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Utilizing a cause-effect model to identify factors linked to fruit yield in okra (*Abelmoschus esculentus* L. Moench)

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Abstract

The current study employed 50 distinct okra genotypes to explore genetic diversity, the intricate relationships among key yield parameters, and their direct and indirect contributions to overall yield. ANOVA analysis unveiled that the mean squares of all attributes linked to genotypes were statistically significant, indicating the presence of genetic variation within the experimental dataset. All 13 traits exhibited Principal Component Values (PCV) surpassing Genetic Coefficient of Variation (GCV) values, underscoring the influential role of environmental factors in shaping these traits. The prevalence of additive gene action was indicated by higher GCV, heritability, and genetic progress as a percentage of the mean for traits such as plant height, internode length, number of nodes per plant, number of branches per plant, fruit production, total soluble sugar, total phenol, and total chlorophyll. Fruit yield displayed a substantial positive correlation with both genotypic and phenotypic levels of plant height and fruit weight, underscoring their interconnectedness. Notably, internode length emerged as the primary driver of fruit yield, followed by fruit weight, number of nodes per plant, phenol content, and number of branches per plant, as revealed by path coefficient analysis. Moreover, a concrete association between fruit yield and fruit weight was established. These noteworthy traits could be of significant consideration in the context of an okra selection program.

Keywords: Okra, genetic variability, correlation, path analysis

Introduction

Belonging to the Malvaceae family and possessing a chromosomal count of $2n=130$, Okra (*Abelmoschus esculentus* L. Moench) has gained prominence as a member of the diverse vegetable crop category. It is a desirable fruit vegetable that is widely grown in warmer regions of the world such as some Asian and African countries. Ranked among the prominent vegetable crops in India, Okra (*Abelmoschus esculentus* L. Moench) stands out for its tender green fruits and is cultivated throughout the summer and rainy seasons. This versatile crop offers various edible parts, including fresh leaves, buds, blossoms, pods, stems, and seeds, allowing for diverse culinary applications. The young, unripe okra fruits are commonly consumed as vegetables and can be incorporated into salads, soups, and stews, either fresh, dried, fried, or boiled. The mucilage found in okra offers therapeutic advantages, serving as a blood volume expander or plasma supplement. Notably, it has the ability to trap toxins and bile acids containing cholesterol released by the liver. Immature pods are also used for making pickles. The entire plant is edible and contributes to a range of dishes. Greek okra seeds possess oil content varying from 20% to 40%, depending on the extraction method. Rich in fiber, okra aids in stabilizing blood sugar levels by regulating the absorption rate of sugar from the digestive tract. Okra consumption on a regular basis may aid in the prevention of renal disease. For effective vegetable and seed production, healthy and high-quality seeds must be used. Exploiting variability and identifying yield factors are critical for increasing okra output. The present research investigation aims to evaluate genetic variation, the relation between fruit yield and its attributes, and path coefficient analysis in okra genotypes, permitting breeders to generate superior hybrids and transgressive segregants after crossing from different parents.

Materials and Methods

The primary aim of the present study conducted at MVRs, Anand Agricultural University, Anand, was to assess the genetic diversity of okra (*Abelmoschus esculentus* L. Moench) during the summer of 2022. Anand is situated at an altitude of 45.10 meters above the average sea level, positioned at latitudes 22°35' North and longitudes 72°55' East. At the examination site,

the soil is an alluvial sandy loam that is deep, well-drained, and has a fair capacity to hold moisture. The area has tropical and semi-arid weather. The weather conditions during the growing season were favorable for the typical growth and development of the crops. The study included 50 unique okra genotypes sourced from various geographical origins. These genotypes were acquired from the Main Vegetable Research Station at Anand Agricultural University. In the summer of 2022, an evaluation of fifty okra genotypes took place at MVRS, AAU, Anand, following a randomized block design (RBD) with three replications. Plots measured 1.20 m × 2.40 m and were spaced at 60 cm × 30 cm. Successful cultivation of the crop was achieved by adhering to recommended agronomic practices and essential plant protection measures. Measurements and data collection were carried out on five randomly selected plants, with the intention of using 16 plants per genotype for each replication. Days to 50% flowering, plant height, number of branches per plant, number of nodes on main stem per plant, internodal length, fruit length, fruit girth, fruit weight, fruit yield per plant, total soluble sugar, total phenol, total chlorophyll, and moisture content were all measured. RBD ANOVA analysis was conducted following the methodology outlined by Panse and Sukhatme (1985) [13]. The phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were computed using the formula established by Burton and De Vane (1953) [4]. Heritability and genetic progress were assessed using the formula introduced by Allard (1960) [3]. The calculation of covariance correlation coefficients was performed using the method outlined in the review by Singh and Choudhary (1985) [18]. Path coefficient analysis was carried out utilizing the approach initially proposed by Wright (1921) [25] and later applied by Dewey and Lu (1959) [7].

Results and Discussion

Analysis of genetic variability and heritability

The primary goal of this current research endeavor is to enhance our understanding of the varying characteristics among different okra genotypes. The analysis of variance yielded a remarkably substantial mean sum of squares attributed to the evaluated genotypes across all 13 quantitative traits. These traits include days to 50% flowering, number of nodes per plant, internodal length, number of branches per plant, plant height, fruit length, fruit girth, fruit weight, fruit yield per plant, total soluble sugar, total phenol content, moisture content, total chlorophyll content, and total chlorophyll content. This outcome signifies the presence of notable genetic diversity (see Table 1).

Genetic diversity is extremely valuable to plant breeders since it is essential in developing a successful breeding programme (Wedwesen and Zeleke, 2020) [24]. GCV and PCV are superior indices for measuring genetic variation and comparing the genetic variability present in different phenotypes. GCV quantifies the degree of genetic variability in a crop. It is thought to be more beneficial than PCV since it reflects the heritable fraction of heritability. All of the attributes investigated in the current research had minimal GCV% and PCV% differences, which implies that genotypic part contribute more in the phenotype compared to environment on the traits being studied (Table 2).

The phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) exhibited consistent similarity, though PCV exhibited a higher magnitude than GCV across nearly all traits. Traits such as internode length, fruit yield,

total soluble sugar, total phenol, and total chlorophyll displayed notable and comparable levels of both PCV and GCV. These outcomes are comparable with the results obtained by Kumar *et al.* (2016) [10], Lateef *et al.* (2020) [11] and Mohammed *et al.* (2022) [12] for internode length and Das *et al.* (2012) [6], Duggi *et al.* (2013) [8], Chandramouli *et al.* (2016) [5] and Kumar *et al.* (2016) [10] for fruit yield and Rahul *et al.* (2016) [27] for total soluble sugar, total phenol and total chlorophyll, which is in confirmation with the present study. The time taken to reach 50% flowering, fruit girth, and moisture content exhibited modest variations among the genotypes, yet they displayed low PCV and GCV values. This indicates limited potential for direct enhancement of these traits through simple selection methods. Similar kind of findings were earlier reported by Adiger *et al.* (2011) [1], Ranjit *et al.* (2016) [15] and Sravanthi *et al.* (2017b) [20] for days to 50% flowering and fruit girth and Rahul *et al.* (2016) [27] for moisture content. heritability values were higher (more than 60%) for number of nodes per plant, internodal length, number of branches per plant, plant height, fruit length, fruit yield per plant, total soluble sugar, total phenol content, moisture content and total chlorophyll content. Adiger *et al.* (2011) [1], Reddy *et al.* (2012) [21], Das *et al.* (2012) [6] and Duggi *et al.* (2013) [8] found high heritability for plant height, fruit length, fruit yield and number of branches per plant; Phani *et al.* (2015) [14] and Chandramouli *et al.* (2016) [5] for internode length and number of nodes per plant; Rahul *et al.* (2016) [27] for total soluble sugar, moisture content, total phenol and total chlorophyll content. Since it was not able to completely rule out variance resulting from various genetic components and their interactions when doing this computation, the broad sense heritability values were likely exaggerated. Therefore, it was necessary to keep these restrictions in mind when evaluating the heritability estimates. Nonetheless, traits like plant height, internode length, number of nodes per plant, number of branches per plant, fruit yield, total soluble sugar, total phenol, and total chlorophyll displayed both elevated heritability and substantial genetic advancement (expressed as a percentage of the mean). This suggests a predominant influence of additive genetic factors. Consequently, phenotypic selection is poised to be more efficient for enhancing these particular attributes. These findings align with the discoveries made by Adiger *et al.* (2011) [1] concerning attributes such as plant height, number of branches per plant, internode length, and fruit yield; Duggi *et al.* (2013) [8] for plant height and fruit yield per plant; Rathava *et al.* (2019) [16] for Days to 50% flowering and internode length; Rahul *et al.* (2016) [27] regarding total soluble sugar, total phenol, and total chlorophyll; Raval *et al.* (2018) [17] for plant height, number of branches per plant, internode length, and fruit yield; Lateef *et al.* (2020) [11] for number of nodes per plant, internode length, and fruit yield; Walling *et al.* (2020) [23] for plant height and fruit yield; and Alam *et al.* (2020) [2] for plant height, number of branches per plant, internode length, number of nodes per plant, and fruit yield. Traits such as days to 50% flowering exhibited moderate heritability coupled with low genetic advance as a percentage of the mean. Fruit girth displayed moderate heritability along with moderate genetic advance, indicating the interplay of both additive and non-additive genetic factors in influencing these traits' inheritance. This underscores the potential for improving these traits through progeny selection or adapted selection techniques aimed at harnessing additive gene effects.

Table 1: Analysis of variance (ANOVA) showing the mean sum of squares for 13 traits in okra

Sr. No.	Source of variation	Replications	Genotypes	Error
	df	2	49	98
1.	Days to 50% flowering	0.09	14.99**	4.92
2.	Number of nodes per plant	2.12*	9.86*	0.48
3.	Internodal length	0.25*	2.58**	0.13
4.	Number of branches per plant	6.30**	0.83**	0.01
5.	Plant height	45.50	213.09**	18.46
6.	Fruit length	8.91**	3.72**	0.45
7.	Fruit girth	0.01	0.35**	0.07
8.	Fruit weight	0.58	1.14**	0.55
9.	Fruit yield per plant	2747.78**	2021.53**	331.02
10.	Total soluble sugar	0.01	4.39*	0.01
11.	Total phenol content	234.00	4175.20*	82.80
12.	Moisture content	12.25	26.02*	1.25
13.	Total chlorophyll content	0.004	4.61*	0.02

*, ** Significant at 0.05 and 0.01 levels of probability, respectively

Table 2: Variability parameters for thirteen characters of okra genotypes used in the study

Sr. No.	Characters	Variance components			GCV (%)	PCV (%)	Heritability (%) (h ² _b)	Genetic Advance (GA %)	Genetic Advance (% of Mean)
		σ^2_g	σ^2_p	σ^2_e					
1	Days to 50% flowering	3.36	8.28	4.92	3.90	6.13	40.55	2.40	5.12
2	Number of nodes per plant	3.13	3.61	0.49	18.43	19.82	86.50	3.38	35.31
3	Internodal length (cm)	0.82	0.95	0.13	20.03	21.59	86.11	1.72	38.29
4	Number of branches per plant	0.27	0.29	0.02	19.65	20.28	93.90	1.04	39.22
5	Plant height (cm)	64.88	83.34	18.46	17.16	19.44	77.85	14.64	31.18
6	Fruit length (cm)	1.09	1.54	0.45	10.20	12.13	70.77	1.81	17.67
7	Fruit girth (cm)	0.10	0.17	0.07	6.67	8.76	57.87	0.48	10.44
8	Fruit weight (g)	0.20	0.75	0.55	5.56	10.88	26.11	0.46	5.85
9	Fruit yield per plant (g)	563.50	894.52	331.02	20.48	25.81	62.99	38.81	33.49
10	Total soluble sugar (%)	1.46	1.47	0.01	52.96	53.16	99.23	2.48	108.67
11	Total phenol content (mg/100g)	1364.12	1446.93	82.81	27.95	28.79	94.28	73.87	55.90
12	Moisture content (%)	8.26	9.51	1.25	3.35	3.59	86.86	5.51	6.42
13	Total chlorophyll content (mg/100g)	1.53	1.56	0.03	34.75	35.05	98.34	2.52	70.99

(σ^2_g : Genotypic variance, σ^2_p : Phenotypic variance, σ^2_e : Environmental variance, **GCV**: Genotypic Coefficient of Variation, **PCV**: Phenotypic Coefficient of Variation)

The results are akin with the findings of Adiger *et al.* (2011) [1] for fruit girth; Rathava *et al.* (2019) [16] for fruit length. Moderate heritability combined with modest genetic advancement, expressed as a percentage of the mean, was observed for fruit weight. This suggests a notable impact of environmental factors, potentially diminishing the efficacy of selection. Consequently, the potential for enhancing these traits through selection appears to be constrained. The results obtained were in confirmatory with Adiger *et al.* (2011) [1] for days to 50% flowering; Rathava *et al.* (2019) [16] for DFF and fruit weight; Lateef *et al.* (2020) [11] for days to 50% flowering, Walling *et al.* (2020) [23] for days to 50% flowering and fruit weight. Kumar *et al.* (2023) [9] for days to 50% flowering and Rahul *et al.* (2016) [27] for moisture content having the same results.

Based on the earlier discourse, it is evident that traits like plant height, number of nodes per plant, number of branches per plant, internode length, and fruit yield exhibit substantial heritability coupled with significant genetic advancement expressed as a percentage of the mean. This underscores the predominant influence of additive genetic factors, making direct selection for these attributes highly effective.

Character association

Selection is only effective in any improvement programme if there is enough genetic variety. However, in order to explain

character interrelationships and help in the successful identification of probable genotypes, simultaneous selection for several traits must be linked. Understanding the interrelationships between numerous economically significant characteristics is beneficial. The summer period was employed to explore the correlation between various morphological, reproductive, and nutritional traits with the fruit yield of okra genotypes, as well as their interrelationships. Thirteen traits were measured throughout both seasons, and their genotypic and phenotypic correlation coefficients were assessed (as shown in Tables 3 and 4). Among the 13 traits examined in the summer study, both plant height and fruit weight displayed a notable positive correlation coefficient with fruit yield per plant, evident at both the genotypic and phenotypic levels. Our outcomes were comparable with the findings of Thulasiram *et al.* (2017) [22] and Yadav *et al.* (2017) [26] for plant height and internode length and Adiger *et al.* (2011) [1] and Sravanthi *et al.* (2021a) [19] for significant positive and negative relation of fruit weight with fruit yield. Furthermore, the trait of the number of nodes per plant demonstrated a meaningful positive correlation solely at the phenotypic level with fruit yield per plant. Our outcomes were in harmony with the findings of Alam *et al.* (2020) [2]. During the summer season, the correlation analysis revealed that traits such as plant height and fruit weight not only displayed a highly favourable

correlation coefficient with fruit yield per plant, but they were also positively and significantly linked to each other. Consequently, selecting based on either of these strongly correlated traits was anticipated to lead to a corresponding positive effect in the other traits. Fruit yield, which holds economic significance, demonstrated a significantly positive connection with both plant height and fruit weight per plant, evident at both the genotypic and phenotypic levels. This underscores the importance of prioritizing these attributes when implementing selection strategies aimed at enhancing fruit yield in okra.

Path analysis

The path coefficient, as introduced by Wright (1921) [25], represents a standardized partial regression coefficient that elucidates causality and assesses the relative importance of individual traits. Consequently, in conjunction with correlation analysis, path coefficient analysis plays a pivotal role in elucidating relationships and quantifying both direct and indirect influences of yield-contributing characteristics on overall grain yield. These path coefficient estimates provide crucial insights for enhancing our comprehension of the crop

dynamics. The objective of the path coefficient analysis was to dissect the genotypic relationship between yield components and fruit yield per plant, discerning the direct effects of attributes and the indirect effects mediated through other traits across the 13 factors. Path coefficient analysis revealed that internode length had maximum direct contribution (1.074) towards fruit yield followed by fruit weight (1.05), number of nodes per plant (0.965), total phenol (0.195) and number of branches per plant (0.179). However, plant height exhibited highest negative direct effect (- 0.862) followed by fruit girth` (-0.434) and total soluble sugar (- 0.0344). These crucial qualities may be taken into consideration in a selection procedure for the further development of okra. These critical characteristics may be considered in a selection programme for future okra improvement. Fruit weight had a real association with a strong positive direct effect and a substantial positive correlation. The path coefficient analysis revealed the real relationship between the traits in question. For calculating the genuine correlation, the route coefficient analysis approach is offered, which will be beneficial for indirect selection for fruit production in okra.

Table 3: Estimates of genotypic correlation coefficients among yield and yield contributing traits in okra

Traits	FY	DFF	PH	IL	FW	FG	NPP	BPP	FL	TSS	TP	MC	TC
FY	1	-0.2536	0.4388**	0.2693	0.8598**	0.0231	0.1055	0.124	-0.0954	0.0853	0.113	0.0951	-0.1764
DFF		1	-0.1195	0.0487	-0.4246**	-0.1295	-0.1108	0.0547	0.0829	-0.0546	-0.3933**	0.2347	-0.1073
PH			1	0.7108**	0.2354	-0.0705	0.2438	-0.0144	0.0774	-0.01	0.1952	0.1433	0.0313
IL				1	0.1373	-0.2112	-0.5338**	-0.0717	0.1006	-0.1281	0.0738	0.1019	-0.2547
FW					1	0.4297**	0.1018	-0.0719	-0.0996	0.1476	0.1366	0.0194	-0.0529
FG						1	0.2157	-0.2808*	0.3161*	0.2329	-0.1298	0.0027	-0.0374
NPP							1	0.0035	-0.0227	0.1685	0.0817	0.0762	0.3404*
BPP								1	-0.0304	-0.1072	-0.2851*	-0.0031	-0.0421
FL									1	0.1134	-0.2337	0.0842	-0.0088
TSS										1	0.4494**	0.1003	0.1982
TP											1	-0.0907	0.5089**
MC												1	-0.0832
TC													1

* and ** Significant at 5% and 1% levels respectively, DFF: Days to 50% Flowering, NPP: Number of nodes per plant, IL: Internode length, BPP: No of branches per plant, PH: Plant height, FL: Fruit length, FG: Fruit girth, FW: Fruit weight, FY: Fruit yield, TSS: Total soluble sugar, TP: Total phenol MC: Moisture content, TC: Total chlorophyll

Table 4: Estimates of phenotypic correlation coefficients among yield and yield contributing traits in okra

Traits	FY	DFF	PH	IL	FW	FG	NPP	BPP	FL	TSS	TP	MC	TC
FY	1	-0.1223	0.3288**	0.1689*	0.3549**	0.0546	0.1054	0.1184	-0.0587	0.0658	0.0846	0.0579	-0.1361
DFF		1	-0.058	0.0478	-0.1286	0.0244	-0.0991	0.0069	0.119	-0.0399	-0.2630**	0.1593	-0.0752
PH			1	0.5744**	0.1039	-0.0003	0.2814**	-0.0168	0.0801	-0.0055	0.1606 *	0.1139	0.0246
IL				1	0.0388	-0.1362	-0.5125**	-0.0531	0.0898	-0.1194	0.059	0.1013	-0.2347**
FW					1	0.2404**	0.056	-0.0479	0.0008	0.0719	0.0776	0.0393	-0.032
FG						1	0.1673*	-0.2221**	0.1670*	0.1756*	-0.1162	-0.0084	-0.0238
NPP							1	-0.0096	-0.0055	0.1608*	0.0772	0.0616	0.3097 **
BPP								1	-0.0274	-0.1	-0.2702**	-0.0081	-0.0366
FL									1	0.096	-0.1989*	0.0524	-0.0231
TSS										1	0.4378**	0.1	0.196*
TP											1	-0.0811	0.4899**
MC												1	-0.0764
TC													1

* and ** Significant at 5% and 1% levels respectively, DFF: Days to 50% Flowering, NPP: Number of nodes per plant, IL: Internode length, BPP: No of branches per plant, PH: Plant height, FL: Fruit length, FG: Fruit girth, FW: Fruit weight, FY: Fruit yield, TSS: Total soluble sugar, TP: Total phenol MC: Moisture content, TC: Total chlorophyll

Table 5: Genotypic path coefficient analysis showing direct and indirect effects of different characters on fruit yield in okra

	DFE	PH	IL	FW	FG	NP	BP	FL	TSS	TP	MC	TC	r _g with FYPP
DFE	0.11873	0.10309	0.05236	-0.44601	0.05624	-0.10692	0.00983	0.01429	0.00188	-0.07704	-0.0056	0.02553	-0.2536
PH	-0.01419	-0.86273	0.76402	0.24722	0.03062	0.23539	-0.00258	0.01335	0.00034	0.03823	-0.00342	-0.00746	0.4388**
IL	0.00578	-0.61326	1.07481	0.14416	0.09174	-0.5154	-0.01288	0.01735	0.00441	0.01446	-0.00243	0.06059	0.2693
FW	-0.05041	-0.20305	0.14752	1.05037	-0.18665	0.09829	-0.01292	-0.01717	-0.00509	0.02677	-0.00046	0.01259	0.8598**
FG	-0.01537	0.06082	-0.227	0.45138	-0.4344	0.20826	-0.05046	0.05449	-0.00803	-0.02543	-0.00007	0.0089	0.0231
NPP	-0.01315	-0.21034	-0.57379	0.10694	-0.09369	0.96545	0.00062	-0.00392	-0.00581	0.016	-0.00182	-0.08096	0.1055
BPP	0.00649	0.01238	-0.07702	-0.07555	0.12199	0.00335	0.17969	-0.00524	0.00369	-0.05584	0.00007	0.01002	0.1240
FL	0.00984	-0.06679	0.10815	-0.10462	-0.13729	-0.02196	-0.00546	0.17238	-0.00391	-0.04578	-0.00201	0.00209	-0.0954
TSS	-0.00648	0.00863	-0.13767	0.15499	-0.10117	0.16267	-0.01926	0.01955	-0.03446	0.08804	-0.00239	-0.04714	0.0853
TP	-0.04669	-0.16837	0.07932	0.14352	0.05638	0.07884	-0.05122	-0.04029	-0.01549	0.19589	0.00217	-0.12103	0.1130
MC	0.02786	-0.12367	0.10953	0.02043	-0.00119	0.07355	-0.00055	0.01451	-0.00346	-0.01777	-0.02388	0.01978	0.0951
TC	-0.01274	-0.02705	-0.27379	-0.05562	0.01625	0.32862	-0.00757	-0.00152	-0.00683	0.09968	0.00199	-0.23784	-0.1764
Residual	0.7238												

* and ** Significant at 5% and 1% levels respectively, DFE: Days to 50% Flowering, NPP: Number of nodes per plant, IL: Internode length, BPP: No of branches per plant, PH: Plant height, FL: Fruit length, FG: Fruit girth, FW: Fruit weight, FY: Fruit yield, TSS: Total soluble sugar, TP: Total phenol MC: Moisture content, TC: Total chlorophyll

Conclusion

The present study leveraged the inherent genetic diversity within the genetic material under investigation. Notably, traits such as number of nodes per plant, internodal length, number of branches per plant, plant height, fruit length, fruit yield per plant, total soluble sugar, total phenol content, moisture content, and total chlorophyll content exhibited substantial variability in terms of both genotypic and phenotypic variance, along with notable heritability and genetic advancement as a percentage of the mean. This pattern indicates the influence of additive gene action in governing the inheritance of these attributes, suggesting their potential for improvement through straightforward selection methods. The correlation analysis underscored the significance of plant height, internode length, and fruit weight in positively enhancing fruit yield. Additionally, the path-coefficient analysis elucidated that internode length, fruit weight, and node number held prominence as major yield components, warranting careful consideration in the selection process due to their significant direct impact and positive correlation with fruit yield. Path coefficient analysis emerged as the most effective approach for unraveling genotypic correlations.

Conflict of Interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

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