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## Genetic variability studies in the indigenous and exotic accessions of okra (*Abelmoschus* spp.) under Konkan conditions

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### Abstract

Twenty six genotypes of okra including indigenous and exotic lines were evaluated for fourteen yield and yield attributing traits during *summer* 2018 in randomized block design with three replications at Education and Research Farm, Department of Agricultural Botany, College of Agriculture, Dr. Balasaheb Sawant Konkan Krishi Vidyapeeth, Dapoli, Ratnagiri, Maharashtra, India. The analysis of variance (ANOVA) revealed significant differences for all the fourteen traits under study suggesting the existence of required genetic variation in the breeding material. Higher PCV and GCV estimates were recorded by plant height, fruit length, fruit yield per plant, shoot and fruit borer incidence on fruits, number of fruits per plant and yellow vein mosaic virus percent disease incidence. Moderate PCV and GCV was registered by fruit weight, internodal length, fruit diameter, number of nodes at first flowering, days to initiation while days to 50% flowering, number of locules per fruit and number of ridges per fruit recorded low PCV and GCV. High to very high heritability (broad sense) was observed for all the traits except number of ridges per fruit, number of locules per fruit and individual fruit weight. These three traits registered moderate heritability. High Genetic Advancement as percent of mean was recorded by some of the traits except internodal length, fruit diameter, Number of nodes at first flowering, fruit weight, days to initiation, number of ridges per fruit, number of locules per fruit and days to 50% flowering. The presence of variability in the germplasm helps in progressing the elite genotypes to utilise in breeding programme.

**Keywords:** Variability, heritability, genetic advance, okra

### Introduction

Okra [*Abelmoschus esculentus* (L.) Moench], is an imperial vegetable crop of the Malvaceae family in the tropics, sub-tropics and warmer portions of the temperate region of the world on a varying scale. Globally, India enjoys the first place in the area and production of okra with an annual production of 6094.9 metric tons (70% of the total world production) from over 509-thousand-hectare area with a productivity of 12 metric tons per hectare area (Horticulture Statistics at a glance, 2018). Although the productivity of okra in India is higher (11.6 tonnes ha<sup>-1</sup>) than world average productivity (7.35 tonnes ha<sup>-1</sup>), it is lower than that of Ghana (21 tonnes ha<sup>-1</sup>) (Horticultural Statistics at a glance, 2018). Low yielding potential of current varieties was due to yield plateau and reduction in yield. Frequent attacks of pests and diseases, especially the fruit and shoot borer (FSB) and yellow vein mosaic virus (YVMV) has become one of the serious problem for yield reduction in okra. Further, being a potentially self pollinated crop, the cultivated okra has a narrow genetic base and concerned efforts, are therefore, required for exploring the full potential of available okra germplasm resources in the gene bank. Hence the present research was carried out to evaluate the variability in the unexploited germplasm of okra collected from NBPGR and use the elite germplasm among them for further breeding.

### Materials and Methods

Twenty six accessions (including both indigenous and exotic) were sown in a randomized block design of three replication during *summer* 2018 at the Botany Farm, D.B.S.K.K.V., Dapoli. Each entry was sown in two rows of 3 m length with a row to row spacing of 45 cm and plant to plant spacing of 30 cm (45cm × 30cm) in broad beds. All the recommended agronomic package of cultivation practices were followed timely for successful raising of crop. The data were subjected to analysis of variance as per the method described by Panse

and Sukhatme (1985) [20]. The observations were recorded from the five randomly selected plants of each replication for fourteen yield and its attributing characters viz., days to first flower initiation, days to 50% flowering, plant height (cm), first flowering node, internodal length (cm), number of locules per fruit, fruit length (cm), number of ridges per fruit, fruit diameter (cm), individual fruit weight (g.), number of fruits per plant, fruit yield per plant (g.), yellow vein mosaic virus percent disease incidence and percent fruit infestation by okra shoot and fruit borer. Various variability parameters like mean, range, coefficient of variation, PCV, GCV, genetic advance and heritability were calculated using their respective formulae.

**Estimation of mean and range:** The mean values for each character were worked out by dividing the total by corresponding number of observations:

$$\bar{X} = \frac{\sum_{i=1}^n X_i}{n}$$

Where,  $\bar{X}$  = Mean of character

$\sum X_i$  = Total of all the observations for character

N = Number of observations

The lowest and highest values of mean of each character represented the range.

**Estimation of coefficient of variation:** The genotypic and phenotypic coefficients of variation were calculated by using following formulae given by Burton, (1952).

i) Genotypic coefficient of variation (GCV)

$$GCV (\%) = \frac{\sigma^2_g}{\bar{X}} \times 100$$

**Where**

$\sigma^2_g$  = Genotypic variance and,  $\bar{X}$  = Mean of character

ii) Phenotypic coefficient of variation (PCV)

$$PCV (\%) = \frac{\sigma^2_p}{\bar{X}} \times 100$$

Where,  $\sigma^2_p$  = Phenotypic variance and,  $\bar{X}$  = Mean of character  
GCV and PCV estimates were classified as

Low: < 10 per cent,

Medium: 10 to 20 per cent

High: > 20 per cent.

**Estimation of heritability (B.S.):** Heritability in broad sense was estimated for various characters as suggested by Hanson *et al.* (1956).

$$h^2 = \frac{\sigma^2_g}{\sigma^2_p} \times 100$$

Where,  $h^2$  = Heritability  $\sigma^2_g$  = Genotypic variance  $\sigma^2_p$  = Phenotypic variance

The high, medium and low heritability estimates were classified on the basis of following:

Low heritability = < 10%

Moderate heritability = 10-30%

High heritability = > 30%

### Genetic advance (G.A.)

Genetic advance (at 5% selection intensity) was calculated using the formula given by Allard (1960).

i) Genetic advance (G.A.)

$$G.A. = k \times \frac{\sigma^2_g}{\sigma^2_p} \times \sqrt{\sigma^2_p}$$

Where,  $\sigma^2_g$  = Genotypic variance

$\sigma^2_p$  = Phenotypic variance

k = Selection differential (at 5% selection = 2.06)

ii) G.A. as percentage of means (GAM):

$$GAM = \frac{GA}{\bar{X}} \times 100$$

Where, G.A. = Genetic advance  $\bar{X}$  = Character mean

GA (As percentage of mean) was classified as

Low: 10 per cent

Medium: 10 to 20 per cent

High: > 20 per cent

### Results and Discussion

The analysis of variance (ANOVA) for twenty six genotypes of okra revealed significant differences for all the fourteen traits under study (Table 1). These results are in agreement with Khajuria *et al.* (2016) [16], Patil *et al.* (2017) [21], Singh *et al.* (2017) [25], Makhdoomi *et al.* (2018) [17], Syfullah *et al.* (2018) [26], Kumar *et al.* (2019) and Shashikala (2019) [24]. Significant differences among the genotypes of okra justified the presence of variability as depicted by ANOVA. The presence of variability encouraged the selection of above material for further breeding activities in okra.

**Table 1:** Analysis of variance for yield, yield attributes in twenty six (26) genotypes of okra

S. No.	Traits	Mean Sum of Squares		
		Replication	Genotypes	Error
		2 (DF)	25 (DF)	50 (DF)
1.	Days to flower initiation	1.50	50.37**	3.18
2.	Days to 50% flowering	1.63	42.45**	2.65
3.	Plant height	190.22	1567.17**	62.77
4.	First flowering node	0.15	1.00**	0.08
5.	Internodal length (cm)	0.14	2.05**	0.24
6.	Number of ridges per fruit	0.04	0.98**	0.16
7.	Fruit length (cm)	0.37	14.26**	0.33
8.	Number of locules per fruit	0.04	0.98**	0.16
9.	Fruit diameter (cm)	0.06	0.18**	0.02
10.	Fruit weight (gm)	4.37	15.12**	2.71
11.	Number of fruits per plant	4.04	89.07**	1.68
12.	Fruit yield per plant (g)	976.05	8900.62**	745.41
13.	FSB infestation on fruits (%)	7.82	175.19**	3.67
14.	YVMV incidence (%)	2.24	777.18**	11.91

\*-0.05% significant \*\*-0.01% significant

Table F value:

Replications- 3.18 (0.05%) 5.06 (0.01%)

Treatments- 1.718 (0.05%) 2.15 (0.01%)

### Genetic variability parameters

Knowledge of nature and magnitude of variation existing in the available breeding materials are requisite to choose characters for effective selection of desirable genotypes to undertake planned breeding programme (Akotkar *et al.* 2010) [2]. The information regarding the mean, range, coefficient of

variation, heritability and genetic advance is presented in table 2, figure 1 and figure 2.

For the trait, days to flower initiation, moderate PCV (12.52), moderate GCV (11.42), high heritability (83.18%) and low GAM (21.46) were observed. The evaluated germplasm had their first flower initiation within the range of 29 to 42 days. High heritability of this trait suggests that selection for this trait would be effective. The results are in agreement with the findings reported by Mishra *et al.* (2015)<sup>[18]</sup>, Makhdoomi *et al.* (2018)<sup>[17]</sup>, Syfullah *et al.* (2018)<sup>[26]</sup>, Alake *et al.* (2019)<sup>[3]</sup>. Low PCV (8.45), low GCV (7.71), high heritability (83.32%) and low GAM (14.50) were recorded for the trait days to 50% flowering. Between 43 days to 55 days the evaluated germplasm were at their 50% flowering stage. The results were in agreement with those reported by Prakash and Pitchaimuthu (2010)<sup>[22]</sup>, Mishra *et al.* (2015)<sup>[18]</sup>, Patil *et al.* (2017)<sup>[21]</sup>, Singh *et al.* (2017)<sup>[25]</sup>.

The trait plant height recorded a range of 68.00 cms to 135.50 cms, higher PCV (23.09), high GCV (21.77), high heritability (88.88%) and high GAM (42.27). Burton (1952) has suggested that GCV together with heritability estimates would give the best option expected for selection. These findings are in agreement with Prakash and Pitchaimuthu (2010)<sup>[22]</sup>, Majid *et al.* (2013)<sup>[16]</sup>, Barche *et al.* (2014)<sup>[7]</sup>, Bello *et al.* (2015), Bagwale *et al.* (2016), Badiger *et al.* (2017), Patil *et al.* (2017)<sup>[21]</sup>, Singh *et al.* (2017)<sup>[25]</sup>, Syfullah *et al.* (2018)<sup>[26]</sup>, Agbowura *et al.* (2019), Alake *et al.* (2019)<sup>[3]</sup>, Kumar *et al.* (2019).

Moderate PCV (14.18), moderate GCV (12.60), high heritability (78.97%) and low GAM (23.07) was observed for the trait first flowering node. The evaluated germplasm had their first flowering node within the range of 3.13 to 5.63. The results are in agreement with Patil *et al.* (2017)<sup>[21]</sup>.

The trait internodal length has reported a range of 4.07 to 7.07 cms, moderate PCV (16.96), moderate GCV (14.31), high heritability (71.19%) and low GAM (24.87). These findings are in confirmation with those of Jindal *et al.* (2010).

Low PCV (12.20), low GCV (9.71), moderate heritability (63.30) and low GAM (15.91) were reported by the trait of number of ridges per fruit. These results are in accordance with Patil *et al.* (2017)<sup>[21]</sup>. Moderate PCV and low GAM were reported for this trait by Khajuria *et al.* (2016)<sup>[14]</sup>.

For the trait, fruit length, range of 6.87 to 13.87cms, high

PCV (21.29), high GCV (20.57), high heritability (93.41%) and high GAM (40.96) were observed. These findings are in accordance with those of Reddy *et al.* (2012), Bello *et al.* (2015), Muluken *et al.* (2016).

Number of locules per fruit has recorded low PCV (12.20), low GCV (9.71), moderate heritability (63.30) and low GAM (15.91).

Moderate PCV (16.11), GCV (13.82), high heritability (73.57%) and low GAM (24.52) was observed for fruit diameter. The fruit diameter of the evaluated germplasm ranged from 1.40 to 2.30 cms. Exotic germplasm had highest fruit diameter when compared to indigenous germplasm. These findings are in accordance with the results of Jindal *et al.* (2010), Patil *et al.* (2017)<sup>[21]</sup>, Makhdoomi *et al.* (2018)<sup>[17]</sup>.

Fruit weight has recorded moderate PCV (17.96), moderate GCV (13.96), moderate heritability (60.42) and low GAM (22.36). The trait fruit weight of the evaluated 26 germplasm lines ranged from 10.93 to 19.32gms. Low GAM was reported by Jindal *et al.* (2010), Chandramouli *et al.* (2016), Singh *et al.* (2017)<sup>[25]</sup>, Makhdoomi *et al.* (2018)<sup>[17]</sup>.

High PCV (35.80), high GCV (34.81), high heritability (94.55%) and high GAM (69.72) was observed for number of fruits per plant. The number of fruits per plant ranged from 8.70 to 24.83. The results are in conformation with those of Reddy *et al.* (2012), Majid *et al.* (2013)<sup>[16]</sup>, Khajuria *et al.* (2016)<sup>[14]</sup>, Badiger *et al.* (2017), Patil *et al.* (2017)<sup>[21]</sup>, Syfullah *et al.* (2018)<sup>[26]</sup>.

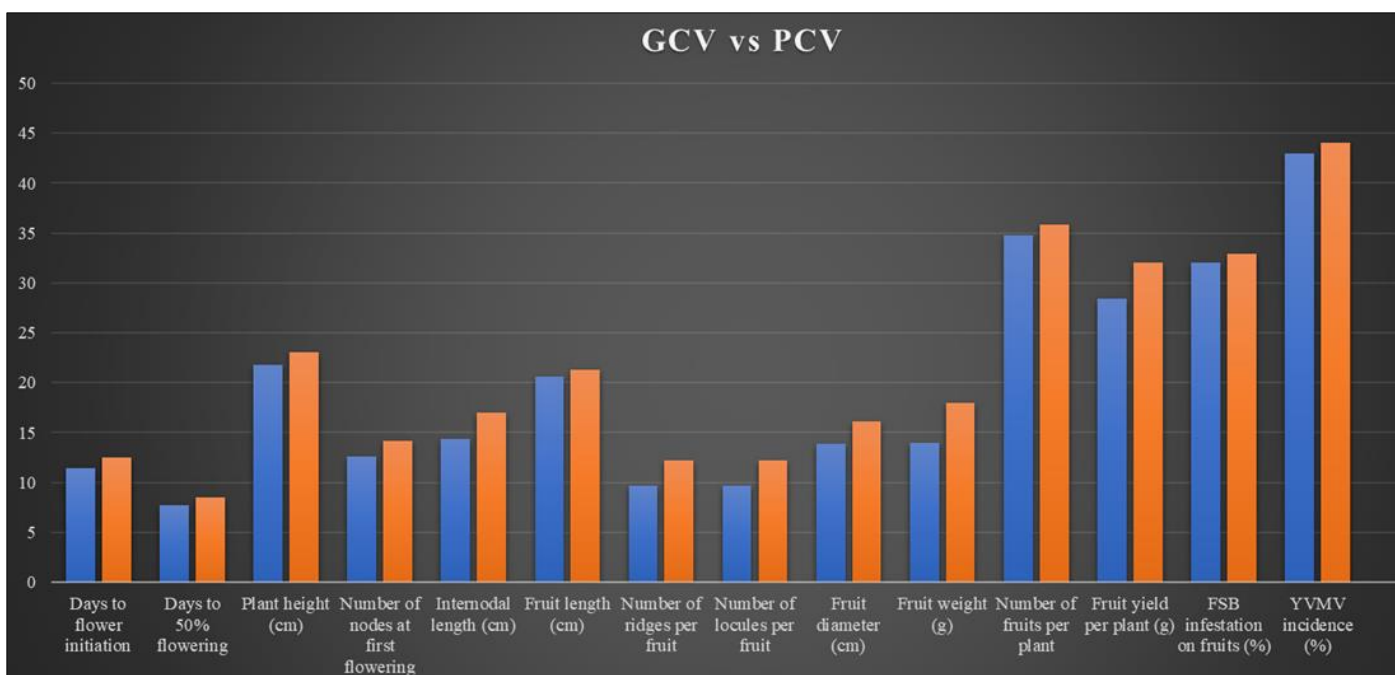
Fruit yield per plant has recorded high PCV (32.07), high GCV (28.41), high heritability (78.48%) and high GAM (51.85). The fruit yield per plant ranged from 278.85 g. to 85.70 g. High heritability and high GAM was reported by Jindal *et al.* (2010). This indicates presence of additive gene effects which indicated the effectiveness of selection for these traits. Similar results were reported by Reddy *et al.* (2012), Bagwale *et al.* (2016), Chandramouli *et al.* (2016), Muluken *et al.* (2016), Badiger *et al.* (2017), Patil *et al.* (2017)<sup>[21]</sup>, Syfullah *et al.* (2018)<sup>[26]</sup>, Alake *et al.* (2019)<sup>[3]</sup>.

High PCV (32.95; 44.93), GCV (32.03; 42.93), high heritability (94.50%; 95.10%) and high GAM (64.14; 85.65) was observed for the trait fruit and shoot borer infestation on fruits and yellow vein mosaic virus disease incidence (%) respectively. Similar results for YVMV were reported by Reddy *et al.* (2012) and Shashikala (2019)<sup>[24]</sup>.

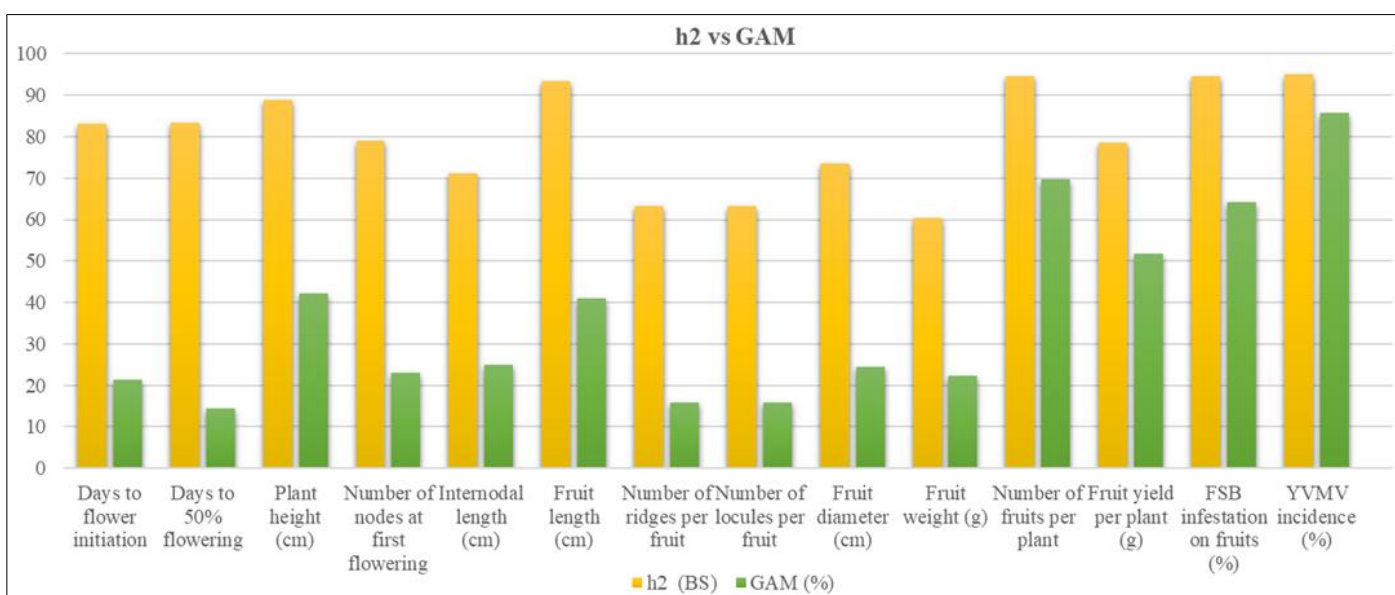
**Table 2:** Genetic parameters for yield and yield attributes in twenty six genotypes of okra

S. No.	Trait	Mean	Minimum	Maximum	h <sup>2</sup> (BS)	GCV (%)	PCV (%)	GAM (%)
1.	Days to flower initiation	34.73	29.33	42.67	83.18	11.42	12.52	21.46
2.	Days to 50% flowering	47.22	43.00	55.00	83.32	7.71	8.45	14.50
3.	Plant height (cm)	102.88	68.00	135.50	88.88	21.77	23.09	42.27
4.	Number of nodes at first flowering	4.39	3.13	5.63	78.97	12.60	14.18	23.07
5.	Internodal length (cm)	5.43	4.07	7.07	71.19	14.31	16.96	24.87
6.	Fruit length (cm)	10.48	6.87	13.87	93.41	20.57	21.29	40.96
7.	Number of ridges per fruit	5.38	5.00	7.33	63.30	9.71	12.20	15.91
8.	Number of locules per fruit	5.38	5.00	7.33	63.30	9.71	12.20	15.91
9.	Fruit diameter (cm)	1.69	1.40	2.30	73.57	13.82	16.11	24.42
10.	Fruit weight (g)	14.57	10.93	19.32	60.42	13.96	17.96	22.36
11.	Number of fruits per plant	15.51	8.70	24.83	94.55	34.81	35.80	69.72
12.	Fruit yield per plant (g)	183.51	85.70	278.85	78.48	28.41	32.07	51.85
13.	FSB infestation on fruits (%)	11.68 (0.34)	5.15 (0.23)	32.91 (0.61)	94.50	32.03	32.95	64.14
14.	YVMV incidence (%)	19.49 (0.44)	6.67 (0.26)	66.67 (0.96)	95.10	42.93	44.03	85.65

Note: h<sup>2</sup> (BS) = Heritability (Broad Sense) GCV = Genotypic coefficient of variance, GAM = Genetic advance as percent of mean PCV = Phenotypic coefficient of variance



**Fig 1:** Graph representing the GCV vs PCV parameters for fourteen traits of okra



**Fig 2:** Graph representing heritability (broad sense) and Genetic Advancement as per cent of mean for fourteen traits of okra

**Conclusion**

The analysis of variance (ANOVA) for 26 genotypes of okra during summer 2018 revealed significant differences for all the fourteen traits under study suggesting the existence of required genetic variation in the breeding material. The values of PCV were of higher magnitude than those of GCV for all the characters indicating influence of environment over the genotype. Higher PCV and GCV estimates were recorded by plant height, fruit length, fruit yield per plant, shoot and fruit borer incidence on fruits, number of fruits per plant and yellow vein mosaic virus percent disease incidence. Moderate PCV and GCV was registered by fruit weight, internodal length, fruit diameter, number of nodes at first flowering, days to initiation while days to 50% flowering, number of locules per fruit and number of ridges per fruit recorded low PCV and GCV. High to very high heritability (broad sense) was observed for all the

traits except number of ridges per fruit, number of locules per fruit and individual fruit weight. These three traits registered moderate heritability. High Genetic Advancement as percent of mean was recorded by some of the traits except internodal length, fruit diameter, Number of nodes at first flowering, fruit weight, days to initiation, number of ridges per fruit, number of locules per fruit and days to 50% flowering. High heritability combined with high genetic advance as a percent of the mean (GAM) conveyed the governance of additive gene on trait expression while high heritability and low GAM elucidated the non-additive gene action governing the trait. The presence of variability in the germplasm conveyed that this germplasm can be advanced to carry out the breeding programme.

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## References

1. Agbowuro GO, Salami AE, Awoyemi SO, Ogunwale GI, Kehinde-Fahare AF, Olajide OO. Genetic variation, heritability and genetic advance studies among okra accessions grown in different agro-ecological zones in Nigeria. *International Journal of Food Science and Agriculture*. 2019;3(1):130-135.
2. Akotkar PK, De DK, Dubey UK. Genetic studies on fruit yield and yield attributes of okra (*Abelmoschus esculentus* (L.) Moench). *Electronic Journal of Plant Breeding*. 2014;5(1):38-44.
3. Alake CO. Genetic variability and diversity in okra landraces using agro morphological traits and seed elemental minerals. *International Journal of Vegetable Science*, 2019, 1-23. DOI: 10.1080/19315260.2019.1610926.
4. Allard RW. *Principles of Plant Breeding*. John Wiley and Sons Inc., New York, 1960, 485.
5. Badiger M, Pitchaimuthu M, Pujer P. Genetic variability, heritability, genetic advance and correlation studies among quantitative traits in okra (*Abelmoschus esculentus* (L.) Moench). *Global Journal of Bioscience and Biotechnology*. 2017;6(2):314-319.
6. Bagwale SB, Jawale LN, Deosarkar DB, Jadhav RA. Genetic variability studies for yield, yield contributing and quality traits in okra [*Abelmoschus esculentus* (L.) Moench.]. *Indian Journal of Agricultural Research*. 2016;50(6):614-618.
7. Barche S, Nair R, Ramgiri M, Jain PK. Genetic variability in okra [*Abelmoschus esculentus* (L.) Moench.]. *The Ecoscan*. 2014;6:153-156.
8. Bello OB, Aminu D, Gambo BA, Azeez AH, Lawal M, Agbolade JO, *et al.* Genetic diversity, heritability, genetic advance in okra [*Abelmoschus esculentus* (L.) Moench.]. *Bangladesh Journal of Plant Breeding and Genetics*. 2015;28(2):25-38.
9. Burton GW. Quantitative inheritance in grasses. *Proceedings of Sixth Inter Grassland Congress*. 1952;1:277-283.
10. Chandramouli B, Srihari D, Rao AVDD, Rao MP. Studies on genetic variability, heritability and genetic advance in okra [*Abelmoschus esculentus* (L.) Moench.] genotypes. *Plant Archives*. 2016;16(2):679-682.
11. Hanson CH, Robinson HR, Comstock RS. Biometrical studies of yield in segregating population of Korean Lespedeza. *Agronomy Journal*. 1956;48:268-272.
12. Horticulture Statistics Division, Department of Agriculture, Cooperation and Farmers Welfare. *Horticulture Statistics at a glance*, 2018.
13. Jindal SK, Arora D, Ghai TR. Variability studies for yield and its contributing traits in okra. *Electronic Journal of Plant Breeding*. 2010;1(6):1495-1499.
14. Khajuria RK, Sharma JP, Samnotra RK, Kumar S, Ranjit K. Variability studies in okra [*Abelmoschus esculentus* (L.) Moench.]. *Electronic Journal of Plant Breeding*. 2016;7(2):226-234.
15. Kumar A, Kumar M, Sharma VR, Singh MK, Singh B, Chand P. Genetic variability, heritability and genetic advance studies in genotypes of okra [*Abelmoschus esculentus* (L.) Moench.]. *Journal of Pharmacognosy and Phytochemistry*. 2019;8(1):1285-1290.
16. Majid SMSAMA, Mohir MN, Jadhav RS. Genetic variability, heritability and genetic advance in okra [*Abelmoschus esculentus* (L.) Moench.]. *Electronic Journal of Plant Breeding*. 2013;4(3):1255-1257.
17. Makhdoomi MI, Kouser PW, Khan SH, Bhat MA, Husain K, Afroza B, *et al.* Combining ability analysis in okra (*Abelmoschus esculentus* (L.) Moench). *Journal of Pharmacognosy and Phytochemistry*. 2018;7(2):460-465.
18. Mishra A, Mishra HN, Senapati N, Tripathy P. Genetic variability and correlation studies in okra [*Abelmoschus esculentus* (L.) Moench.]. *Electronic Journal of Plant Breeding*. 2015;6(3):866-869.
19. Muluken D, Wassu M, Endale G. Variability, heritability and genetic advance in Ethiopian okra [*Abelmoschus esculentus* (L.) Moench] collections for tender fruit yield and other agro-morphological traits. *Journal of Applied Life Sciences International*. 2016;4(1):1-12.
20. Panse VG, Sukhatme PV. *Statistical Methods for Agril. Workers*, ICAR, New Delhi, 1985.
21. Patil BT, Rode VR, Bhalekar MN, Shinde KG. Studies on genetic variability, heritability and genetic advance in okra [*Abelmoschus esculentus* (L.) Moench.]. *International Journal of Agricultural and Environmental Research*. 2017;3(2):197-201.
22. Prakash K, Pitchaimuthu M. Nature and magnitude of genetic variability and diversity studies in okra (*Abelmoschus esculentus* L. Moench). *Electronic Journal of Plant Breeding*. 2010;1(6):1426-1430.
23. Reddy MT, Babu HK, Ganesh M, Reddy CK, Begum H, Reddy PB, *et al.* Genetic variability analysis for the selection of elite genotypes based on pod yield and quality from the germplasm of okra (*Abelmoschus esculentus* L. Moench). *Journal of Agricultural Technology*. 2012;8(2):639-655.
24. Shashikala Kolakar S. Studies on heterosis for fruit yield, quality and Yellow Vein Mosaic Virus resistance in Okra (*Abelmoschus esculentus* L. Moench.) Thesis submitted to University of Agricultural & Horticultural Sciences, Shivamogga, 2019.
25. Singh N, Singh DK, Sati UC, Rawat M, Pandey P. Genetic analysis studies in okra [*Abelmoschus esculentus* (L.) Moench.]. *International Journal of Pure and Applied Bioscience*. 2017;5(4):361-367.
26. Syfullah K, Sani MNH, Nasif SO, Parvin S, Rony MM, Islam MS, *et al.* Genetic variability, heritability, character association and morphological diversity in okra (*Abelmoschus esculentus* L. Moench). *International Journal of Plant & Soil Science*. 2018;25(6):1-11.