7	57.29	6.74	531.25
IV	146.00	12.86	45.00	60.00	16.39	22.06	22.98	11.33	50.66	48.00	7.38	612.50
V	174.16	12.45	44.83	60.16	17.58	20.36	23.07	11.66	55.16	35.50	6.63	654.16
VI	194.33	11.30	55.33	65.66	18.74	18.81	23.84	9.66	37.83	69.50	5.18	433.33
VII	179.33	11.33	45.00	60.00	16.25	19.26	21.26	11.50	36.50	79.16	6.46	570.83
VIII	141.33	11.51	44.61	60.66	17.58	25.81	22.24	9.95	55.61	76.04	6.45	547.57
IX	142.5	12.66	49.00	65.66	15.44	19.06	23.54	10.16	43.5	72.83	4.93	456.66
X	184.83	14.40	44.66	60.33	14.59	19.56	21.89	9.00	33.83	57.16	7.01	454.16
XI	128.00	8.46	44.83	60.33	14.28	19.56	29.64	11.00	55.33	86.33	6.30	516.66
XII	143.77	10.05	50.44	64.00	16.96	19.65	23.01	9.22	39.22	55.11	5.66	438.88
% contribution of each trait in total divergence	0.53	1.58	35.62	0.74	0.00	4.02	2.01	0.63	8.14	17.23	28.44	1.06

Legend:

PH: Plant height (cm)
No.SPFr: Number of seeds/fruit
No.FrPP: Number of fruits/plant
Fr.L: Fruit length (cm)
80% MAT: Days to 80% maturity
INL: Inter-nodal length (cm)
AFr.W: Average fruit weight (g)
100SW: 100 seed weight (g)
Fr.G: Fruit girth (mm)
SG: Stem girth (mm)
50% FLG: Days to 50% flowering
Yl.PP: Yield per plant (g)