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Genetic Variability and Diversity for Yield and Yield Components in Okra

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Abstract The experiment was laid out in a randomized complete block design with 3 replications including 35 okra genotypes. Analysis of variance revealed that highly significant differences were observed among the genotypes for yield and seed quality traits indicating existence of genetic variability in the genotypes. The estimate of phenotypic coefficient of variation (PCV) was higher that the genotypic coefficient of variation (GCV) with narrow differences indicated most of the characters were less influenced by the environment which provides scope for improvement through simple selection. High heritability coupled with high genetic advance as per cent mean was observed for total chlorophyll content and number of branches per plant indicating predominance of additive gene action and amenability for phenotypic selection in early generations. Based on Mahalanobis D^2 analysis, 35 genotypes were grouped into 3 clusters and the cluster I (26) consisted highest number of genotypes. Among the traits studied plant height (21.18%), days to 50% flowering (17.14%), fruit weight (16.13%) and number of branches (10.08%) contributed maximum to the total genetic diversity.

Keywords Diversity, PCV, GCV, Heritability, Genetic advance.

Introduction

Okra [*Abelmoschus esculentus* (L.) Moench] is an annual herbaceous plant belongs to the family *Malvaceae* having a chromosome number of 2n=130. It is commonly known as 'bhendi' or lady's finger and is a priced vegetable grown for its tender fruits in India as vegetable. Okra being an often cross-pollinated crop, out-crossing to an extent of 20% by insects is reported which renders a considerable amounts of variability. Tender fruits of okra are used as vegetable or in culinary preparation as sliced and fried pieces. It has good nutritive value viz. 86.10%,water 2.20% protein, 0.20% fat, 9.70% carbohydrate, 1.0% fiber and 0.80% ash (Saifullah and Rabbani 2009) and also rich in vitamin C (30 mg/100 g), calcium (90 mg/ 100 g) and iron (1.5 mg/100 g) con 10t (Pal et al. 1952).

Genetic variability in the population is the most important pre-requisite of any breeding program. Higher variability has better chance for selecting the desirable genotypes. Further, the partitioning of total variability into its heritable and non-heritable components enables us to know the effectiveness of selection (Fisher 1918). Heritability which indicates the transmissibility of the character from parent to

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offspring is a useful measure for considering the ratio of genetic variance to the total variance. Heritability coupled with genetic advance is more useful and as heritability and phenotypic variation increases, the genetic advance also increases. Generally diverse plants expected to give high hybrid vigor and hence it necessitates study of genetic diversity among the existing germplasm collection for identification of more divers' parents for hybridization programs. The D^2 analysis is useful in choosing the parents for hybridization to recover superior transgressive segregants and it can further results into release of improved open pollinated varieties for commercial cultivation.

Materials and Methods

The experimental material comprised of 35 lines of okra collected from different sources were evaluated in a randomized complete block design with 2 replications at the College of Agriculture, Shivamogga, Karnataka during 2017-2018. The seeds were sown at the spacing of 45 cm between rows and 30 cm between plants. Protective irrigation, weed control and other cultural practices were followed as per the package of practices in order to raise good crop. The observations on plant height, number of branches per plant, inter nodal length, days to 50% flower, number of fruits per plant, fruit length, fruit diameter, number of ridges per fruits, number of vacuoles per fruit, fruit weight, fruit yield per plant, total chlorophyll content, crude fiber were recorded for statistical analysis to draw the conclusion. The mean data were subjected to estimate genetic components and divergence utilizing Mahalanobis D^2 statistic as suggested by Mahalanobis (1936) using statistical software *WINDOSTAT* 9.1 developed by *INDOSAT* services Ltd. Hyderabad, India. Accessions ground into various clusters following the Tocher's method as suggested by Rao (1952).

Results and Discussion

Analysis of variance revealed highly significant difference among genotypes for all the yield and yield attributing characters. The lines showed wide range of variation which provides ample scope for selection superior and desired lines for further improvement in okra. The range of values reflects the amount of phenotypic variability which is not reliable, since it includes genotypic,environmental and genotype × environment interaction components and does not reveal as to which character is showing higher degree of variability (Table 1). Further, the phenotype of crop is influenced by additive gene effect (heritable), dominance (non--heritable) and epistasis (non-allelic interaction). Hence, it becomes necessary to split the observe variability into phenotypic coefficient of variation and genotypic coefficient of variation, which ultimately indicates extent of variability existing for various traits. The estimation of heritability has greater role to play in determining effectiveness of selection for a character, provided it is considered

Table 1. Mean, range, genetic components of variance, heritability and genetic advance for yield and yield parameters in okra.PCV: Phenotypic coefficient variation, GCV : Genotypic coefficient variation, h^2 : Heritability in a broad sense, GA : Genetic advance, GAM : Genetic advance as per cent mean.

Characters	Mean ± SEm	Range	GCV (%)	PCV (%)	h^2(%)	GAM (%)
Plant height (cm)	75.99 ± 2.91	59.35-86.02	10.44	11.81	78	19.03
Number of branches per plant	1.48 ± 0.09	1.05-2.00	13.51	16.58	66	22.69
Inter nodal length (cm)	5.99 ± 0.18	5.45-6.29	2.86	5.28	29	3.19
Days to 50% flower	44.82 ± 1.52	41.00-48.00	3.06	5.77	28	3.34
Number of fruits per plant	21.23 ± 0.81	15.75-23.75	7.63	9.39	66	12.77
Fruit length (cm)	12.75 ± 0.47	11.50-14.15	5.56	7.67	52	8.29
Fruit diameter (cm)	13.18 ± 0.11	1.28-1.99	7.66	11.75	42	10.28
Number of ridges per fruits	5.27 ± 0.18	5.00-6.15	3.09	5.89	27	3.34
Number of vacuoles per fruit	5.26 ± 0.17	5.00-6.10	2.97	5.67	27	3.21
Fruit weight (g)	12.18 ± 0.38	11.46-14.37	5.73	7.12	64	12.77
Fruit yield per plant (g)	275.59 ± 14.25	208.73-321.89	7.15	10.31	48	10.23
Total chlorophyll content	45.94 ± 2.39	39.99-50.83	14.51	15.65	86	27.744
Crude fiber (mg/100g)	1.25 ± 1.61	0.95-1.55	6.21	8.01	60	9.92

Table 2. Clustering pattern of 35 okra genotypes.

Cluster number	Number of genotypes	Genotypes name
I	26	OkraB-5, OkraB-6, OkraB-4, Arka anamika, KRCCH-L37, KRCCH-L39, OkraB-2, OkraB-7, KRCCH-L43, UHSB-L21, KRCCH-L53, UHSB-L19, OkraB-1, KRCCH-L42, KRCCH-L50, UHSB-25, UHSB-L31, OkraB-3, UHSB-L30, UAHS-Line 2, UHSB-L28, UHSB-L35, UAHS-L1, KRCCH-L36, KRCCH-L31
II	8	KRCCH-L23, KRCCH-L24, KRCCH-L17, KRCCH-L5, KRCCH-L14, UHSB-L26, UHSB-L33
III	1	KRCCH-L16

in conjumction with the predicted genetic advance as suggested.

Moderate (10-20%) phenotypic coefficient of variance (PCV) and genotypic coefficient of variance (GCV) for number of branches per plant followed total chlorophyll content, plant height, fruit diameter, fruit yield per plant suggested that little influence of environment indicating the existence of limited variability in the genotypes evaluated for these traits (Table 1). Similar finding supported most of the characters by Daggi et al. (2013) and Shivaramegowda et al. (2016). The variance gives a measure of variation within a particular trait but it fails to provide areal measure for comparison of variances among different traits. The estimates of coefficient of variation provide a relative measure of variance among the different traits. Low (<10%) phenotypic coefficient of variance (PCV) and genotypic coefficient of variance (GCV) were recorded for characters like days to 50% flowering, number of ridges per fruits, number of vacuoles per fruit and fruit weight (Table 1). Similar results were observed by Dhankar and Dhankar (2002).

The phenotypic coefficient of variation was higfer than their respective genotypic coefficient of variation for all the traits under study (Table 1) which is in accordance with the studies of Das et al. (2012), and Duggi et al. (2013). In the present investigation high heritability estimates were recorded for plant height, number of branches per plant, fruit weight and total chlorophyll content. Similar results were reported by Panda Singh (1997). Moderate heritability was noted for fruit length, fruit yield per plant and crude fiber. Low heritability was noticed for days to 50% flowering, number of ridges per plant and number vacuoles per plant.Similar results were reported by Gandhi et al. (2002) and Dhankar and Dhankar (2002). Moderate to high heritability with high genetic advance as percentage of mean was observed for number of branches per plant, total chlorophyll content and plant height indicated predominance of additive gene component. Thus, there is an ample scope for improving these characters by direct selection. These results are in line the earlier reports.

Table 3. Intra (diagonal) and inter cluster distance (D^2) among different okra genotypes.

	Cluster I	Cluster II	Cluster III
Cluster I	**15.18**	29.71	60.88
Cluster II	29.71	**9.93**	28.90
Cluster III	60.88	28.90	**00**

Table 4. Cluster means for 11 characters among 35 genotypes of okra.

Characters	Cluster I	Cluster II	Cluster III
Plant height (cm)	80.03	64.95	59.35
Number of branches per plant	1.56	1.29	1.30
Inter nodal length (cm)	5.96	6.06	6.28
Days to 50% flower	44.48	45.63	47.50
Number of fruits per plant	21.96	19.56	15.75
Fruit length (cm)	13.04	11.91	11.84
Fruit diameter (cm)	1.70	1.82	1.47
Number of ridges per fruits	5.21	5.49	5.00
Number of vacuoles per fruit	5.21	5.48	5.00
Fruit weight (g)	12.97	13.09	15.75
Fruit yield per plant (g)	284.06	256.44	208.73

The study of genetic divergence among the 35 genotypes of okra genotypes was carried out by using Mahalanobis D^2 statistics. Thirty five genotypes of okra were grouped into 3 distinct non-overlapping clusters by using Mahalanobis D^2 statistics (Table 2). This indicated the presence of considerable genetic diversity among the genotypes. The major clusters in the above mentioned genetic divergence analysis contained frequently the genotyped of heterogeneous origin. Although of same origin or geographic region were also found to be grouped together in the same cluster. The instances of grouping genotypes of different origin or geographic region in same cluster

Table 5. Per cent contribution of different parameters towards the total divergence in okra.

Characters	Time ranked I[st]	Contribution (%)
Plant height (cm)	126	21.18
Number of branches per plant	60	10.08
Inter nodal length (cm)	14	2.35
Days to 50% flowering	102	17.14
Number of fruits per plant	46	7.73
Fruit length (cm)	57	9058
Fruit diameter (cm)	11	1.85
Number of ridges per fruits	42	7.06
Number of vacuoles per fruit	29	4.87
Fruit weight (g)	96	16.13
Fruit yield (g/plant)	12	2.02

were frequently observed. This suggested that there is no parallelism between genetic and geographical diversity. Cluster I had higest number of genotypes (26) followed by cluster II (8), whereas cluster III presented only one genotype (Table 2).

Intra-cluster distance revealed that cluster 1 with 26 lines showed maximum intra-cluster diversity(D^2= 15.18) followed by cluster II (D^2 = 9.93) with 8 lines. The clusters III had no intra-cluster distance (D^2 = 0.00) because it possess single line. Maximum intra-cluster distance was observed in cluster I indicating existence of wide genetic divergence among the constituent advanced lines in it as compared to other cluster. High degree of divergence among the advanced lines 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 observed by Prakash and Pitchaimuthu (2010), Akotkar and Pal (2010) Jeyapandi and Balakrishnan (1990). Based on distance between clusters (inter-cluster distances), the maximum divergence was observed between cluster I and cluster III (D^2=60.88) followed by between cluster I and cluster II (D^2 =29.71). Maximum inter-cluster D^2 values was observed between the clusters 1 and III indicating that the lines in these clusters can be used as a parents in hybridization program to get higher heterotic hybrids and segregating population contribution of characters (Table 3). Similar results were reported by Prakash and Pitchaimuthu (2010) and Sangamoni et al. (2014).

Cluster means for different presented in Table 4. The highest cluster mean for plant height was observed in the cluster 1 (80.03 cm) followed by cluster II (64.95 cm). Cluster III (6.28 cm) showed maximum cluster mean for intermodal length followed by cluster II (6.06 cm). Highest cluster mean for number of branches per plant was noticed in the cluster 1 (1.56 cm) and the maximum cluster mean for fruit length was noticed in cluster 1 (13.04 cm) followed by cluster II (11.91 cm), cluster II (13.09 cm) showed maximum cluster mean for fruit weight followed by cluster I (12.97 cm) and lowest cluster mean was observed in cluster II (12.23 cm). Cluster I (21 cm) showed maximum cluster mean for number of fruits per plant followed by cluster II (19.56 cm) and maximum cluster mean for days to 50% flowering was observed in cluster III (47.50 cm). Cluster I (284.06 cm) showed maximum cluster mean for yield per plant followed by cluster II (256.4 cm) and the lowest cluster mean was observed in cluster III (208.73 cm).

Among 11 characters included for D^2 analysis, plant height (21.18%) contributed maximum to the total genetic diversity among the genotypes followed by days 50% flowering (17.14%), fruit weight (16.13%), number of branches (10.08%), fruit length (9.58%), number of fruit (7.73%) and number of ridges (Table 5).

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