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S1 melon characterization

Article

Morphological characterization of first selfing generation melon (*Cucumis melo* L.) genotypes

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Abstract

The first selfing generation (S1) in melon breeding may still exhibit phenotypic variation because the materials are not yet genetically fixed. Morphological characterization at this stage is therefore useful to document visible variation before further evaluation in later generations. This study characterized qualitative and quantitative morphological traits of ten S1 melon genotypes. The experiment was conducted from May to August 2025 under greenhouse and laboratory conditions, using a Completely Randomized Design with 10 genotypes and 3 replications. Qualitative traits were characterized using melon descriptors, while quantitative traits were analyzed using analysis of variance followed by the Honestly Significant Difference test at the 5% level. Representative external and internal images of fruit were used to support visual documentation. The evaluated genotypes showed variation in fruit shape, fruit base and apex shape, rind ground color, groove and netting characteristics, flesh color, and seed color. Significant differences among genotypes were observed for internode length, leaf blade area, fruit harvest age, fruit diameter, fruit length, fruit weight, and flesh thickness. These findings show that the evaluated S1 melon genotypes remained phenotypically variable and require further evaluation in later selfing generations.

Keywords: *Cucumis melo*; fruit morphology; morphological characterization; phenotypic variation; S1 generation.

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1. Introduction

Melon (*Cucumis melo* L.) is an important horticultural crop with wide variation in fruit morphology, quality, and consumer preference. Melon fruit may differ in shape, rind color, rind texture, netting pattern, flesh color, and sweetness (Herwibawa et al., 2026). This diversity makes melon an important crop for breeding and cultivar development (Chikh-Rouhou et al., 2021a; Xu et al., 2022). In melon breeding, self-pollination is commonly used to develop more uniform breeding materials over successive generations. During repeated selfing, heterozygosity is gradually reduced and homozygosity increases (Maitan et al., 2025). However, the first selfing generation remains an early-generation line and should not be considered a stable or fixed line. At this stage, plants may still show considerable phenotypic variation because segregation may continue. Therefore, evaluation of early generation materials is more appropriately used to document morphological

variation and identify materials that require further evaluation in later generations (Bokmeyer et al., 2009; Akpertey et al., 2022).

Morphological characterization is an important initial step in evaluating early-generation breeding materials (Akdogan et al., 2025). Qualitative traits, such as leaf shape, lobe development, flower sex expression, fruit shape, rind color, groove characteristics, netting pattern, flesh color, seed shape, and seed color, can provide visible information on phenotypic differences among genotypes. Quantitative traits, such as internode length, flowering time, leaf area, harvest age, fruit diameter, fruit length, fruit weight, flesh thickness, soluble solids content, and seed weight, can further describe vegetative growth, reproductive development, and fruit-related performance. In early selfing generations, morphological data should be interpreted cautiously. Observed differences among S1 genotypes describe phenotypic variation under the tested conditions and should not be directly interpreted as line stability, genetic distance, or final breeding value. Additional evaluation in subsequent selfing generations and, where necessary, across environments is required before stable lines or superior breeding materials can be confirmed. This study aimed to characterize qualitative and quantitative morphological traits of 10 first selfing-generation melon genotypes. Representative external and internal fruit images were also included to visually document fruit morphological variation among the evaluated S1 materials. The information obtained from this study is expected to provide a descriptive basis for further selection, breeding, and evaluation in later generations.

2. Materials and Methods

2.1. Study site and plant materials

The study was conducted from May to August 2025 in a greenhouse at H. Moenadi State Vocational High School, West Ungaran District, Semarang (7°06'42.8"S 110°24'50.0"E) and at the Laboratory of Plant Physiology and Breeding, Universitas Diponegoro, Semarang. The plant materials consisted of ten first selfing generation melon genotypes, namely S1_AC, S1_AP, S1_D1, S1_GR, S1_GT, S1_IN, S1_LV, S1_MD, S1_RC, and S1_SN. These genotypes were obtained from the melon breeding collection of the Laboratory of Plant Physiology and Breeding. Because the materials were still in the first selfing generation, they were treated as early-generation breeding materials rather than fixed or stable inbred lines. Cultivation materials included melon seeds, peat moss, planting media consisting of soil, compost, and rice husk in a 1:1:1 ratio, polybags, fertilizers, fungicides, bactericides, and insecticides. Standard greenhouse and laboratory equipment were used for seedling preparation, transplanting, crop maintenance, manual self-pollination, fruit harvesting, seed extraction, and morphological measurements.

2.2. Experimental design

The experiment was arranged in a Completely Randomized Design with genotype as the treatment factor. The experiment consisted of 10 S1 melon genotypes with 3 replications, yielding 30 experimental units. Each experimental unit consisted of one plant. The design was used to support descriptive comparison of morphological traits among genotypes under the tested greenhouse conditions. Because each experimental unit consisted of a single plant and the study was conducted in a single environment, the results were interpreted as preliminary phenotypic information rather than as confirmation of line stability or breeding value.

2.3. Crop management and self-pollination

Melon seeds were germinated before transplanting. Seedlings were transplanted into polybags at 21 days after sowing. Crop management was conducted under greenhouse conditions and included irrigation, fertilization, pruning, training, weed control, and pest

and disease management, in accordance with standard melon cultivation practices. Manual self-pollination was performed by transferring pollen from male flowers to the stigma of female or hermaphroditic flowers on the same plant. Pollinated flowers were observed to confirm fruit set. Fruits were harvested at physiological maturity based on external maturity indicators, including rind appearance, net development, cracking near the fruit stalk, and fruit aroma. After harvest, the fruits were used for morphological observation and seed extraction. Seeds produced from the evaluated S1 plants were considered seeds of the next selfed generation and were used only for seed-related observations, including seed shape, seed color, and 100-seed weight.

2.4. Morphological characterization

Morphological characterization was conducted using qualitative and quantitative traits. Qualitative traits were recorded visually using melon descriptor-based characterization according to IPGRI and UPOV descriptors. The qualitative traits included leaf shape, lobe development, terminal lobe length, flower sex expression, fruit longitudinal shape, fruit base shape, fruit apex shape, position of maximum fruit diameter, rind ground color, fruit groove color, fruit groove depth, fruit groove width, fruit netting pattern, netting thickness, netting density, main flesh color, seed shape, and seed color. Quantitative traits included internode length, male flower emergence, female flower emergence, fruit harvest age, leaf blade area, stem thickness, fruit diameter, fruit length, fruit weight per fruit, flesh thickness, soluble solids content, and 100-seed weight. Leaf blade area was measured using ImageJ. Stem thickness was measured on the main stem between the 10th and 11th nodes. Fruit diameter, fruit length, fruit weight, and flesh thickness were measured at harvest. Soluble solids content was measured from fruit juice using a refractometer and expressed as °Brix. The 100-seed weight was measured from cleaned and dried seeds produced by the evaluated S1 plants. Representative external and internal fruit images were documented to support morphological characterization based on descriptors.

2.5. Data analysis

Qualitative traits were summarized descriptively based on descriptor states observed in each replication. Descriptor data were presented by genotype and replication to show within-genotype variation when different descriptor states were observed among replications. Missing observations were indicated using a dash. Quantitative traits were summarized as genotype means. Analysis of variance was conducted using a Completely Randomized Design to determine whether quantitative traits differed among genotypes under the tested conditions. The statistical model was:

$$Y_{ij} = \mu + G_i + \varepsilon_{ij}$$

where Y_{ij} is the observed value of the *i*-th genotype in the *j*-th replication, μ is the overall mean, G_i is the effect of the i-th genotype, and ε_{ij} is the experimental error. When genotype effects were significant, mean comparisons were performed using the Honestly Significant Difference test at the 5% significance level. Descriptive summaries and statistical analyses were conducted using R version 4.6.0 (R Core Team, Vienna, Austria; https://www.r-project.org/). Leaf blade area was measured using ImageJ (National Institutes of Health, USA; https://imagej.net/ij/). All statistical results were interpreted as phenotypic differences among S1 genotypes within a single greenhouse environment. No inference was made regarding genetic distance, kinship, line stability, or final breeding value.

3. Results

3.1. Qualitative morphological variation

The ten S1 melon genotypes showed visible variation in external and internal fruit morphology (Figure 1; Table 1). External fruit variation was mainly observed in fruit longitudinal shape, fruit base and apex shape, rind ground color, groove characteristics, and netting pattern. Fruit longitudinal shape varied among oblate, obvate, medium elliptic, broad elliptic, and circular. Several genotypes, including S1_AC, S1_AP, S1_GT, S1_IN, and S1_RC, consistently showed an oblate fruit shape across replications, whereas S1_D1, S1_GR, and S1_LV showed variation among replications. S1_MD showed a consistent medium elliptic shape, while S1_SN showed an obvate shape in the available observations.

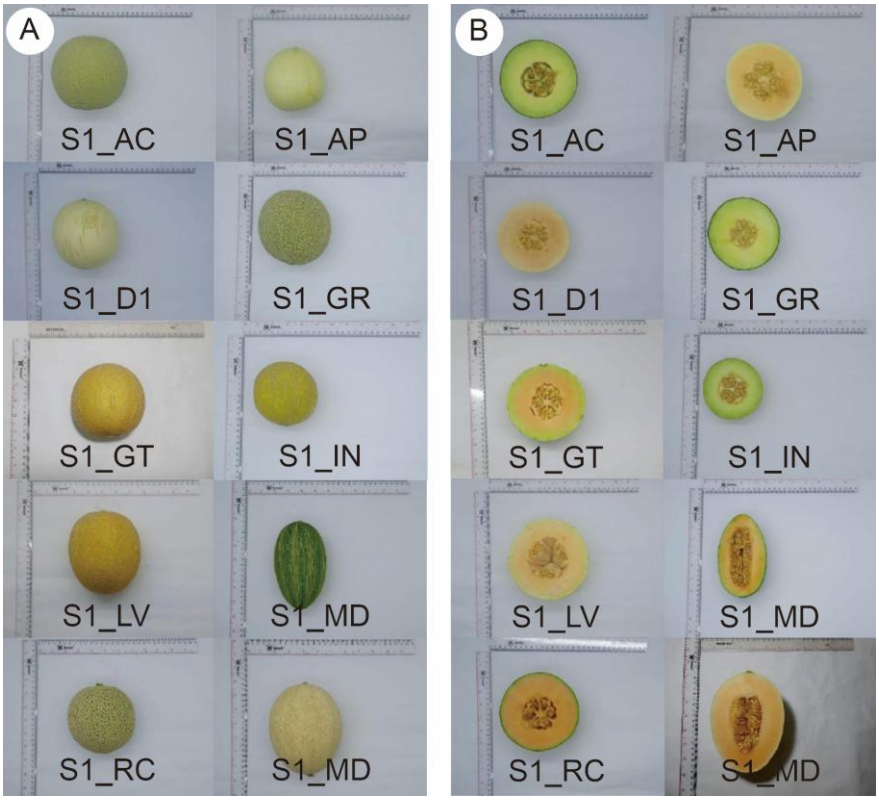

Figure 1. Representative fruit morphology of ten S1 melon genotypes. (A) External fruit morphology showing variation in fruit shape, rind color, groove pattern, and netting characteristics. (B) Internal fruit morphology showing variation in flesh color, flesh thickness, and seed cavity appearance. Images represent selected fruits.

Variation was also observed in fruit base and apex shape. Truncate base and apex were common in S1_AC, S1_GT, S1_IN, and S1_RC, while S1_MD had a rounded fruit base and pointed fruit apex. S1_LV and S1_SN generally showed rounded fruit apexes, whereas S1_D1 and S1_GR showed variation in fruit base or apex shape among replications. The position of maximum fruit diameter was mostly located in the middle of the fruit, except for S1_MD, which consistently showed the maximum diameter toward the stem end. Rind ground color varied among greenish, greyish, whitish, yellowish, and ochre. S1_IN and S1_LV showed ochre rind color in most observations, while S1_AP and S1_SN were whitish. Groove characters were absent in most genotypes, but groove color, depth, and width were observed in S1_AC, S1_AP, and S1_D1. Netting characters also differed among genotypes, ranging from linear only to linear and netted or netted only. S1_AC consistently showed a netted-only fruit surface with medium netting thickness and very dense netting density, while S1_MD showed linear-only netting with mostly very

sparse density. Flesh color varied among greenish white, green, yellowish white, orange, and greenish orange. Seed color varied between whitish and cream yellow, while seed shape was uniform as a pine-nut shape in all available observations.

Table 1. Qualitative fruit and seed morphological descriptors of ten S1 melon genotypes..

Genotypes	Rep	FLS	FBS	FAS	PFD	RGC	GC	GD	GW	NP	NT	ND	FC	SC
S1_AC	R1	Ob	T	T	Mid	Gn	Gr	VS	Wi	NO	Med	VD	GWht	CY
	R2	Ob	T	T	Mid	Gn	A	A	A	NO	Med	VD	GWht	CY
	R3	Ob	T	T	Mid	Gy	A	A	A	NO	Med	VD	GWht	CY
S1_AP	R1	Ob	T	T	Mid	Wt	A	A	A	LO	VT	Sp	YW	Wt
	R2	Ob	T	T	Mid	Wt	Wh	VS	Med	A	A	A	YW	Wt
	R3	Ob	R	T	Mid	Wt	Wh	S	Med	A	A	A	YW	Wt
S1_D1	R1	BE	R	T	Mid	Wt	Wh	VS	N	LO	VT	VSp	YW	Wt
	R2	Ob	T	T	Mid	Wt	Wh	VS	N	LN	Tn	VSp	YW	CY
	R3	Ob	T	T	Mid	Wt	Wh	S	N	DO	Tn	VSp	YW	CY
S1_GR	R1	Ob	T	T	Mid	Gy	A	A	A	NO	Med	VD	GO	CY
	R2	Ov	T	R	SE	Y	A	A	A	LN	Tn	D	GWht	CY
	R3	Ob	T	T	Mid	Gn	A	A	A	NO	Tn	VD	Gr	Wt
S1_GT	R1	Ob	T	T	Mid	Y	A	A	A	LN	Tn	Med	GO	Wt
	R2	Ob	T	T	Mid	Y	A	A	A	NO	Tn	D	GO	CY
	R3	Ob	T	T	Mid	Y	A	A	A	LN	Tn	Med	GO	Wt
S1_IN	R1	Ob	T	T	Mid	Oc	A	A	A	NO	Tk	VD	GWht	CY
	R2	Ob	T	T	Mid	Oc	A	A	A	LN	Tk	D	GWht	CY
	R3	Ob	T	T	Mid	Oc	A	A	A	NO	Tk	VD	Gr	CY
S1_LV	R1	C	R	R	Mid	Oc	A	A	A	LO	Tn	VSp	Or	CY
	R2	BE	T	R	SE	Oc	A	A	A	NO	Med	D	YW	CY
	R3	C	R	R	Mid	Y	A	A	A	LN	VTk	VSp	YW	CY
S1_MD	R1	ME	R	P	SE	Gn	A	A	A	LO	VT	VSp	GO	CY
	R2	ME	R	P	SE	Gn	A	A	A	LO	Tk	Med	GO	CY
	R3	ME	R	P	SE	Gn	A	A	A	LO	VT	VSp	GO	CY
S1_RC	R1	Ob	T	T	Mid	Gy	A	A	A	LN	Tk	VD	GO	Wt
	R2	Ob	T	T	Mid	Gn	A	A	A	NO	VTk	VD	GO	CY
	R3	Ob	T	T	Mid	Gn	A	A	A	NO	VTk	VD	GO	CY
S1_SN	R1	–	–	–	–	–	–	–	–	–	–	–	–	–
	R2	Ov	R	R	Mid	Wt	A	A	A	LN	Tn	D	YW	CY
	R3	Ov	R	R	Mid	Wt	A	A	A	NO	Tn	VD	YW	CY

Rep., replication; R1, first replication; R2, second replication; R3, third replication. "–" indicates unavailable observation. FLS, fruit longitudinal shape; FBS, fruit base shape; FAS, fruit apex shape; PFD, position of maximum fruit diameter; RGC, rind ground color; GC, groove color; GD, groove depth; GW, groove width; NP, netting pattern; NT, netting thickness; ND, netting density; FC, flesh color; SC, seed color. Seed shape was uniform as pine-nut shape in all available observations and is not shown. Abbreviations: A, absent; BE, broad elliptic; C, circular; CY, cream yellow; D, dense; DO, dots only; Gn, greenish; Gr, green; GO, greenish orange; GWht, greenish white; Gy, greyish; LN, linear and netted; LO, linear only; Med, medium; ME, medium elliptic; Mid, middle; N, narrow; NO, netted only; Ob, oblate; Oc, ochre; Or, orange; Ov, obvate; P, pointed; R, rounded; S, shallow; SE, toward stem end; Sp, sparse; T, truncate; Tk, thick; Tn, thin; VD, very dense; VS, very shallow; VSp, very sparse; VT, very thin; VTk, very thick; Wh, white; Wt, whitish; Wi, wide; Y, yellowish; YW, yellowish white.

3.2. Quantitative morphological variation

The quantitative traits of the ten S1 melon genotypes are presented in Table 2. Significant differences among genotypes were observed for internode length, leaf blade area,

fruit harvest age, fruit diameter, fruit length, fruit weight, and flesh thickness. In contrast, stem thickness, male flower emergence, female flower emergence, soluble solids content, and 100-seed weight did not differ significantly among genotypes under the tested conditions. These results indicate that the main quantitative variation among the evaluated S1 genotypes was associated with vegetative growth and fruit-related traits. Internode length ranged from 6.80 to 12.70 cm. S1_D1 and S1_AP had the longest internodes, whereas S1_IN had the shortest internodes. Leaf blade area ranged from 183.91 to 410.99, with the highest values observed in S1_D1 and S1_AC and the lowest value in S1_IN. Fruit harvest age varied from 40.00 to 65.33 days after planting. S1_MD showed the earliest harvest age, whereas S1_GR showed the latest harvest age. Fruit-related traits showed clear variation among genotypes. Fruit diameter ranged from 28.07 to 41.90, with the highest value in S1_GR and the lowest value in S1_MD. Fruit length ranged from 8.82 to 15.05, with S1_SN showing the longest fruit and S1_IN the shortest. Fruit weight ranged from 441.38 to 1204.16 g, with S1_GR having the highest mean fruit weight and S1_MD the lowest. Flesh thickness ranged from 1.95 to 3.84, with S1_AC showing the highest value and S1_MD the lowest. Soluble solids content ranged from 11.83 to 16.17 °Brix, although the differences among genotypes were not significant. The 100-seed weight ranged from 2.33 to 3.66 g and also did not differ significantly among genotypes. Overall, the qualitative and quantitative observations showed that the evaluated S1 melon genotypes still expressed morphological variation, particularly in fruit shape, rind appearance, netting characteristics, flesh color, fruit size, fruit weight, and flesh thickness. These results provide descriptive information on the morphological characteristics of S1 melon materials under the tested greenhouse conditions.

Table 2. Quantitative morphological traits of ten S1 melon genotypes.

Genotypes	IL (cm)	ST (cm)	MFE (DAP)	FFE (DAP)	LBA	FHA (DAP)	FD	FL	FW (g)	FT	SSC (°Brix)	HSW (g)
S1_AC	8.53^{ab}	0.75	8.67	23.33	410.48^{a}	53.33^{ab}	40.63^{a}	11.56^{abc}	1034.70^{ab}	3.84^{a}	12.67	3.09
S1_AP	12.10^{a}	0.71	6.80	22.67	361.15^{ab}	42.00^{b}	35.23^{abc}	11.19^{bc}	641.49^{bc}	2.76^{bcd}	13.23	2.80
S1_D1	12.70^{a}	0.77	9.23	22.67	410.99^{a}	49.00^{ab}	37.17^{ab}	11.74^{abc}	858.16^{abc}	3.24^{ab}	13.23	3.48
S1_GR	8.93^{ab}	0.66	9.20	22.33	298.92^{ab}	65.33^{a}	41.90^{a}	13.51^{ab}	1204.16^{a}	3.66^{a}	16.17	3.29
S1_GT	8.67^{ab}	0.60	12.70	18.00	297.59^{ab}	42.67^{b}	36.27^{ab}	12.17^{abc}	810.94^{abc}	3.21^{ab}	13.33	3.27
S1_IN	6.80^{b}	0.58	12.10	20.33	183.91^{b}	50.67^{ab}	31.87^{bc}	8.82^{c}	482.21^{c}	2.34^{cd}	13.17	2.73
S1_LV	8.50^{ab}	0.71	8.53	24.00	320.00^{ab}	47.33^{ab}	39.20^{ab}	13.67^{ab}	1011.72^{ab}	3.19^{ab}	14.50	3.66
S1_MD	9.20^{ab}	0.71	8.50	22.67	334.40ab	40.00^{b}	28.07^{c}	14.00^{ab}	441.38^{c}	1.95^{d}	11.83	3.13
S1_RC	9.23^{ab}	0.73	9.00	22.33	332.86ab	59.33^{ab}	40.07^{a}	11.90^{abc}	1020.43^{ab}	3.03^{abc}	13.33	3.26
S1_SN	9.00^{ab}	0.65	8.93	21.67	238.62ab	45.50^{ab}	37.05^{ab}	15.05^{a}	1031.17^{ab}	3.46^{ab}	15.70	2.33

Values are means. IL, internode length; ST, stem thickness; MFE, male flower emergence; FFE, female flower emergence; LBA, leaf blade area; FHA, fruit harvest age; FD, fruit diameter; FL, fruit length; FW, fruit weight; FT, flesh thickness; SSC, soluble solids content; HSW, 100-seed weight; DAP, days after planting. Different superscript letters within the same column indicate significant differences according to the Honestly Significant Difference test at $p < 0.05$. Columns without superscript letters were not significantly different among genotypes.

4. Discussion

The present study showed that the ten S1 generations of melon genotypes still exhibited observable morphological variation in qualitative and quantitative traits. This variation was particularly evident in fruit shape, rind ground color, groove and netting characteristics, flesh color, fruit size, fruit weight, and flesh thickness. Such variation is expected in early selfing generations because S1 materials are not yet genetically fixed and may still show segregation for several morphological characters (Yang, 2009). Therefore,

the observed differences should be interpreted as phenotypic variation under the tested greenhouse conditions rather than as evidence of stable line performance. Qualitative fruit descriptors provided useful information for distinguishing the evaluated genotypes. Fruit longitudinal shape varied from oblate to obvate, medium elliptic, broad elliptic, and circular, indicating that fruit shape remained variable among the S1 materials. Variation in fruit base, fruit apex, and position of maximum fruit diameter further supported the presence of diverse fruit morphology. Fruit shape is an important descriptor in melon characterization because it is visually distinctive and directly related to market preference and cultivar identity (Chikh-Rouhou et al., 2021b; Shahwar et al., 2023; Herwibawa et al., 2026). However, because several genotypes showed different descriptor states among replications, these characters should not yet be considered fixed at the S1 stage.

Rind and netting traits also showed clear variation among genotypes. Rind ground color ranged from whitish and greenish to yellowish, greyish, and ochre, while netting pattern varied from linear only to linear and netted or netted only. These rind-related traits are commonly used in melon classification and cultivar description because they are readily observed and strongly influence external fruit appearance (Xu et al., 2024). In this study, S1_AC consistently showed a netted-only fruit surface with medium netting thickness and very dense netting density, whereas S1_MD showed linear-only netting with mostly very sparse density. These differences indicate that rind appearance can be a useful visual trait for documenting variation among early-generation melon materials. Internal fruit traits also differed among the evaluated genotypes. Flesh color varied among greenish white, green, yellowish white, orange, and greenish orange. Flesh color is an important fruit quality descriptor in melon because it is associated with consumer preference and may reflect differences in pigment accumulation, particularly chlorophylls and carotenoids (Tadmor et al., 2010; Diao et al., 2023). In the present study, several genotypes showed consistent flesh color across replications, whereas others showed within-genotype variation. This result supports the interpretation that some S1 genotypes may still be segregating for internal fruit traits. Seed color varied between whitish and cream yellow, while seed shape was uniform as pine-nut shape in all available observations, suggesting that seed shape was less variable than fruit external and internal traits in the evaluated materials.

Quantitative traits further confirmed the presence of phenotypic variation among the S1 genotypes. Significant differences were observed for internode length, leaf blade area, fruit harvest age, fruit diameter, fruit length, fruit weight, and flesh thickness. These traits describe vegetative growth, fruit development, and fruit morphology, and are commonly used in melon characterization studies (Maghfiroh et al., 2023; Wang et al., 2025). In contrast, stem thickness, male flower emergence, female flower emergence, soluble solids content, and 100-seed weight did not differ significantly among genotypes. This indicates that not all measured traits were equally informative for distinguishing the evaluated S1 materials under the tested environment. Fruit-related quantitative traits showed some of the clearest differences among genotypes. Fruit diameter, fruit length, fruit weight, and flesh thickness varied considerably, indicating that fruit morphology and yield-related attributes were still variable in the S1 materials. S1_GR had the highest mean fruit weight and fruit diameter, whereas S1_MD had the lowest fruit diameter, fruit weight, and flesh thickness but showed the earliest fruit harvest age. S1_SN showed the longest fruit length, while S1_AC showed the highest flesh thickness. These observations describe phenotypic performance under the tested conditions, but they should not be interpreted as definitive evidence of superiority, as the materials were evaluated only in the first selfing generation and in a single environment. The absence of significant differences in soluble solids content and 100-seed weight suggests that these traits were less variable among the evaluated genotypes under the present conditions. Soluble solids content can be influenced by ge-

netic background, fruit maturity, environmental conditions, and crop management practices (Scalisi and O'Connell, 2021; Silva et al., 2022; Kasampalis et al., 2025). Therefore, non-significant differences in soluble solids content in this study may reflect limited variation among the evaluated materials, environmental effects, or the small number of plants per genotype. Similarly, 100-seed weight may require larger sample sizes or more stable generations to detect consistent differences among lines.

The results emphasize the importance of careful interpretation when evaluating S1 materials. Although the genotypes showed clear morphological differences, the first selfing generation is still an early stage in line development. At this stage, observed variation may arise from segregation, residual heterozygosity, and environmental influence (Song et al., 2006; Adamski et al., 2014). Therefore, the present study should be viewed as a descriptive morphological characterization rather than a final selection study. The information obtained can help document variation among early-generation materials and guide further selfing and evaluation in subsequent generations. Further evaluation in later selfing generations is necessary to determine whether the observed morphological traits become more uniform and stable. Multi-environment testing would also be needed to confirm whether quantitative traits such as fruit size, fruit weight, flesh thickness, and harvest age are consistently expressed across growing conditions. In addition, molecular marker analysis could be considered in future studies if the objective is to infer genetic diversity or genetic relationships among genotypes. Without molecular or pedigree-based evidence, the present results should be limited to phenotypic and morphological interpretation. The evaluated S1 melon genotypes showed observable qualitative and quantitative morphological variation, particularly in fruit-related traits. The combination of descriptor-based characterization, quantitative measurements, and representative fruit images provided useful documentation of phenotypic diversity among the early-generation materials. These findings provide a descriptive basis for further selfing, selection, and evaluation, but confirmation in later generations is required before stable lines or breeding value can be established.

5. Conclusions

The 10 S1-generation melon genotypes showed observable morphological variation in qualitative and quantitative traits under greenhouse conditions. Qualitative variation was mainly observed in fruit longitudinal shape, fruit base and apex shape, rind ground color, groove and netting characteristics, flesh color, and seed color. Quantitative variation was observed in several vegetative and fruit-related traits, particularly internode length, leaf blade area, fruit harvest age, fruit diameter, fruit length, fruit weight, and flesh thickness. These findings indicate that the evaluated S1 melon genotypes were still phenotypically variable and should be regarded as early-generation breeding materials rather than stable lines. The morphological information obtained in this study can serve as a descriptive basis for further selfing, selection, and evaluation in subsequent generations. Further evaluation across subsequent selfing generations and environments is needed to confirm trait uniformity, stability, and breeding value.

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References

Adamski, T., Krystkowiak, K., Kuczyńska, A., Mikołajczak, K., Ogrodowicz, P., Ponitka, A., Surma, M. and Ślusarkiewicz-Jarzina, A. (2014). Segregation distortion in homozygous lines obtained via anther culture and maize doubled haploid methods in comparison to single seed descent in wheat (*Triticum aestivum* L.). Electronic Journal of Biotechnology, 17(1), 6–13. https://doi.org/10.1016/j.ejbt.2013.12.002

Akdogan, G., Benlioglu, B., Ahmed, H. A. A., Bilir, M., Ergun, N., Aydogan, S., Türkoğlu, A., Demirel, F., Nowosad, K. and Bocianowski, J. (2025). Agro-morphological characterization and machine learning-based prediction of genetic diversity in six-row barley genotypes from Türkiye. Euphytica, 221, 69. https://doi.org/10.1007/s10681-025-03522-7

Akpertey, A., Anim-Kwapong, E., Adu-Gyamfi, P. K. K. and Ofori, A. (2022). Genetic variability for vigor and yield of robusta coffee (*Coffea canephora*) clones in Ghana. Heliyon, 8(8), e10192. https://doi.org/10.1016/j.heliyon.2022.e10192

Bokmeyer, J. M., Bonos, S. A. and Meyer, W. A. (2009). Broad-sense heritability and stability analysis of brown patch resistance in tall fescue. HortScience, 44(2), 289–292. https://doi.org/10.21273/HORTSCI.44.2.289

Chikh-Rouhou, H., Mezghani, N., Mnasri, S., Mezghani, N. and Garcés-Claver, A. (2021a). Assessing the genetic diversity and population structure of a Tunisian melon (*Cucumis melo* L.) collection using phenotypic traits and SSR molecular markers. Agronomy, 11(6), 1121. https://doi.org/10.3390/agronomy11061121

Chikh-Rouhou, H., Tlili, I., Ilahy, R., R'Him, T. and Sta-Baba, R. (2021b). Fruit quality assessment and characterization of melon genotypes. International Journal of Vegetable Science, 27(1), 3–19. https://doi.org/10.1080/19315260.2019.1692268

Diao, Q., Tian, S., Cao, Y., Yao, D., Fan, H. and Zhang, Y. (2023). Transcriptome analysis reveals association of carotenoid metabolism pathway with fruit color in melon. Scientific Reports, 13, 5004. https://doi.org/10.1038/s41598-023-31432-y

Herwibawa, B., Anwar, S., Kusmiyati, F., Sas, M. G. A. and Saputro, T. B. (2026). Fruit morphology and clustering analysis reveals diversity among commercial melons (*Cucumis melo* L.) in Indonesia. International Journal of Agriculture and Biosciences, 15(1), 115–124. https://doi.org/10.47278/journal.ijab/2025.137

Kasampalis, D. S., Tsouvaltzis, P. and Siomos, A. S. (2025). Assessment of melon fruit nutritional composition using VIS/NIR/SWIR spectroscopy coupled with chemometrics. Horticulturae, 11(6), 658. https://doi.org/10.3390/horticulturae11060658

Maghfiroh, R. N., Suwarno, W. B., Sobir and Gunawan, E. (2023). Assessment of relationship among traits and genotypes for melon (*Cucumis melo*) breeding. Biodiversitas Journal of Biological Diversity, 24(8). https://doi.org/10.13057/biodiv/d240833

Maitan, M. Q., Viana, A. P., Silva, F. A. da and Vieira, H. D. (2025). Estimation of inbreeding depression in *Psidium guajava* through seed attributes using S0, S1, and S2 families. Acta Scientiarum. Agronomy, 47, e71675. https://doi.org/10.4025/actasciagron.v47i1.71675

Scalisi, A. and O'Connell, M. G. (2021). Relationships between soluble solids and dry matter in the flesh of stone fruit at harvest. Analytica, 2(1), 14–24. https://doi.org/10.3390/analytica2010002

Shahwar, D., Khan, Z. and Park, Y. (2023). Molecular marker-assisted mapping, candidate gene identification, and breeding in melon (*Cucumis melo* L.): A review. International Journal of Molecular Sciences, 24(20), 15490. https://doi.org/10.3390/ijms242015490

Silva, J. M. C., Viana, E. R. C., Morais, P. L. D., Tomaz, F. L. S., Martins, A. F. and Nunes, G. H. S. (2022). Inheritance of soluble solids content and sucrose in melon. Horticultura Brasileira, 40(3), 295–301. https://doi.org/10.1590/s0102-0536-20220308

Song, X.-L., Sun, X.-Z. and Zhang, T.-Z. (2006). Segregation distortion and its effect on genetic mapping in plants. Chinese Journal of Agricultural Biotechnology, 3(3), 163–169. https://doi.org/10.1079/CJB2006110

Tadmor, Y., Burger, J., Yaakov, I., Feder, A., Libhaber, S. E., Portnoy, V., Meir, A., Tzuri, G., Sa'ar, U., Rogachev, I., Aharoni, A., Abeliovich, H., Schaffer, A. A., Lewinsohn, E. and Katzir, N. (2010). Genetics of flavonoid, carotenoid, and chlorophyll

pigments in melon fruit rinds. Journal of Agricultural and Food Chemistry, 58(19), 10722–10728. https://doi.org/10.1021/jf1021797

Wang, Q., Tang, L., He, Y., Xu, Y., Zhang, J., Kong, W., Hu, K., Garcia-Mas, J., Pujol, M. and Zhao, G. (2025). Comprehensive analysis of transcriptome and metabolome identified the key gene networks regulating fruit length in melon. BMC Plant Biology, 25(1), 442. https://doi.org/10.1186/s12870-025-06332-0

Xu, L., He, Y., Tang, L., Xu, Y. and Zhao, G. (2022). Genetics, genomics, and breeding in melon. Agronomy, 12(11), 2891. https://doi.org/10.3390/agronomy12112891

Xu, S., Shen, J., Wei, Y., Li, Y., He, Y., Hu, H. and Feng, X. (2024). Automatic plant phenotyping analysis of melon (*Cucumis melo* L.) germplasm resources using deep learning methods and computer vision. Plant Methods, 20, 166. https://doi.org/10.1186/s13007-024-01293-1

Yang, R.-C. (2009). When is early generation selection effective in self-pollinated crops? Crop Science, 49, 2065–2079. https://doi.org/10.2135/cropsci2009.01.0029