



Assessment of Genetic Heterogeneity in Okra [*Abelmoschus esculentus* (L.) Moench.] Genotypes

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Abstract: Okra is one of the most significant and widely grown vegetables of the family Malvaceae in India. It is often seen that the growth and yield of okra is constrained by genetic variability and environmental conditions. There has been limited studies on the genetic parameters influencing key horticultural traits in okra under valley conditions of Uttarakhand. Considering this, the present investigation aimed to analyze the extent of genetic variability, heritability, and genetic advance among 26 okra genotypes for major growth and yield attributes under valley conditions of Uttarakhand, with the aim of identifying superior genotypes for growth and yield improvement. The field experiment was carried out during the summer season of 2019 at the Horticultural Research Centre, Department of Horticulture, H.N.B. Garhwal University, Srinagar (Garhwal), Uttarakhand, India. A Randomized Block Design with three replications was employed, and data were recorded on five randomly selected plants from each replication. The genetic analysis revealed that the phenotypic coefficient of variation (PCV) consistently exceeded the genotypic coefficient of variation (GCV) across all the traits, indicating minor environmental influence. The coefficients of variation for both phenotypic and genotypic measurements were significantly high for yield per plot and yield per hectare. Observations showed that traits such as plant height, internodal length, yield (per plot and per hectare) exhibited high heritability estimates along with substantial genetic gain, suggesting that these traits are influenced by additive gene effects and are thus more dependable for efficient selection. Hence, the results indicate that these characters can serve as effective selection criteria in okra breeding programs aimed at yield enhancement and adaptability improvement under valley conditions of Uttarakhand.

Keywords: Heritability • Genetic advance • Genetic gain • Okra • Variability and Valley conditions.

Introduction

Okra [*Abelmoschus esculentus* (L.) Moench.] is an economically and nutritionally vital vegetable crop cultivated extensively across tropical and subtropical regions of the world (Kumari et al., 2019). Thought to have originated in Africa, particularly in Ethiopia and Sudan, it later spread to Asia, Europe, and the Americas (Khajuria et al., 2015). It is important member of family malvaceae which was formerly known as *Hibiscus esculentus* L. (Joshi et al. 2021; Kumar & Joshi, 2024). Most commonly cultivated okra is believed to be an amphidiploid (allotetraploid) derived from *Abelmoschus ficulneus* with ploidy level

$2n=72$ and *Abelmoschus tuberculatus* with ploidy level $2n = 58$ (Singh & Bhatnagar, 1975; Joshi et al., 2020). The crop adapts well to diverse environmental conditions, making it suitable for both tropical and subtropical climates (Chandramouli et al., 2016). It is rich in carbohydrates, fats, vitamins A, B1, and C, minerals such as Ca, Mg and K and dietary fiber, which contribute to its medicinal properties (Sawant et al., 2014; Rajesh et al., 2018). It is known for its high Iodine content, making it beneficial for thyroid health and its mucilage has been used for treating ulcers and inflammations (Prakash & Pitchaimuthu, 2010; Nwangburuka et al., 2012). Wild



relatives of okra, such as *Abelmoschus caillei* and *Abelmoschus manihot* are found in various parts of Africa and Asia, providing valuable genetic resources for breeding programmes (Chaukhande et al., 2011; Badiger et al., 2017). These wild species possess traits such as resistance to pest and diseases, tolerance to abiotic stresses and diverse morphological characteristics that can be utilized for genetic improvement (Sawant et al., 2014; Kandasamy, 2015).

The crop exhibits substantial genetic diversity which is crucial for plant breeding and crop improvement programmes (Patro & Ravisankar, 2004; Akotkar et al., 2010). Genetic variability is a prerequisite for any programme related to breeding, as it gives the basis for selecting superior genotypes for further improvement (Pachiyappan & Saravannan, 2016). Various studies have highlighted the importance of genetic parameters *i.e.*, GCV, PCV, heritability (h^2) and genetic advance (GA) in evaluating the extent of genetic diversity within okra genotypes (Fisher, 1918; Wright, 1935). Despite its importance, the extent of genetic variability in okra remains underexplored, leading to challenges in selecting high yielding and resilient genotypes. The main problem is the lack of detailed characterization of available genetic resources, which limits breeder's ability to develop superior varieties (Reddy et al., 2012). Therefore, the present study was undertaken to estimate the magnitude of genetic variability, heritability, and genetic advance among diverse okra genotypes, focusing on yield and yield-contributing traits, to identify promising varieties suitable for future breeding programs under the specific agro-climatic conditions of Uttarakhand.

Material and methods

The present investigation was carried out during the summer season of 2019 at the Horticultural Research Centre (H.R.C.), Department of Horticulture, H.N.B. Garhwal

University, Srinagar (Garhwal), Uttarakhand located at North terrace valley of Alaknanda River with longitude 78° 47'30" E & latitude 30°13'9" N, at 540 m above elevation, in the lower Himalayan region. The maximum and minimum temperatures ranged between 42.16° C to 20.7°C, while the relative humidity was between 11.76% to 95.41% during the entire experimental period. The average maximum rainfall (0.158 mm) was received in the July month. The field trial constituted 25 genotypes with one check cultivar (Arka Anamika). The genotypes used were Agri Bahar, Hisar Naveen, Chanda, Kashi Kranti, Hisar Unnat, Kashi Pragati, Kashi Mohini, Kashi Kaveri, Vibhuti, King Bhindi, Lucky-666, LC-1 to LC-6, Parbhani Kranti, Pusa A-4, Punjab-8, Pusa Sawani, Vandana-241, Varsha Uphar, VL Bhindi-2 and Super Anamika. In the course of the experiment, five plants from every treatment in each replication were randomly chosen and labeled for data collection, and the average was calculated for all the pertinent yield and attributing characteristics being examined.

The statistical analysis was performed using MS Excel and SPSS (version 26). The phenotypic and genotypic components of variance were computed according to Lush's formulae (1940). The GCV and PCV in percentage were determined following the methods outlined by Burton and De Vane (1953). The values of PCV and GCV were then classified based on the criteria established by Sivasubramanian and Madhavamenon (1973), which categorizes them as Low (0 - 10%), Moderate (11 - 20%), and High (above 20%). The heritability in broad-sense (h^2b) was estimated using the formula given by Hansen et al. (1956) and it has the three categories: Low, Moderate and High with its ranges of 0 - 50%, 51 - 70% and above 70%, respectively. The genetic advance was determined using the approach recommended by Johnson et al. (1955). The was classified according to the criteria proposed by Johnson



et al. (1955) into three categories: Low (0 - 10%), Moderate (11 - 20%), and High (above 20%). All these statistical measures were utilized to assess the extent of variability, heritable portion of genetic variance, and expected genetic improvement under selection for the evaluated traits in okra genotypes.

Result and discussion

Genetic variability

The analysis of genetic variability parameters, including phenotypic and genotypic coefficients of variation (PCV and GCV), heritability (h^2), genetic advance (GA), and genetic advance as a percentage of mean (GAM), is summarized in Table 1. These parameters offer an understanding of the genetic variability and potential for selection among the okra genotypes under study. The

calculation of PCV and GCV gave a picture clearly of the present variations of germplasm. For all observed traits, the PCV values were marginally higher than the corresponding GCV values, indicating that the environment exerted a minimal influence on the expression of these characters. This trend was consistent with earlier findings by Prakash et al. (2011), Khajuria et al. (2015), Chandramouli et al. (2016) and Kerure et al. (2017) in okra. Thus, showing that environmental factors less influence these traits. The coefficients of variation exhibited different magnitudes for each character, ranging from low to moderate to high. This suggested that there was significant diversity in the experimental materials utilized.

Table 1: Estimates of phenotypic and genotypic coefficients of variation, heritability, genetic advance, and genetic advance over mean for growth and yield traits in okra.

SN	Characters	Mean	Range	Coefficients of Variation		Heritability (%)	GA	GA as % of the mean
				GCV (%)	PCV (%)			
1.	Days taken to first germination	5.77	4.67-7.67	11.13	17.18	41.96	0.86	14.85
2.	Plant height (cm)	220.89	138.20-277.87	13.11	13.18	98.99	59.37	26.88
3.	Internodal length (cm)	7.86	4.71-10.05	17.12	17.74	93.21	2.68	34.05
4.	Petiole length (cm)	35.59	31.49-40.01	4.66	6.41	52.84	2.48	6.98
5.	Number of Epicalyx segments	11.02	10.07-11.93	5.06	5.41	87.58	1.08	9.76
6.	Days taken to first flowering	48.94	44.87-53.87	4.79	5.90	65.99	3.92	8.02
7.	Number of nodes bearing first flower	6.20	4.80-7.47	8.78	12.99	45.72	0.76	12.23
8.	Flower diameter (cm)	8.17	6.77-9.50	9.51	9.71	95.93	1.57	19.19
9.	Pedicel length (cm)	4.65	3.53-5.57	12.87	13.57	89.99	1.17	25.15
10.	Pedicel diameter (mm)	6.43	5.61-7.43	5.84	7.44	61.57	0.61	9.43
11.	Days taken to first fruit set	50.46	46.00-54.87	4.50	4.92	83.93	4.29	8.50
12.	Days taken to first fruit harvest	56.29	52.47-60.80	3.71	4.43	70.07	3.60	6.40
13.	Fruit length (cm)	17.78	14.10-22.32	7.99	9.57	69.73	2.44	13.74
14.	Average fruit weight (g)	19.58	17.91-23.16	4.28	7.75	30.48	0.95	4.87
15.	Number of fruits per plant	53.95	42.40-70.87	10.97	15.77	48.40	8.48	15.72
16.	Yield per plot (Kg)	6.72	3.76-10.02	23.99	24.63	94.84	3.23	48.13
17.	Yield per hectare (q)	155.55	86.95-231.87	23.99	24.64	94.84	74.88	48.13

Genotypic and phenotypic coefficients of variation

Variations among all the genotypes for the various traits examined arise from the

combined influence of both genotype and environment. Typically, variations related to environment cannot be fixed. The GCV and PCV serve as straightforward indicators of



variability, frequently utilized to evaluate differences within a genetic population. The magnitude of GCV and PCV serves as an indicator of the amount of genetic variability present in the population (Badiger et al., 2017). In the present study, high GCV and PCV values were recorded for the yield per plot (23.99% and 24.63%) and yield per hectare (23.99% and 24.63%) signifying that these characters might be controlled by additive genes, which makes these character more reliable for selection in the selection process. These results were following the findings of Khajuria et al. (2015), Chandramouli et al. (2016), Deepanshu and Shamd (2017), Kerure et al. (2017) and Kumari et al. (2019) in okra. The GCV and PCV were moderate for internodal length (17.12% and 17.74%), plant height (13.11% and 13.18%), pedicel length (12.87% and 13.57%), days taken to first germination (11.13% and 17.18%) and number of fruits per plant (10.97% and 15.77%). Earlier researchers like Khajuria et al. (2015), Chandramouli et al. (2016) and Badigre et al. (2017) also conducted similar studies and results obtained by them were following the present findings in okra. However, the traits viz., flower diameter (9.51% and 9.71%), fruit length (7.99% and 9.57%), pedicel diameter (5.84% and 7.44%), number of epicalyx segments (5.06% and 5.41%), days taken to first flowering (4.79% and 5.90%), petiole length (4.66% and 6.41%), days taken to first fruit set (4.50% and 4.92%), average fruit weight (4.28% and 7.75%) and days taken to first fruit harvest (3.71% and 4.43%) revealed low GCV and PCV. The current results aligned with those of Ahamed et al. (2015) in okra.

Heritability

The GCV alone does not completely reflect the heritable variations, making the estimation of heritability essential. According to Burton and De-Vane (1953), combining GCV with heritability estimates provides a dependable

indication of the potential improvement achievable through selection. In the present study, broad-sense heritability values varied from 24.67% to 98.99% across the various traits examined. High heritability estimates were obtained for the parameters including plant height (98.99%), flower diameter (95.93%), yield per plot (94.84%), yield per hectare (94.84%), internodal length (93.21%), number of epicalyx segments (87.58%), pedicel length (89.99%), days to first fruit harvest (83.93%) and days taken to first fruit set (70.07%) which was also supported by the findings of Patel et al. (2014), Ahamed et al. (2015), Chandramouli et al. (2016) and Kumari et al. (2019) in okra. Such high estimates indicate that these traits are largely controlled by additive gene effects, suggesting that phenotypic selection would be highly effective for their improvement. Moderate heritability was estimated in fruit length (69.73%), days taken to first flowering (65.99%), pedicel diameter (61.57%) and petiole length (52.84%). Comparable findings were also reported by Goswami et al. (2012) and Umesh et al. (2013) in okra. However, heritability was found to be low for number of fruits per plant (48.40%), number of nodes bearing first flowering (45.72%), days taken to first germination (41.96%) and average fruit weight (30.48%) (Kerure et al. 2017) in okra genotypes which indicated that environmental conditions positively influence these traits hence there is a need of testing these traits under diverse environmental conditions for the effective selection procedure.

Genetic advance over mean (GAM)

The estimates of genetic gain provide further insight into the degree of expected improvement through selection. Genetic gain varied from low to high (from pedicel diameter to yield per hectare) for the various traits examined in the study. It was observed high for the yield per plot (48.13%), yield per hectare (48.13%), internodal length (34.05%), plant height (26.88) and pedicel length



(25.15%) which was also reported by Shaikh et al. (2013), Patel et al. (2014), Ahamed et al. (2015), Mishra et al. (2015) and Deepanshu and Shamd, (2017) but contradicted by Umesh et al. (2013) in okra. The genetic gain was found moderate for flower diameter (19.19%), number of fruits per plant (15.72%), days taken to first germination (14.85%), fruit length (13.74%) and number of nodes bearing first flower (12.23%) which was similar with the findings of Ahamed et al. (2015) and Chandramouli et al. (2016) in okra. However, traits viz., the number of epicalyx segments (9.76%), pedicel diameter (9.43%), days taken to first fruit set (8.50%), days taken to first flowering (8.02%), petiole length (6.98%), days taken to first fruit harvest (6.40%) and average fruit weight (4.87%), were recorded with a low genetic gain which was supported with the findings of Kerure et al. (2017) in okra.

High heritability along with high genetic gain suggests a larger share of additive genetic variance, leading to a high anticipated genetic improvement from selection. The characteristics that show high heritability but have a low genetic advance relative to the mean seem to be influenced by non-additive gene action, making selection for these traits potentially ineffective (Panse & Sukhatme 1984). High genetic advance suggests that these traits are primarily influenced by additive genes, making selection an effective strategy for increasing (Harish, 2018). A high heritability paired with a moderate genetic advance implies the involvement of both additive and non-additive genes (Chandramouli et al. 2016), as found for flower diameter. Hence, direct selection might be having a limited scope in future improvement of these traits. High heritability estimates coupled with high genetic gain were observed for plant height, internodal length, pedicel length, yield per plot and yield per hectare. Similar results were also obtained by Goswami et al. (2012), Mishra et al. (2015),

Deepanshu and Shamd (2017) and Kumari et al. (2019) in okra which suggested that these characters are influenced by additive gene effects, proving them more appropriate for the effective selection. Thus, the results clearly demonstrate that selection based on these characters would be advantageous for developing high-yielding and stable okra genotypes adapted to the valley conditions of Uttarakhand.

Conclusion

In conclusion, the present research demonstrated significant genetic variability present in the okra varieties studied, that was also indicated by the PCV and GCV, as well as the estimates of heritability and genetic advance. High heritability combined with high genetic advance for characteristics like plant height, internodal length, pedicel length, yield per plot and per hectare indicate that these traits are largely controlled by additive gene effects, making them dependable targets for selection in future breeding programs. Conversely, traits with low genetic advance despite high heritability are likely influenced by non-additive gene action, indicating limited effectiveness of direct selection. These results offer important guidance for targeted selection and the enhancement of genetic traits of okra, emphasizing the potential for enhancing yield related traits through targeted breeding strategies.

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