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Morphological characterization of long melon genotypes

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Abstract
A study was conducted to assess the genetic diversity of fifteen long melon genotypes collected from different parts of India, which were examined for variation in seventeen phenotypic characters during 2024-2025. Twelve characters such as predominant fruit skin colour, flesh colour, taste, fruit size, skin texture, ovary shape, seed weight, fruit ribbing, blossom end shape, placenta colour, fruit length width ratio and fruit hairiness were polymorphic, while the remaining traits were monomorphic. The variation observed among polymorphic traits indicates differing levels of morphological differentiation, with fruit length width ratio and fruit size showing the highest diversity. Overall, the diversity patterns underline the importance for trait based selection and provide valuable guidance for long melon germplasm improvement and breeding programmes.

Keywords: *Cucumis melo* var. *utilissimus*, diversity, long melon, fruit

Introduction
Melon (*Cucumis melo* L.), a member of the family Cucurbitaceae, is a highly diverse species exhibiting extensive morphological variation, particularly in fruit characteristics. The species encompasses numerous botanical varieties that differ widely in size, shape, flavour, texture and biochemical composition, making it one of the most polymorphic cultivated cucurbits (Fanourakis *et al.*, 2000; Forouzandeh *et al.*, 2010) [5, 6]. Within this complex species, long melon (*Cucumis melo* var. *utilissimus*) represents a distinct horticultural type, cytogenetically a diploid with chromosome number, 2n = 2x = 24. It is widely known by several vernacular names, such as tar, kakri, serpent melon, snake melon, oriental cucumber, snake cucumber and Armenian cucumber reflecting its elongated fruit form and diverse regional uses.

Long melon is considered as the second most important salad cucurbit after cucumber, valued for its tender texture, refreshing taste and culinary versatility. The genus *Cucumis* includes more than 50 species (Poonia *et al.*, 2025) [11] underscoring its taxonomic richness. However, classification within *C. melo* remains complex and sometimes ambiguous (Pitrat *et al.*, 2000); therefore, varieties such as *C. melo* var. *utilissimus* require precise morphological and taxonomic characterization to support accurate identification, breeding programmes and germplasm conservation (Poonia *et al.*, 2025) [11].

The phenotypic diversity of long melon was documented through several morphological descriptors, including fruit length, diameter, shape index, rind colour, surface texture, taste, and internal characteristics by Stepansky *et al.*, (1999) [13]. Despite this variability, reliance solely on external morphological traits is often insufficient for distinguishing closely related genotypes. The widespread adoption of high yielding commercial cultivars has accelerated the displacement of indigenous varieties, leading to the loss of valuable local diversity. In this context, the characterization and conservation of long melon genotypes are essential for sustainable utilization, varietal improvement and long term genetic resource management (Ali Shtayeh *et al.*, 2015) [2].

Long melon differs markedly from most cultivated melon types, which typically bear fruits with varied fruit length to width ratios. In many genotypes, fruits grow beyond 50 cm in length and around 5 cm in diameter and immature fruits may appear light green, dark green, or variegated (Merheb *et al.*, 2020) [9] with different depths of ribbing. This pronounced morphological diversity further highlights the genetic complexity and adaptive potential of the variety.

Systematic research on the phenotypic characterization of long melon is limited and remains relatively scarce. A comprehensive evaluation of the morphological variability among long melon genotypes is essential to enhance their utility in breeding and conservation. The present study aimed to assess morphological diversity among fifteen long melon genotypes and to analyse the diversity of the key morphological traits.

Materials and Methods

The study comprised evaluation of fifteen long melon genotypes collected from various sources during 2024-2025. A comprehensive set of morphological data was recorded, including traits of flowers, stems, fruits, and seeds. The descriptor list used for this study was based on the predefined morphological characters for melons outlined by Stepansky *et al.* (1999) [13], the International Plant Genetic Resources Institute (IPGRI, 2003) [8] and Soltani (2010) [6]. These descriptors were refined and applied to characterise long melon genotypes, assessing seventeen morphological traits (Table 1).

Observations of the characters were recorded from ten plants in the field evaluation study. The immature fruits were harvested from each genotype and the following traits were scored which included fruit shape, fruit length from stem end to blossom end, width at the broadest point, predominant skin colour (covering the largest surface area of the fruit), skin texture, fruit flesh colour, taste, fruit weight and the presence or absence of fruit hair.

For the floral data, five plants from each genotype were evaluated for sex type and ovary shape. For stem characterization, hair density was recorded. The genotypes were also harvested upon maturity at which seeds were extracted from the mature fruits and recorded hundred seed weight and number of seeds per fruit.

Table 1: Morphological characters measured in long melon genotypes

S. No	Character code	Character	Descriptive value	Reference
1	PFSC	Predominant fruit skin colour	1. White 2. Light-yellow 3. Cream 4. Pale green 5. Green 6. Dark green 7. Blackish-green	IPGRI (2003) [8]
2	FC	Flesh colour	1. White 2. Pale green	Stepansky *et al.*, (1999) [13]
3	T	Taste	1. Non sweet 2. Sweet	Stepansky *et al.*, (1999) [13]
4	FS	Fruit size	1. <100 g 2. 100-150 g 3. 150-200 g	IPGRI (2003) [8]
5	FLWR	Fruit length and width ratio	1. <15 cm 2. 15-20 cm 3. >20 cm	IPGRI (2003) [8]
6	FSH	Fruit shape	1. Oblate 2. Elongate	IPGRI (2003) [8]
7	ST	Skin texture	1. Wrinkled 2. Ribbed	Stepansky *et al.*, (1999) [13]
8	FH	Fruit hairs	1. Presence 2. Absence	Soltani (2010) [6]
9	STY	Sex type	1. Monoecious 2. Andromonoecious	Stepansky *et al.*, (1999) [13]
10	OS	Ovary shape	1. Flat 2. Round 3. Long 4. Very long	IPGRI (2003) [8]
11	HD	Hair density	1. Sparse 2. Medium 3. Dense	Stepansky *et al.*, (1999) [13]
12	SW	Seed weight	1. 1.0-2.0 g 2. 2.1-3.0 g 3. 3.1-4.0 g	IPGRI (2003) [8]
13	FR	Fruit ribbing	1. 3-Superficial 2. 5-Intermediate 3. 7-Deep	IPGRI (2003) [8]
14	BES	Blossom end shape	1. Depressed 2. Flattened 3. Rounded 4. Pointed	IPGRI (2003) [8]
15	FB	Flesh bitterness	1. Low bitterness 2. Intermediate 3. 7-High bitterness	IPGRI (2003) [8]
16	PC	Placenta colour	1. White 2. Green 3. Yellow 4. Orange (yellow-red) 5. Salmon (pink-red) 6. 99-Other	IPGRI (2003) [8]
17	NSPF	Number of seeds per fruit	1. Low (< 10) 2. Intermediate (10-100) 3. High (> 100)	IPGRI (2003) [8]

Results and Discussion

The assessment of the data revealed that out of the seventeen traits studied, five were monomorphic and twelve were polymorphic (Table 2).

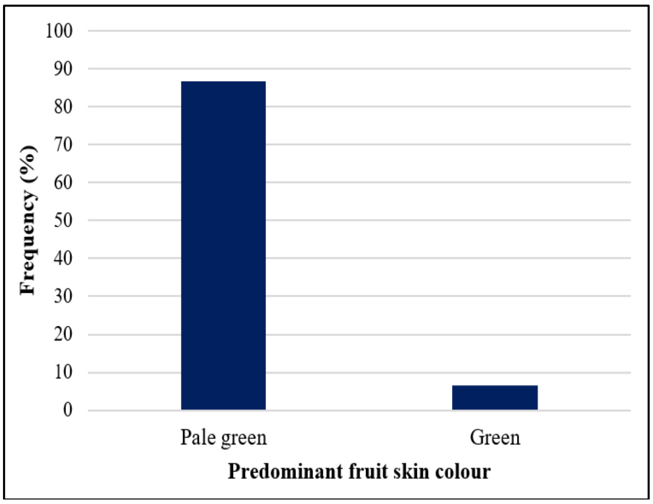
Five traits such as fruit shape, sex type, flesh bitterness, number of seeds per fruit and stem hair density were monomorphic, showing uniform expression across all accessions. Fruit shape was consistently elongate across all the genotypes and sex type was uniformly monoecious with sparse stem hair density. The characters like flesh bitterness and seed number per fruit were also largely uniform, with all genotypes exhibiting low bitterness and high seed count. These consistent patterns highlight strong monomorphism for the morphological traits within the collected materials. These stable traits are commonly reported in *Cucumis melo* subsp. *flexuosus*, where elongated fruit shape, ribbed skin, monoecious sex type, and pubescent ovaries represent stable diagnostic features of the group (Stepansky *et al.*, 1999; IPGRI, 2003) [13, 8]. Similarly, the uniform expression of low flesh bitterness and high seed number per fruit aligns with earlier observations in snake melon landraces, which tend to maintain stable qualitative traits under farmer selection (Soltani *et al.*, 2010) [6].

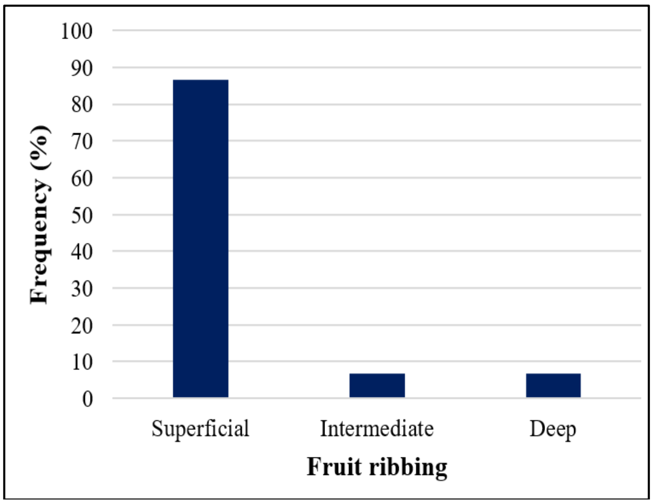
The polymorphic qualitative traits including predominant fruit skin colour, flesh colour, taste, fruit size, skin texture, ovary shape, seed weight, fruit ribbing, blossom end shape, placenta colour, fruit length: width ratio, and fruit hairiness were exhibited measurable diversity, with overall phenotypic variation being substantial, reflecting broad variability among the studied genotypes. Within these traits, the white and pale green skin colour with predominantly ribbed and non sweet pale green fleshed fruits appeared most frequently. Similarly, the ovary shape remained long or very long in most of the genotypes.

The study recorded that the predominant fruit skin colour showed greater variability. Three distinct classes such as white, pale green and green were reported for this trait. Among these, the pale green colour was the most common across the genotypes (86.67%), while green colour fruit with intermediate ribbing was observed only in LM 3 among the genotypes (6.67%). Comparable diversity in fruit skin pigmentation has been reported in Middle Eastern snake melon collections, where white and pale green colours dominate regional landraces (Stepansky *et al.*, 1999) [13]. The pale green colour flesh non sweet fruits was dominant among the genotypes.

Fruit length to width ratio (FLWR) showed substantial variation, with three distinct classes. This degree of size and proportion variability aligns with the results of Staub *et al.* (2004) [12], who reported wide variation in fruit dimensions among Greek snake melon accessions. The shortest fruits belonging to Class 0 were the least frequent. Class 1 was predominant, representing nearly half of the accessions, while Class 2 accounted for a moderate proportion of genotypes. Most of the genotypes had fruit weight ranging from 150 g to 250 g with rounded blossom end shape. Among the 15 genotypes, placenta colour ranged from white to yellow, and white placenta colour was observed more frequently. Similar patterns of morphological variation in snake melon accessions have been documented in Greece (Staub *et al.*, 2004) [12] and Jordan (Abdel-Ghani and Mahadeen, 2014) [1], where traditional landraces exhibit broad phenotypic ranges due to natural cross-pollination and limited breeding for uniformity.

Fruit weight (150 g-250 g range) and blossom end shape also exhibited moderate diversity, mirroring patterns documented in Palestinian and Middle Eastern collections (Stepansky *et al.*, 1999; Soltani *et al.*, 2010) [13, 6]. Placenta colour ranged from white to yellow, with white being more common; variation in internal fruit colour traits has likewise been reported as moderately polymorphic in multiple studies on *C. melo* landraces.





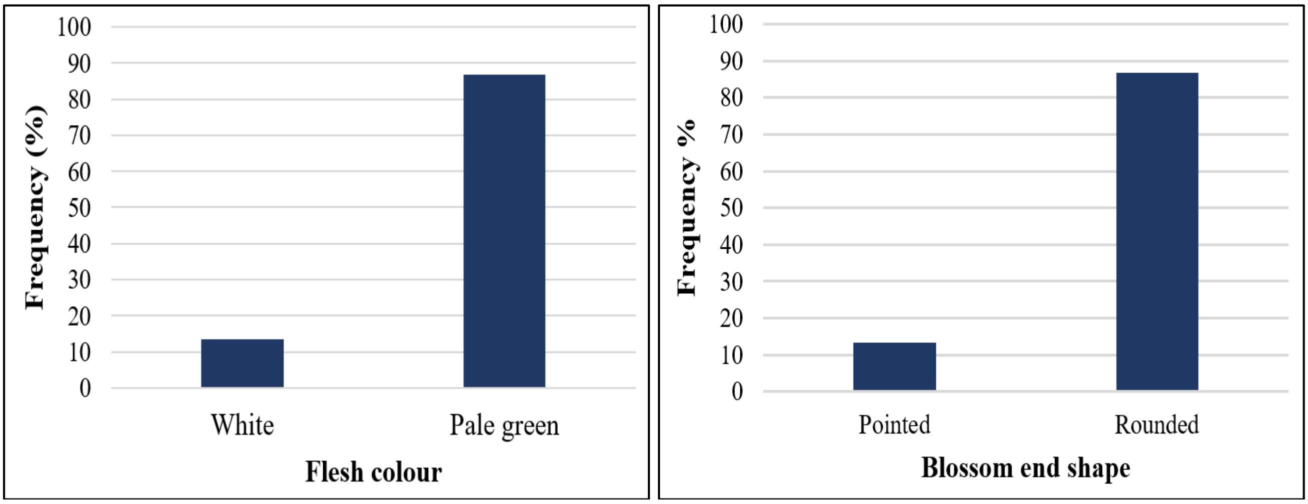


Fig 1: Frequency distribution for fruit related traits recorded from the long melon genotypes

Table 2: Morphological characters of long melon genotypes evaluated

Genotypes	Predominant fruit skin colour	Flesh colour	Taste	Fruit size	Fruit length and width ratio	Fruit shape	Skin texture	Fruit hairs
LM 1	Pale green	Pale green	Non sweet	1	1	Elongate	Ribbed	Presence
LM 2	Pale green	Pale green	Non sweet	2	3	Elongate	Ribbed	Absence
LM 3	Green	White	Non sweet	3	2	Elongate	Ribbed	Absence
LM 4	Pale green	Pale green	Non sweet	3	3	Elongate	Ribbed	Presence
LM 5	Pale green	Pale green	Non sweet	3	3	Elongate	Ribbed	Absence
LM 6	Pale green	Pale green	Sweet	2	2	Elongate	Ribbed	Presence
LM 7	Pale green	Pale green	Non sweet	3	1	Elongate	Ribbed	Presence
LM 8	Pale green	White	Non sweet	3	1	Elongate	Wrinkled	Absence
LM 9	Pale green	Pale green	Non sweet	3	2	Elongate	Ribbed	Absence
LM 10	Pale green	Pale green	Non sweet	3	2	Elongate	Ribbed	Absence
LM 11	Pale green	Pale green	Sweet	3	2	Elongate	Ribbed	Absence
LM 12	Pale green	Pale green	Non sweet	2	1	Elongate	Ribbed	Absence
LM 13	Pale green	Pale green	Non sweet	3	1	Elongate	Ribbed	Absence
LM 14	Pale green	Pale green	Non sweet	3	1	Elongate	Ribbed	Absence
LM 15	Pale green	Pale green	Non sweet	3	2	Elongate	Ribbed	Absence

Table 2: Morphological characters of long melon genotypes evaluated (continued)

Genotypes	Sex type	Ovary shape	Hair density	Seed weight	Fruit ribbing	Blossom end shape	Flesh bitterness	Placenta colour	Number of seeds per fruit
LM 1	Monoecious	Long	Sparse	1	Superficial	Pointed	Low bitterness	White	High
LM 2	Monoecious	Long	Sparse	1	Superficial	Rounded	Low bitterness	White	High
LM 3	Monoecious	Long	Sparse	1	Intermediate	Rounded	Low bitterness	White	High
LM 4	Monoecious	Long	Sparse	1	Superficial	Rounded	Low bitterness	White	High
LM 5	Monoecious	Long	Sparse	1	Superficial	Rounded	Low bitterness	White	High
LM 6	Monoecious	Very long	Sparse	1	Superficial	Rounded	Low bitterness	White	High
LM 7	Monoecious	Long	Sparse	1	Superficial	Rounded	Low bitterness	Yellow	High
LM 8	Monoecious	Long	Sparse	1	Superficial	Rounded	Low bitterness	White	High
LM 9	Monoecious	Long	Sparse	2	Superficial	Rounded	Low bitterness	White	High
LM 10	Monoecious	Long	Sparse	1	Superficial	Rounded	Low bitterness	Yellow	High
LM 11	Monoecious	Very long	Sparse	2	Intermediate	Pointed	Low bitterness	Yellow	High
LM 12	Monoecious	Long	Sparse	1	Superficial	Rounded	Low bitterness	White	High
LM 13	Monoecious	Long	Sparse	1	Deep	Rounded	Low bitterness	White	High
LM 14	Monoecious	Long	Sparse	1	Superficial	Rounded	Low bitterness	White	High
LM 15	Monoecious	Long	Sparse	2	Superficial	Rounded	Low bitterness	White	High

Conclusion

The study revealed a combination of highly uniform and markedly variable traits among the long melon genotypes. The traits such as fruit shape, sex type, flesh bitterness, seed number per fruit and stem hair density were predominantly monomorphic, indicating a high degree of genetic uniformity. In contrast, traits including predominant skin colour, flesh colour, taste, fruit size, seed weight, ribbing, skin texture, placenta colour, ovary shape, and the fruit length: width ratio exhibited substantial polymorphism. Overall, the long melon genotypes demonstrated considerable phenotypic diversity, providing meaningful variability for selection, facilitating the identification of promising parental lines, and guiding future breeding strategies for crop improvement.

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