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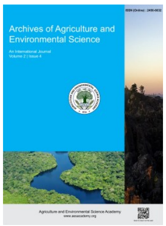

ORIGINAL RESEARCH ARTICLE

Morphological and genetic diversity of local Sudanese lines of snake melon (*Cucumis melo* var. *flexuosus*)

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ABSTRACT

Snake melon (*Cucumis melo* var. *flexuosus*), an underutilized cucurbit with nutritional and cultural significance, is widely cultivated in Sudan but lacks comprehensive morphological and genetic characterization. This study aimed to assess the morphological diversity and genetic relationships among seven Sudanese snake melon genotypes using standardized descriptors and Principal Component Analysis (PCA). Field experiments were conducted during the 2022 winter season in Khartoum North under arid-zone conditions. Both qualitative traits (fruit skin and flesh colour, shape, pubescence,) and quantitative traits (fruit number, weight, size, stem length, and node count) were recorded. Significant ($p<0.05$) morphological variation was observed among genotypes. Genotype HsD11644 exhibited the highest fruit weight (635.33 g), length (48.57 cm), and vegetative vigor (stem length 181.4 cm), while HsD11555, though compact (stem length 84.67 cm), produced the same number of fruits per plant (11.00) as HsD11644. PCA revealed that the first two principal components explained 97.1% of the total phenotypic variation, with PC_1 (81.96%) correlating strongly with fruit size and vegetative traits, and PC_2 (15.16%) with fruit number. The PCA biplot showed distinct clustering, effectively differentiating genotypes based on their trait profiles. This study provides the first integrated morphological and multivariate analysis of local snake melon lines in Sudan. The identified genetic variability will support the conservation and genetic enhancement of snake melon in Sudan and similar agro-ecological conditions.

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INTRODUCTION

The snake melon (*Cucumis melo* var. *flexuosus*), also known as the Armenian cucumber or yard-long cucumber, is a unique variety of melon cultivated and consumed as a vegetable. Unlike dessert melons, they are harvested at an immature stage and are prized for its crisp texture and mild, non-sweet flavour. It holds cultural and culinary significance across the Middle East and North Africa (MENA) region, where it is known by various local names that reflect its deep-rooted heritage. The crop spread particularly in Palestine, Lebanon, Syria, Iran, Jordan, Turkey, Egypt and Sudan. It is commonly called *Faqqus* in Palestine, Lebanon, and Syria; in Iraq and neighboring regions, it may be referred to as *Qitha'*; in Iran, *Khiar-e-sabz-e-deraz* ("long green cucumber"); in Turkey, *Acur*; in Sudan, *Ajjour*; and in Egypt, *Qitha' baladi* ("local cucumber"). These diverse vernacular names underscore the widespread use and cultural integration of the crop across the region. The origin of *Cucumis melo* is debated, some evidence suggests Africa as the center of origin due to the frequent occurrence of wild Cucumis species with the same basic chromosome number (n=12). The oldest findings of *Cucumis melo* seeds from Lower Egypt date to 3700–3500 BC. Wild types are commonly found in the Sudano-Sahelian area of Africa. The wild ancestors of *Cucumis melo*, including snake melon, seem to have been native to the region extending from Egypt to Iran and Northwest India (Endl *et al.*, 2018; Bezirganoglu, 2018; Pandey *et al.*, 2021). It is noted as an ancient crop in the Middle East and Middle Asia. It is also an important cucurbit crop in the Southeastern and Mediterranean regions of Turkey and is grown in pockets in India. In Sudan, snake melon holds a particularly important role in traditional vegetable farming, especially in the states of Khartoum, Gezira, and River Nile. It is grown in both the winter and autumn seasons, and farmers maintain a wide array of local varieties, particularly the '*baladi*' types—that display significant variation in fruit length, shape, skin texture and colour, as well as flesh colour. This morphological diversity represents a valuable genetic reservoir for crop improvement and the development of climate -resilient cultivars. The average yield in Sudan is approximately 20 tons per hectare (Mirghani & El Tahir, 1997).

Despite its deep-rooted cultural and agronomic relevance across the Middle East and North Africa (MENA), snake melon remains underutilized and under-researched. Most cultivars are landraces conserved by smallholder farmers, with limited scientific characterization or inclusion in formal breeding programs (Yousif *et al.*, 2011). This neglect is partly due to the lack of systematic morphological evaluation and genetic diversity assessments using advanced tools. Principal Component Analysis (PCA), a multivariate statistical method, is particularly valuable for unravelling complex trait interactions, reducing dimensionality, and identifying patterns of variation across genotypes. PCA enables breeders to capture and visualize genetic structure among accessions, supporting targeted selection and conservation. Therefore, a rigorous morphological assessment coupled with PCA can unlock the hidden potential of snake melon landraces for modern cultivar development, particularly in regions facing climate stress and resource scarcity (Mohammadi & Prasanna, 2003; Ali-Shtayeh *et al.*, 2017). This study aims to assess the morphological variation and genetic diversity among selected snake melon genotypes cultivated in Sudan, using standardized descriptors and multivariate statistical approaches. This study provides the first integrated morphological and multivariate characterization of Sudanese snake melon (*Cucumis melo* var. *flexuosus*), contributing novel insights to an area where scientific knowledge is notably scarce. By uncovering significant phenotypic diversity and genotype clustering among local lines, the research fills a critical gap in understanding this underutilized crop. The results are expected to support germplasm conservation efforts, guide parental selection for breeding programs, and facilitate the development of improved cultivars adapted to the agroecological conditions of Sudan, the African drylands, and the broader Middle East.

MATERIALS AND METHODS

The study was conducted during the 2022 winter season at the Faculty of Agriculture's demonstration plots, University of Al Zaeim Al Azhari at Khartoum North locality, a region characterized by minimal rainfall, daytime temperatures of 31.4–37.5°C, and 10–11 hours of sunshine daily. Seed sowing was carried out on November 6, 2022, the most productive period for snake melon (Cucumis melo var. flexuosus) cultivation in Sudan. Seven genotypes including, HsD11644, HsD11079, HsD11649, HsD11641, HsD18234, HsD15763, and HsD11555 were selected based on morphological diversity in fruit shape, color, flesh tone, and pubescence. The soil was ploughed twice, harrowed, levelled, and formed into 2 × 3 m ridges. Pre-irrigation was applied before sowing. Seeds were planted 50 cm apart with 3–4 seeds per hole at 2 cm depth, then thinned to two plants per hole after 2–3 weeks. Irrigation followed every 7–10 days based on soil and weather conditions. A basal dose of 30 m^3/ha of well-decomposed manure was incorporated, along with 100 kg/ha single dose superphosphate (15.5% P_2O_5). Urea (46% N) was applied at 250 kg/ha in two equal splits: two weeks after thinning and before fruit set. Data were collected on qualitative (fruit skin and flesh colour, shape, pubescence, hair density) and quantitative traits (fruit weight, length, diameter; number of fruits per plant; stem length; node count). Fruit traits were based on the average of 10 fruits, and plant traits from 5 randomly selected plants per plot, across three replications. Trait descriptors followed as per IPGRI (2003) for skin and flesh colour; a modified Stepansky *et al.* (1999) descriptors for hair density and Soltani *et al.* (2010) for fruit hairs. Data were analyzed using ANOVA via OPSTAT (Sheoran, 2010), following the approach of Gomez & Gomez (1984). Principal Component Analysis (PCA) was performed to assess trait divergence, variability, and genotype clustering, following the methodology of Pearson (1901) and Hotelling (1933).

RESULTS AND DISCUSSION

Morphological characterization

The morphological variation among the seven snake melon genotypes studied is summarized in Table 1. The assessment included qualitative descriptors such as fruit skin colour (primary and secondary), flesh colour, fruit shape, and hairiness and hair density. Green was the predominant fruit skin colour in six of the seven genotypes (85.71%), while white appeared in one genotype (HsD11649). Genotypes HsD11649, HsD11641, HsD18234 and HsD15763 exhibited white as a secondary colour, suggesting possible introgression from white-skinned genetic backgrounds or environmental influences during fruit development. Pale green was observed as a secondary colour in one genotype (HsD11555). Skin colour, specifically predominant fruit skin colour (PFSC) and secondary fruit skin colour (SFSC) are identified as principal characters for discriminating melon accessions in both Palestine and Lebanon as reported in Ali-Shtayeh *et al.* (2017) and Merheb *et al.* (2020), respectively. In the Palestine collection, the recognized phenotypic classes for predominant fruit skin colour (PFSC) include white and green. White PFSC was more predominant among all genotypes. Both authors reported three classes' including white, pale green, and green as Secondary Fruit Skin Color (SFSC). Snake melon skin colour, including its predominant hue, secondary colour, and pattern, is a fundamental morphological trait used to categorize and distinguish landraces and accessions.

Flesh colour varied from yellow-green to pale green, with yellow -green (3 genotypes), followed by pale green (3 genotypes), and white found only in HsD11649. This trait is important for consumer preference and potential nutritional value, especially as pale green and yellow-green flesh are often associated with different carotenoid content levels. A distinct variation in fruit shape was observed, with three genotypes (HsD11644, HsD11641 and HsD15763) exhibiting elongated cylindrical or curved (flexuous) shapes—morphotypes typical of traditional landraces in arid regions (Pitrat, 2008). The other four genotypes presented a straight to slightly curved shape, indicating a trend toward more uniform or commercially desirable types. Genotype HsD15763 had a unique curved (flexuous) form, which is often preferred in traditional markets but may be less suitable for mechanical harvest. In a broader collection of *Cucumis melo* genotypes, several studies have reported a wide variety of flesh colours. These include white and pale green (Ali-Shtayeh *et al*., 2017), green, creamish white, orange, and yellowish green (Singh *et al*., 2020), as well as yellow and brown from a collection in Jordan by Abdel-Ghani & Mahadeen (2014). In Palestine, specific landraces are associated with particular flesh colours, and accessions tend to cluster together based on fruit colour (Ali-Shtayeh *et al*., 2017). Moreover, different countries have varying consumer preferences regarding fruit flesh colour; for instance, in Sudan, the preferred colours are white to pale green.

Fruit pubescence showed notable diversity, with HsD11644 having no visible hair (glabrous), while all other genotypes exhibited the presence of hairs, mainly with dense hair density. Only HsD11079 showed medium density. The expression of fruit hairs and their density may be linked to genotype and environmental conditions and can affect pest resistance and post-harvest handling characteristics (Gillman *et al*., 1999). Glabrous or sparsely haired fruits like HsD11644 and HsD11079 may have enhanced market appeal but reduced resistance to sunburn or insect pressure. The analysis of qualitative traits is a fundamental aspect of characterizing and understanding the diversity within snake melon populations. These traits, alongside quantitative traits, provide crucial information for classification, conservation, and breeding efforts. This qualitative trait analysis highlights substantial genetic variability within the studied germplasm and reflects a valuable genetic base for selection in breeding programs. HsD11644, being glabrous and uniform in shape, could serve as a parent for improved commercial lines. The flexuous form of HsD15763 may be preserved in local cultivar development programs where traditional preferences dominate. Multivariate tools like PCA, along with these descriptors can significantly support genotype classification, parent selection, and improvement strategies for yield, quality, and adaptability.

Mean performance of genotypes

Indicated marked differences in genotype performance. HsD11644 emerged as the most vigorous and productive genotype, recording the highest values in fruit weight (635.33 g), fruit diameter (32.20 cm), fruit length (48.57 cm), number of fruits per plant (11.00), stem length (181.40 cm), and number of nodes per plant (28.50). In contrast, HsD11555 had the lowest values for most of these traits, yet notably matched HsD11644 in the number of fruits per plant (11.00), suggesting a high fruit count despite its small fruit size and shorter growth habit (Table 2). Other genotypes such as HsD11079 and HsD11641 demonstrated moderate performance across traits. The coefficient of variation across traits ranged from approximately 10 to 15%, indicating moderate phenotypic variability within the evaluated material.

Table 1. Morphological traits variation and character descriptors in snake melon genotypes.

Traits	Pre-Dominant fruit skin color	Secondary fruit skin color	Flesh color	Fruit shape	Fruit hairs	Hair density
HsD11644	Green	Green	Yellow green	Elongated Cylindrical	Absence	Spare
HsD11079	Green	Green	Yellow green	straight slightly curved	Sparse	Medium
HsD11649	White	white	white	straight or slightly curved	Presence	Dense
HsD11641	Green	white	Pale green	Elongated Cylindrical	Presence	Dense
HsD18234	Green	white	Pale green	straight or slightly curved	Presence	Dense
HsD15763	Green	white	Yellow green	Curved (Flexuous)	Presence	Dense
HsD11555	Green	Pale green	Pale green	straight or slightly curved	Presence	Dense

Table 2. Mean performance of genotypes yield and growth traits in snake melon genotypes.

Traits	Fruit weight (g)	Fruit diameter (cm)	Fruit length (cm)	Number of fruit per plant	Stem length (cm)	Number of nodes per plant
HsD11644	635.33^{a}	32.20^{a}	48.57^{a}	11.00^{a}	181.40^{a}	28.50^{a}
HsD11079	478.33^{b}	27.13^{b}	36.57^{bc}	6.33^{c}	130.267^{bc}	22.30^{bc}
HsD11649	243.33^{d}	18.73^{cd}	28.60^{cd}	8.67^{b}	104.63^{de}	17.67^{d}
HsD11641	356.67^{c}	27.43^{b}	41.97^{ab}	10.33^{ab}	151.00^{b}	26.23^{ab}
HsD18234	262.00^{d}	20.17^{c}	30.80^{c}	4.67^{c}	109.37^{cd}	17.93^{cd}
HsD15763	250.00^{d}	19.20^{c}	29.40^{cd}	5.33^{c}	110.00^{cd}	18.40^{cd}
HsD11555	186.67^{d}	14.40^{d}	21.97^{d}	11.00^{a}	84.67^{e}	14.00^{d}
Mean	344.62	22.75	33.98	8.19	124.48	20.72
Min	186.67	14.40	21.97	4.67	84.67	14.00
Max	635.33	32.20	48.57	11.00	181.40	28.50
CV	14.72	11.028	14.28	11.511	10.127	12.173
SE(d)	41.41	2.049	3.962	0.77	10.293	2.059
SE(m)	29.28	1.449	2.802	0.544	7.278	1.456
LSD 5%	90.23	4.46	8.633	1.677	22.426	4.487

Diversity and variability among genotypes

The principal component analysis presented in Tables 3 and 4, further clarified the structure of variation. The first principal component (PC1) recorded an Eigenvalue of (4.92) and it accounted for 81.96% of the total variance (Table 3.), with high contributions from fruit length, fruit diameter, stem length, number of nodes per plant and fruit weight, confirming its association with vegetative vigour and fruit size traits (Table 5). Similar higher values were recorded for the first principal component (PC1) by Ali-Shtayeh *et al.* (2017), and Merheb *et al.* (2020). The second principal component (PC2), explaining an additional 15.16% of the variance, was dominated almost exclusively by the number of fruits per plant, indicating its independence from the traits grouped in PC1. Together, PC1 and PC2 explained over 97% of the total variability among the genotypes. These findings are consistent with those reported by Ali-Shtayeh *et al.* (2017) and Yildiz *et al.* (2014). Correlation analysis, confirmed strong associations between PC1 and traits such as stem length (r = 0.993), fruit length (r = 0.991), fruit diameter (r = 0.985), number of nodes per plant (r = 986) and fruit weight (r = 0.94), while PC2 was closely linked to fruit number per plant (r = 0.936). Overall, the data show that genotypic differences in snake melon are well captured through both univariate performance metrics and multivariate techniques like PCA. The contrasting strengths of genotypes such as the large-fruited, vigorous HsD11644 versus the highly productive but compact HsD11555 genotype highlight the potential for selecting parent lines based on specific breeding objectives. The clear partitioning of traits between PCs suggests opportunities for designing complementary crosses that combine high fruit numbers with desirable fruit size and vegetative growth characteristics. Principal Component Analysis (PCA), particularly the first two components (PC1 and PC2), is widely used to identify genetically or phenotypically distinct groups in a simplified, interpretable form (Jolliffe & Cadima, 2016). The biplot based on principal component one (PC1) and principal component two (PC2) displays the spatial distribution of the accessions, revealing potential clustering patterns. PC1 and PC2 together explain the largest portion of the total variation in the dataset and are used to capture and visualize the main differences among genotypes. In Figure 1, accessions such as HsD11555, HsD11649, HsD15763, and HsD18234 cluster on the negative side of PC1 indicating they share similar traits contributing negatively to PC1. At the same time, HsD11844 is separated clearly from cluster one along the positive side of PC1, indicating contrasting trait profiles. Meanwhile, accessions like HsD11641 and HsD11079 are separated along PC2, further supporting variability along secondary traits.

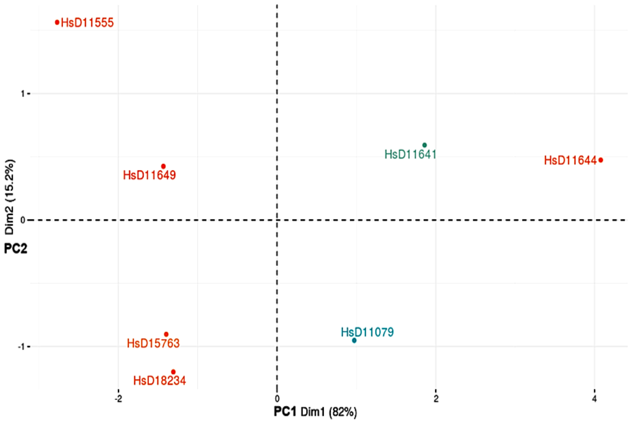

Figure 1. *Biplot using PC_1–PC_2 showing the spatial distribution of snake melon accessions.*

Table 3. Eigen values and percentage of variance.

Principle components	Eigenvalue	Percentage of variance	Cumulative percentage of variance
PC1	4.917	81.955	81.955
PC2	0.909	15.156	97.112
PC3	0.150	2.499	99.610
PC4	0.020	0.341	99.951
PC5	0.003	0.048	99.999
PC6	0	0.001	100.00

Table 4. Percent contribution of each of the variables on PCs.

Variables	PC1	PC2	PC3	PC4	PC5	PC6
Fruit weight (g)	17.97	0.86	72.152	1.413	2.505	5.1
Fruit diameter (cm)	19.746	2.115	0.167	45.451	7.635	24.885
Fruit length (cm)	19.975	0.543	7.153	3.943	43.791	24.595
Number of fruit per plant	2.502	96.38	0.267	0.548	0.291	0.012
Stem length (cm)	20.047	0.014	3.672	41.713	2.213	32.342
Number of nodes per plant	19.76	0.088	16.59	6.931	43.565	13.066

Table 5. Correlation between variables and PCs.

Variables	PC1	PC2	PC3	PC4	PC5	PC6
Fruit weight (g)	0.94	-0.088	0.329	-0.017	-0.008	0.001
Fruit diameter (cm)	0.985	-0.139	0.016	0.096	0.015	-0.003
Fruit length (cm)	0.991	-0.07	-0.104	-0.028	0.036	0.003
Number of fruit per plant	0.351	0.936	0.02	0.011	0.003	0
Stem length (cm)	0.993	-0.011	-0.074	-0.092	-0.008	-0.003
Number of nodes per plant	0.986	-0.028	-0.158	0.038	-0.035	0.002

Conclusion

This study revealed substantial morphological diversity among seven snake melon (*Cucumis melo* var. *flexuosus*) genotypes cultivated in Sudan. The combined use of standardized morphological descriptors and Principal Component Analysis (PCA) effectively distinguished genotypes based on key agronomic and qualitative traits. The clear partitioning of accessions, particularly along fruit size, vegetative vigour, and fruit number traits, highlights the presence of distinct phenotypic groups within the local germplasm pool. Genotype HsD11644 demonstrated superior fruit and vegetative characteristics, making it a strong candidate for use in breeding programs targeting yield and commercial quality. Conversely, HsD11555, with its compact growth and high fruit number, offers the potential for space-efficient or high-density cultivation systems. These contrasting attributes provide opportunities for designing complementary crosses that combine desirable fruit traits with adaptability to local growing conditions. The results underscore the value of PCA as a powerful tool in early-generation selection and genetic resource management. By enabling trait-based clustering, PCA facilitates the identification of genetically divergent parents, supports heterosis exploitation, and informs core collection development for future breeding efforts. Furthermore, the documented morphological variation serves as a foundation for on-farm conservation of traditional varieties and the integration of local landraces into formal breeding pipelines. This is particularly critical in the face of climate variability, where resilient, locally adapted cultivars are increasingly needed across arid and semi-arid agroecologies.

DECLARATIONS

Author contribution statement: Conceptualization: A.I.A. ; Methodology: A.I.A.; Software and validation: A.I.A, A.I.M.,M.M.I. and M.A; Formal analysis and investigation: A.I.A; Resources: A.I.A.; Data curation: A.I.A; Writing—original draft preparation: A.I.A; Writing—review and editing: A.I.A.; Visualization: A.I.A.; Supervision: A.I.A; Project administration: A.I.A; Funding acquisition: A.I.M., M.M.I., and M.I. All authors have read and agreed to the published version of the manuscript.

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