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Genetic Variability, Trait Correlation, and Path Analysis in Snake Melon *Cucumis melo* var. flexuosus (L.) Naudin

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ABSTRACT

This study investigated the genetic variability, correlation, and path analysis of key morphological and agronomic traits in snake melon (*Cucumis melo* var. flexuosus) to identify optimal traits for breeding programs. Seven Sudanese landrace genotypes were evaluated in a completely randomized block design with three replications. Traits such as plant height, fruit weight, fruit dimensions (length, diameter, length-to-diameter ratio), and yield-related parameters were analysed. Results revealed high genotypic and phenotypic variability for fruit weight (GCV = 45.63%, PCV = 47.95%) and number of fruits per plant (GCV = 32.63%, PCV = 34.60%), with high broad-sense heritability (H^2_b =0.89) and genetic advance (GA=63.40%), indicating strong potential for selective improvement. In contrast, the length-to-diameter ratio exhibited low variability (GCV = 3.85%, PCV = 5.72%) and heritability (H^2_b = 0.46), suggesting limited genetic control. Correlation analysis showed strong positive associations between fruit weight and traits like fruit diameter (0.947), fruit length (0.907), and stem length (0.915), implying pleiotropic or linked genetic regulation. Path analysis identified fruit diameter (direct effect = 6.491) and stem length (4.003) as primary contributors to fruit number, while fruit weight and length had compensatory indirect effects. The study underscores fruit weight, diameter, and stem length as priority traits for yield enhancement, while highlighting the need to explore additional physiological or molecular traits to account for residual variation. These findings provide a robust framework for targeted breeding strategies to improve snake melon productivity and adaptability.

Keywords: *Cucumis melo* var. flexuosus, genetic variability, heritability, path analysis, correlation, yield improvement.

1. Introduction

Snake melon (*Cucumis melo* var. flexuosus), a distinctive vegetable melon traditionally grown across the Middle East and North Africa (MENA), holds considerable agronomic, cultural, and historical value (Branca *et al*., 2023). It is a staple in local diets and farming systems in countries such as Sudan, Egypt, Turkey, and Iran. Despite its importance, snake melon remains underrepresented in modern research and breeding efforts. Existing landrace cultivars, maintained by smallholder farmers, show notable variation in key morphological traits such as fruit size, shape, skin texture, and colour which constitute a valuable genetic resource for developing improved, regionally adapted cultivars (Omari *et al*., 2018; Lahy *et al*., 2020).

To harness this genetic diversity effectively, it is essential to understand how morphological traits relate to each other and contribute to yield and adaptability. Correlation analysis serves to quantify the strength and direction of associations among traits, while path analysis further clarifies their direct and indirect effects on yield components. Together, these complementary statistical approaches provide a comprehensive view of trait interactions influencing fruit yield, quality, and environmental resilience (Yousif *et al*., 2011; Ibrahim and Ramadan, 2013; Nanthakumar *et al*. 2021).

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This study investigates morphological variation and genetic structure among selected snake melon genotypes cultivated in Sudan. By applying correlation and path analysis, we aim to identify the key traits that most strongly affect crop performance, supporting both targeted breeding and germplasm conservation. Ultimately, this work will contribute to the development of climate-resilient snake melon cultivars suited to the challenging agroecological conditions of the MENA region.

2. Materials and Methods

2.1 Materials

The study was conducted at the demonstration farm of the Faculty of Agriculture, Al Zaeim Al Azhari University, located in Khartoum North, Sudan. Seven genotypes of snake melon (*Cucumis melo* var. flexuosus), representing common landraces cultivated in the northern, Gezira, and Khartoum states of Sudan, were evaluated. The genotypes included HsD11644, HsD11079, HsD11649, HsD11641, HsD18234, HsD15763, and HsD11555. These genotypes were selected based on their widespread cultivation and adaptation to local agroecological conditions.

2.2 Methods

The experimental site was prepared by ploughing the soil deeply twice in perpendicular directions to ensure proper tilth and aeration. This process was followed by harrowing to level the ground. The experiment was arranged in a completely randomized block design (CRBD) with three replications. Each plot consisted of one bed that measured three meters long and two meters wide. Seeds were planted 50 cm apart, with 3 to 4 seeds per hole at a depth of 2 cm, which were then thinned to two plants per hole after three weeks. Irrigation was administered every 7 to 10 days based on soil moisture and weather conditions. A basal dose of 30 m^3/ha of well-decomposed manure was incorporated, along with a single dose of 100 kg/ha of superphosphate (15.5% P_2O_5). Urea (46% N) was applied at a rate of 250 kg/ha in two equal splits. Data collection focused on important morphological and agronomic traits to evaluate the genotypic variation among the landraces. The measured traits included plant height (cm), recorded from the base to the apex of each plant, and the number of nodes per plant, determined by counting the total number of nodes on the main stem. Additionally, the total number of mature fruits produced by each plant was recorded. For fruit-related characteristics, fresh fruit weight (g) was measured immediately after harvest using a precision balance. Fruit length (cm) was measured from the stem end to the blossom end of each fruit, while fruit diameter (cm) was measured at the widest point. The length-to-diameter (L/D) ratio was also calculated to assess fruit shape uniformity across the genotypes.

2.3. Statistical analysis

The collected data were subjected to analysis of variance (ANOVA) using the Grapes 1.1.0 software package (Gopinath *et al*., 2021) to identify significant differences among the genotypes. The procedures for ANOVA followed the methods outlined by Gomez and Gomez (1984). To assess the extent of variation among the genotypes, the genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were calculated according to the formula proposed by Broad-sense heritability (H^2_b) was estimated using the method described by Johnson *et al*. (1955), based on the genetic model developed by Lush (1949), to determine the proportion of total phenotypic variance attributable to genetic factors. The genetic advance as a percentage of the mean was computed using the formula developed by Comstock and Robinson (1952), providing insight into the expected gain from selection. Interrelationships among traits and Pearson's correlation coefficients were calculated for all possible trait combinations, following the methodologies of Miller *et al.* (1958), Hanson *et al*. (1956), and Johnson *et al.* (1955). These correlations were further analysed to distinguish between direct and indirect effects through path coefficient analysis, allowing for a better understanding of the interrelationships among traits and their contributions to yield. This analysis was conducted according to the path analysis approach first introduced by Wright (1921, 1923) and later refined by Dewey and Lu (1959).

3. Results and Discussion

3.1. Traits variance components in snake melon

The coefficient of variation (CV%) (Table 1) provides crucial insight into the relative variability of each trait, allowing comparison across traits with different measurement scales. In snake melon, traits exhibit varying levels of variability, with fruit weight (CV=14.72%) and stem length (CV=10.13%) showing moderate to high relative variability, indicating that these traits naturally fluctuate more within the population. In contrast, the length-to-diameter ratio (CV=4.22%) displays very low variability, suggesting this trait is highly consistent across individuals with minimal inherent variation.

The phenotypic coefficient of variation (PCV%) reveals the total observable variation for each trait. High PCV values in fruit weight (47.95%) and number of fruits per plant (34.60%) demonstrate that these traits exhibit substantial phenotypic diversity, offering excellent potential for selection. The relatively lower but still significant PCV in fruit diameter (28.98%) and stem length (27.50%) indicates these traits also show meaningful variation that breeders could exploit. The exceptionally low PCV in length-to-diameter ratio (5.72%) confirms it as the most uniform trait with limited scope for improvement through conventional selection.

The genotypic coefficient of variation (GCV%) uncovers the genetic component underlying trait variability. The remarkably high GCV for fruit weight (45.63%) highlights exceptional genetic diversity, making this trait particularly responsive to breeding efforts. Similarly, the number of fruits per plant (32.63%) and stem length (25.57%) show strong genetic variation that breeders can capitalize on. The minimal GCV for length-to-diameter ratio (3.85%) reinforces previous findings that this trait has little genetic basis for improvement, suggesting it may be better addressed through alternative approaches like mutagenesis if modification is desired.

Table 1: Trait variance components in snake melon

Traits	CV (%)	PCV (%)	GCV (%)	Heritability	Genetic adv. (%)
Fruit weight (g)	14.72	47.95	45.63	0.91	89.46
Fruit diameter (cm)	11.03	28.98	26.79	0.86	51.04
Fruit length (cm)	14.28	28.98	25.23	0.76	45.20
Length/diameter ratio	4.22	5.72	3.85	0.46	5.35
Number of fruits per plant	11.51	34.60	32.63	0.89	63.40
Stem length (cm)	10.13	27.50	25.57	0.86	48.96
Number of nodes per plant	12.17	26.91	23.10	0.80	44.08

CV: Coefficient of variation**, PCV:** Phenotypic coefficient of variation, **GCV:** Genotypic coefficient of variation

3.2. Heritability and genetic advance (%)

Broad-sense heritability (H^2_b) estimates clarify the proportion of phenotypic variation attributable to genetic factors. The extremely high heritability of fruit weight (0.91) and number of fruits per plant (0.89) confirms that visual selection for these traits will be highly effective. Strong heritability in fruit diameter (0.86) and stem length (0.86) also promises a good selection response. The moderate heritability of fruit length (0.76) indicates some environmental influence, while the low heritability of length-to-diameter ratio (0.46) suggests it's predominantly environmentally controlled.

The expected genetic advance (GA%) predicts potential improvement from selection. The high GA% (89.46%) for fruit weight indicates potential for dramatic enhancement in just a few generations. Substantial GA% for the number of fruits per plant (63.40%) and stem length (48.96%) suggests these traits can be rapidly improved. The minimal GA % for length-to-diameter ratio (5.35%) confirms it as the most challenging trait to modify through conventional breeding.

These results provide a clear hierarchy of selection priorities. Fruit weight emerges as the premier target due to its exceptional genetic variability and heritability, followed by the number of fruits per plant and stem length. Traits with moderate values, like fruit diameter and number of nodes, represent secondary objectives. The length-to-diameter ratio, with its consistently low values across all parameters, may require different approaches if modification is essential. This analysis powerfully guides resource allocation in snake melon breeding programs, emphasizing traits with the greatest potential for genetic gain while identifying those needing alternative improvement strategies. The results obtained are consistent with previous studies of snake melon landraces and consistently highlight significant variability for morphological and fruit-related traits (Shtayeh *et al*., 2017; Abdel-Ghani and Mahadeen, 2014; Merheb *et al*., 2020; Singh *et al*., 2020). The genetic basis of fruit shape-related traits, such as the length-to-diameter ratio, is often reported as recessive (Jose *et al*., 2005). This explained the low CV%, GCV, and heritability scored by this trait.

3.3 Genotypic and phenotypic correlations among traits

The genotypic and phenotypic correlation analysis (Table 2) revealed strong positive associations between fruit weight and fruit diameter (0.947), fruit length (0.907), stem length (0.915), and number of nodes per plant (0.892). Fruit weight is an important characteristic studied in various melons, including snake melon, muskmelon, long melon, and oriental pickling melon. This trait is of great interest to growers and is crucial for efficient packing and transportation (Shtayeh *et al*., 2017; El-Magawry and El-Tahawey, 2023). Numerous studies highlight the correlations between fruit weight and several other traits, such as yield, fruit dimensions, seed characteristics, and plant vigour. Fruit weight is a valuable selection criterion for improving melon cultivars for different purposes. It is identified as a primary component contributing to yield in oriental pickling melon (Rakhi and Rajamony, 2005).

Table 2: Genotypic (above diagonal) and phenotypic (below diagonal) correlation coefficients among agronomic traits in snake melon.

Traits	Fruit weight (g)	Fruit diameter (cm)	Fruit length (cm)	Fruit Length/diameter ratio	Number of fruit per plant	Stem length (cm)	Number of nodes per plant
Fruit weight (g)	**1**	0.947**	0.907**	-0.683**	0.248	0.915**	0.892**
Fruit diameter (cm)	0.934**	**1**	0.990**	-0.550**	0.215	0.971**	0.984**
Fruit length (cm)	0.900**	0.972**	**1**	-0.425	0.275	1.006**	1.014**
Fruit Length/diameter ratio	-0.261	-0.235	-0.003	**1**	0.221	-0.291	-0.322
Number of fruits per plant	0.264	0.222	0.288	0.250	**1**	0.334	0.309
Stem length (cm)	0.905**	0.967**	0.978**	-0.066	0.339	**1**	0.994**
Number of nodes per plant	0.852**	0.963**	0.958**	-0.119	0.330	0.977**	**1**

Correlation coefficients were tested for significance at the 5% and 1% probability levels, and are marked with * and **, respectively.

Additionally, fruit weight and fruit yield per plant are positively correlated and are recommended as selection criteria for enhancing yield in melons (Taha *et al*., 2003; Babu *et al.,* 2013). In oriental pickling melons, fruit weight shows a significant correlation with both fruit length and fruit girth. This indicates that increasing fruit length contributes to higher fruit weight (Iathet and Piluek, 2006). In snake cucumbers, a moderate positive correlation exists between fruit weight and fruit length (El-Magawry and El-Tahawey, 2023). Lines of snake cucumber that have the highest fruit weight also show the highest fruit length and diameter (AbdRabou *et al.*, 2021). According to Taha *et al.* (2003), fruit weight is significantly correlated with plant length, suggesting that greater plant length and enhanced photosynthesis may contribute to larger fruit weights. This near-perfect genotypic correlation with high correlation values suggests pleiotropy or linkage between genes governing these traits, as observed in other melon cultivars (Yashiro *et al.,* 2005). The study by Monforte *et al.* (2004) identified quantitative trait loci (QTLs) on linkage groups II and V that simultaneously affect fruit weight, diameter, and length, suggesting pleiotropic control. A study by Eduardo *et al.* (2007) also found overlapping QTLs for fruit size traits in melons, supporting the idea that a shared genetic mechanism regulates these traits. Díaz *et al.* (2011) reported that dwarfing genes in melon influence both stem elongation and node production, indicating pleiotropic effects.

Fruit diameter and length (0.990**) imply that selection for one trait will likely enhance the other, which is advantageous for breeding programs targeting fruit size. Fruit diameter and length dimensions are crucial for defining fruit shape, contributing to fruit weight, and influencing overall yield. The relationship between fruit diameter (or width) and fruit length can vary significantly depending on the specific melon variety or species, indicating diverse fruit shapes. In one study on snake cucumber, a low positive correlation (0.21) was reported between fruit diameter and fruit length (El-Magawry and El-Tahawey 2023).

This study also reported a significant negative correlation between fruit weight and the length-to-diameter ratio (-0.683**). The length-to-diameter ratio is an important fruit descriptor that determines fruit shape. The results indicate that heavier fruits tend to be rounder rather than elongated. This aligns with previous studies on snake melon, where fruit shape and weight are often inversely related (Yetişir *et al*., 2008; El-Magawry and El-Tahawey, 2023). Weak correlations between the length-to-diameter ratio and other traits suggest it is governed by distinct genetic mechanisms, making it an independent selection criterion for fruit morphology.

3.4. Path coefficient analysis of traits influencing fruit number

Path coefficient analysis (Table 3) was performed to examine the direct and indirect effects of morphological traits on the number of fruits per plant, which is a key determinant of yield. Fruit diameter had the highest direct positive effect (6.491), followed by stem length (4.003). Similar findings were reported by Reddy *et al*. (2007) in snap melon concerning vine length and fruit diameter. In contrast, fruit weight, fruit length, and the number of nodes per plant showed negative direct effects (-0.651, -4.681, and -4.366, respectively), indicating that selecting for increased fruit weight, length, or number of nodes may inversely affect the number of fruits produced. However, these traits demonstrated a positive correlation with fruit number, suggesting strong compensatory indirect effects, particularly through fruit diameter (6.145) and stem length (3.663 and this reinforces their importance in yield improvement. A study on oriental pickling melon by Iathet and Piluek (2006) reported similar relatively low values for the direct effect of fruit length on yield per vine. The high residual effect suggests that while some of the studied traits (especially the number of nodes per plant and stem length) are useful for indirect selection, additional traits should be incorporated in future studies to better understand and predict fruit number. Incorporating more physiological, morphological, or molecular traits could improve model predictability and breeding efficiency.

Table 3: Direct effect, bold diagonal, and indirect effects on the number of fruits per plant in snake melon.

Trait	Fruit weight (g)	Fruit diameter (cm)	Fruit length (cm)	Fruit Length/ diameter ratio	Stem length (cm)	Number of nodes per plant	Gen. corr. with No of fruit per plant
Fruit weight (g)	**-0.651**	6.145	-4.248	-0.766	3.663	-3.895	0.248
Fruit diameter (cm)	-0.617	**6.491**	-4.634	-0.616	3.887	-4.295	0.215
Fruit length (cm)	-0.591	6.425	**-4.681**	-0.476	4.027	-4.429	0.275
Fruit Length/diameter ratio	0.446	-3.577	1.994	**1.119**	-1.168	1.408	0.221
Stem length (cm)	-0.596	6.303	-4.71	-0.326	**4.003**	-4.34	0.334
Number of nodes per plant	-0.581	6.386	-4.749	-0.361	3.98	**-4.366**	0.309

Residual effect value 0.8177

4. Conclusion

This study highlights fruit weight, number of fruits per plant, and stem length as key targets for genetic improvement in snake melon due to their high genotypic variability, heritability, and genetic advance. These traits also exhibit strong positive correlations with each other and with yield-related parameters, confirming their central role in productivity. In contrast, the length-to-diameter ratio showed low variability and broad-sense heritability, indicating limited potential for improvement via conventional selection. The high residual effect from path analysis also signals that yield is influenced by additional, unmeasured traits. Fruit weight stands out as the primary selection criterion, offering the highest response to selection. Breeding programs should prioritize multi-trait selection for fruit weight, diameter, and stem length, given their pleiotropic or linked genetic control. Future breeding should incorporate broader trait spectra, including physiological and molecular markers, to better capture the complexity of yield determination and maximize genetic gain.

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