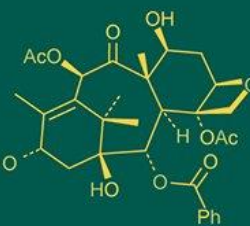
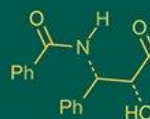
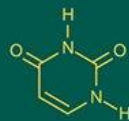


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Assessment of genetic variability, heritability and genetic advance for yield and yield contributing traits in okra (*Abelmoschus esculentus* L. Moench)

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Abstract

The present study was carried out to estimate the variability, heritability and genetic advance by using 13 genotypes under line x tester mating design at Vegetable Research Farm, Department of Vegetable Science Kalyanpur, CSAUA&T, Kanpur during the *Summer Season* of 2024-2026. The result showed that the value of phenotypic coefficients of variance (PCV) was higher than the genotypic coefficients of variance (GCV) for all the characters. The highest phenotypic and genotypic coefficients of variance was observed in fruit yield per plant followed by fruit yield per plot, plant height at final harvest, number of primary branches per plant, self-life of fresh fruits, mucilage content, length of internodes and vitamin-C. The moderate PCV and GCV was recorded in length of fruits followed by total soluble solids, number of fruits per plant, node at which first flower appears, average fruit weight, days to first flowering, number of nodes per plant and fruit diameters. While, low PCV and GCV was measured in days to first picking followed by crude fiber content and days to 50% flowering. The result revealed that the most of the characters show high heritability in broad sense except days to first picking which indicated moderate heritability. The high genetic advance was observed in fruit yield per plant followed by fruit yield per plot, plant height at final harvest, number of primary branches per plant, self-life of fresh fruits, mucilage content, length of internodes, vitamin-C, length of fruits, total soluble solids, number of fruits per plant, node at which first flower appears, average fruit weight, number of nodes per plant, days to first flowering and fruit diameters, whereas moderate genetic advance was recorded in days to 50% flowering and crude fiber content and remaining trait days to first picking was expressed as low genetic advance.

Keywords: Okra, genetic variability, heritability, genetic advance

Introduction

Okra (*Abelmoschus esculentus* L.) is the most important vegetable crop which belongs to the class dicotyledonae, order malvales and family Malvaceae. Okra is a polyploidy in nature having chromosome number of $2n=2x=130$. It is commonly known as *Lady's Finger* in England, *Gumbo* in USA and *Bhindi* in India. It is also known as *Kacang*, *Quiabos*, *Quiabo*, *Bamieh*, *Bamya*, *Kopi Arab*, in other different region. According to Vavilon (1951), it was believed that the main center of origin of okra is South Africa near Ethiopia. The origin of okra can be traced back to the Hindustan region, where it was mostly grown in India, Pakistan and Burma (Zeven and Zhuckovsky, 1975).

Okra is an often cross pollinated crop generally pollinated by insect. The occurrence of out crossing to an extent of 4 to 19% with the maximum of 42.2% is noticed. Okra is generally multiplied by seed generation after generation Bambhaniya *et al.*, 2024. The okra can be grown in variable type of soil but having better drainage property with good amount of organic matter is suitable. The optimum pH range 6-6.5 is reported for suitable okra cultivation. The okra mostly cultivated in tropical, subtropical and warm temperate regions around the world. It is day neutral plant which requires warm temperature and is unable to withstand low temperature for long time. The optimum temperature required for seed germination is 25-32 °C. the optimum minimum and maximum temperature required for better growth between 21-30 °C and 18-35 °C respectively Shewta *et al.*, 2022 [28, 29, 3, 27].

Tender okra fruits are utilized as cooked vegetable in nations like India, Brazil, West Africa and it is also found as dehydrated and canned forms. Sterilized, frozen and sun-dried fruits are

various other significant market product of okra. The mature fruits and stems of okra are used in paper industries because it contains crude fiber. The other important uses of okra, its roots and stem are used for clearing juice in sugar industries Rajani *et al.*, 2021 [22].

The success of a breeding programme for the genetic improvement of quantitative traits depends on the magnitude of genetic variability present in the germplasm and the extent to which the desirable traits are heritable. The total genetic variability dividing it into heritable and non-heritable constituents using the genetic parameters such as genotypic and phenotypic coefficient variation (GCV and PCV), heritability and genetic advance is necessary to have an insight into genetic nature of yield and its components on which selection can be effectively carried out Priyanka *et al.*, 2018 [21].

Heritability denotes the proportion of phenotypic variation due to genotypes, which helps the breeders to choosing the best genotype for a certain traits. However, it is unable to provide the expected genetic gain in a single selection cycle. Genetic advance signifies the improvement in the mean genotypic values of selected population over the parental population and thus helps the breeder to choose the progenies in the earlier generation itself Kute *et al.*, 2023 [14].

Material and Methods

The experiment was conducted in Randomized Block Design with three replications during *summer season* 2024-26 at Vegetable Research Farm, Department of Vegetable Science, Chandra Shekhar Azad University of Agriculture and Technology, Kanpur, (U.P.) 208002. The experiment was conducted using Line x Tester mating design suggested by Kempthorne (1957) [10]. In the present investigation 73 treatments (13 parents, 30 F₁S hybrids and 30 F₂S progenies) were evaluated for the study of genetic analysis of various traits in okra. The five randomly selected plants were tagged and labeled properly of each genotype were used to record the various observations from each plot and each replication. The 19 yields and quality parameters *viz.*, Days to first flowering, Node at which first flower appears, Days to 50% flowering, Length of internodes (cm), Number of primary branches per plant, Number of nodes per plant, Plant height at final harvest (cm), Days to first picking, Length of fruits (cm), Fruit diameters (cm), Average fruit weight (g), Number of fruits per plant, Fruit yield per plant (g), Fruit yield per plot (kg), Vitamin-C (mg/100g fresh fruit), Total soluble solids (^oBrix), Self life of fresh fruits, Crude fiber content (%), Mucilage content (g/100g) were recorded during the experimental period.

Statistical analysis

The analysis of variance can be calculated by using the model recommended by Panse and Sukhatme (1967). The genotypic coefficient of variation and phenotypic coefficient of variation were estimated as per the formula given by Burton and Devane (1953). The heritability in broad sense as a ratio of genotypic variance to phenotypic variance was computed by the following formula given by Hanson *et al.*, (1956). The genetic advance is improvement in mean genotypic value of selected plants over the parental population and estimated by the formula given by Lush (1949), Johnson *et al.*, (1955) and Allard (1960) [20, 10, 4, 6, 17, 8, 2].

Result and Discussion

Estimation of genetic variability parameters

The estimation of genetic variability parameters of various components for yield and it contributes traits showed a wide range of variation for the character studied. The result showed that the value of phenotypic coefficients of variance (PCV) was higher magnitude than the genotypic coefficients of variance (GCV) for all the characters. It was indicating that the environment had an important role in influencing the expression of the characters, however some minor variations were recorded between PCV and corresponding GCV for all the characters. The value of PCV and GCV were <10% considered as low, 10-20% as moderate and >20% were considered as high. The estimate of different characteristics of variability like genotypic coefficients of variance (GCV), phenotypic coefficients of variance (PCV), heritability (h²), genetic advance (GA), genetic advance as percent of mean (GAM) were statistically analysed for different yield and quality traits has. The coefficient of variation at phenotypic and genotypic level was described below in the following heads.

Coefficient of variation

Phenotypic coefficient of variation

The result revealed that the range of phenotypic coefficients of variance (PCV) was varies from 5.19% to 33.07%. The high phenotypic coefficients of variance (>20%) was observed in fruit yield per plant and fruit yield per plot (33.07%) followed by plant height at final harvest (29.61%), number of primary branches per plant (29.29%), self-life of fresh fruits (26.14%), mucilage content (25.98%), length of internodes (20.88%) and vitamin-C (20.31%). The moderate phenotypic coefficients of variance (10-20%) was recorded in length of fruits (18.62%) followed by total soluble solids (18.20%), number of fruits per plant (17.57%), node at which first flower appears (17.12%), average fruit weight (14.39%), days to first flowering (12.79%), number of nodes per plant (12.65%) and fruit diameters (12.05%) while, low phenotypic coefficients of variance (<10%) was measured in days to first picking (5.19%) followed by crude fiber content (7.53%) and days to 50% flowering (9.53%). Similar results were also indicated to support the study with earlier findings of Goudara *et al.*, (2024), Setu (2023), Reddy *et al.*, (2022), Jibung *et al.*, (2021), Lateef *et al.*, (2020) [5, 26, 24, 7, 16].

Genotypic coefficient of variation

The result indicated that the range of genotypic coefficients of variance (GCV) was varies from 4.09 to 32.78. The high genotypic coefficients of variance (>20%) was observed in fruit yield per plant (32.78%) followed by fruit yield per plot (32.77%), plant height at final harvest (29.38%), number of primary branches per plant (29.17%), self life of fresh fruits (26.02%), mucilage content (24.85%), length of internodes (20.70%) and vitamin-C (20.05%). The moderate genotypic coefficients of variance (10-20%) was recorded in length of fruits (18.43%) followed by total soluble solids (18.01%), number of fruits per plant (17.34%), node at which first flower appears (16.92%), average fruit weight (14.11%), days to first flowering (12.09%), number of nodes per plant (12.09%) and fruit diameters (11.15%) whereas, low genotypic coefficients of variance (<10%) was seen in days to first picking (4.09%) followed by crude fiber content (7.11%) and days to 50% flowering (9.15%). The same findings were also reported by Bambhaniya *et al.*, (2024),

Setu (2023), Reddy *et al.*, (2022), Lateef *et al.*, (2020), Kumar *et al.*, (2019) [3, 26, 24, 16].

Heritability (%)

The heritability was calculated for all the characters by the different constituent for estimating their relative magnitude of genotypic and phenotypic variability contributed through environmental factors. It was divided as high heritability value >70% considered as high, 50-70-% as moderate and <50% as low heritability. The heritability estimates in broad sense were ranged from 62.05% to 99.20%. The result revealed that the most of the characters show high heritability in broad sense. Among the characters under study, highest heritability was observed for number of primary branches per plant (99.20%) followed by self-life of fresh fruits (99.08%), mucilage content (98.96%), plant height at final harvest (98.46%), length of internodes (98.30%), fruit yield per plant (98.25%), fruit yield per plot (98.21%), total soluble solids (97.89%), length of fruits (97.88%), node at which first flower appears (97.61%), vitamin- C (97.45%), number of fruits per plant (97.41%), average fruit weight (96.02%), days to 50% flowering (92.25%), number of nodes per plant (91.37%), days to first flowering (89.31%), crude fiber content (89.13%) and fruit diameters (85.59%), whereas moderate heritability was recorded in days to first picking (62.05%). The result was also found earlier by Bambhaniya

et al., (2024), Kute *et al.*, (2023), Ranga *et al.*, (2021), Alam *et al.*, (2020), Kumar *et al.*, (2019) [3, 14, 23, 1].

Genetic advance (%): The genetic advance as percent of mean can be divided into three categories viz., <10% were considered as low, 10-20% as moderate and >20% as high genetic advance. The result expressed that the range of genetic advance as percentage of mean was from 6.63% to 66.93%. According to the statistical data, the high genetic advance as percentage of mean was observed in fruit yield per plant (66.93%) followed by fruit yield per plot (66.91%), plant height at final harvest (60.06%), number of primary branches per plant (59.85%), self life of fresh fruits (53.36%), mucilage content (50.93%), length of internodes (42.28%), vitamin- C (40.77%), length of fruits (37.55%), total soluble solids (36.70%), number of fruits per plant (35.25%), node at which first flower appears (34.43%), average fruit weight (28.47%), number of nodes per plant (23.81%), days to first flowering (23.53%) and fruit diameters (21.24%), whereas moderate genetic advance as percentage of mean was recorded in days to 50% flowering (18.11%) and crude fiber content (13.82%) and remaining trait days to first picking (6.63%) was expressed as low genetic advance as percentage of mean. The result of the present study are in accordance with the finding of Mishra *et al.*, (2024), Mohammed *et al.*, (2022), Kumar *et al.*, (2021), Katiyar (2020), Samim *et al.*, (2018) [18, 19, 13, 9, 25].

Table 1: Estimation of genetic variability parameters for different yield and quality parameters in Okra

S.No.	Characters	Mean	Min.	Max	var (g)	var (p)	Heritability (%)	Genetic advance	GA (% mean)	GCV (%)	PCV (%)
1.	Days to first flowering	36.02	27.14	43.18	18.95	21.22	89.31	8.47	23.53	12.09	12.79
2.	Days to 50% flowering	45.92	37.48	56.82	17.67	19.15	92.25	8.32	18.11	9.15	9.53
3.	Days to first picking	61.41	54.21	66.32	6.29	10.14	62.05	4.07	6.63	4.09	5.19
4.	Node at which first flower appears	4.49	3.10	6.53	0.58	0.59	97.61	1.55	34.43	16.92	17.12
5.	Length of internodes (cm)	4.94	3.39	7.26	1.04	1.06	98.30	2.09	42.28	20.70	20.88
6.	Number of branches per plant	2.50	1.19	4.23	0.53	0.54	99.20	1.50	59.85	29.17	29.29
7.	Number of nodes per plant	20.29	14.18	24.52	6.02	6.58	91.37	4.83	23.81	12.09	12.65
8.	Plant height at final harvest (cm)	103.28	61.87	178.02	921.00	935.45	98.46	62.03	60.06	29.38	29.61
9.	Length of fruits (cm)	13.09	8.39	18.32	5.81	5.94	97.88	4.91	37.55	18.43	18.62
10.	Fruit diameters (cm)	1.50	1.15	1.82	0.03	0.03	85.59	0.32	21.24	11.15	12.05
11.	Average fruit weight (g)	16.06	11.49	20.85	5.13	5.34	96.02	4.57	28.47	14.11	14.39
12.	Number of fruits per plant	17.77	11.32	22.14	9.49	9.74	97.41	6.26	35.25	17.34	17.57
13.	Vitamin- C (mg/100 gm. fresh fruit)	14.52	9.69	21.33	8.48	8.70	97.45	5.92	40.77	20.05	20.31
14.	Total Soluble Solids (°Brix)	2.75	2.13	3.98	0.24	0.25	97.89	1.01	36.70	18.01	18.20
15.	Crude fiber content (%)	13.86	12.60	16.50	0.97	1.09	89.13	1.92	13.82	7.11	7.53
16.	Mucilage content (g/100g)	3.36	2.15	5.78	0.70	0.70	98.96	1.71	50.93	24.85	24.98
17.	Self-life of fresh fruits	3.50	2.23	5.35	0.83	0.84	99.08	1.87	53.36	26.02	26.14
18.	Fruit yield per plant (g)	272.10	143.25	455.77	7955.39	8096.72	98.25	182.13	66.93	32.78	33.07
19.	Fruit yield per plot (kg)	6.80	3.58	11.39	4.97	5.06	98.21	4.55	66.91	32.77	33.07

Conclusion

The analysis of variance revealed that mean square due to genotypes was found significant for all the 19 traits studied which indicated that the presence of adequate variability for all the traits studied. The magnitude of PCV was higher than the GCV for all the characters. The highest to moderate phenotypic and genotypic coefficients of variance was observed in fruit yield per plant followed by fruit yield per plot, plant height at final harvest, number of primary branches per plant, self-life of fresh fruits, mucilage content, length of

internodes and vitamin-C, length of fruits, total soluble solids, number of fruits per plant, node at which first flower appears, average fruit weight, days to first flowering, number of nodes per plant and fruit diameters. The high heritability was observed for all the traits except days to first picking. The genetic advance expressed as percentage of mean was obtain high for sixteen characters and remaining three traits such as days to 50% flowering, crude fiber content show moderate and days to first picking show low genetic advance.

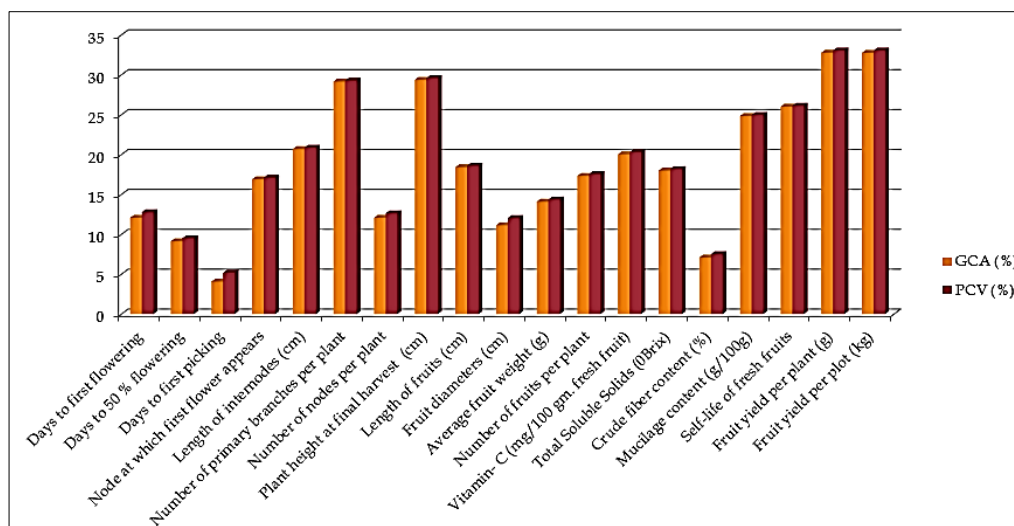


Fig 1: Genotypic Coefficient of Variation and Phenotypic Coefficient of Variation

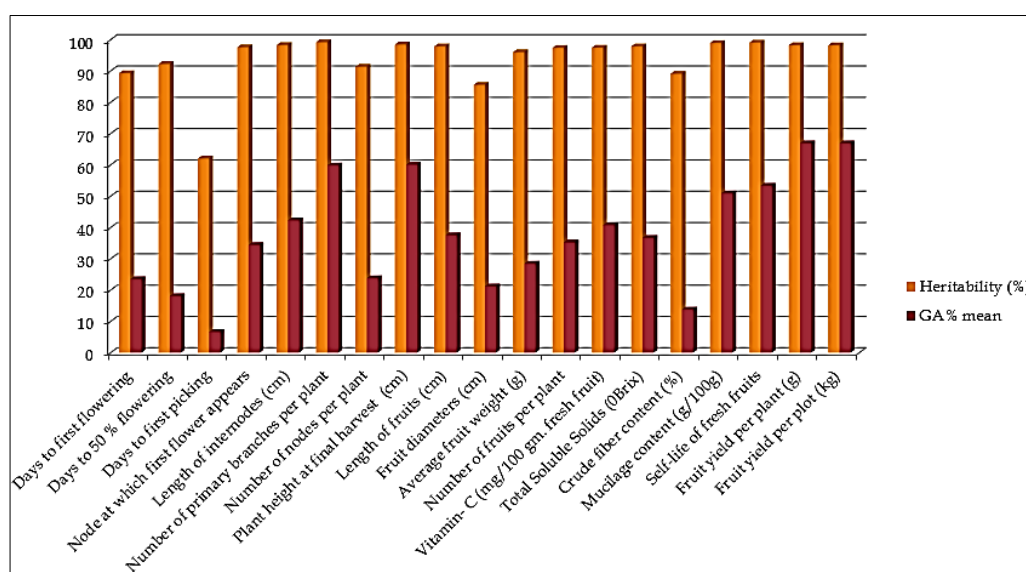


Fig 2: Heritability and Genetic Advance as (%) of mean.

References

1. Alam K, Singh MK, Kumar M, Singh A, Kumar V, Ahmad M, Keshari D. Genetic variability, heritability and genetic advance for selection parameters of genotypes in *Abelmoschus esculentus* (L.) Moench. International Journal of Chemical Studies. 2020;8(6):1016-1022.
2. Allard RW. Principles of Plant Breeding. New York: John Wiley and Sons; 1960. p. 227-228.
3. Bambhaniya UB, Makwana SM, Armi P, Raval LJ. Studies on genetic variability, heritability and genetic advance in *Abelmoschus esculentus* (L.) Moench. International Journal of Advanced Biochemistry Research. 2024;8(SP-7):536-540.
4. Burton GW, Devane EH. Estimating heritability in tall fescue (*Festuca arundinacea*) from replicated clonal material. Agronomy Journal. 1953;45:478-481.
5. Goudara R, Shantappa T, Wani P. Genetic variability, heritability and genetic advance for yield and yield attributing traits in *Abelmoschus esculentus* (L.) Moench genotypes. International Journal of Advanced Biochemistry Research. 2024;8(SP-10):813-816.
6. Hanson GH, Robinson HF, Comstock RE. Biometrical studies of yield in segregating populations of Korean lespedeza. Agronomy Journal. 1956;48:268-272.
7. Jibung GG, Manggoel W. Genetic variation and heritability studies in some *Abelmoschus* spp. varieties. International Journal of Science and Applied Research. 2021;4(1-2):1-2.
8. Johnson HW, Robinson HF, Comstock RE. Estimates of genetic and environmental variability in soybean. Agronomy Journal. 1955;47:314-318.
9. Katiyar AS. Genetic component and variance analysis of *Abelmoschus esculentus* (L.) Moench. Journal of Rural and Agricultural Research. 2020;20(2):55-57.
10. Kempthorne O. An Introduction to Genetic Statistics. New York: John Wiley and Sons; 1957. p. 468-471.
11. Kumar A, Kumar M, Sharma VR, Singh MK, Singh B, Chand P. Genetic variability, heritability and genetic advance studies in genotypes of *Abelmoschus esculentus* (L.) Moench. Journal of Pharmacognosy and Phytochemistry. 2019;8(1):1285-1290.
12. Kumar A, Kumar M, Sharma VR, Singh MK, Singh B, Chand P. Genetic variability, heritability and genetic advance studies in genotypes of *Abelmoschus esculentus*

- (L.) Moench. Journal of Pharmacognosy and Phytochemistry. 2019;8(1):1285-1290.
13. Kumar A, Singh AK, Singh BK, Pal AK. Estimation of variability, heritability and genetic advance studies in okra. The Pharma Innovation Journal. 2021;10(9):1279-1281.
 14. Kute KG, Zate DK, Ghadage AP, Mitkari SB, Deshmukh SD. Estimating genetic variability, heritability and genetic advance for yield and yield contributing traits in *Abelmoschus esculentus* (L.) Moench genotype. The Pharma Innovation Journal. 2023;12(12):2864-2870.
 15. Kute KG, Zate DK, Ghadage AP, Mitkari SB, Deshmukh SD. Estimating genetic variability, heritability and genetic advance for yield and yield contributing traits in *Abelmoschus esculentus* (L.) Moench genotype. The Pharma Innovation Journal. 2023;12(12):2864-2870.
 16. Lateef A, Afroza B, Hamid I, Ali G. Genetic analysis in *Abelmoschus esculentus* (L.) Moench. International Journal of Chemical Studies. 2020;8(2):2241-2244.
 17. Lush JL. Heritability of quantitative characters in farm animals. Hereditas. 1949;35(1):356-375.
 18. Mishra B, Tiwari A, Pandey SK, Ramgiry M. DUS-based agro-morphological characterization and genetic variability in *Abelmoschus esculentus* (L.) Moench. Vegetable Science. 2024;51(1):78-85.
 19. Mohammed J, Mohammed W, Shiferaw E. Performance and genetic variability of *Abelmoschus esculentus* (L.) Moench genotypes in Ethiopia for agro-morphological and biochemical traits. Advances in Agriculture. 2022;2022:5521151.
 20. Panse VG, Sukhatme PV. Statistical Methods for Agricultural Workers. 2nd ed. New Delhi: Indian Council of Agricultural Research; 1967. p. 381.
 21. Priyanka VM, Reddy T, Begum H, Sunil N, Jayaprada M. Studies on genetic variability, heritability and genetic advance in genotypes of *Abelmoschus esculentus* (L.) Moench. International Journal of Current Microbiology and Applied Sciences. 2018;7(5):401-411.
 22. Rajani A, Naidu NL, Reddy RVSK, Srikanth D, Kumari RN, Babu RD. Studies on combining ability for yield and quality attributing traits in *Abelmoschus esculentus* (L.) Moench. The Pharma Innovation Journal. 2021;10(10):1398-1400.
 23. Ranga AD, Kumar S, Mayur SD. Variability among different yield and yield contributing traits of *Abelmoschus esculentus* (L.) Moench genotypes. Electronic Journal of Plant Breeding. 2021;12(1):74-81.
 24. Reddy JP, Anbanandan V, Kumar BS. Genotypic and phenotypic variability and evaluation of *Abelmoschus esculentus* (L.) Moench genotypes for yield components. Journal of Applied and Natural Science. 2022;14(1):180-187.
 25. Samim S, Sood S, Singh A. Genetic assessment for fruit yield and horticultural traits in *Abelmoschus esculentus* (L.) Moench. International Journal of Current Microbiology and Applied Sciences. 2018;7(10):947-957.
 26. Setu H. Genetic variability analysis for traits in *Abelmoschus esculentus* (L.) Moench genotypes. International Journal of Food Science and Agriculture. 2023;7(1):95-104.
 27. Shweta, Sood S, Sood VK, Chadha S. Heterotic expression for fruit yield and component traits in intervarietal hybrids of *Abelmoschus esculentus* (L.) Moench. Himachal Journal of Agricultural Research. 2022;48(2):225-233.
 28. Vavilov NI. The origin, variation, immunity and breeding of cultivated plants. Chronica Botanica. 1951;13(6):36-37.
 29. Zeven AC, Zhukovsky PM. Dictionary of Cultivated Plants and Their Centres of Diversity. Wageningen, The Netherlands: Centre for Agricultural Publishing and Documentation; 1975. p. 219.