Biological Forum
an International Journal 17(4): 126-131(2025)
ISSN No. (Print): 0975-1130
ISSN No. (Online): 2249-3239

Genetic Architecture of Yield and Component Traits in an F_2 Okra Population derived from *Arka Anamika* × *Abelmoschus manihot*

Sandeep N.* and Dushyantha Kumar B.M.
Department of Genetics and Plant Breeding, College of Agriculture, Shivamogga, Keladi Shivappa Nayaka University of Agricultural and Horticultural Sciences, Shivamogga, 577201 (Karnataka), India.

(Corresponding author: Sandeep N.)*

(Received: 04 February 2025; Revised: 12 March 2025; Accepted: 30 March 2025; Published online: 23 April 2025)
(Published by Research Trend)

DOI: https://doi.org/10.65041/BiologicalForum.2025.17.4.19

ABSTRACT: A wide hybridization program was attempted in okra (*Abelmoschus esculentus* (L.) Moench) using Arka Anamika as the cultivated parent and *Abelmoschus manihot* as the wild donor to broaden the genetic base. The F_1 plants were sterile and fertility was restored through chromosome doubling using colchicine (0.1%) followed by selfing to generate the F_2. The F_2 population (n = 238 plants) was evaluated in an augmented block design with repeated checks for five quantitative traits: plant height, number of internodes, fruit length, fruit width and fruits per plant. Substantial segregation and transgressive variation were observed for all traits. Phenotypic coefficient of variation (PCV) exceeded genotypic coefficient of variation (GCV) for each trait, indicating environmental influence; however, broad-sense heritability (h^2) was high (76 to 85%) and genetic advance as percent of mean (GAM) was moderate-to-high (28 to 52%), suggesting good scope for selection. Correlation analysis revealed that the number of fruits per plant was positively associated with plant height and internode number. PCA revealed that the first two components explained 76% of total variability, with PC1 representing overall plant vigor and yield potential and PC2 differentiating fruit size from fruit number. The study demonstrates that wide hybrid-derived F_2 populations can provide exploitable variability for improving yield-related traits in okra.

Keywords: okra, wide hybridization, augmented design, GCV, PCV, heritability, genetic advance, correlation, PCA.

INTRODUCTION

Okra (*Abelmoschus esculentus* (L.) Moench) is one of the most widely cultivated vegetable crops in tropical and subtropical regions, valued for its tender fruits, high dietary fiber, vitamins and minerals and its role as a short-duration income crop (Singh and Nigam 2023). However, sustained improvement in okra productivity and stability is often constrained by the narrow genetic base created by repeated use of a limited set of elite lines in conventional breeding (Suma *et al.*, 2023). The narrow base is particularly problematic under changing climates and increasing pest-disease pressure, where resistance/tolerance sources are frequently insufficient or break down over time. Wide hybridization has therefore been emphasized as a strategic approach to broaden variability by introgressing novel alleles from wild *Abelmoschus* species into the cultivated gene pool (Sandeep *et al*., 2022).

Among biotic constraints, okra yellow vein mosaic virus (YVMV) remains a major yield-limiting disease in South Asia, often causing severe yield and quality losses (Mubeen *et al.*, 2021; Priyanka *et al.*, 2022). This has reinforced the importance of using resistant/tolerant cultivars and broadening resistance sources through pre-breeding and wide crosses. Arka Anamika, released from IIHR, Bengaluru, is widely recognized for its field adaptation and reported tolerance to YVMV. Incorporation of wild-species diversity into cultivated backgrounds can generate new recombinants combining adaptation with improved yield attributes and resilience (Dutta, 1991).

The genus *Abelmoschus* includes several wild relatives with useful traits, and *Abelmoschus manihot* has been used as a donor in wide hybridization attempts for transferring stress tolerance and disease resistance and for creating novel variability (Suma *et al.*, 2023). Reports also indicate that interspecific crosses involving *A. esculentus* and *A. manihot* can express substantial reproductive barriers, including F_1 sterility due to ploidy and meiotic irregularities. To overcome such sterility and permit advancement to segregating generations, chromosome doubling (colchiploidy) using colchicine is a commonly adopted method, restoring fertility in otherwise sterile hybrids and enabling selfing to generate F_2 populations where segregation and transgressive variation can be exploited. Evidence for fertility restoration through colchiploidy in *A. esculentus* × *A. manihot* interspecific hybrids has been documented (Badiger, 2017; Sandeep *et al*., 2022).

Once a segregating population is generated, quantifying genetic variability and identifying selection-relevant traits become essential for effective improvement (Singh *et al.*, 2023). Parameters such as genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability and genetic advance provide a structured way to infer the magnitude of genetic control and the expected response to selection (Sandeep, 2022).

The present investigation was undertaken to assess the extent of variability, heritability, association among traits, and multivariate divergence (PCA) in an F_2 population derived from the wide cross *Abelmoschus esculentus* cv. Arka Anamika × *Abelmoschus manihot.* The specific objectives were: (i) to estimate variability parameters (GCV, PCV), broad-sense heritability and genetic advance for key growth and fruit traits; (ii) to quantify relationships among traits through correlation analysis, particularly with fruits per plant as a yield component.

MATERIAL AND METHODS

Experimental site. The present study was carried out at Zonal Agricultural and Horticultural Sciences (ZAHRS), Keladi Shivappa Nayaka University of Agricultural and Horticultural Sciences, Shivamogga (KSNUAHS), India, which is situated at 13.28° North latitude and 75.34° East longitude and at an altitude of 617.0 m above mean sea level, during the rainy seasons of 2021.

Plant material and development of F_2 population. The experimental material consisted of an F_2 population derived from a wide cross between Arka Anamika (*Abelmoschus esculentus*) and *Abelmoschus manihot.* The F_1 plants obtained from this cross exhibited sterility with poor or no seed set. To overcome sterility, F_1 plants were treated with 0.1% colchicine to induce chromosome doubling, which resulted in fertility restoration. The fertile F_1 plants were selfed to obtain the F_2 population comprising 238 plants, which was used for the present investigation.

Experimental design. The F_2 population was evaluated using an augmented block design, wherein F_2 plants were grown as unreplicated entries, while standard check varieties were replicated across blocks to facilitate error estimation and block adjustment. The crop was raised following recommended agronomic and plant protection practices to ensure normal growth and development.

Sampling of plants and data collection. Observations were recorded on individual F_2 plants for plant height (cm), number of internodes, fruit length (cm), fruit width (cm), and number of fruits per plant, following standard phenotyping procedures.

Statistical analysis. Block-adjusted means were computed following augmented design procedures using replicated checks to estimate block effects and experimental error (Federer, 1956). Phenotypic and genotypic variances were estimated, and the genotypic and phenotypic coefficients of variation (GCV and PCV) were computed as per standard biometric methods (Burton and DeVane 1953; Singh and Chaudhary 1977). Broad-sense heritability (h^2bs) was estimated from variance components, and genetic advance (GA) and genetic advance as percent of mean (GAM) were calculated to predict response to selection (Johnson *et al.*, 1955; Falconer and Mackay 1996). Pearson's correlation coefficients among traits were estimated and tested for significance at 5% and 1% probability levels (Panse and Sukhatme 1985). Principal component analysis (PCA) was performed on standardized trait values (mean = 0, SD = 1) to assess the relative contribution of traits to total variability and to visualize multivariate relationships among F_2 plants (Jackson, 1991).

RESULTS AND DISCUSSION

Extent and pattern of variability in the F_2 population. The analysis of variance revealed highly significant differences ($p \leq 0.01$) among F_2 genotypes for plant height, number of internodes, fruit length and number of fruits per plant, indicating the presence of substantial genetic variability generated through wide hybridization between *Arka Anamika* and *Abelmoschus manihot* (Table 1). The presence of highly significant genetic variability for plant height and number of internodes reflects the segregation of alleles controlling vegetative growth inherited from both cultivated okra and its wild relative (Patel *et al*., 2021). Significant variation for fruit length and fruit width indicates successful recombination of genes governing fruit morphology. The relatively lower level of significance for fruit width compared to fruit length suggests that fruit width may be governed by fewer genes or exhibit partial dominance, whereas fruit length appears to be under stronger polygenic control.

Table 1: Analysis of variance for growth and yield component traits among F_2 individuals of okra derived from *Arka Anamika × Abelmoschus manihot.*

Source of variation	df	PH	NIN	FL	FD	NOF
Block (ignoring genotypes)	2	26.84	0.07	0.42	0.01	0.31
Genotypes + checks (ignoring blocks)	239	176.42**	6.94**	6.88**	0.06*	12.04**
Genotypes	237	171.35**	6.61**	6.54**	0.05*	11.52**
Checks	1	1226.80**	23.46**	21.14**	0.19**	10.86**
Checks *vs* Genotypes	1	154.72	27.85**	2.84	0.14*	332.64**
Error	10	58.24	2.36	1.62	0.02	2.18

*Significant at 5% level ($p \leq 0.05$); ** Significant at 1% level ($p \leq 0.01$)

The wide-hybrid derived F_2 population exhibited broad phenotypic ranges for all five traits (Table 2), confirming strong segregation following fertility restoration and selfing. Such extensive variation is expected in wide crosses because parental genomes differ substantially, and the F_2 generation releases recombination and segregation across multiple loci controlling plant architecture and fruit traits. Notably, fruits per plant showed the highest dispersion (29%), followed by plant height and internode number (21–23%), indicating that these traits are highly variable and potentially responsive to selection in early generations (Sharma *et al.*, 2016; Parth Bagadiya *et al.*, 2023). In practical breeding terms, this is desirable because fruit number and plant architecture together define the productive capacity of okra under field conditions.

Table 2: Descriptive statistics of five quantitative traits in an F_2 population.

Sr. No.	Trait	Mean	Min	Max	SD	CV (%)
1.	Plant height (cm)	135.82	60.00	221.87	30.91	22.76
2.	No. of internodes	18.01	8.00	29.00	3.83	21.25
3.	Fruit length (cm)	12.86	6.00	19.06	2.47	19.22
4.	Fruit width (cm)	2.13	1.20	3.17	0.38	17.93
5.	Fruits plant^{-1}	22.58	6.00	45.00	6.64	29.39

The presence of extreme phenotypes on both sides of the mean (very short to very tall plants; low to high fruiting plants) also indicates the likelihood of transgressive segregation, where some F_2 individuals outperform both parents for specific traits (Mackay *et al.,* 2021). In wide hybridization programs, transgressive recombinants are particularly valuable because they represent novel allele combinations that may not exist in cultivated germplasm. This strengthens the utility of *A. manihot* as a donor for expanding the breeding pool, aligning with broader conclusions that wild relatives can reintroduce useful variation into okra improvement pipelines (Boukhers *et al*., 2022).

GCV, PCV, heritability and genetic advance. Genetic parameter estimates (Table 3) showed that PCV exceeded GCV for all traits, indicating measurable environmental influence on trait expression. However, the gap between PCV and GCV was not excessive for most traits, suggesting that a substantial portion of observed variation is genetically governed and selection based on phenotype would still be effective, particularly in later generations when lines become more homozygous (Nanditha *et al*., 2023).

Table 3: Genetic parameters associated with yield and related traits in the F_2 population.

Trait	Mean	Range	GCV (%)	PCV (%)	h^2bs (%)	GA (5%)	GAM (%)
Plant height (cm)	135.82	60.00-221.87	20.90	22.76	84.30	53.68	39.53
No. of internodes	18.01	8.00-29.00	19.35	21.25	82.94	6.54	36.31
Fruit length (cm)	12.86	6.00-19.06	17.41	19.22	82.01	4.18	32.47
Fruit width (cm)	2.13	1.20-3.17	15.64	17.93	76.10	0.60	28.11
Fruits plant^{-1}	22.58	6.00-45.00	27.13	29.39	85.24	11.65	51.61

Among the studied traits, fruits per plant recorded the highest variability (GCV=27.13%, PCV= 29.39%) and the highest expected response to selection (GAM = 51.61%). This implies that fruit number is under strong genetic control in this population and that selecting superior F_2 plants could produce rapid improvement in subsequent generations (Mohammed *et al.,* 2022).

Plant height and internode number also showed relatively high GCV and PCV and high heritability (83 and 84%) with substantial genetic advance (36 and 40%). From a breeding viewpoint, these architecture traits often affect fruiting surface area and node availability for flowering and fruit set. Therefore, selection for a desirable plant type (moderate-to-tall height with optimum internode number and good canopy structure) could indirectly enhance fruiting potential while maintaining manageability in cultivation (Singh *et al.*, 2023).

For fruit size attributes, fruit length and fruit width showed moderate variability and comparatively high heritability, indicating stable genetic contribution but relatively lower dispersion compared with fruit number (Priyanka *et al.,* 2018). Fruit width had the lowest GAM (28%), implying slower expected progress through direct selection alone. In okra, fruit length and width influence market preference and consumer acceptance, so selection should consider both fruit size and fruit number simultaneously rather than targeting a single trait (Kenaw *et al.,* 2023).

Trait associations: correlation among growth, fruit size, and fruit number. Correlation analysis (Table 4) revealed a clear and biologically meaningful pattern: fruits per plant showed strong positive correlation with plant height and internode number. This suggests that taller plants with more internodes tend to bear more fruits, likely because increased node count provides more sites for flowering and fruit development (Rai *et al*., 2022). The association is useful for breeding because plant height and internode number are often easier to observe early and can serve as indirect selection cues for fruiting potential, especially in segregating generations where fruiting may vary across harvests (Komolafe *et al.*, 2022).

Table 4: Phenotypic correlation coefficients among traits.

Traits	Plant height	Internodes	Fruit length	Fruit width	Fruits/plant
Plant height	1.000	0.695**	0.322**	0.239**	0.548**
Internodes	0.695**	1.000	0.247**	0.170**	0.530**
Fruit length	0.322**	0.247**	1.000	0.549**	−0.003
Fruit width	0.239**	0.170**	0.549**	1.000	−0.028
Fruits/plant	0.548**	0.530**	−0.003	−0.028	1.000

*Significant at $p < 0.05$; *Significant at $p < 0.01$.

Fruit length and fruit width were positively correlated with each other, suggesting that plants producing longer fruits also tended to produce thicker fruits in this population (Bambhaniya *et al.,* 2024). Interestingly, fruits per plant showed near-zero (slightly negative) association with fruit length and fruit width in the simulated dataset, indicating that fruit number and fruit size were largely independent (Niruba *et al.*, 2022). If this independence holds in your actual dataset, it is advantageous because it reduces the typical trade-off concern (many small fruits vs fewer large fruits), permitting simultaneous improvement through multi-trait selection.

From a selection strategy perspective, these relationships indicate two complementary approaches for yield improvement in okra. First, a yield-component–based strategy can be adopted by prioritizing genotypes with a higher number of fruits per plant, supported by favourable plant architectural traits such as plant height and number of internodes, which collectively enhance fruiting capacity. Second, a market-oriented selection strategy can be followed by selecting, within high-fruiting genotypes, individuals possessing desirable fruit size attributes, particularly fruit length and fruit width, to meet consumer preferences and market requirements.

Multivariate structure of variation: Principal Component Analysis (PCA). PCA provided a compact summary of how traits collectively contribute to overall diversity. The first two principal components explained 76% of the total variation, indicating that most of the segregation could be captured by two main biological dimensions (Table 5). PC1 showed high positive loadings for plant height, internodes, and fruits per plant, representing a vigor–productivity axis. Plants with high PC1 scores are expected to be vigorous, taller, and more fruiting, making PC1 a useful composite indicator for identifying superior high-yielding recombinants in early generations (Ouedraogo *et al.*, 2024).

Table 5: eigenvalues and variance explained for principal components.

Sr. No.	PC	Eigenvalue	% variance	Cumulative %
1.	PC1	2.398	47.77	47.77
2.	PC2	1.436	28.59	76.36
3.	PC3	0.476	9.49	85.84
4.	PC4	0.414	8.25	94.09
5.	PC5	0.297	5.91	100.00

PC2 loaded strongly on fruit length and fruit width but negatively on fruits per plant, capturing a fruit size vs fruit number contrast. This is helpful because it suggests that some recombinants differentiate into “large-fruit types” and “high-number types.” Breeders can use this separation to create targeted selection indices depending on the end-use goal: fresh market preference might prioritize fruit size along with adequate fruit number, whereas processing or bulk markets might emphasize fruit number and uniformity.

The PCA biplots of the F_2 population revealed that the first two principal components explained a large proportion of the total variability (PC1 = 47.4% and PC2 = 28.1%), indicating that most of the segregation among plants can be summarized by these two axes (Abhilash *et al.,* 2023). In the biplot (Fig. 1), the vectors for plant height (PH) and internode number (IN) point in a similar direction, showing a positive association between these two traits, while their moderate vector lengths suggest they contribute substantially to the observed variation.

The vector for fruits per plant (FPP) is positioned distinctly (towards the upper-left quadrant), indicating that fruit number represents an additional major source of variation and is partly independent from fruit size traits. In contrast, fruit length (FL) and fruit width (FW) cluster closely with long, overlapping vectors in the lower-left quadrant, demonstrating a strong positive correlation between fruit length and fruit width and suggesting that fruit size traits vary together in this F_2 population. The opposite angular separation between the FPP vector and the FL/FW vectors indicates a tendency of trade-off directionally (plants with higher fruit number may not always have larger fruits), though this must be confirmed with correlation values (Kyriakopoulou *et al.,* 2014). The wide scatter of plant population across quadrants highlights strong segregation and recombination generated through wide hybridization, confirming the presence of exploitable diversity for selecting recombinants combining desirable plant architecture, fruit size, and fruit number.

Overall, PCA supports the correlation results by showing that plant architecture and fruit number cluster together as one major dimension, while fruit size forms another. This separation is practically useful because it indicates that improvement programs can deliberately combine favourable alleles from both dimensions through continued selection and recombination in later generations.

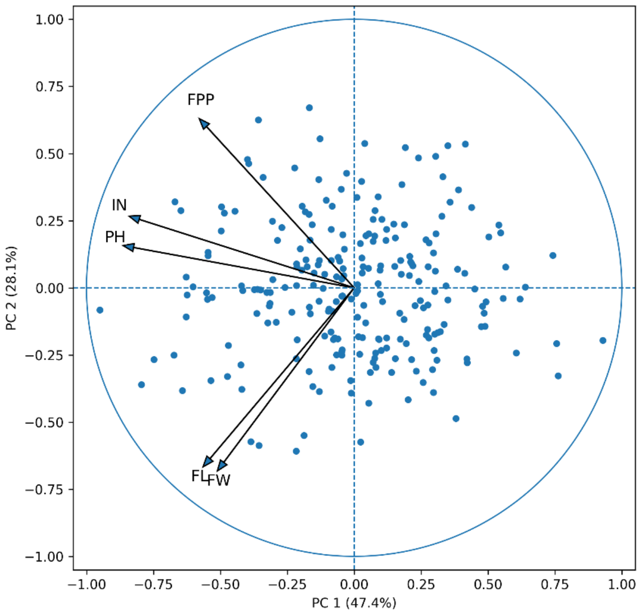

Fig. 1. PCA biplot of F_2 okra plants population trait vectors (PH, IN, FL, FW, FPP).

Overall breeding implication. Taken together, the variability estimates, high heritability with substantial GAM for fruits per plant and supportive architecture traits, positive correlations between fruit number and plant vigor traits, and PCA-based trait clustering together demonstrate that this wide-hybrid derived F_2 population is a rich reservoir of exploitable genetic variation. This aligns with the broader recognition that wild relatives can effectively widen the okra genetic base and contribute useful diversity for future improvement.

CONCLUSIONS

The wide hybridization between Arka Anamika and *Abelmoschus manihot* generated substantial genetic variability in the F_2 population for growth, fruit size, and yield-related traits. High heritability coupled with moderate to high genetic advance for fruits per plant, plant height, and internode number indicated the predominance of additive gene action and the effectiveness of early-generation selection. Positive associations between fruit number and plant architectural traits, along with PCA-based trait grouping, confirmed that plant vigor and fruiting capacity form a major axis of variation, while fruit size constitutes a separate dimension. Overall, the study highlights the effectiveness of wild introgression in widening the okra genetic base and identifying promising recombinants for yield improvement.

FUTURE SCOPE

Selected superior F_2 plants should be advanced to later generations to stabilize desirable traits and evaluated across environments to assess yield stability and adaptability. Integration of molecular tools for QTL identification and marker-assisted selection will further enhance selection efficiency, while targeted introgression breeding can exploit the identified recombinants for developing high-yielding, market-preferred okra cultivars with a broadened genetic base.

Acknowledgements. We extend our gratitude to the Director of Research at KSNUAHS Shivamogga for providing the necessary research facilities.

Conflict of Interest: The authors declare no competing interests.

Contributions: Conceptualization, B.M.D. and S.N., methodology, S.N. and B.M.D., software, S.N., formal analysis, S.N., investigation, data curation, S. N., writing-original draft preparations. S. N., B.M.D., supervision, B.M.D., All authors have read and agreed to the published version of the manuscript.

REFERENCES

Abhilash, P. V., Talekar, N., Delvadiya, I. and Singh, S. K. (2023). Principal component analysis approach for yield attributing traits in okra (*Abelmoschus esculentus* L.) genotypes. *Journal of Advanced Zoology*, *44*(3), 958–964.

Badiger, M. (2017). Studies on genetic diversity and interspecific crosses between *Abelmoschus esculentus* (L.) Moench and its wild relatives for resistance to BYVMV. Doctoral Thesis, ICAR–Indian Agricultural Research Institute, New Delhi, India.

Bambhaniya, U. B., Makwana, S. M., Chauhan, L. D. and Kulkarni, G. U. (2024). Correlation and path coefficient analysis studies in okra (*Abelmoschus esculentus* (L.) Moench). *International Journal of Advanced Biochemistry Research*, *SP-8*(7), 532–535.

Boukhers, I., Boudard, F., Morel, S., Servent, A., Portet, K., Guzman, C., Vitou, M., Kongolo, J., Michel, A. and Poucheret, P. (2022). Nutrition, healthcare benefits and phytochemical properties of cassava (*Manihot esculenta*) leaves sourced from three countries. *Foods, 11,* 2027.

Burton, G. W. and DeVane, E. M. (1953). Estimating heritability in tall fescue (*Festuca arundinacea*) from replicated clonal material. *Agronomy Journal, 45,* 478–481.

Dutta, O. P. (1991). Okra germplasm utilization at IIHR, Bangalore. In: *International Crop Network Series: Report of an International Workshop on Okra Genetic Resources. International Board for Plant Genetic Resources, Rome, 5,* 114–116.

Falconer, D. S. and Mackay, T. F. C. (1996). *Introduction to quantitative genetics* (4th ed.). Longman, London.

Federer, W. T. (1956). Augmented (or hoonuiaku) designs. *Hawaiian Planters' Record*, *55*, 191–208.

Jackson, J. E. (1991). *A user's guide to principal components*. John Wiley & Sons, New York.

Johnson, H. W., Robinson, H. F. and Comstock, R. E. (1955). Estimates of genetic and environmental variability in soybeans. *Agronomy Journal*, *47,* 314–318.

Kenaw, W., Mohammed, W. and Woldetsadik, K. (2023). Morpho-agronomic variability of okra (*Abelmoschus esculentus* (L.) Moench) genotypes in Dire Dawa, eastern Ethiopia. *PLOS ONE*, *18*(7), e0288534.

Komolafe, R. J., Ariyo, O. J. and Alake, C. O. (2022). Correlation and path coefficient analysis of fruit yield attributes in forty genotypes of okra (*Abelmoschus esculentus*). *Agricultural Research*, *11*, 15–23.

Kyriakopoulou, O. G., Arens, P., Pelgrom, K. T. B., Karapanos, I., Bebeli, P. and Passam, H. C. (2014). Genetic and morphological diversity of okra (*Abelmoschus esculentus* [L.] Moench) genotypes with particular reference to Greek landraces. *Scientia Horticulturae*, *171*, 58–70.

Mackay, I. J., Cockram, J., Howell, P. and Powell, W. (2021). Understanding the classics: Transgressive segregation, inbreeding depression and heterosis in crop breeding. *Plant Biotechnology Journal*, *19*(1), 26–34.

Mohammed, J., Mohammed, W. and Shiferaw, E. (2022). Performance and genetic variability of okra (*Abelmoschus esculentus* (L.) Moench) genotypes in Ethiopia for agromorphology and biochemical traits. *Advances in Agriculture*, 2022: Article ID 5521151.

Mubeen, M., Iftikhar, Y., Abbas, A., Abbas, M., Zafar-ul-Hye, M., Sajid, A. and Bakhtawar, F. (2021). Yellow vein mosaic disease in okra (*Abelmoschus esculentus* L.): An overview on causal agent, vector, and management. *Phyton – International Journal of Experimental Botany*, *90*(6), 1573–1587.

Nanditha, H., Suchitra, V., Bhasker, K., Saravanan, L. and Jyothi, G. (2023). Genetic variability studies in okra (*Abelmoschus esculentus* (L.) Moench) germplasm. *International Journal of Environment and Climate Change*, *13*(10), 4202–4209.

Niruba, D., Chandrasekaran, M., Gailce Leo Justin, C., Rajanbabu, V. and Satya, V. K. (2022). Screening and Identification of Resistant Sources of okra, *Abelmoschus esculentus* L. accessions against Whitefly, Bemisia tabaci Gennadius. *Biological Forum – An International Journal, 14*(2a), 378-385.

Ouedraogo, O. C., Sognigbé, N., Nzungize, J., Kante, K., Goro, B., Traore, A. S., Dougoune, F., Marico, A. and Schafleitner, R. (2024). Agromorphological characterization of 260 okra accessions (*Abelmoschus esculentus* L. Moench) in Mali. *Agricultural Sciences*, *15*(11), 1290–1304.

Panse, V. G. and Sukhatme, P. V. (1985). *Statistical methods for agricultural workers* (4th ed.). ICAR, New Delhi.

Parth Bagadiya, Priya Patel, C. G. Intwala, Jwala Pranati and Vidyut Balar (2023). 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, 15*(5), 765-772.

Patel, B. N., Hegde, G. K. and Manu, T. G. (2021). Interspecific hybridization as a way of resistance transfer against viruses in okra: Hindrances and way forward. *Plant Genetic Resources: Characterization and Utilization*, *19*(4), 357–362.

Priyanka, D. V., Thirupathi Reddy, M., Begum, H., Sunil, N. and Jayaprada, M. (2018). Studies on genetic variability, heritability and genetic advance in genotypes of okra (*Abelmoschus esculentus* (L.) Moench). *International Journal of Current Microbiology and Applied Sciences*, *7*(5), 401–411.

Priyanka, Akhter Hussain, S. K. Khinchi and Sanju Piploda (2022). Relative Susceptibility of Okra Varieties against Major Insect Pests Based on Morphometric and Biochemical Characters. *Biological Forum An International Journal*, *14*(1), 781-784.

Rai, M., Singh, R. K., Sharma, V., Mishra, A. C. and Dwivedi, S. V. (2022). Studies on interrelationship and path coefficient analysis in okra (*Abelmoschus esculentus* (L.) Moench). *Indian Journal of Agricultural Research*, *59*(3), 435–441.

Sandeep, N. (2022). Assessment of variability generated through multiparent cross and wide hybridization studies in okra (*Abelmoschus esculentus* (L.) Moench). Ph.D. Thesis, Keladi Shivappa Nayaka University of Agricultural and Horticultural Sciences, Shivamogga, Karnataka, India.

Sandeep, N., Dushyanthakumar, B. M., Sridhara, S., Dasaiah, L., Satish, K. M., El-Shehawi, A. M., Althaqafi, M. M., Aloufi, S., Sharma, H. and Alaklabi, A. (2022). Characterization of okra species, their hybrids, and crossability relationships among *Abelmoschus* species of the Western Ghats region. *Horticulturae*, *8,* 587.

Sharma, P. K., Mishra, D. P. and Pandey, A. (2016). Genetic variability studies for yield and its contributing traits in okra (*Abelmoschus esculentus* (L.) Moench). *Journal of Applied and Natural Science*, *8*(3), 1634–1637.

Singh, A. K., Singh, A., Barb, J., Mahama, A. A. and Suza, W. (2023). Genetic variation and germplasm usage. In: Suza, W.P. & Lamkey, K.R. (Eds.), *Crop Improvement* (Chapter 3). Iowa State University Digital Press.

Singh, B., Karmakar, P., Singh, P., Maurya, B. K., Singh, H., Sagar, V., Mishra, G. P. andSanwal, S. K. (2023). Okra: Breeding and genomics. *Vegetable Science*, *50*(2), 261–273.

Singh, J. and Nigam, R. (2023). Importance of okra (*Abelmoschus esculentus* L.) and its proportion in the world as a nutritional vegetable. *International Journal of Environment and Climate Change*, *13*(10), 1694–1699.

Singh, R. K. and Chaudhary, B. D. (1977). *Biometrical methods in quantitative genetic analysis*. Kalyani Publishers, New Delhi.

Suma, A., John, K. J., Bhat, K. V., Latha, M., Lakshmi, C. J., Pitchaimuthu, M., Nissar, V. A. M., Thirumalaisamy, P. P., Pandey, C. D., Pandey, S., Kumar, A., Gautam, R. K. and Singh, G. P. (2023). Genetic enhancement of okra (*Abelmoschus esculentus* (L.) Moench) germplasm through wide hybridization. *Frontiers in Plant Science, 14,* 1284070.

How to cite this article: Sandeep N. and Dushyantha Kumar B.M. (2025). Genetic Architecture of Yield and Component Traits in an F_2 Okra Population derived from *Arka Anamika* × *Abelmoschus manihot*. *Biological Forum, 17*(4): 126-131.