



ISSN (E): 2277-7695  
ISSN (P): 2349-8242  
NAAS Rating: 5.23  
TPI 2023; 12(7): 2430-2434  
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[www.thepharmajournal.com](http://www.thepharmajournal.com)  
Received: 07-04-2023  
Accepted: 16-06-2023

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## Enhancement of heritability and genetic advance with respect to yield and yield contributing characters in Okra [*Abelmoschus esculentus* (L.) Moench.]

**Mousmi Syed, Somdutt Tripathi, Akansha Gupta, Shwetank Singh, Isha Ojha, Gaurav Mishra and Rajan Singh**

### Abstract

Sixty-eight okra as in access were evaluated for genetic variability, heritability, and genetic advance in okra at the Research Farm, Department of Agricultural Science, Shridhar University, Pilani (Rajasthan), during 2019-2020 respectively. Genetic variability analysis on 68 genotypes of okra disclosed high magnitude of genetic variability for the traits viz., pod yield and plant height under study. High magnitude of genotypic coefficient of variation for number of pod yield and plant height indicated high degree of genetic variability offering great scope for selection of these characters. The genotypes under study showed bearable heritability showed the environmental impact. High heritability coupled with high genetic gene action and more chances of fixing by selection to improve such traits. The genotypes viz., B -02, KS - 442 are noticed with great quiescent and can be utilized for enhancement of okra germplasm.

**Keywords:** Okra, *Abelmoschus esculentus*, genetic variability, heritability, genetic advance

### Introduction

Okra [*Abelmoschus esculentus* (L.) Moench.], 2n= 130, belonging to the family Malvaceae, is an vegetable crop cultivated throughout India. It is commonly known as Lady's finger (English), Bhindi (Hindi, Punjabi), Gandhamula (Sanskrit), Dheras (Bengali), Vendi (Tamil) and Venda (Telugu). It is native to Ethiopia from where it proliferated into Arabia and Europe. India is also considered its native place as ancestral wild forms have been found here (Yawalkar, 1965) [31].

Okra prefers warm- moist season and thrives successfully both in the plains and the hills. It is a short duration crop and grown as spring- summer and rainy season crop in northern India. In south India, where winter is mild and frost free, it is possible to grow okra throughout the year. Its immature and tender green fruits are used as vegetable. It is rich in carbohydrate (6.4%), protein (1.9%), fibre (1.2%), minerals and vitamins- A & B. Juice of stem and mature fruits are used for purifying cane juice in the manufacturing of jaggery. Decoction of immature fruits is emollient, demulcent and diuretic and useful in catarrhal affections, ardor urinae, dysuria and gonorrhoea. Mucilage of fruits and seeds is also emollient and demulcent and useful in gonorrhoea (Chopra *et al.* 1956) [6].

Okra is an erect growing and 1-2 m tall herbaceous annual. Leaves are alternate, broadly cordate, palmately 3-7 lobed and serrate. Flowers borne solitary and axillary with about 2 cm long peduncle. Calyx split longitudinally as flower opens. There are 5-7 cm long five petals of white colour with yellow- crimson spots on claw. Staminal column is united to the base of petals with numerous stamens, superior ovary and 5-7 deep red stigma. Capsule (fruit) light green, 10-30cm long, pyramidal oblong, longitudinally furrowed and dehiscent longitudinally when ripe. A flower bud takes about 22-26 days from initiation to full bloom. Anthesis and stigma receptivity occurs around 8-10am. Flowers remain open for short duration and wither late in afternoon. Okra is basically a self-pollinated crop but natural cross pollination to an extent of 8.75% may occur (Purewal and Randhawa, 1947) [23]. Hence, it is classified as often cross- pollinated crop.

Since okra is an autogamous crop, the breeding methods suitable for the self-pollinated crops can usefully be employed in this crop also. The crop offers several features viz adaptability to wide range of climatic conditions, erect growing habit, short life span, large size flower and monoadelphous and epipetalous nature of stamens which have a great value to breeder in achieving quick genetic results.

Large size flowers and monoadelphous condition of stamens facilitate hand emasculation. Its capsule produces a large number of seeds which is also a desirable feature for hybrid seed production. Being a short duration crop, it is possible to grow two generations in a year. Despite these qualities, no systematic studies have been made to generate information on quantitative traits which may be directly or indirectly related to yield and further improvement of this crop.

Genetic variability in the population is the most important prerequisite of any breeding programme. Variability, hidden or observable, among the different genotypes of a species is known as genetic diversity. Variability, only accounts for the observable phenotypic differences, which may be of genetic and/or environmental. Higher variability has better chance for selecting the desirable genotypes. Furthermore, the partitioning of total variability into its heritable and non-heritable components enables us to know the effectiveness of selection. Heritability, which indicates the transmissibility of the character from parent to offspring, is an useful measure for considering the ratio of genetic variance to the total variance. It may be based on total genetic variance and additive genetic variance, where latter is more important in selection breeding. Heritability indicates the possibility and extent to which improvement can be brought about through selection and it may be of broad and narrow senses (Robinson, 1966) [26].

However, heritability alone does not provide the true picture of genetic improvement to be made in subsequent generations. It is the genetic advance which predicts speed of genetic improvement for a particular intensity of selection. Heritability coupled with genetic advance is more useful, and as heritability and phenotypic variation increases, the genetic advance also increases. Thus, the primary requirement of a plant breeder is to have information on the genetic advances and direct and indirect influences of the plant characters on yield. The nature and degree of association between yield and its attributes claims distinct importance which assist the breeder to ascertain the actual yield components and furnish an effective basis of phenotypic selection.

## Materials and Methods

The present research work was conducted at the Research Farm, Department of Agricultural Science, Shridhar University, Pilani (Rajasthan), during 2019 – 2020 respectively. The genotypes which were chosen for the present study were grown in a randomized block design with three replications. Standard cultural and agronomic practices were followed to maintain healthy crop growth. Ten observations were recorded on five randomly selected plants in each replication for the morphological traits *viz.*, Days to 50% flowering, Plant height (cm), Number of fruits per plant, Fruit Length (cm), Fruit width (cm), Number of branches per plant, Number of fruiting nodes per plant, Number of first fruiting node, Tapering length of fruit (cm) and Pod yield per plant (g). The data were statistically analyzed the analysis of variance as per the standard statistical procedure (Panse and Sukhatme, 1985) [20]. Phenotypic and genotypic components of variance were estimated as per the formulae suggested by (Lush, 1940) [17]. The broad sense heritability was estimated by following the procedure suggested by Weber and Moorthy. Estimates of phenotypic and genotypic coefficients of variation were calculated as per the standard formulae (Burton and Devane, 1953) [3]. Genetic advance for each character was

predicted by the formula given by (Johnson *et al.*, 1955) [11].

## Results and Discussion

Analysis of variance disclose that the genotypes under study were highly significant for all characters studied indicating the presence of competent amount of genetic variability among the germplasm. Generally, the significant differences explain among the morphological traits may be diversified source of materials and also the result of environmental significance affecting okra genotypes. This substantiate findings of Ariyo (1993) [2] and Adeniji (2003) [1] who mentioned the role of environmental factors as well as differences in the genetic makeup of different varieties in yield determination of okra.

The mean range could give a rough estimate of the variability among the genotypes. The characters with high variability have more room for improvement. All the 18 characters under study showed high variability from the mean values. However, the characters marketable pod yield per plant, plant height, number of fruits per plant and number of first fruiting nodes having wide range of variation in mean values indicated the presence of high variability for these characters and thus more scope for the selection of desirable genotypes. Based on mean performance the accession no. 648-4-1 showed early for days to 50% flowering (40 days). Plant height showed high significant variance compared to the other traits. C1081 obtained maximum height of 112 cm while the genotype Arka Anamika obtained maximum height of 78 cm. Number of fruits per plant were obtained from accession no. 37 and least number of fruits per plant were obtained from accession no. 5135. Similarly, the genotype with maximum fruit length and fruit width was obtained from accession B-02 (14cm) while Parbhani Kranthi showed minimum among the genotypes (12.8 cm) for fruit length and 155-1-1-2-3 showed minimum for fruit width. Likewise, the maximum no of branches per plant and number of first fruiting node/ plan were obtained from KS-442 and genotypes SK4/8R/RS-8S showed minimum no of branches per plant and accession no 409 showed minimum number of first fruiting node/ plan respectively. Likewise, the maximum number of nodes per plant were obtained from 137-10-12 and genotypes SK4/8R/RS-8S minimum no of nodes per plant. Furthermore, Maximum pod yield was obtained from accession B-02 and minimum was from accession no. 446. These findings are in consonance with the findings of earlier workers (Dhankar and Dhankar, 2002; Singh *et al.*, 2006; Mohapatra *et al.*, 2007; Prakash *et al.* 2011; Reddy *et al.*, 2012; Khajuria *et al.* 2015; Jadhav *et al.* 2016; Shivaramgowda *et al.* 2016; Kerure *et al.* 2017) [8, 30, 19, 22, 25, 14, 10, 29, 13] in okra. For all the characters under study, phenotypic variances were higher than the corresponding genotypic variances showing the environmental factors influence the expression. The phenotypic variance was highest for number of branches per plant followed by number of first fruiting nodes per plant. Similarly, the genotypic variance was also highest for tapering length of fruit followed by pod yield per plant. Whereas the phenotypic and genotypic coefficient of variance was maximum for pod yield per plant followed by plant height and phenotypic and genotypic coefficient of variance was minimum obtained from width of the fruit followed by length of the fruit. High magnitude of PCV and GCV for above characters suggested greater phenotypic and genotypic variability among the populations and indicated that these

characters can be improved through phenotypic selection. The similar high PCV and GCV values were observed by (Kumar and Kumar, 2014; Patel *et al.* 2014; Saryam *et al.* 2015 Jadhav *et al.* 2016) <sup>[15, 21, 27, 10]</sup> for number of branches/plant at final harvest; (Kandasamy *et al.*, 2015; Jadhav *et al.*, 2016; Shivaramgowda *et al.*, 2016; Kerure *et al.*, 2017) <sup>[12, 10, 29, 13]</sup>; for fruit yield/plant; (Chaukhande *et al.*, 2011; Prakash *et al.* 2011) <sup>[5, 22]</sup>; for internodal length; (Kandasamy *et al.*, 2015; Khajuria *et al.*, 2015; Kerure *et al.*, 2017) <sup>[12, 14, 13]</sup> for number of fruits/plant and (Kandasamy, 2015; Khajuria *et al.*, 2015; Jadhav *et al.* 2016 and Shivaramgowda *et al.*, 2016) <sup>[12, 14, 10, 29]</sup> for plant height at final harvest. Heritability measures how important genetics is to a trait. A high heritability, close to 1, indicates that genetics explain a lot of the variation in a trait between different germplasm; a low heritability, near zero, indicates that most of the variation is not genetic. In addition broad-sense heritability, defined as  $H^2 = VG/VP$ , captures the proportion of phenotypic variation due to genetic values that may include effects due to dominance and epistasis. On the other hand, narrow-sense heritability,  $h^2 = VA/VP$ , captures only that proportion of genetic variation that is due to additive genetic values (VA). The estimates of heritability showed moderate magnitude for plant height, number of fruits per

plant, width of fruit, number of branches per plant, number of first fruiting nodes per plant, tapering length of fruit and pod yield per plant. This denotes the effect of environmental influence. Heritability depends on the range of typical environments in the population that is studied. If the environment of the population is fairly uniform, then heritability may be high, but if the range of environmental differences is very large, then heritability may be low. The heritability estimate provide the information on the magnitude of inheritance of quantitative characters but does not indicate the magnitude of genetic gain obtained by selection of best individual from the best population. So, heritability along with genetic advance is more useful than the heritability alone. In present study, high genetic advance coupled with high heritability was observed for pod yield and plant height. It indicated that additive gene action was more important for these characters which was in accordance to the findings of (Mazid *et al.*, 2013; Patel *et al.*, 2014; Deo, 2014; Saryam *et al.*, 2015; Khajuria *et al.*, 2015; Rao *et al.*, 2015; Shivaramgowda *et al.* 2016; Jadhav *et al.*, 2016; and Kerure *et al.* (2017) <sup>[18, 21, 7, 27, 14, 24, 29, 10, 13]</sup>. Therefore, improvement in these traits would be more effectively be done through selection in the present material.

**Table 1:** Mean performance of 68 genotypes of okra for different quantities character

Germplasm	Days to 50% Flowering	Plant Height (cm)	Fruits/Plant	Fruit Length (cm)	Fruit Width (cm)	Branches/Plant	Nodes/Plant	First Fruiting Node/Plant	Tapering Length of Fruit	Yield/Plant (g)
IC-28872	42.7000	89.57	9.37	14.05	1.79	2.16	6.55	2.32	193.66	192.65
IC-306053	42.4533	87.61	9.65	14.32	1.70	2.01	7.64	2.04	196.56	196.56
1773	41.7667	85.67	10.44	14.26	1.82	1.94	7.50	2.06	185.13	185.13
648-4-1	40.50	84.50	40.33	13.91	1.86	2.05	7.03	2.33	167.77	167.77
67-10-3	41.33	81.02	9.57	13.82	1.66	2.23	6.33	2.28	202.63	202.63
5135	41.93	81.64	8.88	13.44	1.88	2.04	6.90	2.34	179.44	179.43
10/21/2001	43.90	85.04	9.38	13.92	1.85	2.04	5.90	2.06	166.91	166.93
282-10-1	42.05	82.37	9.70	14.11	1.76	2.17	7.23	1.99	165.66	165.75
317-10-1	42.40	84.56	9.89	13.06	1.77	2.11	6.80	1.75	165.76	184.56
IC-11527	45.03	81.21	10.39	14.63	1.78	1.91	6.03	7.60	184.56	189.55
138-10-1	43.07	84.34	10.33	13.79	1.76	1.90	13.01	6.46	1.74	196.60
1999	45.32	85.34	10.11	13.55	1.79	2.23	12.20	7.44	1.73	202.40
135-10-1	44.20	84.55	10.55	13.73	1.75	1.82	12.73	7.23	1.71	176.66
155-1-1-23	43.66	87.91	11.33	13.72	1.73	2.06	13.11	6.20	1.87	170.66
68-10-12	41.90	91.66	10.44	13.67	1.71	1.96	13.33	6.70	1.86	186.46
629-7-12-3	41.88	93.21	10.33	13.41	1.84	1.96	13.40	6.66	1.81	170.80
SKX/QR/RS 10-7	42.55	92.72	10.77	13.88	1.88	1.99	13.70	7.52	1.80	182.99
231-10-1	42.70	91.20	10.68	13.42	1.93	1.93	12.80	7.22	1.83	177.33
223	44.60	92.32	10.45	13.85	1.82	1.73	11.80	6.30	1.93	180.16
1875	43.23	93.11	11.04	13.25	1.88	2.13	12.50	6.70	2.23	194.80
212-10-1	43.53	93.01	10.65	13.60	1.86	2.07	13.10	6.66	2.39	184.99
2A	44.46	93.03	12.19	13.77	1.96	1.91	13.45	7.53	2.35	197.01
263	43.22	92.44	12.17	13.17	1.94	2.06	12.30	6.96	2.14	186.55
SKA/TR/RS-113	44.05	92.14	12.16	13.88	1.86	2.34	12.33	6.45	2.00	199.55
454-10-1	42.44	91.44	11.55	13.87	1.80	2.07	13.33	7.63	1.71	202.44
37	44.06	89.01	12.90	13.49	1.95	2.93	13.00	6.28	1.81	191.77
IC-16902	44.42	83.33	12.04	12.92	1.96	2.06	13.40	6.44	1.74	164.72
EC-169367	44.16	89.02	12.33	13.11	1.97	2.30	13.13	7.63	1.77	177.05
307-10-12	43.10	86.03	11.76	13.87	1.86	2.66	13.03	6.28	1.86	186.81
409	44.03	95.01	10.77	14.66	1.79	2.33	12.40	6.90	2.03	171.66
167	46.33	98.11	11.07	14.67	1.80	2.00	14.60	6.77	1.91	176.13
326	46.33	93.89	10.87	14.57	1.78	2.03	12.40	7.66	1.90	184.70
108-10-21	44.33	94.37	10.46	13.44	1.86	2.10	11.63	8.41	1.64	153.66
238	44.43	98.92	10.40	13.04	1.84	1.98	12.88	7.67	1.73	150.80
217-10-1	44.40	88.53	9.99	14.05	1.91	1.99	13.45	7.34	2.15	148.03
446	43.04	91.71	10.91	13.94	1.83	2.03	13.72	7.44	2.28	155.60
1668	47.04	93.77	10.63	13.98	1.75	1.77	12.66	6.96	2.30	167.36

SK4/8R/RS-8S	46.33	93.19	10.93	14.09	1.81	2.16	12.36	7.30	1.87	150.76
770	44.33	96.33	11.00	13.66	1.86	2.33	13.54	5.60	1.95	161.70
118	45.44	95.34	11.54	13.65	1.84	2.46	13.80	6.93	2.07	150.77
177	45.98	105.96	11.54	13.45	1.88	2.56	13.63	7.83	2.25	161.60
SC-108	45.66	101.03	12.01	13.54	1.86	2.98	13.10	8.83	2.43	164.76
332-10-1	43.33	104.87	11.22	13.87	1.80	2.33	13.23	8.4	1.89	212.03
Parbhani	43.28	104.34	10.09	12.99	1.85	2.29	12.26	7.6	2.09	187.43
Kranti	44.60	102.03	11.07	14.65	1.92	2.33	12.86	7.5	2.07	216.00
FB-10	44.61	107.01	12.63	13.87	1.87	2.87	12.36	7.86	2.22	202.41
VR0-5	43.40	112.34	11.33	14.09	1.92	2.99	13.63	7.83	2.29	221.70
C1801 B0-2	42.26	112	12.91	14.82	1.81	2.09	12.35	8.00	2.34	231.83
VR0-03	43.54	107.88	11.22	14.18	1.99	2.83	13.53	8.06	2.28	214.53
KS-310	42.66	91.03	11.32	14.40	1.91	2.33	12.46	8.43	2.11	203.20
KS-404	42.45	93.00	11.98	14.09	1.97	2.54	12.76	9.23	2.17	179.63
Kashi Mohini	43.23	98.03	11.43	13.45	1.93	2.09	13.53	7.80	2.27	180.16
Kashi Lalima	41.71	101.31	10.88	13.09	1.96	2.45	14.03	7.53	2.16	171.80
Kashi Vibhuti	43.61	91.30	10.32	13.98	1.92	2.78	13.60	8.16	2.08	163.93
Kashi Pragati	43.40	94.11	10.09	13.87	1.97	1.77	13.34	8.23	1.85	188.90
Varsha Upkar	43.66	86.32	10.11	14.01	1.88	2.36	14.00	8.43	1.87	189.96
Utkal Gourav (2014)	41.73	79.02	9.89	13.89	1.78	2.98	14.12	7.41	1.74	186.96
Co-2 (2014)	42.53	84.01	12.22	13.99	1.77	2.32	13.06	8.65	1.89	209.06
Pusa Sawni	44.15	89.11	10.98	14.88	1.89	2.09	13.71	7.31	1.77	203.46
Arka Anamika	42.53	78.23	12.77	14.70	1.83	2.45	13.09	8.65	1.76	216.60
KS-442	42.08	91.43	11.23	13.76	1.89	3.07	12.78	7.01	2.16	203.20
KC-11-HR-4	43.88	86.99	12.09	13.77	1.86	2.98	12.11	8.03	2.08	179.63
KS-446	42.93	79.33	11.88	12.68	1.81	2.45	12.12	8.50	2.28	180.16
C8901	42.99	84.30	12.33	13.42	1.80	2.66	13.08	7.41	2.32	173.78
K-311	43.01	88.97	11.13	13.09	1.89	2.55	12.72	8.43	2.06	159.73
307-10-1	43.98	78.65	11.97	13.47	1.82	2.09	12.34	8.16	1.77	184.26
151-101-2-3	43.33	93.39	12.06	13.66	1.80	2.98	12.70	7.53	1.88	171.16
KS- 305 (AB-3)	43.08	91.01	11.56	13.68	1.85	2.03	12.86	7.80	2.03	188.90
Mean	43.48	92.41	10.94	13.84	1.85	2.13	13.09	7.31	2.00	183.33
C.V.	4.27	8.44	10.16	4.51	4.56	3.11	6.84	11.50	9.39	8.63
F ratio	3.10	5.89	3.60	2.32	4.50	3.97	2.89	5.30	7.90	8.64
F Prob.	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
S.E.	0.75	3.18	0.45	0.25	0.03	0.11	0.36	0.34	0.07	6.46
C.D. 5%	2.11	8.86	1.26	0.71	0.09	0.31	1.01	0.95	0.21	17.96
C.D. 1%	2.78	11.67	1.66	0.83	0.12	0.41	1.34	1.25	0.28	23.67
Range Lowest	40.50	78.49	8.93	12.89	1.69	1.70	11.63	5.60	1.64	148.03
Range Highest	47.03	112.69	12.90	14.83	1.99	3.03	14.60	9.23	2.43	231.83

**Table 2:** Analysis of Variance for the characters under study in Okra

Source of Variation	d.f.	X1	X2	X3	X4	X5	X6	X7	X8	X9	X10
Replication	2	0.60	0.53	0.19	0.06	0.37	0.81	2.55	3.12	0.63	0.96
Treatment	67	3.10	5.8	3.60	2.32	4.50	3.97	2.89	5.30	7.90	8.64
Error	335	3.45	60.92	1.23	0.39	0.007	0.78	0.80	0.70	0.035	250.50

\*\*Significant at 1% level; \*Significant at 5% level; d.f = degree of freedom; X1-Days to flowering; X2-plant height (cm); X3-Number of fruits per plant; X4-Length of fruit (cm); X5-Width of fruit (cm); X6-Number of branches per plant; X7-Number of nodes per plant; X8-Number of first fruiting nodes per plant; X9-Tapering length of fruit (cm); X10- Pod Yield per plant (g)

**Table 3:** Estimate of heritability, genetic advance in percent over mean for different characters under study in Okra

Characters	Variance			Co-efficient of variation			h <sup>2</sup> (Board Sense)	Gen. Adv Adv 5%	Gen. Adv 1%	Gen. Adv as % of Mean 5%	Gen. Adv as % of Mean 1%
	ECV $\sigma_e$	GCV $\sigma_e$	PCV $\sigma_e$	Var Env.	Var Genot.	Var Pheno.					
X1	4.27	2.53	4.97	3.45	1.21	4.67	0.26	1.16	1.48	2.66	3.41
X2	8.45	7.63	11.3	60.92	49.75	110.67	0.45	9.74	12.48	10.54	13.51
X3	10.1	6.7	12.8	1.24	0.54	1.78	0.30	0.83	1.06	7.59	9.73
X4	4.52	2.12	4.99	0.39	0.09	0.48	0.18	0.26	0.33	1.86	2.38
X5	4.56	3.49	5.74	0.01	0.00	0.01	0.37	0.08	0.10	4.36	5.59
X6	13.1	9.23	16.0	0.08	0.04	0.12	0.33	0.23	0.30	10.95	14.04
X7	6.85	3.84	7.85	0.08	0.25	1.06	0.24	0.51	0.65	3.88	4.97
X8	11.5	9.7	15.0	0.71	0.51	1.22	0.42	0.95	1.22	12.98	16.63
X9	9.39	10.0	13.7	0.04	0.04	0.08	0.54	0.30	0.39	15.19	19.46
X10	8.63	9.75	13.0	250.5	319.2	569.7	0.56	27.5	35.31	15.03	19.26

X1- Days to flowering; X2- plant height (cm); X3- Number of fruits per plant; X4- Length of fruit (cm); X5- Width of fruit (cm); X6- Number of branches per plant; X7- Number of nodes per plant; X8- Number of first fruiting nodes per plant; X9- Tapering length of fruit (cm); X10 – Pod Yield per plant (g).



## Conclusion

Based upon the present investigation, it is suggested that the genetic variability reported for different characters in relation to pod yield will be worthwhile for future genetic improvement of okra and the characters showing high heritability with high genetic advance viz., plant height, pod yield should be utilized in direct selection. The genotypes B-02, KS-442, performed and can be further utilized for breeding programs.

## References

- Adeniji OT. Inheritance studies in West African okra (*Abelmoschus caillei*). Agriculture Thesis, University of Agriculture, Abeokuta, Nigeria; c2003. p. 98.
- Ariyo OJ. Genetic diversity in West African okra (*Abelmoschus caillei* (A. Chev.) Stevels). Multivariate analysis of morphological and agronomic characteristics. Genetic Resource and Crop Evolution. 1993;40:25-32.
- Burton GW, Devane EM. Estimating heritability in fall fescue (*Festuca arundinacea*) from replicated clonal material. Agron. J. 1953;45:478-481.
- Calisir S, Ozcan M, Haciseferogullari H, Yildiz MU. A study on some physico-chemical properties of Turkey okra (*Hibiscus esculentus* L.) seeds. J Food Eng. 2005;68:73-78.
- Chaukhande P, Chaukhande PB, Dod VN. Genetic variability in okra (*Abelmoschus esculentus* (L.) Moench). Asian J Horti. 2011;6(1):241-246.
- Chopra RN, Nayar SL, Chopra CI. Glossary of Indian Medicinal Plants C, S. I. R., New Delhi; c1956.
- Deo C. Genetic analysis of pod yield and its contributing traits in okra (*Abelmoschus esculentus* (L.) Moench). Progressive Horticulture. 2014;46(1):71-75.
- Dhankar BS, Dhankar SK. Genetic variability, correlation and path analysis studies in okra (*Abelmoschus esculentus* (L.) Moench). Vegetable Science. 2002;29(1):63-65.
- Gul MZ, Bhakshu LM, Ahmad F, Kondapi AK, Qureshi ZA, Ghazi IA. Evaluation of *Abelmoschus moschatus* extracts for antioxidant, free radical scavenging, antimicrobial and antiproliferative activities using *in vitro* assays. BMC Complement Altern Med. 2011;11:64-75.
- Jadhav RA, Bagwale SB, Jawale LN, Deosarkar DB. Genetic variability studies for yield, yield contributing and quality traits in okra (*Abelmoschus esculentus* (L.) Moench). Indian J Agric. Res. 2016;50(6):614-618.
- Johnson HW, Robinson HF, Comstock RS. Estimates of genetic and environmental variability in soybeans. Agronomy Journal. 1955; 47:314-318.
- Kandasamy R. Variability studies in okra (*Abelmoschus esculentus* (L.) Moench). The Asian Journal of Horticulture. 2015;10(1):60-63.
- Kerure P, Pitchaimuthu M, Hosamani A. Studies on variability, correlation and path analysis of traits contributing to fruit yield and its components in okra (*Abelmoschus esculentus* (L.) Moench). Elec. J Pl. Bre. 2017;8(1):134-14.
- Khajuria RK, Sharma JP, Samnotra RK, Kumar S, Ranjit K. Variability studies in okra (*Abelmoschus esculentus* L.). Elec. J Pl. Bre; c2015. p. 226-234.
- Kumar P, Kumar R. Variability, heritability and character association in okra (*Abelmoschus esculentus* (L.) Moench). Asian Journal of Bio Science. 2014;9(1):9-13.
- Kumar SJ, Deepak A, Ghai TR. Variability studies for yield and its contributing traits in okra. Elec. J Pl. Bre. 2010;1(6):1495-1499.
- Lush JL. Intersire correlations and regression of offspring on dams as a method of estimating heritability of characters. Proceedings of American Society of Animal Breeding. 1940;33:293-301.
- Mazid, SMS, Mohrir MN, Jadhav RS. Genetic variability, heritability and genetic advance in okra (*Abelmoschus esculentus* (L.) Moench). Elec. J Pl. Bre. 2013;4(3):1255-1257.
- Mohapatra MR, Acharyya P, Sengupta S. Variability and association analysis in okra. The Indian Agriculturist. 2007;51(1, 2):17-26.
- Panse VG, Sukhatme PV. Statistical methods for agricultural workers. Indian Council of Agricultural Research Publication; c1985. p. 87-89.
- Patel R, Sengupta SK, Verma AK. Studies on genetic parameters in okra (*Abelmoschus esculentus* (L.) Moench). Trends in Biosciences. 2014;7(14):1808-1811.
- Prakash K, Pitchaimuthu M, Venugopalan R, Hongal S, Jainag K. Variability, heritability and genetic advances studies in okra (*Abelmoschus esculentus* (L.) Moench). The Asian Journal of Horticulture. 2011;6(1):124-127.
- Purewal SS, Randhawa GS. Studies in *Hibiscus esculentus* (Lady's finger). Chromosome and pollination studies. Indian J Agric. Sci. 1947;17:129-136.
- Rao AM, Kumar S, Phanikrishna M, Begum H. Estimation of heritability and genetic advance in okra (*Abelmoschus esculentus* (L.) Moench). Plant Archives. 2015;15(1):489-491.
- Reddy MT, Haribabu K, Ganesh M, Begum H, Reddy RVSK. Exploitation of heterosis for growth earliness and yield attributes in okra (*Abelmoschus esculentus* (L.) Moench). International Journal of Plant Breeding. 2012;6(1):53-60.
- Robinson HS. Quantitative genetics in relation to breeding on the central of mendalism. The Indian Journal of Genetics and Plant Breeding. 1966;26:171-187.
- Saryam DK, Mitra SK, Prajapati S, Singh OP, Mehta AK. Assessment of genetic variability for various yield and yield attributing traits in okra (*Abelmoschus esculentus* (L.) Moench) under Kymore Plateau & Satpura hills agro-climatic regions of Madhya Pradesh. Current Advances in Agric. Sci. 2015;7(2):177-179.
- Schafleitner R, Kumar S, Lin C, Hegde SG, Ebert A. The okra (*Abelmoschus esculentus*) transcriptome as a source for gene sequence information and molecular markers for diversity analysis. Gene. 2013;17:27-36.
- Shivamegowda KD, Krishnan A, Jayaramu YK, Kumar V, Yashoda, Hee-Jong Koh. Genotypic variation among okra (*Abelmoschus esculentus* (L.) Moench) Germplasms in South India. Plant Breed. Biotech. 2016;4(2):234-241.
- Singh B, Pal AK, Singh S. Genetic variability and correlation analysis in okra (*Abelmoschus esculentus* (L.) Moench). Indian Journal of Horticulture. 2006;63(3):63-66.
- Yawalkar KS. Vegetable crops of India. III Ed. 1965. Agri. Horticultural Publishing House, Nagpur; c1965.