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Genetic variability, correlation, and path analysis in F_3 populations of Okra (*Abelmoschus esculentus* L. Moench)

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Abstract

Okra (*Abelmoschus esculentus* L. Moench) is a nutritionally significant vegetable crop cultivated extensively across tropical and subtropical regions of the world. The present investigation was conducted to assess genetic variability, correlation, and path coefficient analysis in F_3 populations derived from the cross OK-2017-010 × Varsha Uphar during Kharif 2024 at the Department of Biotechnology and Crop Improvement, College of Horticulture, Bengaluru. The experimental material comprised 25 F_3 families evaluated using an Augmented Block Design (ABD), along with two parents and five standard checks. Fourteen quantitative traits related to yield and yield-contributing characters were assessed. Substantial genetic variability was observed among all traits studied. Stem girth, total yield per plant, number of seeds per fruit, internodal length, and number of nodes exhibited high genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV). High heritability coupled with high genetic advance as a percentage of mean (GAM) was recorded for total yield per plant (h^2bs: 96.58%, GAM: 52.01%), stem girth (99.54%, 288.57%), number of seeds per fruit (83.98%, 44.49%), internodal length (86.63%, 42.29%), and number of nodes (98.72%, 39.10%), indicating the predominance of additive gene action and the effectiveness of direct selection for these traits. Correlation analysis revealed that total yield per plant exhibited highly significant positive associations with number of branches per plant (r = 0.964**), fruit length (r = 0.961**), number of fruits per plant (r = 0.725**), and average fruit weight (r = 0.659**). Path coefficient analysis identified number of fruits per plant (0.705), average fruit weight (0.428), and number of branches per plant (0.264) as having the highest positive direct effects on yield. These findings collectively suggest that simultaneous selection for these traits would constitute an effective and efficient breeding strategy for developing high-yielding okra cultivars. The considerable genetic diversity observed in this population offers a valuable genetic resource for future okra improvement programs.

Keywords: Okra, F_3 population, genetic variability, heritability, genetic advance, correlation, path coefficient analysis

Introduction

Okra (*Abelmoschus esculentus* L. Moench, $2n = 2x = 130$) is an important warm-season vegetable crop belonging to the family Malvaceae. It is widely grown in tropical and subtropical countries of Africa, Asia, the Americas, and the Mediterranean region (Gemede *et al.*, 2015) [9]. India is one of the largest producers of okra, contributing significantly to global production with major growing states including West Bengal, Bihar, Odisha, Uttar Pradesh, and Karnataka (NHB, 2022). The tender green pods are consumed as a fresh vegetable and are valued for their high nutritional content, including mucilage, vitamins (A, C, and B6), minerals, dietary fiber, and antioxidants (Mishra *et al.*, 2012) [12]. Beyond nutritional value, okra also holds significant industrial importance, as its stem fibers are used in paper manufacturing and its seeds are a source of edible oil (Arapitsas, 2008) [4].

Despite its socioeconomic importance, okra productivity remains constrained due to limited availability of high-yielding varieties, susceptibility to biotic and abiotic stresses, and a narrow genetic base in many breeding programs. Yield improvement in vegetable crops is a complex task due to the quantitative nature of yield and its dependence on a number of interrelated component traits. In such situations, knowledge of the nature and magnitude of genetic variability present in the breeding population is of paramount importance. The genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) give useful information about the extent of variability, while heritability estimates indicate the degree to which a trait is transmitted from parent to offspring (Burton, 1952; Johnson et al., 1955) [5, 10]. Genetic advance as a percentage of the mean (GAM) provides further insight into the expected gain under selection, especially when interpreted together with heritability (Allard, 1960) [2].

A clear understanding of the inter-relationships among yield and its component traits through correlation analysis helps breeders identify suitable selection criteria. However, since correlation does not distinguish between direct and indirect causes of association, path coefficient analysis as proposed by Wright (1921) [19] and later applied by Dewey and Lu (1959) [6] is used to partition correlation coefficients into direct and indirect effects, providing a clearer picture of cause-and-effect relationships. Several workers have reported significant positive associations of yield with traits such as number of fruits per plant, fruit weight, and number of branches in okra (Reddy *et al.*, 2013; Kumar *et al.*, 2014; Yadav *et al.*, 2019; Singh *et al.*, 2021) [11, 16, 17, 20].

The use of segregating populations such as F_3 families in variability studies is advantageous because they exhibit wide genetic diversity arising from recombination in the preceding generations, and selection in such populations can be highly effective if the traits are governed by additive gene action (Falconer and Mackay, 1996) [8]. The cross OK-2017-010 × Varsha Uphar was chosen for the present study because of the contrasting nature of the parents for several agronomic and yield-related characters. The present investigation was therefore undertaken to: (i) estimate genetic variability parameters including GCV, PCV, heritability, and genetic advance for 14 quantitative traits in F_3 populations of okra; (ii) determine the nature and magnitude of correlation among yield and its component traits; and (iii) identify the traits with significant direct and indirect effects on yield through path coefficient analysis, with the ultimate objective of formulating an efficient selection strategy for yield improvement in okra.

Materials and Methods

Experimental Site and Plant Material

The experiment was carried out at the Department of Biotechnology and Crop Improvement (BCI), College of Horticulture, Bengaluru, Karnataka, India during the *Kharif* 2024 season. The experimental material consisted of F_3 populations derived from biparental crosses developed at the same department. The cross used in the present study was OK-2017-010 × Varsha Uphar. The F_3 families were generated through selfing of selected F_2 individuals from the cross to obtain segregating families exhibiting genetic variation for yield and yield-contributing traits.

Experimental Design

A total of 25 F_3 families with a population size of 250 plants, along with their respective parents and five standard checks (Kashi Pragati, Arka Anamika, Pusa A4, Varsha Uphar, and Parbhani Kranti), were evaluated using an Augmented Block Design (ABD) during *Kharif* 2024. The experiment comprised five blocks, with each family represented by 10 plants spaced at adequate distances to ensure optimal growth. All recommended agronomic practices were followed as per the University of Horticultural Sciences (UHS), Bagalkot package of practices (Anonymous, 2016) [3]. Standard plant protection measures were adopted throughout the crop season.

Statistical Analysis

Statistical analyses were performed following standard procedures. Analysis of variance (ANOVA) was carried out as per the method described by Panse and Sukhatme (1985) [14]. Genotypic and phenotypic coefficients of variation (GCV and PCV) were computed according to Burton (1952) [5]. Broad-sense heritability (h^2bs) and genetic advance as a percentage of mean (GAM) were estimated following Johnson *et al*. (1955) [10]. Correlation coefficients (genotypic and phenotypic) were calculated following the method of Al-Jibouri *et al*. (1958) [1]. Path coefficient analysis was performed as per the methods proposed by Wright (1921) and Dewey and Lu (1959) [6, 19]. Genetic parameters were categorized as high, medium, or low based on mean ± standard deviation as suggested by Diwakar *et al*. (2016) [7]. Data analyses were performed using R STUDIO 4.4.1 (AUGMENTEDRCBD package) and GRAPES 1.0 software.

Results and Discussion

Genetic Variability Parameters

The estimation of genetic variability parameters in the F_3 populations of the okra cross OK-2017-010 × Varsha Uphar is presented in Table 1. The analysis revealed considerable variation among genotypes for all traits studied, reflecting substantial genetic diversity in the population – a prerequisite for effective selection (Allard, 1960) [2]. The mean, range, GCV, PCV, broad-sense heritability (h^2bs), and genetic advance as percent of mean (GAM) were computed for 14 quantitative traits.

Stem girth exhibited exceptionally high values for both GCV (140.20%) and PCV (140.52%), indicating extensive phenotypic and genotypic variation for this trait. The close correspondence between GCV and PCV for stem girth also suggests minimal environmental influence on its expression. Similarly, total yield per plant displayed high GCV (25.65%) and PCV (26.10%), reflecting considerable scope for selection-based improvement. High GCV and PCV for yield have been reported by several workers in okra (Yadav *et al*., 2019; Reddy *et al*., 2013) [16, 20], corroborating the present findings. Other traits with high genetic variability included number of seeds per fruit (GCV: 23.53%; PCV: 25.68%), internodal length (GCV: 22.02%; PCV: 23.66%), and number of nodes (GCV: 19.07%; PCV: 19.20%). The narrow difference between GCV and PCV across most traits suggests that phenotypic expression was predominantly under genetic control, with limited environmental modification – a desirable attribute for reliable selection (Patel *et al*., 2011) [15].

Heritability estimates (h^2bs) ranged from 41.30% for number of ridges on the fruit surface to 99.54% for stem girth (Table 1). High heritability coupled with high genetic advance – the combination indicative of additive gene action – was observed for stem girth (h^2bs: 99.54%, GAM: 288.57%), total yield per plant (96.58%, 52.01%), fruit diameter (91.86%, 13.77%), average fruit weight (95.70%, 36.29%), plant height (99.14%, 27.67%), number of nodes (98.72%, 39.10%), internodal length (86.63%, 42.29%), and number of seeds per fruit (83.98%, 44.49%). These findings are in agreement with those of Kumar *et al*. (2014), Singh *et al*. (2021), and Yadav et al. (2019) [11, 17, 20], who reported high heritability and genetic advance for yield-related traits in okra, suggesting that these traits are amenable to direct selection. The predominance of additive gene action for these traits further validates the utility of selection in early segregating generations. Traits governed by additive effects respond predictably to selection and allow reliable genetic gain across generations (Falconer and Mackay, 1996) [8].

Number of branches per plant showed high heritability (81.01%) with relatively high GAM (26.53%), indicating additive genetic control. Number of fruits per plant exhibited moderate heritability (61.66%) and moderate GAM (21.69%), suggesting the influence of both additive and non-additive gene action, as also reported by Mishra *et al*. (2012) [12]. Days to first flowering and days to 50% flowering exhibited comparatively low GCV and PCV values, with moderate heritability estimates (58.10% and 67.56%, respectively) and low GAM (4.20% and 5.28%, respectively), implying the role of non-additive genetic components and environmental effects in the expression of these traits (Solanki *et al*., 2016) [18].

Table 1: Estimation of genetic variability parameters in F_3 populations of the okra cross OK-2017-010 × Varsha Uphar

Traits	Mean	Min	Max	GCV (%)	PCV (%)	h^2bs (%)	GAM (%)
Days to first flowering	41.77	37.50	44.80	2.67	3.51	58.10	4.20
Days to 50% flowering	43.07	40.00	46.00	3.11	3.79	67.56	5.28
Plant height (cm)	178.55	130.50	255.00	13.47	13.53	99.14	27.67
Number of branches	2.01	1.45	2.81	14.29	15.87	81.01	26.53
Number of nodes	16.70	10.27	23.43	19.07	19.20	98.72	39.10

Internodal length (cm)	8.30	3.51	11.57	22.02	23.66	86.63	42.29
Number of ridges on fruit	5.52	5.00	6.20	4.22	6.57	41.30	5.60
Fruit length (cm)	11.87	14.65	20.58	4.42	5.21	72.10	7.75
Fruit diameter (cm)	1.94	1.64	2.75	6.96	7.26	91.86	13.77
Stem girth (cm)	2.21	1.12	2.11	140.20	140.52	99.54	288.57
Number of fruits per plant	29.39	23.00	40.40	13.39	17.05	61.66	21.69
Average fruit weight (g)	17.60	10.80	22.80	17.98	18.38	95.70	36.29
Number of seeds per fruit	48.20	39.80	81.20	23.53	25.68	83.98	44.49
Total yield per plant (g)	510.29	262.44	832.24	25.65	26.10	96.58	52.01

GCV: Genotypic Coefficient of Variation; PCV: Phenotypic Coefficient of Variation; h^2bs: Broad sense heritability; GAM: Genetic Advance Percent Mean.

Correlation Analysis

Understanding the nature and magnitude of association among yield and its component traits is fundamental for framing an effective selection strategy. Correlation coefficients computed for 14 traits in the F_3 populations are presented in Table 2. Total yield per plant exhibited highly significant positive correlations with number of branches per plant (r = 0.964**), fruit length (r = 0.961**), number of fruits per plant (r = 0.725**), and average fruit weight (r = 0.659**). These results imply that selection pressure applied on any of these traits would result in simultaneous improvement in yield, corroborating earlier reports by Reddy *et al*. (2013), Kumar *et al*. (2014), and Singh *et al*. (2021) [11, 16, 17] in okra.

Significant negative correlations were observed between days to first flowering and total yield per plant (r = −0.49**), indicating that early-flowering genotypes tend to exhibit higher yields. This relationship has practical implications for selection: choosing genotypes with shorter pre-flowering duration may indirectly enhance yield potential by extending the duration of pod production (Patel *et al*., 2011) [15]. Internodal length showed a strong negative association with yield (r = −0.594**), number of fruits per plant (r = −0.932**), and number of branches per plant (r = −0.60**). This negative relationship between internodal length and yield is consistent with findings of Yadav *et al.* (2019) and Solanki *et al*. (2016) [18, 20], who suggested that compact plant architecture with shorter internodes is associated with higher branching and fruiting potential.

Among the component traits, number of branches per plant demonstrated highly significant positive associations with fruit length (r = 0.935**), number of fruits per plant (r = 0.725**), and average fruit weight (r = 0.602**), highlighting its importance as a key yield determinant. Fruit length also exhibited strong positive correlations with number of fruits per plant (r = 0.723**) and average fruit weight (r = 0.59**), emphasizing its dual contribution to yield improvement (Kumar *et al*., 2014) [11]. Number of nodes on the main stem showed positive correlation with yield (r = 0.359**), largely through its indirect association with fruit-bearing nodes (Mishra *et al*., 2012) [12].

Table 2: Correlation coefficients among yield and its attributing traits in the F_3 populations of the cross OK-2017-010 × Varsha Uphar in okra.

	DFF	**D50F**	**PH**	**NBPP**	**NNMS**	**IL**	**NR**	**FD**	**FL**	**SG**	**NFPP**	**AFW**	**NSF**	**TYPP**
DFF	1	0.729**	-0.107	-0.400*	-0.332	0.344	0.074	-0.301	-0.482**	-0.042	-0.373*	-0.333	-0.121	-0.49**
D50F		1	0.016	-0.227	-0.228	0.320	-0.025	-0.186	-0.196	-0.185	-0.353	-0.116	-0.199	-0.265
PH			1	0.260	0.301	-0.226	-0.053	0.287	0.280	0.523**	0.324	-0.113	0.407*	0.180
NBPP				1	0.392*	-0.6**	-0.147	0.361*	0.935**	0.295	0.725**	0.602**	0.349	0.964**
NNMS					1	-0.197	-0.081	0.967**	0.369*	0.103	0.326	0.112	-0.048	0.359
IL						1	-0.118	-0.198	-0.584**	-0.525**	-0.932**	0.084	-0.553**	-0.594**
NR							1	-0.044	-0.156	-0.129	0.025	-0.034	-0.062	-0.097
FD								1	0.330	0.052	0.308	0.095	-0.086	0.339
FL									1	0.302	0.723**	0.59**	0.374*	0.961**
SG										1	0.548**	-0.283	0.873**	0.228
NFPP											1	-0.001	0.542**	0.725**
AFW												1	-0.142	0.659**
NSF													1	0.310
TYPP														1

DFF: Days to first flowering	D50F: Days to 50% flowering	PH: Plant height (cm)	NBPP: Number of branches per plant
NNMS: Number of nodes on the main stem	INL: Inter nodal length (cm)	FD: Fruit diameter (cm)	NFPP: Number of fruits per plant
SG: Stem girth (cm)	NR: Number of ridges on fruits	FL: Fruit length (cm)	AFW: Average fruit weight (g)
NSF: Number of seeds per fruit	TYPP: Total yield per plant (g)		

Fruit diameter was positively and significantly correlated with average fruit weight (r = 0.42**), indicating that pod size uniformity is an important selection criterion for improving marketable yield quality (Gemede *et al*., 2015) [9]. These positive inter-trait correlations suggest that simultaneous multi-trait selection would be more effective than single-trait selection for genetic improvement of okra.

Path Coefficient Analysis

Path coefficient analysis was conducted to partition the observed correlations into direct and indirect causal components, thereby providing a more precise understanding of the traits influencing total yield per plant (Table 3). The analysis revealed that number of fruits per plant exerted the highest positive direct effect on yield (0.705), confirming its paramount importance as a primary yield determinant in okra. This finding is in consonance with reports from Kumar *et al*. (2014), Yadav *et al*. (2019), and Singh *et al*. (2021) [11, 17, 20], who consistently identified number of fruits per plant as the most critical yield component. The high positive direct effect of this trait, combined with its significant positive correlation with yield, provides strong justification for prioritizing it in selection programs.

Average fruit weight exhibited the second highest positive direct effect on yield (0.428), suggesting that pod size and weight are important determinants of final yield (Reddy *et al*., 2013) [16]. This trait also showed significant positive correlation with yield (r = 0.659**), indicating that selection for heavier pods would be a reliable indirect approach to improving total yield per plant. Number of branches per plant recorded a positive direct effect of 0.264 on yield, with a very high positive correlation (r = 0.964**). Its large indirect effects through number of fruits per plant and fruit length further substantiate its role as a key yield contributor, as reported by Patel *et al*. (2011) and Mishra *et al*. (2012) [12, 15].

Internodal length showed a positive direct effect (0.230) on yield but exhibited a large negative indirect effect through number of fruits per plant (−0.657), resulting in an overall negative correlation with yield (r = −0.594**). This discrepancy between direct and indirect effects underscores the importance of path analysis in disentangling true causal relationships from spurious associations (Dewey and Lu, 1959) [6]. Similarly, number of nodes on the main stem exhibited a negative direct effect (−0.183) but a positive correlation (r = 0.359) with yield, mediated through positive indirect effects via fruit diameter (0.195) and number of fruits per plant (0.230). These contrasting direct and indirect effects indicate complex trait interactions that cannot be discerned from simple correlation analysis alone (Wright, 1921) [19].

Fruit length showed a strong positive correlation with yield (r = 0.961**) but a moderate direct effect, with much of its influence being channeled through number of branches per plant and number of fruits per plant. Such traits with high indirect effects serve as important selection indices in indirect selection programs (Allard, 1960) [2]. Days to first flowering exhibited a low but positive direct effect on yield (0.089), with the net negative correlation with yield (−0.49**) being primarily attributable to indirect negative effects through internodal length and number of nodes.

The residual effect in the path analysis was found to be minimal (< 0.10), confirming that the traits included in the study collectively explained most of the variability in total yield per plant and that no major yield-contributing trait was overlooked (Falconer and Mackay, 1996) [8]. These results provide a scientifically sound basis for developing a multi-trait selection index focusing on number of fruits per plant, average fruit weight, and number of branches per plant as the most effective approach to yield improvement in okra breeding programs.

Table 3: Direct and indirect of characters on yield and yield attributing trait in the F_3 populations of the cross OK-2017-010 × Varsha Uphar in okra.

	DFF	D50F	PH	NBPP	NNMS	IL	NR	FD	FL	SG	NFPP	AFW	NSF	TYPP
DFF	-0.136	0.098	0.009	-0.106	0.061	0.079	-0.001	-0.061	-0.02	-0.001	-0.263	-0.142	-0.007	-0.49
D50F	-0.099	0.134	-0.001	-0.06	0.042	0.074	0.001	-0.038	-0.008	0.001	-0.249	-0.049	-0.011	-0.265
PH	0.015	0.002	-0.082	0.069	-0.055	-0.052	0.001	0.058	0.012	0.010	0.229	-0.048	0.022	0.180
NBPP	0.054	-0.030	-0.021	0.264	-0.072	-0.138	0.003	0.073	0.039	0.004	0.511	0.257	0.019	0.964
NNMS	0.045	-0.031	-0.025	0.104	-0.183	-0.045	0.002	0.195	0.015	0.006	0.230	0.048	-0.003	0.359
IL	-0.047	0.043	0.018	-0.158	0.036	0.230	0.002	-0.040	-0.025	-0.003	-0.657	0.036	-0.030	-0.594
NR	-0.010	-0.003	0.004	-0.039	0.015	-0.027	-0.020	-0.009	-0.007	-0.001	0.018	-0.015	-0.003	-0.097
FD	0.041	-0.025	-0.023	0.095	-0.177	-0.046	0.001	0.202	0.014	0.005	0.217	0.041	-0.005	0.339
FL	0.065	-0.026	-0.023	0.247	-0.068	-0.135	0.003	0.067	0.042	0.005	0.510	0.252	0.021	0.961
SG	0.019	0.001	-0.188	0.247	-0.259	-0.179	0.005	0.225	0.051	0.004	0.787	-0.066	0.052	0.697
NFPP	0.051	-0.047	-0.026	0.192	-0.060	-0.215	-0.001	0.062	0.030	0.005	0.705	-0.001	0.030	0.725
AFW	0.045	-0.015	0.009	0.159	-0.021	0.019	0.001	0.019	0.025	-0.001	-0.001	0.428	-0.008	0.659
NSF	0.016	-0.027	-0.033	0.092	0.009	-0.128	0.001	-0.017	0.016	0.004	0.382	-0.061	0.055	0.310

DFF: Days to first flowering	D50F: Days to first fruiting	PH: Plant height (cm)	NBPP: Number of branches per plant
NNMS: Number of nodes on the main stem	INL: Inter nodal length (cm)	FD: Fruit diameter (cm)	NFPP: Number of fruits per plant
SG: Stem girth (cm)	NR: Number of ridges on fruits	FL: Fruit length (cm)	AFW: Average fruit weight (g)
NSF: Number of seeds per fruit	TYPP: Total yield per plant (g)		

Conclusion

The F_3 populations of the okra cross OK-2017-010 × Varsha Uphar exhibited substantial genetic variability for yield and yield-contributing traits, indicating their suitability as a valuable genetic resource for selection-based breeding. High heritability coupled with high genetic advance was observed for traits such as total yield per plant, stem girth, number of seeds per fruit, internodal length, and number of nodes, reflecting the predominance of additive gene action and confirming the efficiency of direct selection for these traits. Correlation analysis established that number of branches per plant, fruit length, number of fruits per plant, and average fruit weight were major contributors to yield, with significant positive associations. Path coefficient analysis identified number of fruits per plant, average fruit weight, and number of branches per plant as the traits with the highest positive direct effects on yield.

Based on these findings, simultaneous selection for number of fruits per plant, average fruit weight, and number of branches per plant is recommended as the most effective breeding strategy for developing high-yielding okra cultivars. The genetic diversity revealed in this population offers substantial scope for the development of superior okra genotypes through systematic selection and further hybridization programs.

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