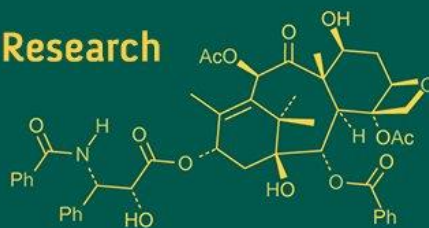


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Ruturaj R Shinde

M.Sc. Scholar, Department of Horticulture (Vegetable Science), College of Agriculture, Latur, Vasantao Naik Marathwada Krishi Vidyapeeth (VNMKV), Parbhani, Maharashtra, India

Raghwendra A Patil

Assistant Professor, Department of Horticulture, College of Agriculture, Dharashiv, Vasantao Naik Marathwada Krishi Vidyapeeth (VNMKV), Parbhani, Maharashtra, India

Shivshankar P Pole

Associate Professor, Department of Genetics and Plant Breeding, College of Agriculture, Dharashiv, Vasantao Naik Marathwada Krishi Vidyapeeth (VNMKV), Parbhani, Maharashtra, India

Kiran S Thorat

Assistant Professor, Department of Extension Education, College of Agriculture, Dharashiv, Vasantao Naik Marathwada Krishi Vidyapeeth (VNMKV), Parbhani, Maharashtra, India

Rohit S Bhujbal

M.Sc. Scholar, Department of Horticulture (Vegetable Science), College of Agriculture, Latur, Vasantao Naik Marathwada Krishi Vidyapeeth (VNMKV), Parbhani, Maharashtra, India

Corresponding Author:**Ruturaj R Shinde**

M.Sc. Scholar, Department of Horticulture (Vegetable Science), College of Agriculture, Latur, Vasantao Naik Marathwada Krishi Vidyapeeth (VNMKV), Parbhani, Maharashtra, India

Assessment of genetic variability and trait association in the F_3 generation of okra derived from Arka Anamika $\times$ IC-42464

Ruturaj R Shinde, Raghwendra A Patil, Shivshankar P Pole, Kiran S Thorat and Rohit S Bhujbal

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Abstract

The present investigation entitled “Assessment of Genetic Variability and Trait Association in the F_3 Generation of Okra (*Abelmoschus esculentus* L. Moench) Derived from Arka Anamika $\times$ IC-42464” was undertaken to assess the extent of genetic variability, heritability, genetic advance, correlation, and path coefficient among yield and yield-contributing traits in the F_3 population of okra. The experimental material comprised ten F_3 progenies derived from the cross Arka Anamika $\times$ IC-42464, along with their parents and standard checks, evaluated during Kharif 2025 at the Instructional-cum-Research Farm, College of Agriculture, Latur, Maharashtra, India, using a Randomized Block Design with two replications. Observations were recorded on twelve quantitative characters related to growth, flowering, fruit attributes, and yield.

Analysis of genetic parameters revealed considerable variability among the F_3 progenies for all the characters studied. The phenotypic coefficient of variation (PCV) was generally higher than the corresponding genotypic coefficient of variation (GCV), indicating the influence of environmental factors on trait expression. High GCV, PCV, heritability, and genetic advance as percent of mean were observed for plant height, number of branches per plant, number of fruits per plant, fruit yield per plant, fruit yield per plot, and fruit yield per hectare, suggesting the predominance of additive gene action and the effectiveness of direct phenotypic selection for these traits. Correlation analysis revealed that plant height, number of branches per plant, and number of fruits per plant exhibited significant positive associations with fruit yield per plant at both genotypic and phenotypic levels. Path coefficient analysis further demonstrated that number of fruits per plant exerted the highest positive direct effect on fruit yield, followed by plant height and number of branches per plant, indicating their major contribution to yield improvement. The results suggest that simultaneous selection for higher fruit number, increased branching, and optimum plant height would be an effective strategy for improving fruit yield in segregating populations of okra. The F_3 population derived from Arka Anamika $\times$ IC-42464 possesses substantial genetic variability and offers promising opportunities for the identification and advancement of superior progenies in future okra breeding programmes.

Keywords: *Abelmoschus esculentus*, F_3 generation, genetic variability, heritability, genetic advance, correlation analysis, path coefficient analysis, fruit yield, trait association, okra breeding

Introduction

Okra (*Abelmoschus esculentus* L. Moench), a member of the family Malvaceae, is one of the most important warm-season vegetable crops cultivated in tropical and subtropical regions of the world. It is valued for its tender immature fruits, which are consumed as vegetables and constitute an important source of vitamins, minerals, dietary fibre, and bioactive compounds. The crop is widely cultivated in countries such as India, Nigeria, Sudan, Pakistan, Turkey, Brazil, and the United States because of its adaptability to diverse agro-climatic conditions, short crop duration, and high market demand. India is the largest producer of okra, contributing more than 60% of the global production, and the crop plays a significant role in improving farmers' income and nutritional security (FAOSTAT, 2023; Anonymous, 2025) [1].

Okra fruits are rich in carbohydrates, proteins, dietary fibre, vitamins A, C and K, folic acid, calcium, potassium, magnesium, and antioxidants, making them an important component of a balanced diet.

The mucilage present in okra fruits has pharmaceutical and industrial applications owing to its antioxidant, hypoglycaemic, antimicrobial, and cholesterol-lowering properties (Gemede *et al.*, 2015; Liu *et al.*, 2021) ^[2, 3]. Besides its nutritional importance, okra is widely utilized in the processing industry for dehydrated products, frozen vegetables, soups, and value-added food products. The increasing demand for fresh and processed okra has created a continuous need for developing high-yielding cultivars possessing superior fruit quality, earliness, and resistance to major biotic and abiotic stresses. Genetic improvement in okra primarily depends on the availability and effective utilization of genetic variability. Since yield is a complex quantitative trait governed by several genes and greatly influenced by environmental factors, direct selection based solely on yield is generally inefficient. Therefore, plant breeders focus on the identification of yield-contributing characters exhibiting substantial genetic variability and favourable associations with fruit yield. The magnitude of variability present in segregating populations determines the effectiveness of selection and the probability of recovering superior recombinants in subsequent generations (Burton and DeVane, 1953; Johnson *et al.*, 1955) ^[4, 5].

The F₃ generation represents an important stage in pedigree breeding because the segregating population begins to attain greater homozygosity while still retaining considerable genetic variation. Evaluation of F₃ progenies enables the identification of desirable segregants carrying favourable combinations of genes inherited from both parents. Selection during this generation is expected to be more efficient than in earlier segregating generations because environmental effects are relatively reduced and superior families can be identified with greater precision. Therefore, the assessment of genetic parameters in F₃ populations provides valuable information for advancing promising progenies and accelerating cultivar development.

Among the available breeding materials, the cross Arka Anamika × IC-42464 possesses considerable breeding potential owing to the contrasting characteristics of its parental lines. Arka Anamika is a widely cultivated commercial variety known for its high yield, adaptability, and desirable horticultural traits, whereas IC-42464 represents a genetically diverse germplasm line capable of contributing novel alleles for yield improvement and other economically important traits. The evaluation of the segregating F₃ population derived from this cross is therefore expected to generate useful information for identifying superior recombinants suitable for future breeding programmes. Estimation of genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability, and genetic advance constitutes an important approach for understanding the nature and extent of genetic variability. The comparison between GCV and PCV provides an estimate of environmental influence on trait expression, whereas heritability together with genetic advance helps predict the effectiveness of selection. High heritability coupled with high genetic advance generally indicates the predominance of additive gene action and suggests that direct phenotypic selection would be effective. Conversely, high heritability associated with low genetic advance indicates the involvement of non-additive gene action, where delayed selection or hybrid breeding may be more appropriate (Johnson *et al.*, 1955; Hanson *et al.*, 1956) ^[5, 6].

In addition to variability studies, understanding the association among different traits is equally important for developing effective selection strategies. Correlation analysis measures the degree and direction of association among characters and helps identify yield-contributing traits that can be used as indirect selection criteria. However, correlation alone does not distinguish between direct and indirect contributions of component traits towards fruit yield. Path coefficient analysis, originally proposed by Wright (1921) ^[7] and later adapted for plant breeding by Dewey and Lu (1959) ^[8], partitions the correlation coefficients into direct and indirect effects, thereby providing a better understanding of the causal relationships among characters influencing yield. This approach enables breeders to identify traits exerting the greatest direct influence on fruit yield and formulate efficient selection indices. Several studies have reported substantial variability and significant associations among yield-related traits in okra. High heritability coupled with high genetic advance has been reported for plant height, number of branches, number of fruits per plant, fruit yield per plant, and fruit weight, suggesting that these traits are predominantly governed by additive gene effects and can be effectively improved through direct selection (Alam *et al.*, 2020; Yadav *et al.*, 2020; Vani *et al.*, 2021; Jadhav *et al.*, 2022; Reddy *et al.*, 2022) ^[9]. Likewise, positive correlations and strong direct effects of traits such as number of fruits per plant, fruit weight, and plant height on fruit yield have been documented in several studies, highlighting their importance in yield improvement programmes (Rathava *et al.*, 2019; Choudhary *et al.*, 2022; Kumar *et al.*, 2022) ^[10].

Although numerous investigations have been conducted on genetic variability in okra, information regarding segregating populations derived from specific parental combinations remains limited. In particular, the genetic behaviour of the F₃ population derived from Arka Anamika × IC-42464 has not been adequately documented. Therefore, evaluating this population for genetic variability and trait association is essential for identifying promising segregants and developing efficient selection strategies for future breeding programmes.

Keeping these considerations in view, the present investigation entitled "Assessment of Genetic Variability and Trait Association in the F₃ Generation of Okra (*Abelmoschus esculentus* L. Moench) Derived from Arka Anamika × IC-42464" was undertaken to estimate genetic variability, heritability, genetic advance, correlation, and path coefficient analysis for fruit yield and its component traits, with the objective of identifying superior F₃ progenies for use in okra improvement programmes.

Materials and Methods

Plant Material and Experimental Site

The present investigation was conducted during the Kharif 2025 season at the Instructionalcum-Research Farm, Department of Horticulture, College of Agriculture, Latur, Vasantao Naik Marathwada Krishi Vidyapeeth (VNMKV), Parbhani, Maharashtra, India. The experimental material comprised ten F₃ progenies developed from the cross Arka Anamika × IC-42464, along with their two parents (Arka Anamika and IC-42464) and two standard checks (Parbhani Kranti and Mahyco-10). The F₃ progenies were developed through pedigree selection from the corresponding F₂

population, and seeds were obtained from the Department of Horticulture, College of Agriculture, Latur.

Experimental Design and Crop Management

The experiment was laid out in a Randomized Block Design (RBD) with two replications. Each F_3 progeny, parental line, and check was grown in individual plots following a spacing of 45 cm $\times$ 30 cm. Standard agronomic and plant protection practices recommended for okra cultivation were followed uniformly throughout the crop growth period. The experimental field was prepared by ploughing, harrowing, and levelling to obtain a fine tilth. A basal dose of 50 kg N, 50 kg P_2O_5 , and 50 kg K_2O ha^{-1} was applied during land preparation, followed by an additional 50 kg N ha^{-1} as top dressing at 30 days after sowing (DAS). Irrigation, intercultural operations, weed management, and plant protection measures were carried out as required to ensure optimum crop growth. Fruits were harvested periodically at the marketable stage.

Data Recording

Observations were recorded from five randomly selected plants in each progeny, parent, and check from every replication, and the mean values were used for statistical analysis. Twelve quantitative traits associated with growth, flowering, fruit characteristics, and yield were recorded:

1. Days to 50% flowering

- Plant height (cm)
- Number of branches per plant
- Node at first flowering
- Internodal length (cm)
- Number of fruits per plant
- Fruit length (cm)
- Fruit diameter (cm)
- Average fruit weight (g)
- Fruit yield per plant (kg)
- Fruit yield per plot (kg)
- Fruit yield per hectare (qha^{-1})

Standard procedures were followed for recording each trait throughout the crop growth period.

Statistical Analysis

The recorded data were subjected to analysis of variance (ANOVA) for a Randomized Block Design following the procedure described by Panse and Sukhatme (1985) ^[11] to determine the significance of differences among genotypes.

Estimation of Genetic Parameters

Phenotypic variance (σ^2_p), genotypic variance (σ^2_g), and environmental variance (σ^2_e) were estimated according to the method of Johnson *et al.* (1955) ^[5]. Genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were calculated following Burton and DeVane (1953) ^[4]. Broad-sense heritability (H^2) was estimated according to Burton and DeVane (1953) ^[4] and Hanson *et al.* (1956) ^[6], while genetic advance (GA) and genetic advance as percentage of mean (GAM) were computed following Johnson *et al.* (1955) ^[5]. The magnitude

of GCV, PCV, heritability, and GAM was classified using standard criteria proposed by Sivasubramanian and Menon (1973) ^[12] and Johnson *et al.* (1955) ^[5].

Correlation Analysis

Genotypic and phenotypic correlation coefficients among yield and its component traits were estimated following the procedure described by Miller *et al.* (1958) ^[13] and Johnson *et al.* (1955) ^[5]. The significance of correlation coefficients was tested at 5% and 1% probability levels according to Snedecor and Cochran (1967) ^[14].

Path Coefficient Analysis

To determine the direct and indirect effects of yield-contributing characters on fruit yield per plant, path coefficient analysis was performed following the method proposed by Wright (1921) ^[7] and adapted for plant breeding by Dewey and Lu (1959) ^[8]. Fruit yield per plant was considered the dependent variable, whereas the remaining quantitative traits were treated as independent variables. The residual effect was estimated to determine the contribution of other unmeasured factors influencing fruit yield.

Results and Discussion

Genetic Variability, Heritability and Genetic Advance

The success of any crop improvement programme depends primarily on the magnitude of genetic variability available in the breeding population. Estimation of genetic parameters such as genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability, and genetic advance provides valuable information regarding the nature of gene action and the effectiveness of selection. In the present investigation, substantial variation was observed among the F_3 progenies of the cross Arka Anamika $\times$ IC-42464 for all the quantitative characters studied, indicating the presence of sufficient genetic variability for effective selection. The estimates of GCV, PCV, broad-sense heritability (H^2), genetic advance (GA), and genetic advance as percentage of mean (GAM) are presented in Table 1.

Growth Characters

Days to 50% flowering exhibited low estimates of GCV (5.88%) and PCV (8.43%), suggesting limited variability for this trait among the F_3 progenies. The moderate heritability (48.53%) coupled with low genetic advance as percentage of mean (8.44%) indicated the predominance of non-additive gene effects and environmental influence on the expression of this trait. Therefore, direct phenotypic selection for earliness may not be highly effective at this generation, and further advancement of progenies would be desirable before imposing selection. Similar observations have been reported by Yadav *et al.* (2020) ^[9], Awasthi *et al.* (2022), and Reddy *et al.* (2022).

Plant height showed a wide range of variation (50.55-118.70 cm) with high GCV (23.38%) and PCV (25.02%). The relatively small difference between GCV and PCV suggested limited environmental influence on the expression of this trait. High heritability (87.31%) together with high GAM (45.07%) indicated that additive gene action predominantly governed plant height, making direct

phenotypic selection effective for improving this character. Comparable findings were reported by Mohammed *et al.* (2020) and Choudhary *et al.* (2022).

The number of branches per plant also exhibited high genetic variability with GCV and PCV values of 23.26% and 24.82%, respectively. The trait recorded high heritability (87.79%) and high genetic advance as percentage of mean (44.95%), indicating the predominance of additive genetic effects. These results suggest that selection for plants with a greater number of branches can be effectively practiced in the F_3 generation. Similar trends have been documented by Ranga *et al.* (2021), Chetana and Deshmukh (2021), and Kute *et al.* (2023).

Node at first flowering and internodal length recorded comparatively low GCV and PCV values along with moderate heritability and low GAM, indicating narrow genetic variability and a greater influence of environmental factors. Such combinations generally reflect the involvement of non-additive gene action, suggesting that these traits are less responsive to direct selection during early segregating generations.

Fruit Characters

Among fruit characters, the number of fruits per plant exhibited moderate to high variability with GCV (18.04%) and PCV (20.12%). High heritability (80.47%) coupled with high GAM (33.40%) suggested that additive gene effects were predominant, making this trait highly amenable to direct selection. Since fruit number contributes directly to marketable yield, this character represents an important selection criterion for yield improvement. Similar findings were reported by Sravanti (2017), Rathava *et al.* (2019), Alam *et al.* (2020), and Kumar *et al.* (2022)^[10].

Fruit length exhibited relatively low GCV (7.25%) and PCV (10.21%) along with moderate heritability (50.39%) and moderate GAM (10.61%). Likewise, fruit diameter recorded low variability, moderate heritability (45.52%), and low

GAM (8.73%). These estimates indicate that both traits are influenced by additive as well as non-additive gene effects with appreciable environmental influence, suggesting that selection for these traits should be practiced in later generations after greater homozygosity has been achieved.

Fruit weight also exhibited low GCV (7.35%) and PCV (10.78%), moderate heritability (46.42%), and moderate GAM (10.33%). The moderate estimates indicate that both genetic and environmental factors contributed to the observed variation. Therefore, moderate progress through selection can be expected for fruit weight in advanced generations. Similar results have been reported by Sharma *et al.* (2016)^[15] and Gangashetty *et al.* (2010).

Yield Characters

Fruit yield per plant exhibited the highest magnitude of genetic variability among all the traits studied, with GCV (31.02%) and PCV (32.27%) indicating substantial variation among the F_3 progenies. The trait also recorded very high heritability (92.40%) together with high GAM (61.51%), demonstrating that additive gene action predominates and that direct phenotypic selection would be highly effective. The close correspondence between GCV and PCV further indicated minimal environmental influence on trait expression. Similar observations have been reported by Vani *et al.* (2021), Jadhav *et al.* (2022), and Reddy *et al.* (2022).

Similarly, fruit yield per plot and fruit yield per hectare recorded high GCV, PCV, heritability, and genetic advance. Fruit yield per plot exhibited GCV and PCV values of 32.74% and 34.00%, respectively, with heritability of 92.76% and GAM of 65.06%. Fruit yield per hectare also recorded high variability (GCV 31.10%; PCV 32.41%), high heritability (92.06%), and high GAM (61.55%). These estimates clearly indicate that the observed variability is primarily governed by additive gene effects and that substantial genetic improvement can be achieved through direct selection of superior F_3 progenies.

Table 1: Estimates of variability parameters for twelve characters in F generation of okra cross I: Arka Anamika × IC-42464 (C1: P1 × P4)

Sr. No.	Characters	Mean	Range	GCV (%)	PCV (%)	h ² bc (%)	GA	GAM (%)
1.	Days to 50 % Flowering	49.38	42.25 - 55.65	5.88	8.43	48.53	4.17	8.44
2.	Plant height (cm)	85.74	50.55 - 118.70	23.38	25.02	87.31	38.64	45.07
3.	No. of branches per plant	2.04	1.36 - 3.92	23.26	24.82	87.79	0.92	44.95
4.	Node at which first flower appear	4.96	4.07 - 5.72	5.79	8.71	44.26	0.39	7.95
5.	Internodal length (cm)	7.01	5.27 - 7.82	5.54	8.31	44.44	0.53	7.62
6.	No. of fruit per plant	11.74	9.22 - 17.51	18.04	20.12	80.47	3.92	33.40
7.	Length of fruit (cm)	12.49	10.90 - 14.70	7.25	10.21	50.39	1.33	10.61
8.	Fruit diameter (cm)	1.24	0.95 - 1.43	6.27	9.30	45.52	0.11	8.73
9.	Fruit weight (g)	13.14	9.63 - 14.89	7.35	10.78	46.42	1.36	10.33
10.	Fruit yield per plant (kg)	0.11	0.07 - 0.19	31.02	32.27	92.40	0.06	61.51
11.	Fruit yield per plot (Kg)	1.80	1.08 - 3.36	32.74	34.00	92.76	1.17	65.06
12.	Fruit yield per hectare (q)	70.56	54.05 - 128.11	31.10	32.41	92.06	43.43	61.55

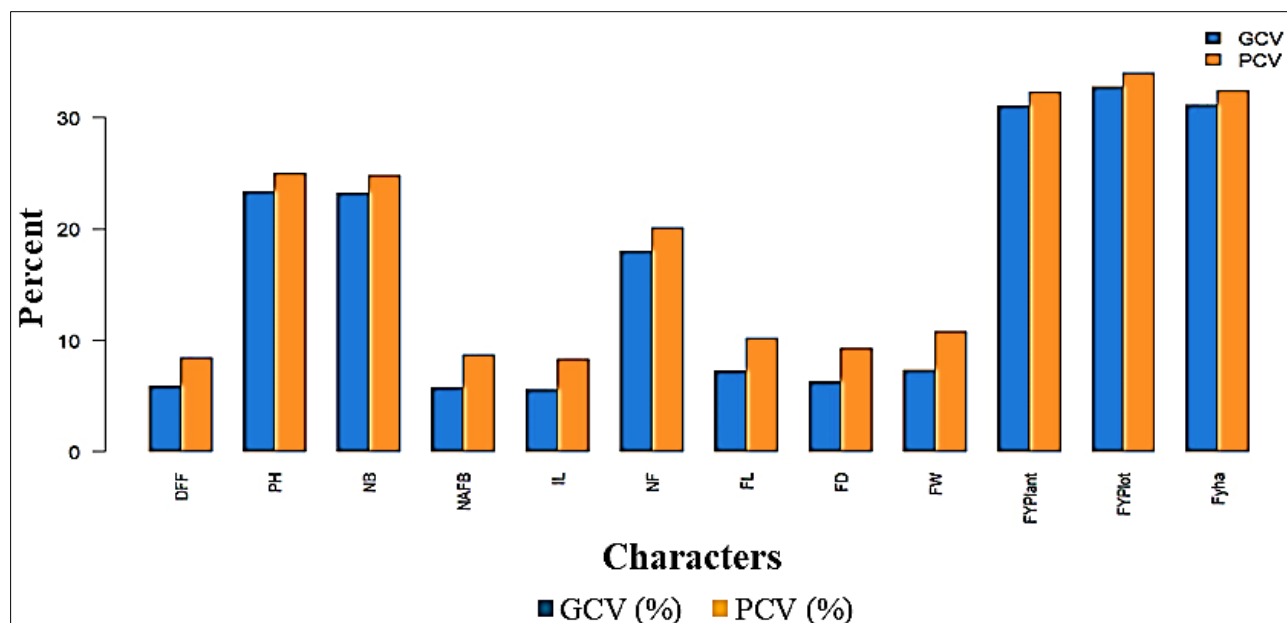


Fig 1: Genotypic coefficient of variation and phenotypic coefficient of variation in F₃ generation of okra cross Arka Anamika × IC-42464

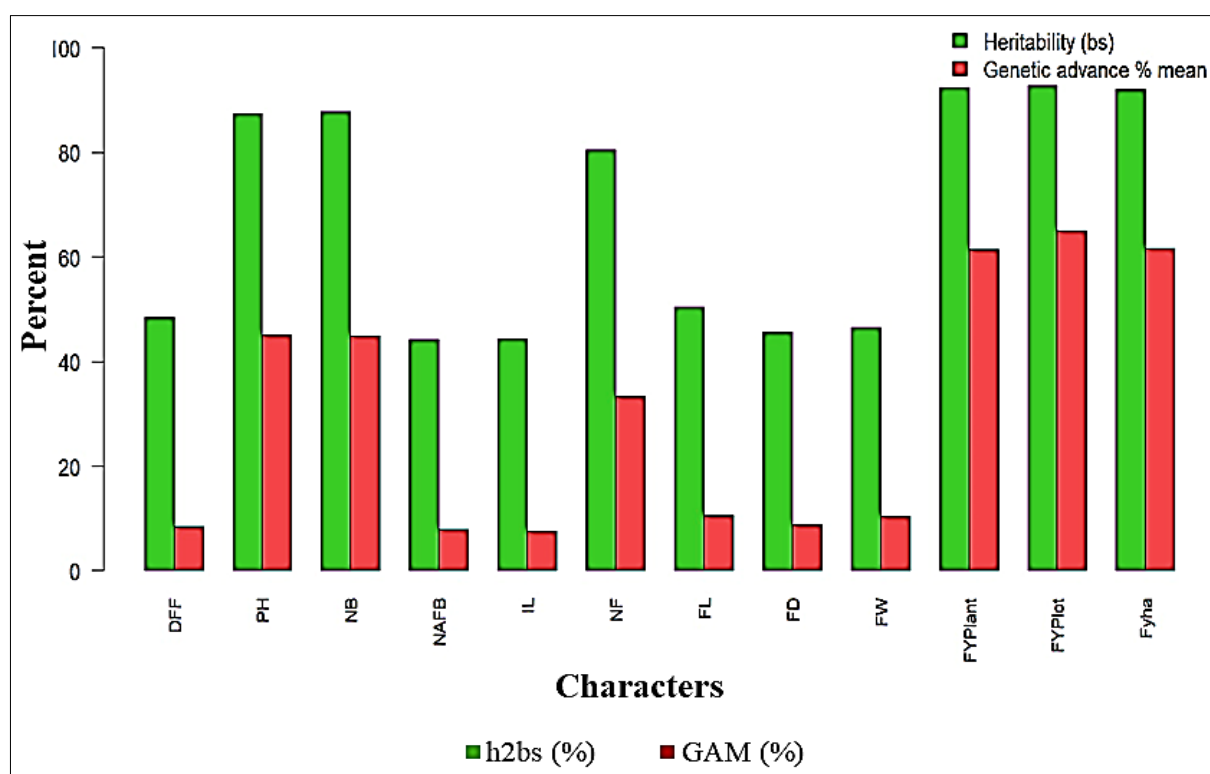


Fig 2: Heritability and percent mean of genetic advance in F₃ generation of okra cross Arka Anamika × IC-42464

Correlation Analysis

Fruit yield is a complex quantitative trait governed by several interrelated characters, and therefore the efficiency of selection can be substantially improved by understanding the relationships among yield-contributing traits. Correlation analysis provides information on the magnitude and direction of association between different characters, thereby enabling plant breeders to identify traits that can be effectively utilized for indirect selection. In the present investigation, both genotypic and phenotypic correlation coefficients were estimated among twelve quantitative characters in the F₃ population derived from the cross Arka Anamika × IC-42464. In general, genotypic correlation coefficients were higher than the corresponding phenotypic

correlations, indicating that environmental factors slightly reduced the expression of the inherent genetic associations among the traits.

Association of Growth Characters

Days to 50% flowering exhibited non-significant positive associations with plant height and internodal length, whereas it showed non-significant negative correlations with fruit length, fruit diameter, fruit weight, fruit yield per plant, fruit yield per plot, and fruit yield per hectare at both genotypic and phenotypic levels. The negative association between flowering time and yield suggests that comparatively earlier flowering progenies tended to produce higher yields, although the relationship was statistically non-

significant. Similar observations have been reported by Rathava *et al.* (2019) and Mishra *et al.* (2015), who also observed negative associations of days to 50% flowering with important yield-related traits in okra.

Plant height exhibited highly significant and positive correlations with internodal length, number of fruits per plant, fruit yield per plot, fruit yield per plant, and fruit yield per hectare at both genotypic and phenotypic levels. Positive but non-significant associations were observed with days to 50% flowering, number of branches per plant, node at first flowering, fruit length, and fruit diameter, whereas fruit weight showed a non-significant negative association. These results indicate that taller plants generally produced more fruits and consequently higher yields, making plant height an important indirect selection criterion in the segregating population. Similar positive associations between plant height and fruit yield have been reported by Gangashetty *et al.* (2010), Rathod *et al.* (2019), and Shinde *et al.* (2023).

The number of branches per plant showed highly significant positive correlations with number of fruits per plant, fruit yield per plant, fruit yield per plot, and fruit yield per hectare, indicating that plants possessing more branches had greater fruit-bearing potential and ultimately produced higher yields. Since branch development determines the number of productive nodes and flowering sites, this association is biologically meaningful and suggests that the number of branches per plant may serve as an efficient indirect selection criterion during pedigree selection.

Association of Fruit Characters

Among fruit-related traits, the number of fruits per plant exhibited the strongest positive association with fruit yield per plant, fruit yield per plot, and fruit yield per hectare at both genotypic and phenotypic levels. This finding indicates that fruit number contributed substantially to overall

productivity and therefore represents one of the most important yield-determining components in the F_3 population. Similar results have been reported by Alam *et al.* (2020), Kumar *et al.* (2022) ^[10], and Vani *et al.* (2021), who also identified the number of fruits per plant as a major determinant of fruit yield in okra.

Fruit length, fruit diameter, and fruit weight generally exhibited positive associations with fruit yield, although the magnitude of these correlations was lower than that observed for number of fruits per plant. These traits collectively contribute to marketable yield through improvement in fruit size and individual fruit weight. Their positive relationship with yield suggests that simultaneous improvement of these characters could further enhance productivity in advanced breeding generations.

Association with Fruit Yield

Fruit yield per plant showed strong positive associations with several economically important traits, particularly plant height, number of branches per plant, and number of fruits per plant. These relationships indicate that improvement in these component traits is likely to result in a corresponding increase in fruit yield. The consistency of positive associations at both genotypic and phenotypic levels further suggests that these relationships are primarily genetic rather than environmental in nature.

The comparatively higher genotypic correlation coefficients than the phenotypic correlations observed for most character combinations indicate that environmental effects slightly reduced the expression of genetic relationships but did not substantially alter the overall association pattern. Therefore, selection based on genotypic relationships would be more reliable for identifying superior recombinants in the segregating population.

Table 2: Genotypic correlation co-efficient for yield and yield contributing characters in F_3 generation. Cross I : Arka Anamika $\times$ IC-42464

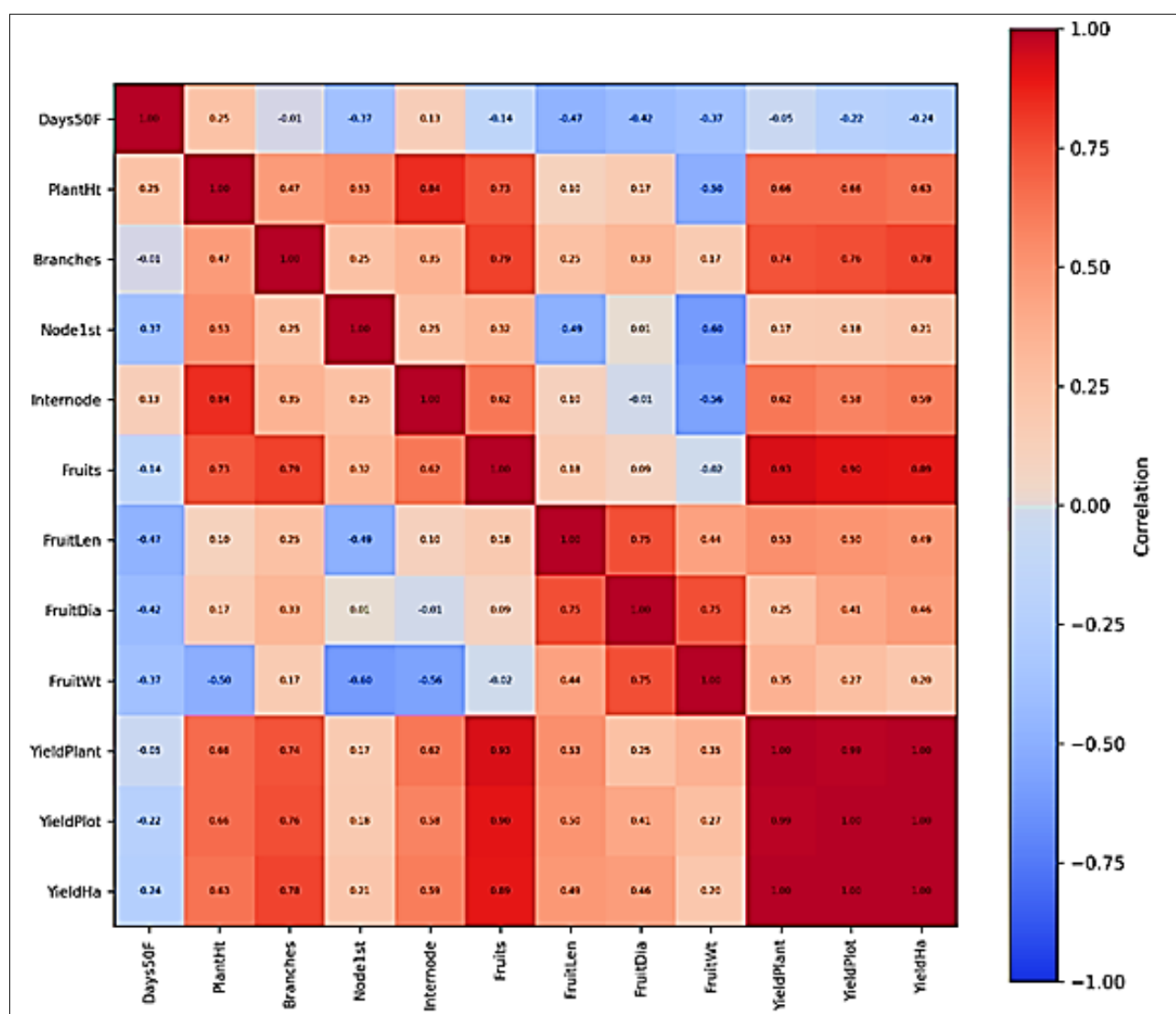
Characters	Days to 50 % Flowering	Plant height	No. of branches per plant	Node at first flower appear	Inter-nodal length	No. of fruit per plant	Length of fruit	Fruit diameter	Fruit weight	Fruit yield per plant	Fruit yield per plot	Fruit yield per hectare
Days to 50 % Flowering	1	0.246	-0.007	-0.373	0.134	-0.141	-0.472	-0.418	-0.368	-0.051	-0.217	-0.238
Plant height		1	0.474	0.529	0.842**	0.731**	0.096	0.171	-0.500	0.658*	0.663**	0.633*
No. of branches			1	0.254	0.346	0.792**	0.250	0.326	0.171	0.737**	0.757**	0.784**
Node at first flower appear				1	0.254	0.321	-0.488	0.007	-0.605*	0.175	0.185	0.211
Internodal length					1	0.619*	0.103	-0.014	-0.564*	0.624*	0.576*	0.594*
No. of fruit per plant						1	0.184	0.085	-0.023	0.931**	0.904**	0.894**
Length of fruit							1	0.750**	0.442	0.530	0.500	0.486
Fruit diameter								1	0.754**	0.253	0.413	0.463
Fruit weight									1	0.352	0.271	0.201
Fruit yield per plant										1	0.992**	0.996**
Fruit yield per plot											1	0.997**
Fruit yield per hectare												1

, : Significance at 5% and 1% respectively

Table 3: Phenotypic correlation co-efficient for yield and yield contributing characters in F₃ generation. Cross I : Arka Anamika × IC-42464

Characters	Days to 50 % Flowering	Plant height	No. of branches	Node at first flower appear	Inter nodal length	No of fruit per plant	Length of fruit	Fruit diameter	Fruit weight	Fruit yield per plant	Fruit yield per plot	Fruit yield per hectare
Days to 50 % Flowering	1	0.284	0.132	0.029	0.275	0.120	0.252	0.002	-0.108	-0.023	-0.036	-0.032
Plant height		1	0.457	0.379	0.680**	0.710**	0.200	0.166	-0.202	0.611*	0.669**	0.633*
No. of branches			1	0.357	0.342	0.775**	0.326	0.294	0.026	0.686**	0.750**	0.764**
Node at first flower appear				1	0.244	0.340	0.017	0.092	-0.458	0.109	0.197	0.246
Internodal length					1	0.612*	0.283	0.264	-0.200	0.487	0.512	0.509
No of fruit per plant						1	0.336	0.094	-0.024	0.873**	0.884**	0.875**
Length of fruit							1	0.564*	0.281	0.419	0.463	0.465
Fruit diameter								1	0.112	0.308	0.372	0.382
Fruit weight									1	0.129	0.148	0.155
Fruit yield per plant										1	0.963**	0.950**
Fruit yield per plot											1	0.983**
Fruit yield per hectare												1

, : Significance at 5% and 1% respectively

**Fig 3:** Genotypic correlation heatmap illustrating the association among yield and yield-contributing traits in the F₃ population of okra derived from the cross Arka Anamika × IC-42464.

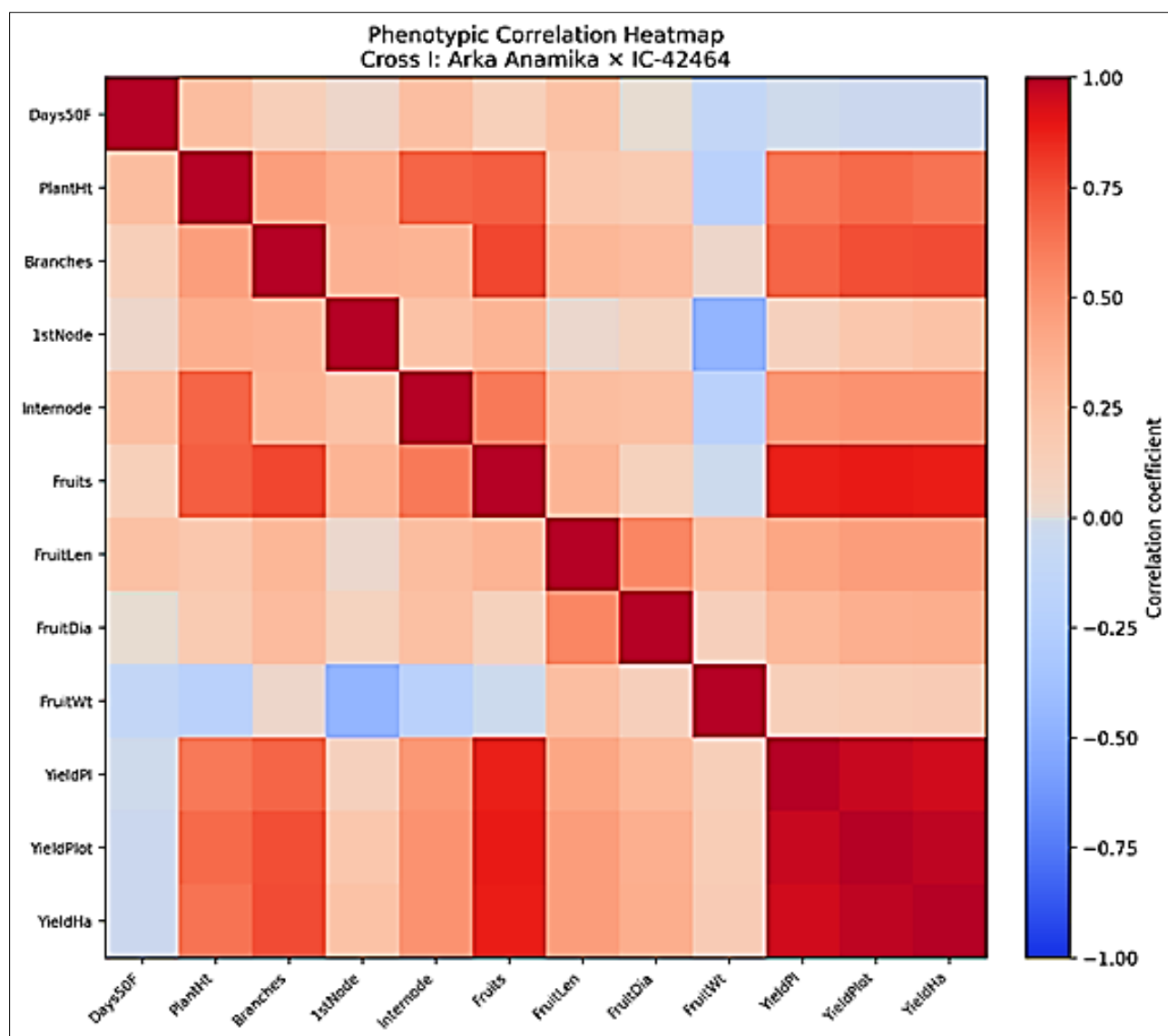


Fig 4: Phenotypic correlation heatmap of yield and yield-contributing traits in the F_3 population of okra (*Abelmoschus esculentus* L. Moench) derived from the cross Arka Anamika × IC-42464.

Path Coefficient Analysis

Although correlation analysis provides valuable information regarding the association among different characters, it does not distinguish whether the relationship is due to a direct influence of a trait on yield or is mediated indirectly through other associated characters. Therefore, path coefficient analysis was carried out at both genotypic and phenotypic levels to partition the correlation coefficients into direct and indirect effects. Fruit yield per plant was considered the dependent variable, while the remaining quantitative characters served as independent variables. This analysis facilitated the identification of the most influential traits contributing directly to fruit yield and provided a reliable basis for formulating effective selection strategies in the F_3 population of Arka Anamika × IC-42464.

Genotypic Path Coefficient Analysis

The genotypic path coefficient analysis revealed that the magnitude of direct effects varied considerably among the characters studied, indicating differential contributions of individual traits towards fruit yield. Among all the traits, number of fruits per plant exerted the highest positive direct effect on fruit yield per plant, demonstrating that this character is the primary determinant of productivity in the

segregating population. The strong positive direct effect, together with its significant positive correlation with fruit yield, indicates that selection based on higher fruit number would be highly effective for improving yield in subsequent generations.

Plant height also exhibited a substantial positive direct effect on fruit yield. In addition to its own direct contribution, plant height influenced yield indirectly through its positive association with number of fruits per plant and other growth characters. These findings indicate that vigorous plants possessing greater vegetative growth tend to produce a larger number of fruits, thereby contributing significantly to higher productivity.

The number of branches per plant recorded another important positive direct effect on fruit yield. Since branching determines the number of productive nodes and flowering sites, plants with a greater number of branches are capable of producing more fruits, ultimately resulting in increased yield. The combined evidence from variability, correlation, and path analyses therefore identifies number of branches per plant as an important indirect selection criterion for yield improvement.

Fruit weight also contributed positively towards fruit yield, although its direct effect was comparatively lower than that

observed for number of fruits per plant. The contribution of fruit weight was supplemented through favourable indirect effects via other yield-related characters, indicating that simultaneous improvement in fruit number and fruit weight would maximize overall productivity.

In contrast, traits such as days to 50% flowering, node at first flowering, internodal length, fruit length, and fruit diameter exhibited comparatively low or negative direct effects on fruit yield. Their contribution to productivity was largely indirect through associations with other yield components. Consequently, direct selection based on these characters alone is unlikely to produce substantial improvement in fruit yield.

Phenotypic Path Coefficient Analysis

The phenotypic path coefficient analysis showed trends largely similar to those observed at the genotypic level, although the magnitude of direct and indirect effects was comparatively lower due to environmental influence. Nevertheless, number of fruits per plant, plant height, and number of branches per plant consistently exhibited positive direct effects on fruit yield, confirming the stability of these relationships under field conditions.

The similarity between genotypic and phenotypic path

coefficients indicates that the expression of these major yield-contributing traits was only marginally affected by environmental factors. Therefore, phenotypic selection for these characters is expected to be reliable and effective during pedigree selection in the F_3 generation.

Breeding Implications

The combined results of variability, correlation, and path coefficient analyses clearly indicate that **number of fruits** per plant, plant height, and number of branches per plant are the principal yield-determining characters in the F_3 population derived from Arka Anamika $\times$ IC-42464. These traits exhibited favourable genetic variability, high heritability, strong positive associations with fruit yield, and substantial direct effects on productivity, demonstrating that they are predominantly governed by additive gene action.

The integration of these genetic parameters suggests that simultaneous selection for increased branching ability, optimum plant height, and higher fruit number would substantially improve fruit yield while maintaining desirable agronomic characteristics. Such an integrated selection strategy is expected to accelerate the identification of superior segregants and enhance the efficiency of pedigree breeding in okra.

Table 4: Direct and indirect genotypic effect of nine variables on fruit yield in the F_3 generation of okra. Cross I: Arka Anamika $\times$ IC-42464

Characters	Days to 50 % Flowering	Plant height	No. of branches	Node at first flower appear	Inter nodal length	No of fruit per plant	Length of fruit	Fruit diameter	Fruit weight	Fruit yield per plant
Days to 50 % Flowering	-0.0380	0.0184	-0.0199	-0.0066	-0.0574	0.1364	-0.0107	0.0008	0.0001	0.0232
Plant height	-0.0108	0.0647	-0.0688	-0.0849	-0.1421	0.8059	-0.0085	0.0553	0.0003	0.6111
No. of branches	-0.0053	0.0296	-0.1506	-0.0799	-0.0724	0.8799	-0.0138	0.0983	0.0014	0.6896
Node at first flower appear	-0.0011	0.0245	-0.0538	-0.2238	-0.0531	0.3855	-0.0007	0.0306	0.0006	0.1088
Internodal length	-0.0104	0.0441	-0.0522	-0.0568	-0.2090	0.6954	-0.012	0.0881	0.0003	0.4873
No. of fruit per plant	-0.0046	0.0459	-0.1167	-0.0762	-0.1281	1.1354	-0.0143	0.0316	-0.0013	0.8724
Length of fruit	-0.0096	0.0132	-0.0491	-0.0039	-0.0592	0.3818	-0.0424	0.1883	-0.0004	0.4186
Fruit diameter	-0.0001	0.0107	-0.0443	-0.0205	-0.0551	0.1073	-0.0239	0.3342	-0.0001	0.3079
Fruit weight	0.0041	-0.0131	-0.0038	0.1026	0.0418	-0.0268	-0.0119	0.0373	-0.0013	0.1288

Residual = 0.348

Table 5: Direct and indirect phenotypic effect of nine variables on fruit yield in the F_3 generation of okra Cross I : Arka Anamika $\times$ IC-42464

Characters	Days to 50 % Flowering	Plant height	No. of branches	Node at first flower appear	Inter nodal length	No of fruit per plant	Length of fruit	Fruit diameter	Fruit weight	Fruit yield per plant
Days to 50 % Flowering	-0.0380	0.0184	-0.0199	-0.0066	-0.0574	0.1364	-0.0107	0.0008	0.0001	0.0232
Plant height	-0.0108	0.0647	-0.0688	-0.0849	-0.1421	0.8059	-0.0085	0.0553	0.0003	0.6111
No. of branches	-0.0053	0.0296	-0.1506	-0.0799	-0.0724	0.8799	-0.0138	0.0983	0.0014	0.6896
Node at first flower appear	-0.0011	0.0245	-0.0538	-0.2238	-0.0531	0.3855	-0.0007	0.0306	0.0006	0.1088
Internodal length	-0.0104	0.0441	-0.0522	-0.0568	-0.2090	0.6954	-0.012	0.0881	0.0003	0.4873
No. of fruit per plant	-0.0046	0.0459	-0.1167	-0.0762	-0.1281	1.1354	-0.0143	0.0316	-0.0013	0.8724
Length of fruit	-0.0096	0.0132	-0.0491	-0.0039	-0.0592	0.3818	-0.0424	0.1883	-0.0004	0.4186
Fruit diameter	-0.0001	0.0107	-0.0443	-0.0205	-0.0551	0.1073	-0.0239	0.3342	-0.0001	0.3079
Fruit weight	0.0041	-0.0131	-0.0038	0.1026	0.0418	-0.0268	-0.0119	0.0373	-0.0013	0.1288

Residual = 0.338

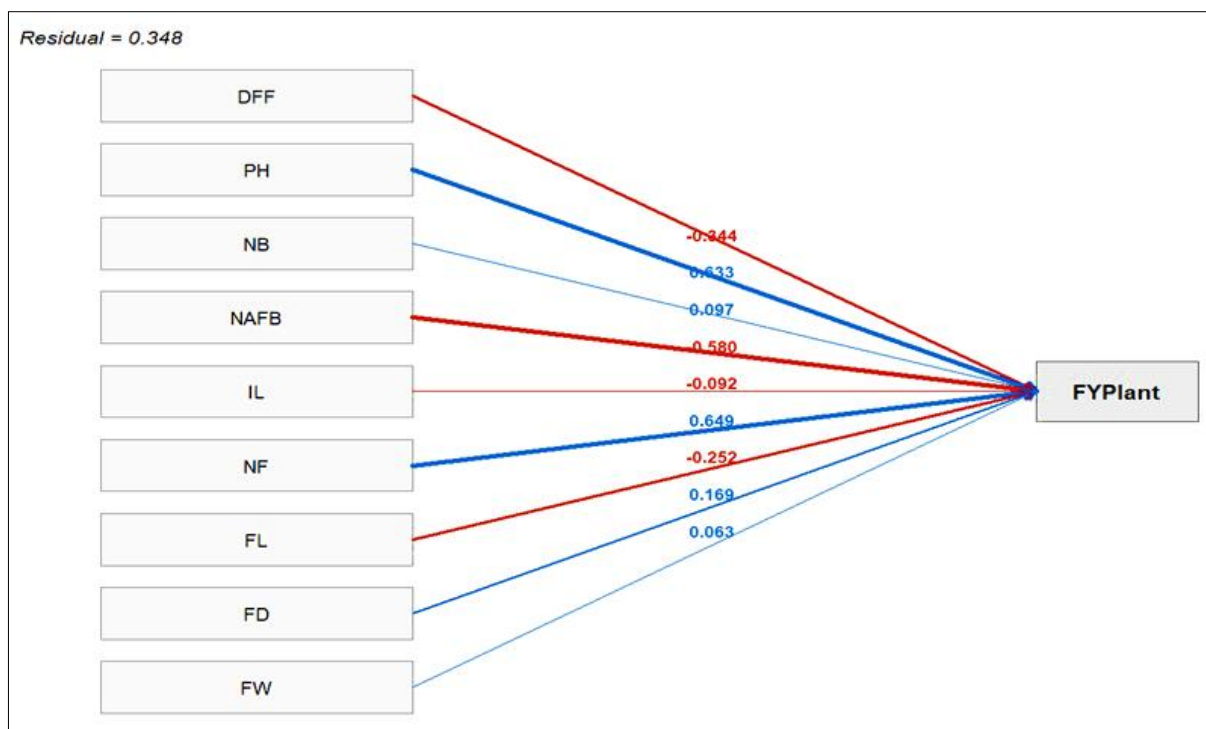


Fig.5: Genotypic Path Diagram for Fruit Yield per Plant in F₃ generation of okra cross Arka Anamika × IC-42464

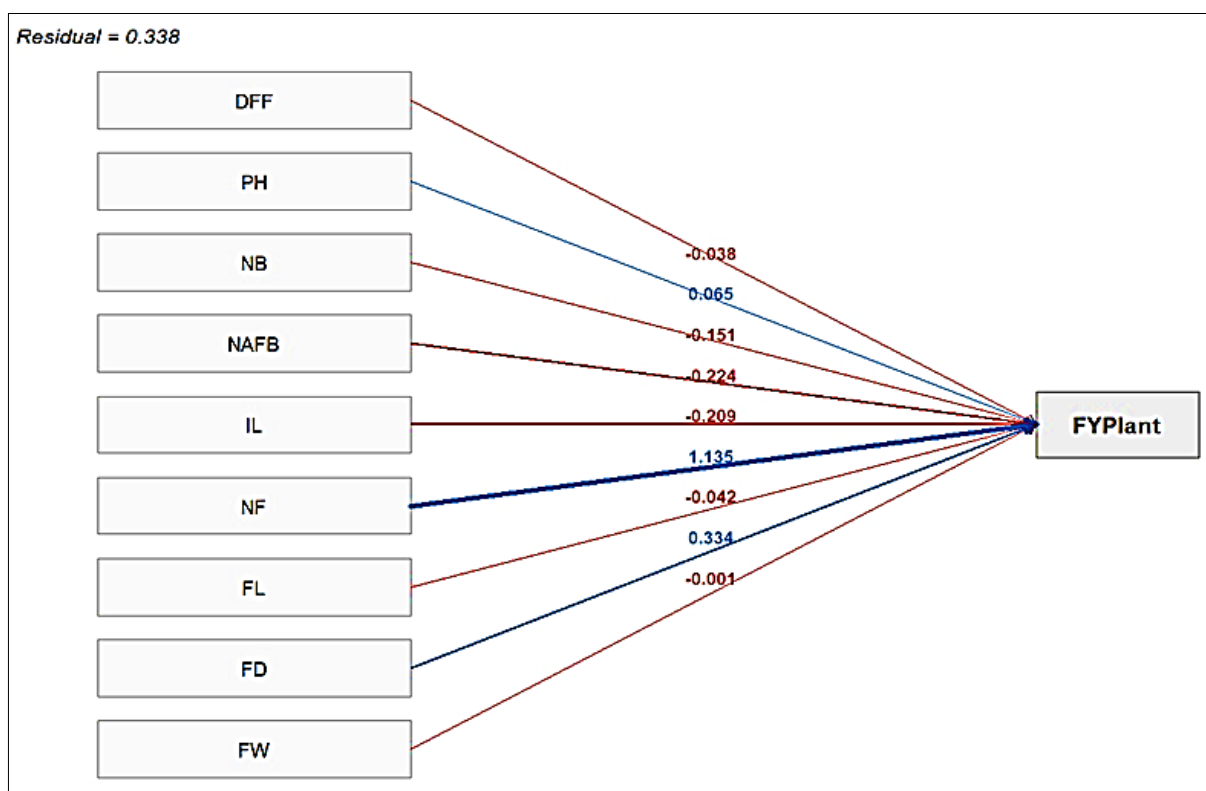


Fig 6: Phenotypic Path Diagram for Fruit Yield per Plant in F₃ generation of okra cross Arka Anamika × IC-42464

Conclusion

The present investigation demonstrated the existence of substantial genetic variability among the F₃ progenies derived from the cross Arka Anamika × IC-42464, indicating considerable scope for genetic improvement through selection. The variability parameters revealed that plant height, number of branches per plant, number of fruits per plant, fruit yield per plant, fruit yield per plot, and fruit yield per hectare exhibited high genotypic and phenotypic coefficients of variation coupled with high heritability and

high genetic advance as percentage of mean. This combination suggests the predominance of additive gene action, indicating that these traits can be effectively improved through direct phenotypic selection in the segregating population. Correlation analysis revealed that plant height, number of branches per plant, and number of fruits per plant were positively and significantly associated with fruit yield, suggesting that these characters are reliable indicators of productivity. The higher magnitude of genotypic correlations compared with phenotypic

correlations further indicated that these associations were primarily governed by genetic factors with relatively limited environmental influence. These relationships provide a useful basis for indirect selection aimed at improving fruit yield in okra breeding programmes.

Path coefficient analysis further clarified the cause-and-effect relationships among yield-contributing traits by partitioning the correlation coefficients into direct and indirect effects. Among all the characters studied, number of fruits per plant exerted the highest positive direct effect on fruit yield, followed by plant height and number of branches per plant. These traits not only showed strong positive associations with yield but also possessed favourable variability and heritability estimates, confirming their importance as primary selection criteria for yield improvement. The integration of variability, heritability, correlation, and path coefficient analyses clearly identified number of fruits per plant, plant height, and number of branches per plant as the most reliable traits for selection in the F_3 generation of Arka Anamika $\times$ IC-42464. Simultaneous selection based on these characters is expected to enhance the efficiency of pedigree breeding by facilitating the identification of superior segregants with high yield potential.

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