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Assessment of genetic variability in F_2 populations of okra [*Abelmoschus esculentus* (L.) Moench] for productivity traits

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Abstract
The present investigation was aimed to assess the extent of genetic variability in two F_2 populations of crosses, L43 × T44 and L22 × T36 with 250 plants each for yield and its component traits along with checks, carried out at the KRCCH Arabhavi. The analysis revealed the existence of significant amount of variation for the traits studied. High genotypic coefficient of variation and phenotypic coefficient of variation were observed for plant height, number of nodes, number of flowers, number of pods and pod yield in both the populations KRCCHO-1 and KRCCHO-2, indicating existence of broad genetic base where selection would be rewarding. Maximum heritability plus high GAM were observed for the characters *viz.*, plant height, days to first flowering, number of flowers days to first picking, in both the populations. This indicates preponderance of additive genes.

Keywords: Variability, genotypic coefficient of variance (GCV), phenotypic coefficient of variance (PCV), heritability, genetic advance over mean (GAM)

Introduction
Okra (*Abelmoschus esculentus* (L.) Moench) is one of the most liked vegetables in tropical and subtropical province around the world. Mainly grown for culinary purpose where green immature tender pods are used. For offseason use, pods are preserved with value addition by making pickles, dried slices or canned. The mucilaginous extract from immature pods used in different recipes like soups, stews and sauces as it adds consistency to the preparation (Guddadamath *et al.*, 2012) [4].

Ethiopia is considered as centre of origin of okra (Sathish & Eswar, 2013) [15]. Okra is herbaceous annual belongs to family Malvaceae. It has somatic chromosome number 2n = 130 and is considered as amphidiploid (Naveed *et al.*, 2009) [9]. In okra about 4-19% cross pollination takes place, of which 42.2 per cent due to insects attracted by its large showy attractive flowers and also because of protogyny nature, hence okra is classified under often cross pollinated crops Vrunda *et al*. (2019) [18]. Okra can be cultivated during both rainy and summer season in major agro-ecological zones of India since it is day neutral in response to photoperiod. In India okra has reached remarkable position, after onion, it shares about 60 per cent of 30 per cent exchange earning from export of fresh vegetables. It covers an area of about 0.511million ha and production around 6.219 million tonnes with productivity of 12.17 MT/ ha in India (2018-2019 1st advance NHB). Karnataka covers an area about 10.91 thousand ha and production around 98.91 thousand MT. Of the total production and area of Karnataka, Belagavi contributing around 162.8 thousand MT from area of 8.09 thousand ha (Anon., 2018) [1]. Key element in any crop improvement programme is the genetic variability. The nature and degree of genotypic and phenotypic variation plays an important role in formulating successful breeding programme for advancement of varieties (Priyanka *et al.*, 2018). The variation which is present naturally in population is considered enough for crop improvement. In case of scarce useful variability, it is essential to create variability through hybrid breakdown is most potential way in okra breeding (Priyanka *et al.*, 2019). The present investigation was aimed to assess the genetic variability in segregating population for yield improvement in okra.

Material and Methods
The experimental materials consist of 250 F_2 plants each in two populations which were developed from the cross, L43 × T44 and L22 × T36 and were compared with two check varieties and parents. Experiment was carried out at experimental block of vegetable science, KRCCH Arabhavi, Gokak taluk, Belagavi district of Karnataka.

All 250 plants along with checks were sown in pattern of unreplicated trials with spacing 60 × 45 cm with RDF given by UHS bagalkote. The observations were recorded on all the individually tagged 250 plants on thirteen characters (Table. 1). The data recorded from the experiment was subjected to various statistical analysis to estimate phenotypic and genotypic coefficients of variation, heritability in broad sense, genetic advance as per cent of mean as per Burton and De vane (1953) [2].

Results and Discussion

The analysis of variability showed that each plant differed significantly among themselves for all the fourteen traits in the material studied. The mean, range, genotypic (GCV) and phenotypic (PCV) coefficients of variation, heritability and genetic advance as per cent of mean for all the traits are presented in Table 1. The magnitude of PCV was higher than that of GCV for all the traits indicating that all the fourteen traits were influenced by the environment. High PCV and moderate GCV was observed for intermodal length (22.71 %, 14.22 %) in the population KRCCHO-1. Whereas the population KRCCHO-2 shown high PCV and moderate GCV for number of branches at final harvest (98.31 %, 14.11 %) and inter nodal length (23.13 %, 16.96 %), Moderate PCV and GCV (10-20 %) were noticed for stem girth (15.69 %, 10.97 %), days to first flowering (34.71 %, 32.73 %), days taken for first picking (11.25 %, 10.68 %) and Pod length (12.18 %, 8.40 %) in the populations KRCCHO-1. Moderate GCV and PCV stem girth (11.36, 14.91 %), days to first flowering (12.95 and 13.31 %), and days taken for first picking (11.85 %, 12.26 %) in population KRCCHO-2. Both the populations recorded Low GCV for pod diameter (KRCCHO-1-7.12 %, KRCCHO-2-4.87 %), pod weight (KRCCHO-1-7.12 %, KRCCHO-2-8.59 %).The low values indicate narrow range of variation for these characters and indicates least scope for improvement through selection. Similar observations were also reported by Gangashetty *et al.* (2010) [7], Prakash and Pitchaimuthu (2010) [10], Kavya *et al.* (2019) [6] and Mahesh *et al.* (2013) [7], Priyanka *et al.* (2019) [12] and Tukaram *et al.* (2019) [17].

The measures of heritability in broad sense and GAM are given in table 1. High heritability coupled with high GAM was observed for traits *viz.*, plant height, days to first flowering, number of flowers, days taken for first picking, pod length, number of pods per plant and pod yield per plant in both the populations KRCCHO-1 and KRCCHO-2. Low to moderate heritability accompanied with high genetic advance over mean was recorded for traits *viz.*, stem girth, inter nodal length, number of branches at final harvest, intermodal length, pod length and per pod in population KRCCHO-1, whereas KRCCHO-2 exhibited for traits stem girth, intermodal length, average pod weight and number of ridges per pod, low heritability along with low GAM was noticed for characters *viz.*, pod diameter, number of ridges per pod and average pod weight in the population KRCCHO-1 whereas, the population KRCCHO-2 exhibited for traits number of branches at final harvest and pod diameter. Results are in close conformity with previous studies of Sanganamoni *et al.* (2015) [14], Mehta *et al.* (2006) [8], Qhureshi (2007) [13], Tukaram *et al.* (2019) [17], Das *et al.* (2012) [3], Kandasamy (2015) [5] and Sharma *et al.* (2017) [16].

A higher value of heritability suggests only the existence of heritable portion but in combination with high GAM, the utility and efficiency increases. Genetic advance provides information regarding gene action, higher values indicates additive gene effects where selection will be rewarding for improvement of such characters. Thus pod yield can be improved by selecting pod length, plant height, days to first flowering, and number of flowers, days taken for first picking, pod length and number of pods per plant simultaneously in the present study.

Table 1: Estimates of mean, range, components of variance, heritability and genetic advance for growth, flowering and yield parameters in two F_2 populations of okra

Sl. No.	Characters	F_2 Population	Mean	Range	GV	PV	GCV (%)	PCV (%)	h^2 (%)	GA (%)	GAM (%)
growth and flowering parameters											
1.	Plant height	KRCCHO-1	125.45	30 to 210	1094.27	1241.56	26.37	28.09	88.14	63.97	51.00
		KRCCHO-2	131.80	31 to 210	899.10	1042.42	22.75	24.50	86.25	57.37	43.52
2.	Stem girth	KRCCHO-1	21.85	13.77 to 33.76	5.74	11.76	10.97	15.69	48.85	3.45	15.79
		KRCCHO-2	20.41	8.25 to 27.00	5.37	9.26	11.36	14.91	58.04	3.64	17.83
3.	Number of branches at final harvest	KRCCHO-1	0.56	0.00 to 3.00	0.02	0.51	27.14	127.69	4.52	0.07	11.88
		KRCCHO-2	0.71	0.00 to 3.00	0.01	0.48	14.11	98.31	2.06	0.03	4.17
4.	Total number of nodes	KRCCHO-1	15.00	5.00 to 26.00	16.15	19.61	26.80	29.53	82.34	7.51	50.09
		KRCCHO-2	15.81	5.00 to 29.00	11.84	15.71	21.76	25.07	75.36	6.15	38.92
5.	Internodal length	KRCCHO-1	9.05	4.40 to 14.20	1.66	4.23	14.22	22.71	39.22	1.66	18.35
		KRCCHO-2	9.00	4.20 to 14.80	2.33	4.33	16.96	23.13	53.77	2.31	25.62
6.	Days to first flowering	KRCCHO-1	54.18	45.00 to 73.00	41.11	42.79	11.83	12.07	96.07	12.95	23.89
		KRCCHO-2	58.16	46.00 to 73.00	56.76	59.92	12.95	13.31	94.73	15.11	25.97
7.	Number of flowers	KRCCHO-1	15.66	7.00 to 32.00	26.27	29.54	32.73	34.71	88.92	9.96	63.58
		KRCCHO-2	20.10	9.00 to 37.00	25.79	30.72	25.26	27.57	83.94	9.58	47.68
8.	Days taken for first picking	KRCCHO-1	60.53	51.00 to 80.00	41.82	46.38	10.68	11.25	90.16	12.65	20.90
		KRCCHO-2	64.82	51.00 to 80.00	59.01	63.13	11.85	12.26	93.47	15.3	23.60
Yield parameters											
9	Pod length (cm)	KRCCHO-1	13.23	6.77 to 19.84	1.23	2.59	8.40	12.18	47.57	1.58	11.93
		KRCCHO-2	14.56	10.25 to 36.55	3.56	4.73	12.96	14.93	75.42	3.38	23.19
10.	Pod diameter (mm)	KRCCHO-1	13.98	7.10 to 19.38	0.31	3.59	3.95	13.55	8.51	0.33	2.37
		KRCCHO-2	15.17	10.88 to 21.84	0.55	3.11	4.87	11.63	17.55	0.64	4.20
11.	Average pod weight (g)	KRCCHO-1	13.88	7.69 to 23.30	0.98	4.15	7.12	14.68	23.55	0.99	7.12
		KRCCHO-2	14.89	10.70 to 20.63	1.64	3.28	8.59	12.17	49.83	1.86	12.49
Sl. No.	**Characters**	**F2 Population**	**Mean**	**Range**	**GV**	**PV**	**GCV (%)**	**PCV (%)**	**h2 (%)**	**GA (%)**	**GAM (%)**
12.	Number of ridges per fruit	KRCCHO-1	5.03	5.00 to 5.60	0.00	0.01	1.35	2.31	33.93	0.08	1.62

		KRCCHO-2	5.03	5.00 to 5.60	0.01	0.01	1.66	2.19	57.72	0.13	2.61
13.	Number of pods per plant	KRCCHO-1	13.71	6.00 to 28.00	22.47	26.57	34.59	37.61	84.58	8.98	65.52
		KRCCHO-2	17.27	7.00 to 35.00	23.54	29.76	28.09	31.59	79.08	8.89	51.45
14.	Fruit yield per plant (kg)	KRCCHO-1	175.17	78.00 to 365.00	3866.92	4947.47	35.50	40.15	78.16	113.25	64.65
		KRCCHO-2	215.26	101.10 to 415.00	3602.28	4521.54	27.88	31.24	79.67	110.36	51.27

Note: PCV= Phenotypic coefficient of variation; h2=Heritability broad sense; GCV=Genotypic coefficient of variation; GAM=Genetic advance as per cent mean

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