# International Journal of Advanced Biochemistry Research

**Beeresha HK**
M.Sc., Scholar, Department of Biotechnology and Crop Improvement, College of Horticulture, Bengaluru, Karnataka, India

**Halesh GK**
Associate Professor, Department of Biotechnology and Crop Improvement, College of Horticulture, Bengaluru, Karnataka, India

**Dhananjaya MV**
Principal Scientist, Division of Vegetable Crops, ICAR-IIHR, Bengaluru, Karnataka, India

**Pitchaimuthu M**
Principal Scientist, Division of Vegetable Crops, ICAR-IIHR, Bengaluru, Karnataka, India

**CN Hanchinamani**
Professor and Head, Department of Vegetable Science, College of Horticulture, Bengaluru, Karnataka, India

**KV Ravishankar**
Principal Scientist, Division of Biotechnology ICAR-IIHR, Bengaluru, Karnataka, India

**Corresponding Author:**
**Dr. Halesh GK**
Associate Professor, Department of Biotechnology and Crop Improvement, College of Horticulture, Bengaluru, Karnataka, India

# Genetic variability analysis in F₂ segregating populations for yield and its contributing traits in okra [*Abelmoschus esculents* (L.) Moench]

## Beeresha HK, Halesh GK, Dhananjaya MV, Pitchaimuthu M, CN Hanchinamani and KV Ravishankar

### Abstract
The current study aimed to assess the genetic variability of yield and its related characteristics in three bi-parental F₂ breeding populations *viz*., OK-2017-010 x Pusa Savani, OK-2017-010 x Varsha Uphar, OK-2017-006 x Pusa A4, along with their respective parental lines and the commercial check Radhika. The internodal length and number of branches per plant showed high phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) values across all three crosses. Traits like plant height, internodal length, number of branches per plant, number of nodes per plant, number of fruits per plant, and number of seeds per fruit exhibited high heritability and genetic advance as a percentage of mean (GAM) in all three segregating populations indicating the influence of additive gene action. This suggests significant potential for genetic enhancement these traits through targeted selection.

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

### Introduction
Okra [*Abelmoschus esculentus* (L.) Moench] is a prestigious and prize value vegetable crop, which has captured a significant position among vegetables in India. It is especially valued for its tender green fresh fruits, which are used as vegetable. Okra is normally cultivated during summer and rainy seasons and it is an important vegetable crop of the tropics and subtropics of the world and has found its place in India since time immemorial Komolafe *et al*. (2023) [10]. Okra is significant herbaceous annual crop, having a somatic chromosome number of 2n=130 and is considered to be an amphidiploid. It is being an often-cross pollinated crop, out crossing occurs to an extent of 4 to 19 per cent (Patil, 1995) [14]. Okra is being cultivated for its fibrous fruits or pods. It has multiple virtues, where tender fruits are used as vegetable, eaten boiled or in culinary preparations as sliced and fried pieces. It is also used in thickening of soups and gravies because of its high mucilage content. Okra fruits are sliced, sundried, canned and dehydrated for off-season use. Fruits are rich source of iodine which is helpful in curing goitre Mohammed *et al.* (2022) [13].

All activities involved in enhancing plants through breeding aim to ultimately increase the genetic yield potential. As yield is a complex trait affected greatly by environmental factors, focusing solely on yield in selection is ineffective. To choose for high yield, a breeder must indirectly consider yield-related and highly heritable characteristics while eliminating environmental influences on observed characteristics Pattnaik *et al.* (2023) [15]. Trying to enhance a trait through selection is fruitless unless a significant portion of the variation is due to genetics, highlighting the need for a thorough quantitative evaluation of the population yield and its contributing traits Priyanka *et al*. (2018) [17]. Study of different variability parameter provides a strong basis for selection of desirable genotype for augmentation of yield and other agronomical attributes. Such study estimates the feasibility of using available genetic resources for effective improvement Shwetha *et al.* (2022) [21]. The F₂ generation is critical for success of the breeding programme, as there are more chances of recovering superior recombinants in advanced generations Hallur *et al*. (2017) [7].

In order to enhance genetic traits related to yield, it is crucial to gather data on the variability, its heritability, and the relationships within the breeding populations. Without proper selection, the chances of identifying superior recombinants in later generations are minimal. This study aimed to assess the level of genetic diversity concerning total yield per plant and its associated traits in $F_2$ okra segregating populations, as well as to determine the potential genetic advancements achievable through selective breeding.

**Materials and Methods**
The experimental material in the present study consisted of five contrasting parental lines *viz*., OK-2017-010, OK-2017-006, Pusa Sawani, Varsha Uphar, Pusa. Three crosses were developed by mating the contrasting parent's *viz*., OK-2017-010 x Pusa Savani (H1), OK-2017-010 x Varsha Uphar (H2), OK-2017-006 x Pusa A4 (H3). The $F_1$ progeny of these three bi-parental crosses was raised to generate $F_2$ populations. The parents and their respective $F_1$'s and Commercial check were sown with replication and $F_2$ populations were sown without replication. The parents and hybrids and $F_2$ populations were evaluated and all the recommended package of practices was carried out to grow a successful crop. The experiment was carried out at Research block, Department of biotechnology and crop improvement, College of Horticulture, Bengaluru, GKVK post, Karnataka (State) during *summer* season of 2023. The observation recorded from five plants per parent and hybrid cross. The mean of these five plants was considered for statistical analysis. With respect to $F_2$, observations were recorded on 377 plants in H1, 372 plants in H2 and 426 plants in H3 on the 13 characters *viz*., plant height (cm), inter-nodal length (cm), number of branches per plant (No.), number of nodes per plant, stem girth (cm), fruit length (cm), fruit diameter (mm) average fruit weight (g), number of fruits per plant, number of seeds per pod, number of ridges per fruit, days to first flowering, total yield per plant (g) as per the DUS guidelines provided by PPV and FRA.

**Statical analysis and estimation of genetic parameters**
The components of genetic variability were estimated by utilizing the variability among the spaced $F_2$ plants in relation to the variability among the spaced plants of the non-segregating parents and check variety as suggested by Mahmud and Kramer (1951) [12].

**Variance**
Variance is defined as the average of the standard deviations of individual observation from the mean. It is expressed as the sum of squares of the deviations of all observations of a sample from its mean and divided by (n-1), where 'n' is the number of observations. It is estimated by the following formula.

$$Variance = \frac{\sum_{Xi} 2 - (\sum_X)^2/n}{(n-1)}$$

a) The total variance of observations for a character in $F_2$, is considered as its phenotypic variance.

Phenotypic variance $\sigma^2p = $ Var $F_2 = \sigma^2 F_2$

b) The environmental variance for each character was estimated from the mean-variance of the non-segregating parental genotypes and check variety.

Experimental error variance= $\sigma^2e$ = (Var $P_1$+Var $P_2$+Var check)/3

c) The genotypic variance was separated from the total phenotypic variance by subtracting the environmental variance as per the method of Mahmud and Kramer (1951) [12].

Genotypic variance $\sigma^2_g = \sigma^2 F_2 - \sigma^2e$
= $\sigma^2 F_2 - $ [Var $P_1$+Var $P_2$+Var check]/3

Genotypic coefficient of variation: $GCV = \frac{\sqrt{v_g}}{\bar{x}} \times 100$

Phenotypic coefficient of variation: $PCV = \frac{\sqrt{vp}}{\bar{x}} \times 100$

Broad-sense heritability and genetic advance as a percentage of the mean were calculated to assess the relative effectiveness of genetic improvement, following the methodology outlined by Johnson *et al*. (1955) [8-9].

**Result and Discussion**
The mean, range, phenotypic and genotypic coefficient of variation, heritability, and genetic advance as per cent of mean for 13 traits are presented in table 1 and figure 1a ,1b for population OK-2017-010 x Pusa Savani, table 2 and figure 2a, 2b for population OK-2017-010 x Varsha Uphar, table 3 and figure 3a, 3b for population OK-2017-006 x Pusa A4. In the present investigation, the phenotypic variance was greater than genotypic variance for all the characters in all three crosses under study which denoting the environmental factors influencing their expression to some degree which is in accordance with findings of Komolafe *et al*. (2023) [10], Singh *et al*. (2023) [22], Setu (2023) [20] and Pattnaik *et al*. (2023) [15]. The higher magnitude of PCV and GCV was observed in $F_2$ populations of OK-2017-010 x Pusa Savani, OK-2017-010 x Varsha Uphar, OK-2017-006 x Pusa A4 for internodal length (55.14% and 50.49%, 39.23% and 33.43%, 55.21% and 43.67% respectively) and number of branches per plant (97.56% and 58.53%, 68.07% and 33.72%, 81.95% and 66.52% respectively). This higher magnitude of PCV and GCV for above characters suggested greater phenotypic and genotypic variability among the $F_2$ segregating populations indicated that these characters can be improved through phenotypic selection. The similar results were obtained by Hallur *et al*. (2017) [7], Priyanka *et al*. (2018) [17], Raval *et al*. (2019) [19], Chavan *et al*. (2019) [5], Rathod *et al*. (2019) [18], Sravanthi *et al*. (2021) [24], Mohammed *et al*. (2022) [13], Shwetha *et al*. (2022) [21] for a number of branches per plant; Singh *et al*. (2017) [23] and Mohammed *et al*. (2022) [13] for internodal length. Selection of those segregating lines having more no of primary branches per plant could be selected due to the fact that primary branches also bear fruits which in turn contribute high yield and lines with shortest internodal length with more no of internodes bear a greater number of fruits produce better yield Anteneh (2017) [2]. In addition, other traits with moderate to low PCV and GCV values suggest the higher influence of environment on these

traits thus, selection on the phenotypic basis would not be effective for the genetic improvement Ehab *et al.* (2013) [6].

As environment plays its role by interacting with genotype in order to give a particular phenotype so heritability estimates in broad sense which contains total genetic variability not additive affect alone therefore, it could not be a true representation of the genotype's genetic potential. As a result, a high heritability in combination with a significant genetic progress as a percentage of the mean can explain the frequency of additive genes. Additionally, given that these traits were controlled by additive genes, it predicts a stronger response for the selection of high yielding genotypes (Bagadiya *et al.* 2023) [4].

High heritability coupled with high genetic advance as per cent of mean was recorded in $F_2$ populations of crosse OK-2017-010 x Pusa Savani for characters like plant height (80.84% and 54.54%), inter nodal length (83.84% and 99.81%), number of branches per plant (36.00% and 75.67%), number of nodes per plant (61.45% and 29.55%), number of fruits per plant (69.03% and 34.44%) and total fruit yield per plant (42.67% and 24.20%) suggested the preponderance of additive genes. It also indicated higher response for selection of high yielding genotypes as these characters were governed by additive genes. Similar results were reported by Bagadiya *et al.* (2023) [4] and Pattnaik *et al.* (2023) [15] for plant height; Mohammed *et al.* (2022) [13] and Shwetha *et al.* (2022) [21] for inter nodal length; Temam *et al.* (2020) [25] and Singh *et al.* (2023) [22] for number of nodes per plant; Shwetha *et al.* (2022) [21] and Pattnaik *et al.* (2023) [15] for number of fruits per plant; Temam *et al.* (2020) [25] and Awasthi *et al.* (2022) [3] for number of seeds per fruit; Temam *et al.* (2020) [25] for days to first flowering. While, in $F_2$ populations of OK-2017-010 x Varsha Uphar, also showed high heritability along with moderate genetic advance for plant height (84.62% and 48.18%), internodal length (72.63% and 61.54%), number of fruits per plant (63.36% and 26.23%), number of seeds per fruit (65.62%

and 24.12%). Similar results were obtained by Awasthi *et al.* (2022) [3], Mohammed *et al.* (2022) [13], Shwetha *et al.* (2022) [21], Bagadiya *et al.* (2023) [4] and Pattnaik *et al.* (2023) [15] for plant height, internodal length, number of fruits per plant; Temam *et al.* (2020) [25] and Awasthi *et al.* (2022) [3] for number of seeds per fruits. The higher estimates of heritability coupled with high genetic advance as per cent of the mean is recorded in the cross OK-2017-006 x Pusa A4 for plant height (82.73% and 56.56%), internodal length (62.56% and 74.53%), stem girth (64.97% and 34.84%) and number of fruits per plant (70.64% and 32.54%) suggested the role of additive gene action and a simple selection can be applied for improvement of these traits. Similar results were obtained by Mohammed *et al.* (2022) [13], Bagadiya *et al.* (2023) [4] and Pattnaik *et al.* (2023) [15] for plant height; Mohammed *et al.* (2022) [13], Shwetha *et al.* (2022) [21] and Pattnaik *et al.* (2023) [15] for inter nodal length; Temam *et al.* (2020) [25] for stem girth; Shwetha *et al.* (2022) [21], Pattnaik *et al.* (2023) [15] and Singh *et al.* (2023) [22] for number of fruits per plant. Heritability provides evidence for genetic control for the expression of a given trait and phenotypic reliability to predict its breeding value. It also estimates genetic advance that a breeder can expect from selection and which breeding method to adopt Ullah *et al.* (2023) [26]. Therefore, selection of high performing genotypes is possible for the improvement of these traits. The high heritability would be a close correspondence between the genotypic and phenotypic variations due to relatively small contribution of the environment to the phenotype expression of the trait Singh *et al.* (2017) [23]. Heritability estimates along with genetic advance provide better information than each parameter alone Johnson *et al.* (1955) [8-9]. Phani *et al.* (2015) [16] suggested that selection based on phenotypic performance of genotypes would be effective to improve the traits for which there is high genetic advance as percent of mean coupled with high heritability estimates.

**Table 1:** Estimates of genetic variability parameters for growth and yield attributes in $F_2$ segregating population of the cross OK-2017-010 × Pusa Sawani

| Sl. No. | Characters | Mean | Range | | PCV (%) | GCV (%) | h² (%) | GAM (%) |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| | | | Min. | Max. | | | | |
| 1 | Plant height (cm) | 93.84 | 30.00 | 180.00 | 31.25 | 28.01 | 80.84 | 54.54 |
| 2 | Inter nodal length (cm) | 8.01 | 0.50 | 20.00 | 55.14 | 50.49 | 83.84 | 99.81 |
| 3 | No. of branches per plant | 0.89 | 0.00 | 3.00 | 97.56 | 58.53 | 36.00 | 75.67 |
| 4 | No. of nodes per plant | 12.74 | 7.00 | 21.00 | 22.28 | 17.46 | 61.45 | 29.55 |
| 5 | Stem girth (cm) | 1.42 | 0.30 | 2.70 | 27.67 | 19.53 | 49.81 | 29.77 |
| 6 | Fruit length (cm) | 14.66 | 10.10 | 21.10 | 13.46 | 9.77 | 52.69 | 15.30 |
| 7 | Fruit diameter (mm) | 15.55 | 10.60 | 22.30 | 10.08 | 6.93 | 47.18 | 10.26 |
| 8 | Average fruit weight (g) | 17.15 | 13.17 | 29.63 | 10.15 | 6.63 | 42.67 | 9.34 |
| 9 | No. of fruits per plant | 11.03 | 6.00 | 19.00 | 23.11 | 19.20 | 69.03 | 34.44 |
| 10 | No. seeds per fruit | 55.28 | 38.00 | 73.00 | 16.20 | 14.90 | 84.62 | 29.60 |
| 11 | No. of ridges per fruit | 5.06 | 5.00 | 6.00 | 4.73 | 2.41 | 25.86 | 2.64 |
| 12 | Days to first flowering | 41.57 | 37.00 | 48.00 | 5.23 | 4.35 | 69.18 | 7.81 |
| 13 | Total yield per plant (g) | 188.85 | 97.90 | 344.00 | 24.57 | 16.59 | 42.67 | 24.20 |

PCV: Phenotypic coefficient of variation GAM: Genetic advance as per cent of mean
GCV: Genotypic coefficient of variation h²(bs): Heritability

**Table 2:** Estimates of genetic variability parameters for growth and yield attributes in $F_2$ segregating population of the cross OK-2017-010 × Varsha Uphar

| Sl. No. | Characters | Mean | Range | | PCV (%) | GCV (%) | $h^2$ (%) | GAM (%) |
|---|---|---|---|---|---|---|---|---|
| | | | Min. | Max. | | | | |
| 1 | Plant height (cm) | 106.00 | 40.00 | 195.00 | 26.37 | 24.25 | 84.62 | 48.18 |
| 2 | Inter nodal length (cm) | 8.45 | 2.00 | 19.00 | 39.23 | 33.43 | 72.63 | 61.51 |
| 3 | No. of branches per plant | 1.23 | 0.00 | 3.00 | 68.07 | 33.72 | 24.54 | 36.02 |
| 4 | No. of nodes per plant | 13.93 | 6.00 | 20.00 | 19.91 | 14.80 | 55.24 | 23.74 |
| 5 | Stem girth (cm) | 1.61 | 0.70 | 2.80 | 21.16 | 15.76 | 55.43 | 25.32 |
| 6 | Fruit length (cm) | 14.56 | 9.40 | 21.30 | 13.53 | 7.32 | 29.23 | 8.75 |
| 7 | Fruit diameter (mm) | 15.33 | 9.60 | 20.60 | 10.69 | 7.18 | 45.09 | 10.39 |
| 8 | Average fruit weight (g) | 17.46 | 13.01 | 22.58 | 8.71 | 4.62 | 28.20 | 5.30 |
| 9 | No. of fruits per plant | 11.27 | 6.00 | 18.00 | 19.19 | 15.27 | 63.36 | 26.23 |
| 10 | No. seeds per fruit | 54.63 | 32.00 | 77.00 | 17.02 | 13.79 | 65.62 | 24.12 |
| 11 | No. of ridges per fruit | 5.06 | 5.00 | 6.00 | 4.66 | 2.27 | 23.67 | 2.38 |
| 12 | Days to first flowering | 42.35 | 37.00 | 49.00 | 5.25 | 3.31 | 39.69 | 4.15 |
| 13 | Total yield per plant (g) | 197.24 | 103.40 | 365.60 | 20.06 | 14.22 | 50.25 | 21.75 |

PCV: Phenotypic coefficient of variation  GAM: Genetic advance as per cent of mean
GCV: Genotypic coefficient of variation $h^2$ (bs): Heritability

**Table 3:** Estimates of genetic variability parameters for growth and yield attributes in $F_2$ segregating population of the cross OK-2017-006 × Pusa A4
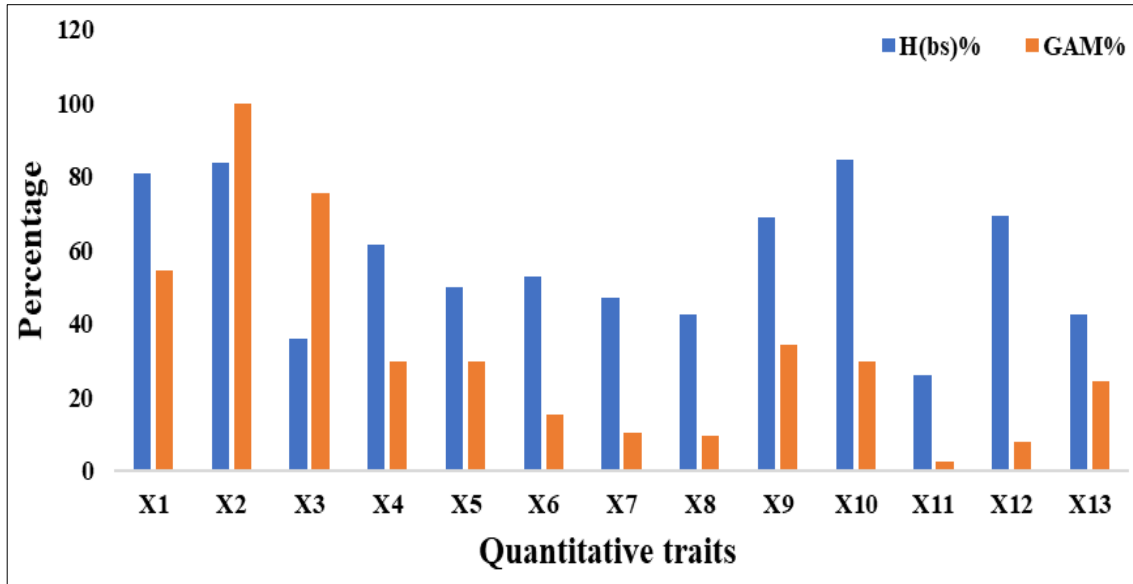
| Sl. No. | Characters | Mean | Range | | PCV (%) | GCV (%) | $h^2$ (%) | GAM (%) |
|---|---|---|---|---|---|---|---|---|
| | | | Min. | Max. | | | | |
| 1 | Plant height (cm) | 88.38 | 32.00 | 189.00 | 31.66 | 28.80 | 82.73 | 56.56 |
| 2 | Inter nodal length (cm) | 3.78 | 0.50 | 12.00 | 55.21 | 43.67 | 62.56 | 74.53 |
| 3 | No. of branches per plant | 1.04 | 0.00 | 3.00 | 81.95 | 66.52 | 49.05 | 86.73 |
| 4 | No. of nodes per plant | 15.40 | 8.00 | 24.00 | 19.00 | 12.30 | 41.88 | 17.15 |
| 5 | Stem girth (cm) | 1.61 | 0.70 | 2.90 | 24.85 | 20.03 | 64.97 | 34.84 |
| 6 | Fruit length (cm) | 14.82 | 10.50 | 19.60 | 13.14 | 9.67 | 54.18 | 15.36 |
| 7 | Fruit diameter (mm) | 15.49 | 9.60 | 21.00 | 11.40 | 6.69 | 34.40 | 8.47 |
| 8 | Average fruit weight (g) | 16.43 | 13.21 | 20.57 | 8.48 | 5.66 | 44.71 | 8.18 |
| 9 | No. of fruits per plant | 11.72 | 6.00 | 24.00 | 21.34 | 17.93 | 70.64 | 32.54 |
| 10 | No. seeds per fruit | 59.96 | 40.00 | 73.00 | 11.51 | 9.53 | 68.51 | 17.03 |
| 11 | No. of ridges per fruit | 5.08 | 5.00 | 6.00 | 3.85 | 3.49 | 45.10 | 5.06 |
| 12 | Days to first flowering | 42.30 | 37.00 | 49.00 | 4.96 | 3.23 | 42.30 | 4.53 |
| 13 | Total yield per plant (g) | 191.53 | 100.10 | 370.00 | 20.77 | 11.85 | 32.59 | 14.58 |

PCV: Phenotypic coefficient of variation GAM: Genetic advance as per cent of mean
GCV: Genotypic coefficient of variation $h^2$ (bs): Heritability
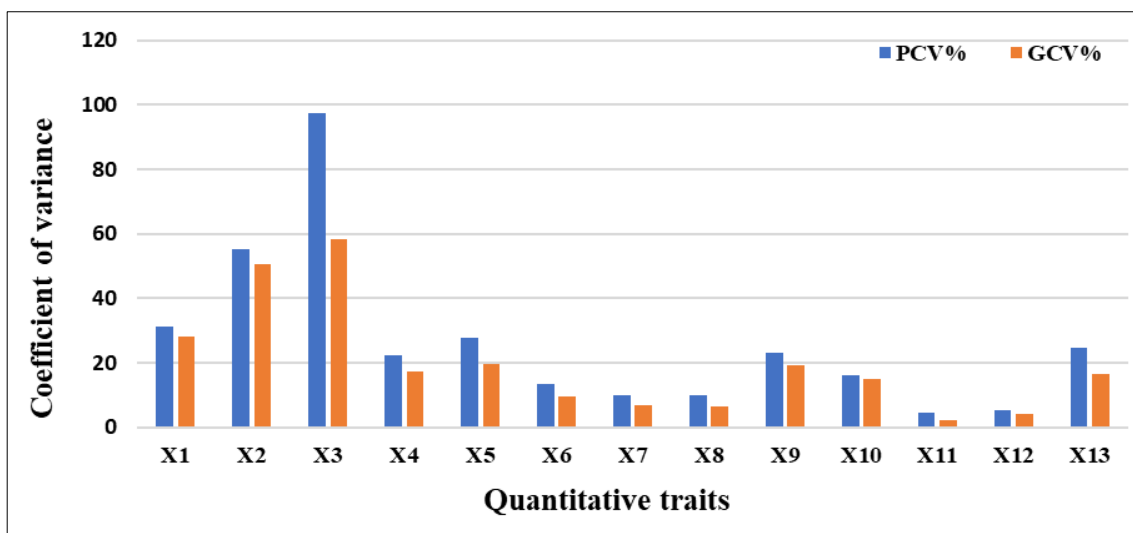


PCV: Phenotypic coefficient of variation GCV: Genotypic coefficient of variation
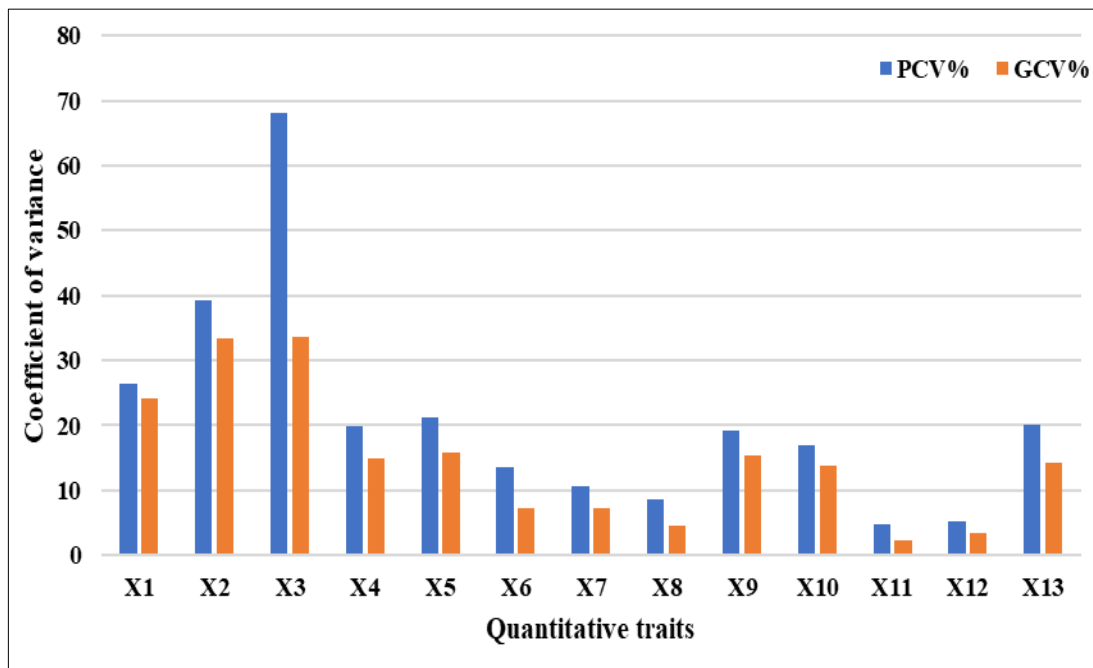
**Fig 1a:** Phenotypic and genotypic coefficient of variances for quantitative characters in F2 segregating population of the cross OK-2017-010 × Pusa Sawani

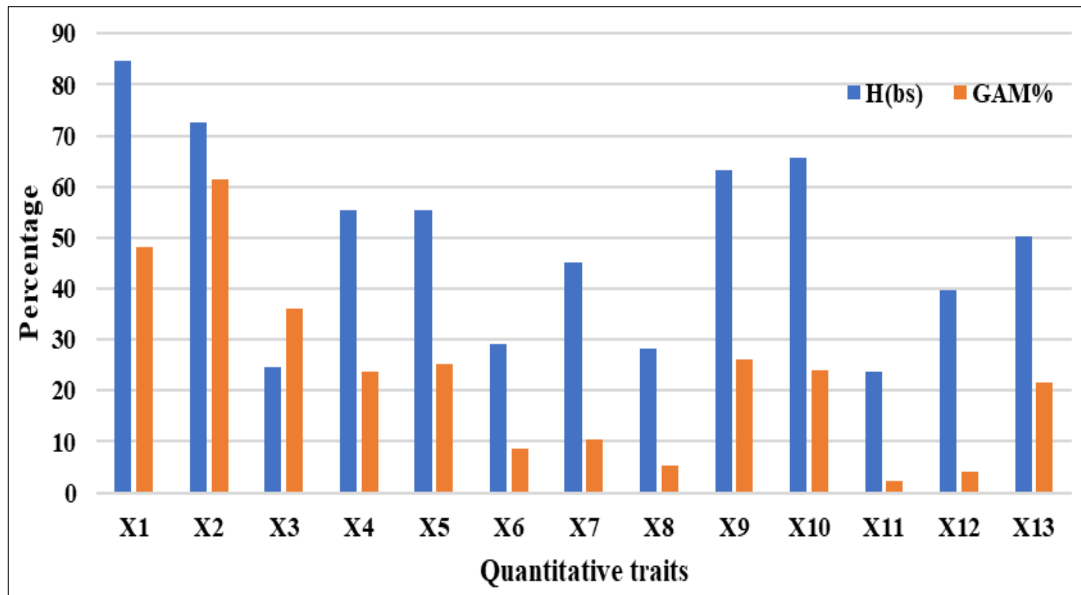H(bs): Broad sense heritability GAM: Genetic advance as percent of mean

| X1: | Plant height (cm) | X6: | Fruit length (cm) | X11: | No. of ridges per fruit |
| X2: | Inter nodal length (cm) | X7: | Fruit diameter (mm) | X12: | Days to first flowering |
| X3: | No. of branches per plant | X8: | Average fruit weight (g) | X13: | Total yield per plant (g) |
| X4: | No. of nodes per plant | X9: | No. of fruits per plant | | |
| X5: | Stem girth (cm) | X10: | No. seeds per fruit | | |

**Fig 1b:** Heritability and genetic advance as percent of mean for quantitative characters in $F_2$ segregating population of the cross OK-2017-010 × Pusa Sawani



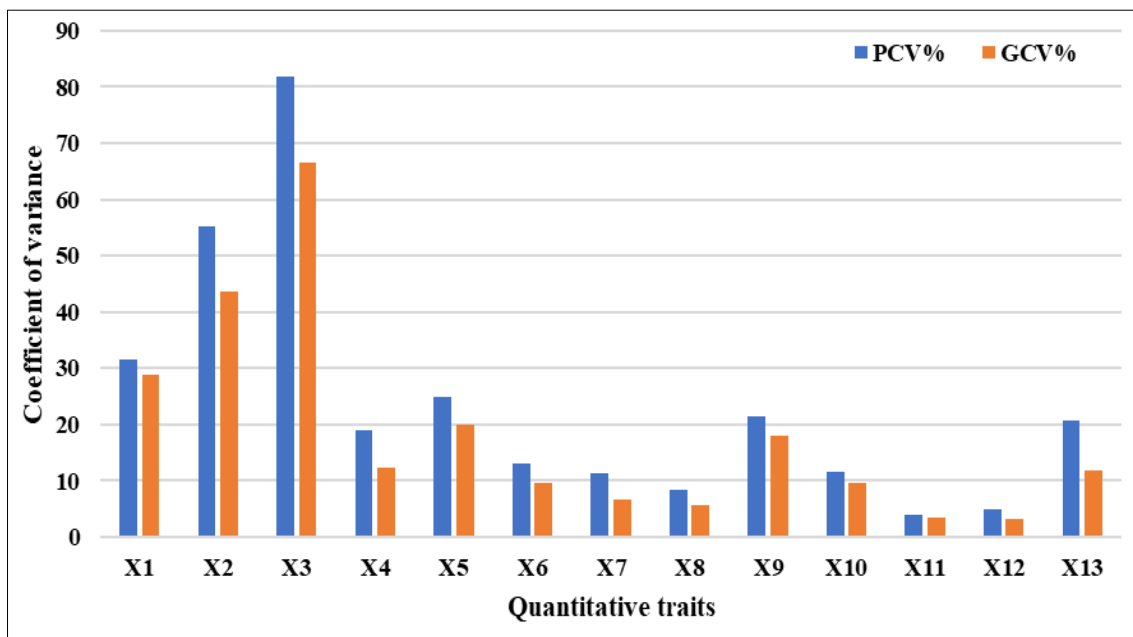PCV: Phenotypic coefficient of variation GCV: Genotypic coefficient of variation

**Fig 2a:** Phenotypic and genotypic coefficient of variances for quantitative characters in $F_2$ segregating population of the cross OK-2017-010 × Varsha Uphar

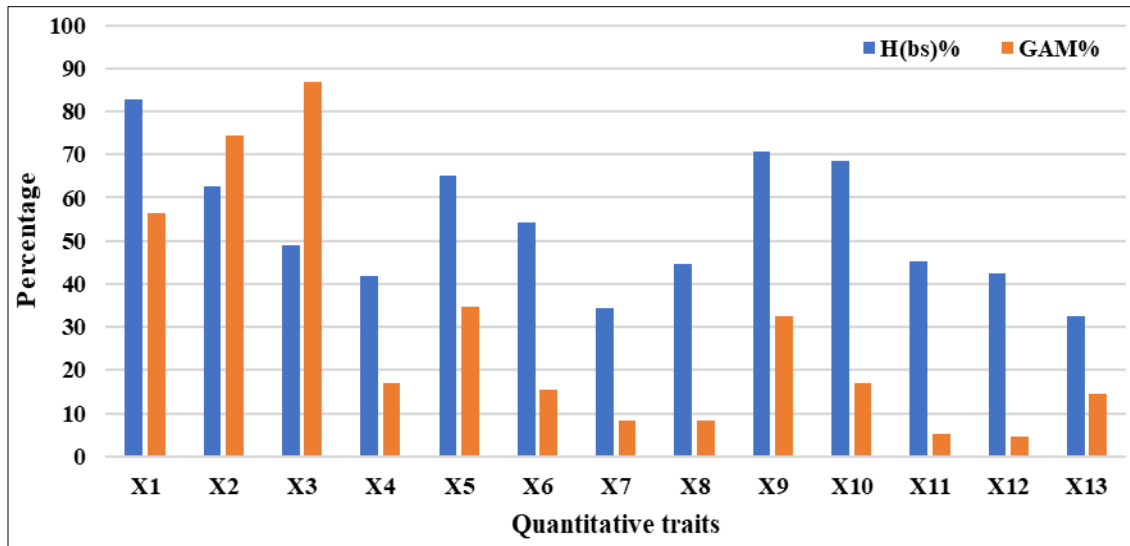H(bs): Broad sense heritability GAM: Genetic advance as percent of mean

| X1: | Plant height (cm) | X6: | Fruit length (cm) | X11: | No. of ridges per fruit |
| X2: | Inter nodal length (cm) | X7: | Fruit diameter (mm) | X12: | Days to first flowering |
| X3: | No. of branches per plant | X8: | Average fruit weight (g) | X13: | Total yield per plant (g) |
| X4: | No. of nodes per plant | X9: | No. of fruits per plant | | |
| X5: | Stem girth (cm) | X10: | No. seeds per fruit | | |

**Fig 2b:** Heritability and genetic advance as percent of mean for quantitative characters in F$_2$ segregating population of the cross OK-2017-010 × Varsha Uphar



PCV: Phenotypic coefficient of variation GCV: Genotypic coefficient of variation

**Fig 3a:** Phenotypic and genotypic coefficient of variances for quantitative characters in F$_2$ segregating population of the cross OK-2017-006 × Pusa A4

H(bs): Broad sense heritability GAM: Genetic advance as percent of mean

| X1: | Plant height (cm) | X6: | Fruit length (cm) | X11: | No. of ridges per fruit |
| X2: | Inter nodal length (cm) | X7: | Fruit diameter (mm) | X12: | Days to first flowering |
| X3: | No. of branches per plant | X8: | Average fruit weight (g) | X13: | Total yield per plant (g) |
| X4: | No. of nodes per plant | X9: | No. of fruits per plant | | |
| X5: | Stem girth (cm) | X10: | No. seeds per fruit | | |

**Fig 3b:** Heritability and genetic advance as percent of mean for quantitative characters in F₂ segregating population of the cross OK-2017-006 × Pusa A4

## Conclusion
The results of the current study showed that the PCV was larger than the matching GCV for all of the characteristics, suggesting that there may be some degree of genotype-environment interaction. Strong genetic advance as a percentage of mean and high heritability estimations gives us idea about the governance of additive genes for the characters. It also suggests selection would be rewarding for high yielding genotypes as those characters mentioned above were governed by additive genes. Thus, we should focus on those yield attributing characters which is giving higher response of high estimates of heritability along with high genetic advance

## Future scope
Okra [Abelmoschus esculentus (L.) Moench] is a highly nutritious vegetable that is rich in fiber, vitamins, and minerals. By advancing the selected segregating lines, we can investigate phenotypic diversity. By assessing the variability of okra genotypes in response to changing climatic conditions, we can study the adaptive traits such as disease resistance and abiotic stress tolerance.

## Acknowledgement
The authors thank the College of Horticulture, Bengaluru, for its facilities.

## Conflict of Interest
The authors have declared that no conflict of interest exists.

## References
1. Anonymous. Protection of Plant Varieties and Farmers' Rights Authority (PPV & FRA); c2022. Available from: https://plantauthority.gov.in/sites/default/files/revised-dus-test-gudeilines-okra-01.04.2022.pdf

2. Anteneh B. Characterization and evaluation of indigenous and exotic okra (*Abelmoschus esculentus* (L.) Moench) genotypes for yield and yield related traits at Dire Dawa, Eastern Ethiopia. Haramaya University, Haramaya, Ethiopia. MSc Thesis; c2017.

3. Awasthi S, Singh DP, Lal B, Singh P, Upadhyay A, Singh PK, Kuswaha C, Pandey S, Maurya PK, Kumar A. Assessment of genetic variability, heritability and genetic advance of okra genotypes (*Abelmoschus esculentus* L. Moench). Assessment. 2022;53(04):450-461.

4. Bagadiya P, Patel P, Intwala CG, Pranati J, Balar V. Exploring variability, heritability and genetic advances: case study in okra (*Abelmoschus esculentus* (L.) Moench) through four distinct crosses in F2. Biological Forum-An International Journal. 2023;15(5):765-772.

5. Chavan J, Seenivasan N, Saidaiah P, Sivaraj N. Estimation of correlation coefficient and path coefficient analysis for yield and yield components in okra (*Abelmoschus esculentus* (L.) Moench). International Journal of Chemical Studies. 2019;7(4):1254-1260.

6. Ehab AA, Mohamed YA, Ali MM. Genetic behaviour of families selected from some local okra (*Abelmoschus esculentus* (L.) Moench) populations in Egypt. Plant Breeding Biotechnology. 2013;1(4):396-405.

7. Hallur RH, Shantappa T, Jagadeesha RC. Studies on genetic variability in segregating populations of okra and their character association. Research Journal of Environmental Sciences. 2017;10(1):71-74.

8. Johnson HW, Robinson HF, Comstock RE. Estimates of genetic and environmental variability in soybeans. Journal of Agronomy. 1955;47(7):314-318.

9. Johnson HW, Robinson HF, Comstock RE. Genotypic and phenotypic correlations in soybeans and their implications in selection. Journal of Agronomy. 1955;47(10):477-483.

10. Komolafe RJ, Ariyo OJ, Alake CO, Oduwaye OA. Genetic variability, heritability, genetic advance, association between fruit yield and yield components of okra (*Abelmoschus esculentus* L. Moench) accessions grown in two different years. Israel Journal of Plant Sciences. 2023;1-13.

11. Kudari GB, Hanchinamani CN, Hadimani HP, Satish D, Bhavidoddi A, Kantharaju V. Assessment of genetic variability in F2 populations of okra (*Abelmoschus esculentus* (L.) Moench) for productivity traits. Journal of Pharmacognosy and Phytochemistry. 2020;9(6):1574-1576.

12. Mahmud I, Kramer HH. Segregation for yield, height and maturity following a soybean cross. Journal of Agronomy. 1951;43:605-609.

13. Mohammed J, Mohammed W, Shiferaw E. Performance and genetic variability of okra (*Abelmoschus esculentus* (L.) Moench) genotypes in Ethiopia for agromorphology and biochemical traits. Journal of Advanced Agricultural Technologies. 2022;14:111-118.

14. Patil YB. Studies on genetic divergence, heterosis and combining ability in okra (*Abelmoschus esculentus* (L.) Moench.). PhD Thesis. University of Agricultural Sciences, Dharwad; c1995.

15. Pattnaik P, Singh AK, Singh BK, Pal AK. Statistical estimation of genetic parameters to study variability in okra (*Abelmoschus esculentus* (L.) Moench) for enhancement in economic and quality attributes. Journal of Pharmaceutical Innovation. 2023;12(8):1505-1508.

16. Phani KM, Hameedunnisa BA, Manohar R, Kumar NS. Estimation of heritability and genetic advance in okra (*Abelmoschus esculentus* (L.) Moench.). Plant Archives. 2015;15(1):489-491.

17. Priyanka VD, Reddy TM, Begum H, Sunil N, Jayaprada M. Studies on genetic variability, heritability and genetic advance in genotypes of okra (*Abelmoschus esculentus* (L.) Moench). International Journal of Current Microbiology and Applied Sciences. 2018;7(5):401-411.

18. Rathod S, Parmar VL, Patel AI. Correlation and path coefficient analysis for quantitative traits in $F_2$ population in okra (*Abelmoschus esculentus* (L.) Moench). International Journal of Chemical Studies. 2019;7(5):1030-1033.

19. Raval V, Patel AI, Vashi CB, Chaudhari BN. Correlation and path analysis studies in okra (*Abelmoschus esculentus* (L.) Moench). International Journal of Chemical Studies. 2019;7(1):1230-1233.

20. Setu H. Genetic variability analysis for traits in okra (*Abelmoschus esculentus* L. Moench) genotypes. International Journal of Agriculture and Food Science. 2023;7(1):95-104.

21. Shwetha A, Basavaraja N, Raghavendra G, Ganiger VM, Jagadeesha RC, Mesta RK, Pitchaimuthu M. Genetic variability studies in okra (*Abelmoschus esculentus* (L.) Moench) for yield and yield contributing traits. Journal of Pharmaceutical Innovation. 2022;11(6):287-290.

22. Singh G, Pathak M, Sharma A. Identification of novel sources of yellow vein mosaic disease resistance in okra (*Abelmoschus esculentus* L. Moench). Euphytica. 2023;219(10):111.

23. Singh N, Singh DK, Sati UC, Rawat M, Pandey P. Genetic analysis studies in okra (*Abelmoschus esculentus* (L.) Moench). International Journal of Pure & Applied Bioscience. 2017;5(4):361-367.

24. Sravanthi U, Prabhakar BN, Saidaiah P, Rao AM, Narayana DL, Sathish G. Studies on genetic variability in okra (*Abelmoschus esculentus* (L.) Moench). Journal of Pharmaceutical Innovation. 2021;10(11):151-155.

25. Temam N, Mohamed W, Aklilu S. Agro-morphological characterization and evaluation of okra (*Abelmoschus esculentus* (L.) Moench) genotypes for yield and other variability components at Melkassa, Central Ethiopia. Journal of Ecology and Environment. 2020;5(2):80-87.

26. Ullah MZ, Hasan MJ, Chowdhury AZMK, Saki AI, Rahman AHMA. Genetic variability and correlation in exotic cucumber (*Cucumis sativus* L.) varieties. Bangladesh Journal of Plant Breeding and Genetics. 2012;25(1):17-23.