Path Analysis and Trait Correlation for Yield and Growth Parameters in Okra [*Abelmoschus esculentus* (L.) Moench]

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ABSTRACT

Understanding genetic relationships among yield-influencing traits is essential for optimizing okra breeding. This study, conducted at the Faculty of Agriculture, Al Zaeim Al Azhari University (Sudan), evaluated 21 F_1 hybrids and ten parental lines of okra [Abelmoschus esculentus (L) Moench] using correlation and path coefficient analyses. Significant genetic variability was observed in traits such as plant height, number of fruits per plant, and seed yield components. Genotypic correlations were generally higher than phenotypic ones, indicating strong genetic control. Traits including number of fruits per plant, fruit fresh and dry weight, number of seeds per fruit, and 100-seed weight positively correlated with yield. Path analysis revealed that fruit length and dry weight had the highest positive direct effects on yield, while the number of seeds per fruit and fruits per plant contributed indirectly. Yield per plant showed high heritability (0.59) and genetic advance (30.39%), supporting effective selection.

Keywords: Okra, variability, correlations, heritability, yield.

Introduction

Okra *Abelmoschus esculentus* (L.) Moench, also known as lady's finger or gumbo, is a widely cultivated vegetable crop in tropical, subtropical, and warm temperate regions. Okra belongs to the Malvaceae family and is believed to have originated in Africa, with Ethiopia, Sudan and West Africa being prominent centres of genetic diversity. The crop's adaptability to diverse climatic conditions, ranging from humid tropics to arid regions, makes it an ideal vegetable for various African agro-ecological zones where it serves as a crucial food source and an important component of subsistence and smallholder farming systems. The major production regions include Nigeria, Sudan, Ghana, Egypt, and Côte d'Ivoire. Nigeria is the largest producer in Africa and globally, with okra playing a significant role in the country's domestic food market [1]. In countries like Sudan, okra is cultivated under both rain-fed and irrigated systems, with different varieties adapted to specific local conditions [2]. The diversity of landraces in these regions highlights the potential for genetic improvement and breeding for resilience to changing climates [3]. It is highly valued in Sudan for its tender, edible pods rich in vitamins, minerals, and dietary fibre, making it a vital contributor to food security and nutrition in the region. Also, it is dried and ground into powder and is used as an additive to several Sudanese dishes, adding consistency to the gravy nature of these recipes. Okra's seeds are also rich in protein and oil, with potential use beyond fresh consumption, including in oil extraction and animal feed production [2, 4].

Genotypic and phenotypic correlation and path analysis are crucial statistical tools in plant breeding, offering valuable insights into the relationships between traits and their underlying genetic and environmental influences.

These methods allow researchers to examine how different traits in crops like okra are interrelated, both genetically (genotypic correlation) and in terms of observable characteristics (phenotypic correlation). Path analysis, developed by Sir Ronald A. Fisher in the early 20th century, is particularly useful for determining direct and indirect effects of various traits on desirable outcomes, such as yield or resistance to disease. In the context of crop breeding, these analyses help breeders identify key traits that should be selected for improvement, thus enhancing the efficiency of breeding programs. In okra (*Abelmoschus esculentus*), a crop valued for its nutritional and economic importance, understanding the genetic and phenotypic associations between growth and yield traits is essential for optimising breeding strategies. This study's significance lies in its potential to advance the development of high-yielding okra varieties, which are crucial for meeting the growing demands of food security and improving farmers' livelihoods in Sudan. Through such analyses, breeding programs can be more targeted and efficient, leading to quicker progress in developing superior cultivars.

Material and Methods

The study was conducted at the demonstration farm of the Faculty of Agriculture, Al Zaeim Al Azhari University, Khartoum North, Sudan. Twenty-one F1 hybrids, along with ten genetically diverse parental lines of okra, composed of seven female lines (HSD1835, HSD1834, HSD1839, HSD2543, HSD2482, HSD1840, and HSD2550) and three male testers (Sinnar, Hjerat, and Clemson Spineless), were used in this study. All genotypes were evaluated in a randomized complete block design (RCBD) with three replications.

Each plot consisted of three ridges, each three meters long, with a spacing of 75 cm between ridges and 30 cm between plants. The experiment was conducted under standard agronomic practices, including irrigation, fertilisation, and pest control, to ensure optimal growth conditions. Data were collected on several key agronomic traits to assess plant growth, development, and yield performance. Days to flowering were recorded as the number of days from sowing to the onset of flowering. Plant height (cm), number of lateral branches, number of nodes per plant, number of fruits per plant, and yield per plant (g) were measured from five randomly selected plants from each plot across the three replicates. Fruit-related traits, including fruit length (cm), fresh and dry fruit weight (g), and the number of seeds per fruit, were recorded as the average of ten randomly selected pods per plot across the three replicates. The weight of 100 seeds (g) was determined as the average weight of 100 seeds across three replicates.

The data were analyzed using analysis of variance (ANOVA) through the Grapes software (version 1.1.0) [5] to determine significant differences among genotypes following the methodology outlined in [6]. Genotypic and phenotypic coefficients of variation (GCV and PCV) were estimated based on the standard equations provided in [7], as shown in Equations (1) and (2), respectively.

$$GCV = \sqrt{\frac{\delta^2 g}{\bar{x}}} \times 100 \ (1)$$

$$PCV = \sqrt{\frac{\delta^2 p}{\bar{x}}} \times 100 \ (2)$$

Where,

$\delta^2 g$ = genotypic variance
$\delta^2 p$ = phenotypic variance
$\bar{x}$ = Grand mean

Broad-sense heritability (h^2) was calculated following the definition outlined in [8], using the formula detailed in [9,10], as presented in Equation (3).

$$h^2 = \frac{\delta^2 g}{\delta^2 p} \ (3)$$

Genetic advance as a percentage of the mean (GAM) was estimated using the formula proposed in [11], as presented in Equation (4):

$$GAM \ \% = \left(\frac{GA}{\bar{x}}\right) \times 100 \ (4)$$

Where,
GA = Genetic Advance
Genotypic and phenotypic correlation coefficients for all possible trait combinations were calculated using the method suggested by [9,10, 12]. Correlation coefficients were further partitioned into direct and indirect effects through path coefficient analysis, originally developed by [13,14]) and later described by [15].

Results and Discussion

The genetic components of variance, heritability, and genetic advance for various agronomic traits in okra are presented in Table 1. The coefficient of variation (CV %) expresses the relative variability of a trait compared to the traits studied. The number of fruits per plant, number of seeds per fruit and number of nodes per plant recorded higher coefficients of variation of (20.66%), (19.73%) and (18.67%), respectively. This indicates that the materials have enough variability concerning those traits.

Table 1. Genetic Components of Variances in Okra

Traits	CV (%)	PCV (%)	GCV (%)	Heritability Broad Sense	Genetic. Advance (%)
Days to flowering	3.75	4.15	1.79	0.19	1.59
Number of lateral branches	14.79	20.26	13.84	0.47	19.49
Plant height (cm)	15.33	21.06	14.45	0.47	20.41
Number of nodes per plant	18.67	21.17	9.99	0.22	9.70
Length of fruit (cm)	14.63	17.41	9.44	0.29	10.55
Number of fruits per plant	20.66	25.32	14.63	0.33	17.42
Fruit dry weight (g)	14.45	17.50	9.87	0.32	11.47
Fruit fresh weight (g)	10.69	11.23	3.43	0.09	2.16
Number of seeds per fruit	19.73	21.58	8.73	0.16	7.27
Weight of hundred seeds (g)	9.86	13.90	9.80	0.50	14.23
Yield per plant (g)	15.82	24.83	19.14	0.59	30.39

The highest phenotypic coefficient of variation (PCV) was observed for the number of fruits per plant (25.32%), followed by yield per plant (24.83%), both traits recorded moderate-to-high Genotypic coefficient of variation (GCV) values of 14.63% and 19.14%, respectively. The difference between PCV and GCV can also be quite small, suggesting that environmental influence is minimal and the trait is mainly under genetic control and highly responsive to selection. Similar results were reported by [16,17,18,19, 20] for the number of fruit per plant and yield per plant. The phenotypic coefficient of variation (PCV) was consistently higher than the genotypic coefficient of variation (GCV) across the remaining traits, indicating that environmental factors play a significant role in the expression of these traits.

Heritability estimates ranged from (0.09) for fruit fresh weight to (0.59) for yield per plant, with the latter also showing the highest genetic advance (30.39%). This indicates that yield per plant has a high potential for genetic improvement through selective breeding, as it is less influenced by environmental factors and more by genetic factors. Heritability estimates for yield per plant in okra are frequently reported as high [21,22,23,24,25]. Several sources emphasise that high heritability is coupled with high genetic advance[21,22,23, 26, 27]. This combination is often indicative of the predominance of additive gene action in controlling the expression of these traits [22, 21,27], which eventually indicates that selection based on phenotypic performance would be effective for improving this trait.

The correlation analysis, presented in Table 2, revealed important relationships among the agronomic traits at both genotypic and phenotypic levels. Generally, genotypic correlation coefficients are higher than phenotypic correlations

for many traits, indicating a strong inherent association between characters, with environmental influence potentially playing a lesser role in reducing the expression of this association. This is in conformity with results and reports by [28, 22, 23, 29].

Table 2. Genotypic (Above Diagonal) and phenotypic (Below Diagonal) Correlation Coefficients among Agronomic Traits

Traits	Days to flowering	Number of lateral branches	Plant height (cm)	Number of nodes per plant	Fruit length (cm)	Number of fruits per plant	Fruit dry weight (g)	Fruit fresh weight (g)	Number of seeds per fruit	Weight of hundred seeds (g)	Yield per plant (g)
Days to flowering	1	-0.824**	-0.277**	-0.809**	-0.657**	0.151	0.009	-0.504**	-0.195	0.373**	-0.127
Number of lateral branches	-0.413**	1	0.056	0.782**	0.208*	0.016	-0.118	-0.046	0.213*	-0.292**	-0.075
Plant height (cm)	-0.430**	0.269**	1	-0.034	0.352**	0.021	-0.458**	-0.540**	0.125	0.136	0.396**
Number of nodes per plant	-0.207*	0.389**	0.200*	1	-0.085	-0.188	-0.441**	-0.709**	0.698**	-0.315*	-0.027
Length of fruit (cm)	-0.164	0.166	0.231*	0.047	1	0.162	-0.097	0.388**	0.827**	-0.041	0.249*
Number of fruits per plant	0.082	0.120	0.014	0.031	0.069	1	0.928**	0.598**	1.169 **	0.542**	0.882**
Fruit dry weight (g)	0.057	0.085	-0.145	-0.047	0.105	0.095	1	0.412**	0.970**	0.373**	0.739**
Fruit fresh weight (g)	0.186	-0.129	-0.197	0.043	0.104	-0.094	0.257*	1	0.497**	-0.210*	0.732**
Number of seeds per fruit	0.039	0.072	0.024	0.005	0.134	0.389**	0.089	0.036	1	0.623**	0.904**
Weight of hundred seeds (g)	0.179	-0.227*	0.034	-0.001	-0.074	0.069	0.283**	0.077	0.105	1	0.557**
Yield per plant (g)	0.048	0.011	0.120	0.027	0.176	0.674**	0.263*	0.096	0.456**	0.261*	1

*Note: Superscript asterisks * and ** on the correlation coefficients signify statistical significance at 5 % and 1% probability levels, respectively*

Days to flowering showed significant negative correlations at the genotypic level, with number of lateral branches, plant height (cm),number of nodes per plant, fruit length (cm) and fruit fresh weight (g) recording (-0.824**), (-0.277*), (-0.809**),(-0.657**), and (-0.504**) respectively. The values at the genotypic level are consistent with the correlation coefficient at the phenotypic level, with traits such as number of lateral branches, plant height (cm) and number of nodes per plant, recording (-0.413**),(-0.430**), and (-0.207*) respectively. The result suggests that early-flowering plants tend to be taller and develop a higher number of lateral branches and nodes, as well as bearing heavier and longer fruits. These traits are crucial determinants of yield. The relationship between "Days to flowering" (which includes the days until the first flower appears and the days until 50% of the plants are flowering) and yield per plant in okra is well-documented. Generally, earlier flowering is associated with higher yield. These findings align with previous studies [30, 31, 32, 33,34].

Yield is a complex character, considered dependent, and is the resultant effect of several component characters [29,35]. Understanding the relationships between yield per plant and other traits is essential for identifying and selecting characteristics that occur simultaneously and positively influence yield in okra [36]. Yield per plant showed significant positive correlations at the genotypic level with traits such as number of fruits per plant (0.882**), number of seeds per fruit (0.904**), fruit dry weight (0.739**) and fruit fresh weight (0.732**). These strong associations suggest that increasing the number of fruits and seeds per plant, as well as improving fruit dry and fresh weight, could directly enhance yield per plant. At the phenotypic level, yield per plant was also positively

correlated with the number of fruits per plant (0.674**) and the number of seeds per fruit (0.456**), reinforcing the importance of these traits in yield improvement and association at both genotypic and phenotypic levels. The number of fruits per plant is frequently highlighted as having a significant and positive correlation with yield per plant [37,38,39,22, 40, 29,40 41,42]. Number of seeds per fruit is typically reported with positive and significant or highly significant correlation with yield per plant, alongside number of fruits per plant [37,39, 43, 44, 45].Fruit weight or (average fruit weight, pod weight, fresh fruit mass),This trait also consistently shows in the literature, positive and significant or highly significant correlation with yield per plant at genotypic and/or phenotypic levels [22, 34, 37, 42,43, 46, 47]. Selection based on the number of pods per plant, number of seeds per fruit and fresh weight will eventually lead to high-yielding varieties in okra.

Number of seeds per fruit showed significant positive correlations at genotypic level with number of nodes per plant (0.698**), length of fruit (0.827**), number of fruits per plant (1.169 **), fruit dry weight (0.962**), fruit fresh weight (0.498**) and yield per plant (0.456**). The number of seeds per fruit emerged as a pivotal trait, reflecting the integration of both vegetative and reproductive attributes in okra. A significant relationship at the genotypic level was observed between seed number and the number of nodes per plant, emphasizing the role of nodal sites as key determinants of fruiting potential. Similar findings were reported by several authors [38,48].

Fruit length showed a strong correlation at the genotypic level with seed number. This is likely attributed to its ability to provide sufficient space for ovule attachment and development,

which, when pollination is successful, enhances the chances of seed development. Similar findings were reported in [39,49].

A positive and significant phenotypic and genotypic correlation coefficient between the number of seeds per fruit and fruit yield per plant during early and late seasons was reported by several researchers,[39, 45, 48, and 50]. This association will amplify seed yield in Okra. Okra seed has several potential uses as an oil crop and animal feed.

Furthermore, a positive correlation at the genotypic level was observed between fruit weight and seeds number per fruit. This suggests that heavier fruits tend to have more developed tissues and allocate a greater amount of dry biomass to seed development. This finding aligns with previous studies [39,51,52], all of which reported strong positive correlations between seed numbers and fruit weight. This pattern supports the hypothesis of Source-Sink Dynamics, which suggests that dry matter partitioning is influenced by the strength of sinks and their ability to attract assimilates [53, 54]. The strength of okra seeds as sinkers is determined by various factors, including genetics, growth stage, and environmental conditions. By understanding the dynamics of partitioning, we can enhance growth models and yield predictions in okra breeding programs. Ultimately, this knowledge will help in selecting cultivars with efficient sink strength, influencing both fruits and seeds, thereby improving the harvest index [54].

The path coefficient analysis, as presented in Table 3, revealed significant variation in the direct and indirect effects of yield-contributing traits in okra at the genotypic level. Notably, fruit length (0.938) and fruit dry weight (0.785) exerted the highest positive direct effects on yield per plant, supported by their respective significant genotypic correlations with yield (r = 0.249* and 0.739**, respectively), indicating that these two traits are crucial determinants of yield and should be prioritized in selection indices. Similar studies reported that fruit dry weight often shows a positive direct effect on fruit yield per plant [29,39, 55]. Fruit length was also reported to have the highest positive direct effects on yield by [39,55].In contrast to these findings, some authors reported a negative direct effect for fruit length [28, 38]. Other findings cited a negligible direct effect and a low direct negative effect at the genotypic level by 50 and 45, respectively. In contrast, the fresh weight of fruit (-1.084), the number of nodes per plant (-1.006), and the 100-seed weight (-0.626) showed strong negative direct effects. This indicates that, despite their positive genotypic correlations (e.g., fruit fresh weight: r = 0.732; hundred seed weight: r = 0.557), their direct contributions to yield operate through compensatory mechanisms or metabolic trade-offs that affect yield potential. Contrary to our findings, previous studies have predominantly reported fruit fresh weight as having a positive direct effect. However, several researchers support our results by noting a negative direct effect of the number of nodes in the main stem and the hundred-seed weight, respectively [24,40].

Table 3. Direct and Indirect Effects of Different Traits on Okra Yield Per Plant at Genotypic Level

	Days to flowering	Number of lateral branches	Plant height (cm)	Number of nodes per plant	Fruit length (cm)	Number of fruits per plant	Fruit dry weight (g)	Fruit fresh weight (g)	Number of seeds per fruit	Weight of hundred seeds	Gen_corr with main variable
Days to flowering	0.054	-0.309	0.024	0.829	-0.632	0.009	0.007	0.553	-0.035	-0.235	-0.127
Number of lateral branches	-0.045	0.375	-0.005	-0.801	0.201	0.001	-0.092	0.051	0.039	0.184	-0.075
Plant height (cm)	-0.015	0.021	-0.085	0.035	0.339	0.001	-0.358	0.591	0.023	-0.086	0.396
Number of nodes per plant	-0.044	0.293	0.003	-1.024	-0.082	-0.012	-0.347	0.778	0.127	0.198	-0.027
Fruit length (cm)	-0.036	0.078	-0.03	0.087	0.963	0.01	-0.076	-0.425	0.15	0.026	0.249
Number of fruits per plant	0.008	0.006	-0.002	0.193	0.156	0.062	0.724	-0.655	0.212	-0.341	0.882
Fruit dry weight (g)	0	-0.044	0.039	0.451	-0.093	0.057	0.787	-0.448	0.175	-0.233	0.733
Fruit fresh weight (g)	-0.027	-0.017	0.046	0.727	0.374	0.037	0.322	-1.095	0.09	0.132	0.733
Number of seeds per fruit	-0.011	0.08	-0.011	-0.715	0.796	0.072	0.757	-0.545	0.182	-0.392	0.904
Weight of hundred seeds	0.02	-0.11	-0.012	0.322	-0.04	0.033	0.291	0.23	0.113	-0.629	0.557

The computation of indirect effects further illuminated complex interrelationships among traits. Number of seeds per fruit exhibited the highest total positive indirect effect on yield (+2.89), primarily through its strong associations with fruit length, fruit dry weight, and number of fruits per plant. Similar findings were reported by [37,50,57]. At the genotypic level some authors noted that the number of seeds per fruit had a positive indirect effect on yield per hectare, mediated through the number of primary branches per plant [56]. The number of seeds per fruit is reported to exerted a negligible positive indirect effect through factors such as stem diameter, the number of nodes at first flowering, leaf blade length, flower length, pedicel length, days to 50% flowering, the number of branches, and plant height [50]. In contrast, a moderate positive indirect effect was observed for the number of seeds per fruit through the number of fruits per plant. Similarly, the number of fruits per plant contributed positively through other key traits, recording a total positive indirect effect of (+1.48), reinforcing its importance as an indirect enhancer of yield. Similar results were observed [37,50,57,58,59]. Traits like days to flowering and number of nodes per plant had negative indirect effects, reflecting their suppressive influence on yield when mediated through other traits. Overall, the results emphasise that while some traits may not exert strong direct effects, their indirect roles via more influential components are substantial. Therefore, integrating both direct and indirect effects is essential for effective selection strategies. Breeders aiming to improve yield in okra should focus on traits such as fruit length, fruit dry weight, number of fruits, and seed number per fruit, which collectively offer high direct and/or indirect gains. The high residual effect (0.865) indicates the influence of additional unexplored variables, highlighting the need for further multivariate studies and genomic approaches to refine trait-based yield improvement models.

Conclusion

This study elucidates the complex interplay of traits influencing yield in okra, emphasising the predominance of genetic control over key agronomic parameters. Fruit length and dry weight emerged as primary drivers of yield, directly enhancing productivity, while the number of seeds per plant and fruits per plant amplified yield indirectly. Negative indirect effects from days to flowering and nodes per plant underscore the need to mitigate traits that delay reproductive phases or divert metabolic resources. High heritability and genetic advance for yield per plant validate its suitability for phenotypic selection. However, the residual effect (0.865) signals the contribution of unexplored variables, advocating for integrated genomic and multivariate analyses in future research. By prioritising traits with robust direct and indirect effects, breeders can accelerate the development of resilient, high-yielding okra varieties adapted to Sudan's agroecological conditions.

Future Scope

This study's findings highlight the need for integrated genomic and phenotypic approaches to validate trait-trait relationships and identify molecular markers for fruit length and dry weight in okra. Future research should explore the stability of these yield-determining traits under climate stress, particularly drought and high temperatures, to enhance breeding for Sudanese agroecologies. The high residual effect (0.865) should be addressed through measuring additional, factors such as environmental conditions or other genetic and physiological

traits play a significant role in determining yield. Future research should therefore expand trait selection, incorporate advanced multivariate analyses, and refine experimental design to capture these influences.

Conflict of Interest: Authors have declared that no competing interests exist.

Author contributions. All authors contributed equally to the conception and design of the analysis, data collection, provision of data or analysis tools, performance of the analysis, and manuscript writing.

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