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Genetic Variability Study in Segregating Generations of Okra (*Abelmoschus esculentus* L.)

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A B S T R A C T

Segregating generations F_2, F_3, BC_1F_2 and BC_2F_2 were evaluated in randomized block design with three replication at Experimental Farm, Department of Agricultural Botany, College of Agriculture, Latur, Vasantrao Naik Marathwada Krishi Vidyapeeth, Parbhani during *kharif* 2017. The observations were recorded for traits days of first flowering (days), plant height (cm), intermodal length (cm), number of branches per plant, number of nodes per plant, fruit length (cm), fruit weight (g), fruit diameter (mm), number of fruits per plant, fruit yield per plant (g) for examine the genetic variability in segregating generations in the cross Arka Bahar x IC31032A. The data pertaining to the analysis of variance revealed that treatment variances were found highly significant for all the characters indicating presence of considerable amount of variability in the experimental material used in the present study. Mean performance revealed the superiority of Arka Bahar for internodal length, number of nodes per plant and length of fruit, IC31032A for fruit diameter, F_1 for plant height and number of branches per plant, BC_2F_1 for number of fruit per plant and fruit yield per plant, F_2 for early flowering, and fruit weight. The estimated of high genotypic and phenotypic coefficient of variation were observed for number of nodes per plant and fruit weight in F_2 generation, internodal length in F_3 generation, plant height, number of branches per plant, fruit diameter, number of fruit per plant and fruit yield per plant in BC_1F_2 generation, length of fruit in BC_2F_2 generation. The estimated of heritability was appreciably moderate for fruit weight in BC_1F_2. Higher heritability indicated less influence of environments. The genetic advance as per cent of mean was appreciably high for fruit yield per plant in BC_1F_2 and moderate for fruit weight and number of fruit per plant in F_2 and BC_1F_2 generation respectively. High GAM indicated influence of additive genetic action.

Introduction

Okra (*Abelmoschus esculentus* L.) is an annual herbaceous important vegetable crop that is grown for its young immature green fruit and fresh leaves in the tropical and subtropical parts of the world. Okra is generally self pollinated and belongs to family Malvaceae with 2n=130 chromosomes and amphidiploids in nature. Out of 34 species of *Abelmoschus*

only the species *Abelmoschus esculentus* is known to be cultivated in extensively as commercial vegetable. Okra is usually consumed for its green tender fruits as a vegetable in a variety of ways. The tender fruits are used as vegetable, eaten boiled or in culinary preparations as sliced and fried pieces. Its average nutritive value is higher than tomato, egg plant and most of the cucurbits Evaluation of potentialities of the existing cultivars is essential because it depicts the genetic diversity of the base materials on which depends the promise for further improvement. The success of a breeding programme for the improvement of quantitative attributes depends to a great extent on the magnitude of genetic variability existing in the germplasm. Burton (1952) suggested that genetic variability along with heritability should be considered for assessing the maximum and accurate effect of selection. Studies on the variability using genetic parameters like genotypic coefficient of variation (GCV), heritability and genetic advance is essential for initiating an efficient breeding programme. High yield can be achieved by selection of those characters that have high heritability values coupled with high genetic advance. Selection is an indispensable component of variety development process.

Materials and Methods

The experimental material was developed by involving two genetic diverse genotype viz. Arka Bahar and IC31032A, maintained through continuous selfing. The cross, Arka Bahar x IC31032A was effected in *kharif*, 2015-16 by hand emasculation and pollination. The F_1's and parents were grown in summer, 2016 to advance the F_2's and to prepare BC_1 and BC_2 crosses. The F_2's, BC_1 and BC_2 were grown and selfed during *Kharif*, 2016 to advance F_3, BC_1F_2 and BC_2F_2 generation. Thus seed of nine generation, P_1, P_2, F_1, F_2, F_3, BC_1, BC_2, BC_1F_2, BC_2F_2 and Parbhani kranti was considered as a local check to evaluate segregating generations during *kharif*, 2017. The experiment was conducted at experimental farm, department of agricultural botany, college of agriculture, Latur. The observations was recorded for characters ten characters on randomly selected five plants in P_1, P_2, F_1, BC_1, BC_2 and Parbhani kranti and each plant in F_2, F_3, BC_1F_2 and BC_2F_2 generation in each replication. Analysis of variance was carried out as per standard method of Panse and Sukhatme, 1954. The variance parameters of variability analysis were carried out as per Burton (1953).

Results and Discussion

Analysis of variance

The analysis of variance for genetic variability, heterosis and inbreeding depression in segregating generations was carried out for all studied ten characters revealed that mean sum of square for treatments in Arka Bahar x IC31032A cross showed highly significant differences for all the characters. This indicated existence of sufficient variation for effective selection for all the characters in the material under studied depicted in table 3.1.

Genetic variability, heritability and genetic advance

Day to first flowering was recorded moderate phenotypic coefficient of variation in BC_1F_2 (13.20%) generation. Low PCV recorded for F_2, F_3, and BC_2F_2 generations. Low genotypic coefficient of variation was observed for all the generations respectively. For days to first flowering, the moderate PCV and GCV values were exhibited by the BC_1F_2 population. Moderate heritability coupled with low genetic advance as per cent mean for BC_1F_2 generation. The result obtained in the present

study was in accordance with report of Badiger *et al.,* (2017), Akotkar *et al.,* (2010), Meena *et al.,* (2013), Guddadamath *et al.,* (2011), Sravanth (2017).

Highest phenotypic coefficient of variation with moderate genotypic coefficient of variation was recorded for plant height (cm) in all segregating generations. The heritability for this trait was low for all generations. Among the different generations F_2 progeny was moderate heritability coupled with low genetic advance as per cent mean and high PCV and moderate GCV. The result obtained confirm the earlier report of Sharma *et al.,*(2014), Guddadamath *et al.,* (2011), Mehta *et al.,* (2006), Sravanth (2017), Kandasamy (2015).

The low heritability for internodal length (cm) was identified in F_3 followed by BC_1F_2, BC_2F_2 and F_2 generations. F_3 progenies had moderate heritability coupled with moderate genetic advance as per cent mean. F_3 was recorded high PCV and moderate GCV followed by F_2, BC_2F_2, and BC_1F_2 population. Similar result reported by Badiger *et al.,* (2017), Simon *et al.,* (2013), Meena *et al.,* (2013), Singh *et al.,* (2017), Goswami (2014), Mallesh (2015).

BC_1F_2 progenies had low heritability coupled with high genetic advance as per cent mean. BC_1F_2 was recorded very high PCV and GCV followed by F_2, F_3, and BC_2F_2 population for the character number of branches per plant. This was in accordance with report of Yonas *et al.,* (2014), Meena *et al.,* (2013), Guddadamath *et al.,* (2011), Shivaramegowda *et al.,*(2016), Singh *et al.,* (2017)

The value of PCV and GCV recoded high and moderate respectively in F_2 for the trait number of nodes per plant. F_2 progenies had low heritability with moderate genetic advance expressed as per cent mean. The result obtained confirm the earlier report of Yonas *et al.,* (2014), Meena *et al.,* (2013), Guddadamath *et al.,* (2011), Singh *et al.,* (2017). Genotypic coefficient of variability was observed for trait length of fruit (cm) 12.66, 16.33, 20.00 and 18.84 percent in F_2, F_3, BC_1F_2 and BC_2F_2 generations respectively. Phenotypic coefficient of variability was observed 28.29, 37.48, 34.41 and 38.02 percent in F_2, F_3, BC_1F_2 and BC_2F_2 generations respectively. Across different population BC_2F_2 was recorded high PCV and moderate GCV. BC_2F_2 progenies had moderate heritability coupled with high genetic advance as per cent mean for length of fruit (cm). The result obtained confirm the earlier report of Singh *et al.,* (2017), Meena *et al.,* (2013), Shivaramegowda *et al.,*(2016).

The fruit diameter (mm) was recorded high and moderate PCV and GCV value respectively by the BC_1F_2 generation. BC_1F_2 progenies had low heritability with moderate genetic advance expressed as per cent of mean for fruit diameter.

The result obtained in the present study was accordance with report of Akotkar *et al.,* (2010), Guddadamath *et al.,* (2011), Yonas *et al.,* (2014), Das *et al.,* (2012), Mehta *et al.,* (2006).

Value of PCV and GCV for number of fruit per plant identified high and moderate respectively in BC_1F_2. BC_1F_2 progenies had low heritability coupled with moderate genetic advance expressed as per cent mean.

The result obtained confirm the earlier report of Guddadamath *et al.,* (2011), Yonas *et al.,* (2014), Sharma *et al.,*(2014), Sala and Shanthi (2016).

Generation F_2 was recorded for fruit weight high PCV and moderate GCV. F_2 progenies had low heritability coupled with moderate genetic advance expressed as per cent mean.

Table.1 Analysis of variance for different characters in okra

Source of variance	d.f.	Days to first flowering	Plant height (cm)	Inter-nodal length (cm)	No. of branches per plant	No. of nodes per plant
Replication	2	0.08	355.45	2.27	0.05	2.83
Treatment	9	8.32**	1062.95**	2.93**	0.14**	15.31**
Error	18	0.92	101.86	0.76	0.02	1.10
Source of variance	**d.f.**	**Length of fruit (cm)**	**Fruit diameter (mm)**	**No. of fruit per plant**	**Fruit Weight (g)**	**Fruit yield per plant(g)**
Replication	2	2.94	2.92	2.35	1.69	1304.71
Treatment	9	34.78**	31.42**	12.95**	8.73**	6645.13**
Error	18	1.97	1.53	2.45	1.50	725.66

** and * indicates significant at 1% and 5%, respectively

Table.2 Estimation of genetic variability parameters for ten quantitative traits in F_2, F_3, BC_1F_2 and BC_2F_2 generation of okra

Generation	Mean	Range	PCV	GCV	h^2 (%)	GA	GAM(%)
1. Days to First Flowering							
F_2	38.13	35.00 to 42.00	8.016	3.36	17.60	1.10	2.90
F_3	38.36	35.30 to 42.00	8.11	3.58	19.50	1.25	3.20
BC_1F_2	43.45	38.00 to 52.00	13.0	7.71	35.20	4.10	9.40
BC_2F_2	39.69	37.00 to 48.00	7.53	4.23	31.50	1.94	4.89
2. Plant Height (cm)							
F_2	150.11	85.00 to 206.66	26.88	11.33	17.80	14.77	9.84
F_3	137.43	95.00 to 190.00	23.83	10.09	17.90	12.10	8.80
BC_1F_2	128.85	91.66 to 181.66	26.51	15.65	34.90	24.54	19.04
BC_2F_2	154.68	101.60 to 203.30	25.29	13.34	27.90	22.45	14.51
3. Internodal Length (cm)							
F_2	8.57	5.30 to 11.60	23.88	10.467	19.20	0.81	9.44
F_3	7.66	5.44 to 11.66	24.23	14.15	34.10	1.30	17.03
BC_1F_2	9.59	7.63 to 12.73	18.84	9.63	26.10	0.973	10.14
BC_2F_2	9.23	6.6 to 11.53	20.63	10.48	25.80	1.01	10.97
4. Number of Branches per plant							
F_2	1.428	0.33 to 3.66	70.5	28.43	16.3	0.337	23.62
F_3	1.78	0.66 to 3.66	62.48	27.91	20.00	0.46	25.69
BC_1F_2	1.60	0.33 to 3.66	73.94	40.03	29.30	0.716	44.65
BC_2F_2	1.71	0.33 to 2.67	47.91	23.87	24.80	0.42	24.50
5. Number of Nodes Per Plant							
F_2	18.08	11.66 to 25.30	29.08	12.48	18.40	1.99	11.03

F_3	16.69	8.00 to 20.66	22.29	10.44	21.90	1.68	10.07
BC_1F_2	14.79	9.66 to 20.33	27.95	15.19	29.60	2.51	17.01
BC_2F_2	15.96	8.00 to 20.66	23.83	11.36	22.70	1.78	11.15
7. Length Of Fruit (cm)							
F_2	11.89	5.56 to 16.33	28.29	12.66	20.00	1.38	11.67
F_3	11.83	7.33 to 18.00	37.48	16.33	19.00	1.73	14.65
BC_1F_2	12.89	9.40 to 23.15	34.41	20.00	33.80	3.09	23.96
BC_2F_2	9.80	6.50 to 15.00	38.02	18.84	24.50	1.89	19.22
8. Fruit Diameter (mm)							
F_2	18.51	13.70 to 23.03	20.00	8.37	17.50	1.34	7.20
F_3	19.00	15.16 to 24.90	19.00	8.99	22.40	1.66	8.77
BC_1F_2	13.66	8.39 to 18.50	29.80	15.39	26.70	2.23	16.37
BC_2F_2	20.29	16.93 to 25.73	14.97	7.87	27.60	1.73	8.53
9. No. Of fruit Per Plant							
F_2	22.18	14.00 to 32.66	28.62	12.64	19.50	2.55	11.51
F_3	21.75	12.00 to 31.66	28.10	12.33	19.30	2.42	11.15
BC_1F_2	19.06	11.33 to 26.00	36.01	18.65	26.80	3.79	19.89
BC_2F_2	20.98	14.33 to 28.30	24.87	11.99	23.30	2.50	11.92
9. Fruit Weight (g)							
F_2	18.60	10.33 to 29.3	36.12	16.06	19.80	2.74	14.72
F_3	22.92	10.33 to 23	25.8	10.78	18.50	1.69	9.54
BC_1F_2	17.36	11.60 to 23.60	27.54	17.88	42.20	4.15	23.92
BC_2F_2	15.98	8.00 to 22.30	30.84	14.58	22.40	2.27	14.21
10. fruit Yield Per Plant (g)							
F_2	305.17	141.60 to 513.3	39.75	16.82	17.90	44.74	14.66
F_3	290.78	140.00 to 475.33	41.46	20.47	24.40	60.57	20.83
BC_1F_2	325.12	178.60 to 547.60	42.04	21.53	26.20	73.83	22.71
BC_2F_2	302.12	130.00 to 451.00	37.48	19.07	25.40	60.41	19.99

The result obtained confirm the earlier report of Meena *et al.,* (2013), Sharma *et al.,*(2014), Guddadamath *et al.,* (2011), Yonas *et al.,* (2014), Singh *et al.,* (2017).

The PCV was observed 39.75, 41.46, 42.04 and 37.48 per cent in F_2, F_3, BC_1F_2 and BC_2F_2 generations respectively for the trait fruit yield per plant (g). Whereas, GCV observed was 16.82, 20.47, 21.53 and 19.07 per cent in F_2, F_3, BC_1F_2 and BC_2F_2 generations respectively. High PCV and GCV values were exhibited by the BC_1F_2 population followed by F_3, F_2 and BC_2F_2 population. The result obtained in the present study were in accordance with report AdeOluwa *et al.,*(2011), Yonas *et al.,* (2014), Ahmad *et al.,*(2017), Akotkar *et al.,* (2010), Meena *et al.,* (2013), Guddadamath *et al.,* (2011), Yonas *et al.,* (2014), Shivaramegowda *et al.,*(2016), Das *et al.,*(2012), Singh *et al.,* (2017).

The estimated of high genotypic and phenotypic coefficient of variation were

observed for number of nodes per plant and fruit weight in F_2 generation, internodal length in F_3 generation, plant height, number of branches per plant, fruit diameter, number of fruit per plant and fruit yield per plant in BC_1F_2 generation, length of fruit in BC_2F_2 generation. The estimated of heritability was appreciably moderate for fruit weight in BC_1F_2. Higher heritability indicated less influence of environments. Hence, selection for this generation would be rewarding. The genetic advance as per cent of mean was appreciably high for fruit yield per plant in BC_1F_2 and moderate for fruit weight and number of fruit per plant in F_2 and BC_1F_2 generation respectively. The high GAM indicated influence of additive genetic action.

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