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Genetic Variability in F_2 Melon (*Cucumis melo* L.) Population from Double Cross of Sex-Distinct Parent Lines

Agus Budi Setiawan[1*], Irna Auliauzzakia[2] and Aziz Purwantoro[1]

[1]Laboratory of Plant Breeding, Department of Agronomy, Faculty of Agriculture, Universitas Gadjah Mada, Yogyakarta, Indonesia; [2]Department of Agronomy, Faculty of Agriculture, Universitas Gadjah Mada, Yogyakarta, Indonesia

[*]*Corresponding author:* setiawanab@ugm.ac.id

Abstract

Melon (*Cucumis melo* L.) is an economically significant crop in Indonesia. Due to the increasing demand for premium melon fruit with high sugar content, firm flesh, extended shelf life, bright peel and flesh color, and round fruit shapes, researchers developed melon lines that align with consumer preferences. This study aimed to determine the segregation pattern and genetic basis of sex expression in F_1 and F_2 populations, estimate genetic parameters for pericarp thickness and total soluble solids, and identify superior F_2 genotypes using a predicted selection response based on a weighted selection index. A total of 137 F_1 individuals derived from crossing 'Inthanon RZ' with 'Glamour Sakata' and 237 F_2 individuals derived from the self-pollinated IG10 line were grown in a greenhouse using a hydroponic drip fertigation system. The F_1 population exhibited genetic variation in sex expression based on the allele-specific marker of *CmACS7*, with a 1:1 phenotypic ratio, consisting of 68 monoecious and 69 andromonoecious individuals. All individuals in the F_2 population showed homozygote andromonoecious expression, indicating that the IG10 progenitor line was homozygous (*aaGG*). Pericarp thickness and total soluble solids exhibited high phenotypic and genotypic coefficients of variation and moderate-to-high broad-sense heritability. Among the genotypes, four displayed high-weighted selection indices based on the two target traits, with IG10-124 achieving the highest selection index. The selection response based on the weighted selection index suggests that pericarp thickness and total soluble solids will show genetic improvement in the next generation.

Keywords: andromonoecious line; *CmACS7* gene; genotype selection; melon breeding; monoecious line

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INTRODUCTION

Melon (*Cucumis melo* L.) is an important horticultural crop because of its high economic value (Sormin et al., 2021). Aside from yield improvement, market demand and customer preferences are essential variables for plant breeders to consider while developing newly improved varieties (Ojwang et al., 2023). In Indonesia, the demand for premium melon fruit with high sugar content, firm flesh, extended shelf life, bright peel and flesh color, and round fruit shape has increased. In melon, sugar content, represented by total soluble solids (TSSs), is associated with fruit sweetness, which determines fruit quality (Sinclair et al., 2006; Andrade et al., 2021). Therefore, researchers started a melon breeding program to develop a new improved variety with high-quality fruit that meets market demand and preferences.

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Most Indonesian farmers grow melon in greenhouses to produce high-quality fruit and use the 'Inthanon RZ' F_1 hybrid. This cultivar has yellow-peeled, green-fleshed, netted fruit with high TSS content and good shelf life (Hai and Thao, 2021). 'Glamour' is a melon hybrid cultivar with orange flesh, netted fruit, moderate fruit firmness, short shelf life (Krarup et al., 2016), and low TSS content (Khairi et al., 2017). Both cultivars have different sex expression traits, i.e., monoecious ('Inthanon RZ') and andromonoecious ('Glamour'). Sex expression is strongly associated with fruit shape (Boualem et al., 2022). Monoecious melon cultivars have several benefits, including low cost and high seed production efficiency for hybrid cultivar development, and a small bottom scar but elongated fruit shape. By contrast, andromonoecious lines have low seed production efficiency and a large bottom scar but a round fruit shape (Noguera et al., 2005; Sakata et al., 2013).

Sex expression in melon is controlled by andromonoecious (*a*) and gynoecious (*g*) genes, and the interaction between these two genes results in several sex expression traits, i.e., monoecious (*A_G_*), andromonoecious (*aaG_*), gynoecious (*AAgg*), and hermaphrodite (*aagg*) (Boualem et al., 2008; Xu et al., 2022). In addition, the 1-aminocyclopropane-1-carboxylic acid synthase gene (*CmACS7*) plays an important role in sex determination in melon (Boualem et al., 2008, 2015, 2016; Pechar et al., 2024; Li et al., 2025) and can be used as a marker to distinguish between andromonoecious and monoecious genotypes. Researchers utilized 'Inthanon RZ' and 'Glamour' for the melon breeding project to develop newly improved cultivars with high TSSs, good fruit firmness and peel color, round fruit shape, and orange flesh color to fulfill the market demand and preferences for melons.

Selection is an important step in plant breeding projects, and pedigree is a selection method that can be applied to produce new inbred lines. In this method, the breeder begins by selecting two or more adapted progenies that perfectly complement each other in several traits (Singh et al., 2021). In addition, selection can be undertaken on a certain generation that exhibits considerable genetic variation (Sintia et al., 2023). The response to selection can be predicted for traits with high heritability values and large genetic variations in advanced generations (Syukur et al., 2012). Selection for a certain genotype can be determined by using a selection index approach for targeted traits, as has been reported for barley (Zali et al., 2023), millet (Sintia et al., 2023), pepper (Yunandra et al., 2017), and wheat (Gholizadeh et al., 2025).

Although sex determination in melon has been studied using genetic markers (Boualem et al., 2008, 2015, 2016), the segregation patterns of sex expression in F_1 and F_2 populations from monoecious × andromonoecious crosses remain unexamined. Additionally, while TSS content and pericarp thickness are key fruit quality traits, their genetic parameters in advanced segregating populations require further investigation. Most studies rely on phenotypic selection, whereas the use of predicted selection response based on a weighted selection index remains underutilized in melon breeding. Furthermore, sustainable agriculture may be supported through the development of melon cultivars adapted to greenhouse conditions in developing countries, including Indonesia.

Breeding cultivars with higher quality traits, such as increased sweetness and pericarp thickness, enhanced fruit firmness, and longer shelf life, can significantly reduce postharvest losses, which are a major challenge in horticultural production (Shipman et al., 2021). Moreover, the utilization of precise genetic information and selection indexes enables breeders to enhance productivity with lower inputs, thereby supporting sustainable intensification of agricultural systems (Fritsche-Neto et al., 2023; Ćeran et al., 2024). The availability of genetically superior cultivars can benefit smallholder farmers in developing countries by increasing economic returns and improving livelihoods sustainably (Kumar, 2024).

In this study, researchers used an F_2 population derived from double-crossed parental lines with distinct sex expression traits and applied pedigree selection in the F_1 generation exhibiting genetic variation in sex expression. This study aimed to examine the segregation pattern and genetic basis of sex expression in F_1 and F_2 populations, estimate genetic parameters for pericarp thickness and TSSs, and identify superior F_2 genotypes using a weighted selection index.

MATERIALS AND METHOD

Plant materials

The research was conducted from February to December 2023. Two cultivars of melon, i.e., the 'Inthanon RZ' F_1 hybrid (monoecious) and 'Glamour Sakata' F_1 hybrid (andromonoecious),

were used to develop an F_1 population through double crossing (Figure 1a-1f). In addition, melon genotypes GM-03, GM-98, GM-107, MF-032, 'Action 434', and 'Prince' were used as andromonoecious checks for sex expression analysis. The 137 F_1 individuals derived from crossing 'Inthanon RZ' with 'Glamour Sakata' were grown in a greenhouse at Pondok Pesantren Madania, Banguntapan, Bantul, Yogyakarta, Indonesia. The F_1 population was selected by utilizing the pedigree method and self-pollinated to develop an F_2 population. A total of 237 F_2 individuals derived from self-pollinated fruit were grown in the same greenhouse by using a hydroponic drip irrigation system.

Melon nutrient solution

Melons were grown in a 35 cm × 35 cm polybag containing 2:1 cocopeat and rice husk charcoal from February to August 2023. Full-strength Enshi nutrient solution was applied throughout melon growth and development, including vegetative, generative, fruit development, and harvest (Asaduzzaman et al., 2018). Electrical conductivity was incrementally adjusted from 1.8 to 2.4 dS m^{-1} at pH 5.9 following melon growth stages. Melon seedlings with two fully expanded leaves were transplanted into a polybag containing cocopeat and rice husk charcoal with a plant spacing of 60 cm × 40 cm. A fan and an exhaust fan were automatically activated to control the air temperature when it exceeded 33 °C.

DNA isolation and *CmACS7* gene amplification

Total DNA was extracted from the 0.5 g leaves of melon genotypes, including the F_1 population, 'Inthanon RZ,' 'Glamour,' 'Action 434,' 'Prince,' GM-03, GM-98, GM-107, and MF-032, by using the hexadecyltrimethylammonium bromide (CTAB) extraction method described by Setiawan et al. (2020). PCR amplification was conducted by using a T100™ thermal cycler (Bio-Rad, USA). A total of 12.5 µl PCR reaction, which consisted of 2.5 µl of 50 ng μl^{-1} DNA, 6.25 µl of 1× PowerPol 2× PCR Mix (ABclonal, USA), 0.25 µl each of 0.2 µm forward and reverse primers, and 2.75 µl of nuclease-free water, was used for PCR. Sex expression in the F_1 population was genotyped using a cleaved amplified polymorphic sequence (CAPS) marker based on the *CmACS7* gene sequence. The primer pair, 5'-ACATTCAATTCAACAAATCTTCAG TTC-3' and 5'-GGGTATAGTAATTACAGT AAAGAGTGG-3', was used as described by Boualem et al. (2008). The PCR program included predenaturation at 95 °C for 3 minutes, 35 cycles of denaturation at 95 °C for 1 minute, annealing at 57 °C for 1 minute, extension at 72 °C for 2 minutes, and the post-extension at 72 °C for 5 minutes. PCR products were stained with FloroSafe DNA Stain (1stBase, Singapore) and visualized on a 1.5% (w/v) agarose gel using a Compact Gel Imaging System Mupid-Scope WD (Mupid Co. Ltd., Japan). The amplified DNA was digested with the *AluI* restriction enzyme (ThermoFisher Scientific, USA) at 37 °C for 3 hours in a 10 µl reaction containing 3 µl of DNA (0.5 µg μl^{-1}), 1 µl of 10× buffer, 1 µl of 10 U μl^{-1} *AluI*, and 5 µl of nuclease-free water.

Phenotypic trait observations

Yield and fruit quality traits, including fruit weight (FW), fruit length (FL), fruit width (FWd), length-to-width ratio (LWR), pericarp thickness (PT), and total soluble solids (TSS), were measured in 137 F_1 and 237 F_2 individuals. TSS content was assessed using a digital refractometer (ATAGO PAL-1, Japan).

Data analysis

The mean and standard deviation of phenotypic traits were calculated for each population and analyzed using a t-test ($\alpha = 0.05$) and correlation analysis in R software. The mean values were then used for further analyses, including variance component estimation and selection parameters. The phenotypic variance (σ^2_P) was estimated as σ^2F_2, while the environmental variance (σ^2_e) was determined as σ^2F_1. Broad-sense heritability (h^2_{bs}) was estimated as $= \frac{\sigma^2F_2-\sigma^2F_1}{\sigma^2F_2} \times 100\%$ (Burton, 1951). The phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were computed using Equation 1 and 2, respectively.

$$PCV = \frac{\sqrt{\sigma^2 p}}{\bar{x}} \times 100\% \quad (1)$$

$$GCV = \frac{\sqrt{\sigma^2 g}}{\bar{x}} \times 100\% \quad (2)$$

(Burton and DeVane, 1953)

Trait standardization (X_n) was performed using Equation 3.

$$X_n = \frac{X_{ij} - \bar{X}_i}{\sigma_i} \quad (3)$$

(Sintia et al., 2023)

Where, $\bar{x}$ = Means of the variable, $\sigma^2 g$ = Genetic variance, X_{ij} = Means of each genotype, $\bar{X}_i$ = Means of the variable, σ_i = Standard deviation of the variable.

The weighted selection index (I) was calculated as $I = \sum b_i P_i$ (Baker, 1986), differential selection (S) as $S = \mu_s - \mu_0$, and predicted selection response (ΔG) as $\Delta G = S \times h^2_{bs}$ (Acquaah, 2012). PCV and GCV were categorized as low (0 to 10%), moderate (10 to 20%), and high (> 20%) following Zaki and Radwan (2022). Broad-sense heritability (h^2_{bs}) was classified as high (60 to 100%), moderate (30 to 60%), and low (0 to 20%) based on Robinson et al. (1949). For molecular analysis, data were transformed into binary format, with DNA bands scored as present (1) or absent (0). Clustering was performed using the unweighted pair group method with arithmetic mean (UPGMA) in the NTSYS-PC program with the Dice coefficient similarity index (Rohlf, 2009).

RESULTS AND DISCUSSION

Genetic variation in the sex expression and fruit shape traits of the F_1 melon population

The sex expression of 137 individuals of the F_1 population derived from the double crossing of the 'Inthanon RZ' F_1 hybrid (*A_G_*) × 'Glamour Sakata' F_1 hybrid (*aaG_*) was observed in this study. The 'Inthanon RZ' and 'Glamour Sakata' are monoecious and andromonoecious. The F_1 population had a phenotypic ratio of 1:1 for sex expression, with 68 and 69 individuals being monoecious and andromonoecious, respectively. This phenotypic ratio of sex expression was supported by the amplification of the *CmACS7* gene in the parental lines, with F_1 progenies exhibiting monoecious, andromonoecious, and other genotypes (Supplemental Figure 1a and 1b). Sex expression was controlled by two alleles, i.e., *a* and *g*, and the interaction between these genes produced four distinct sex expression traits, namely, *A_G_*, *aaG_*, *AAgg*, and *aagg* (Boualem et al., 2008; Xu et al., 2022). A total of 137 individuals in the F_1 population clearly showed genetic variation in their sex expression. These results indicate that the F_1 population derived from a double-cross hybrid exhibited genetic variation. The results of this study were similar to those reported by Matos et al. (2021). In their study, double-cross hybrids were developed by using four distinct inbred lines, creating chromosomal rearrangement events. These events resulted in greater genetic variability and phenotypic variation of double-cross hybrids than those of single-cross hybrids.

CmACS7 was successfully amplified from melon DNA (Supplemental Figure 1a), and specific amplicons were digested with the *Alu1* restriction enzyme (Supplemental Figure 1b). Monoecious melon genotypes exhibited specific DNA amplification at 525, 330, 180, and 116 bp, whereas andromonoecious genotypes were amplified only at 525 and 116 bp. Clustering analysis showed that the F_1 progenies grouped into two major clusters based on their sex expression traits (Figure 1c). Boualem et al. (2008) and (2016) revealed that andromonoecious plants contain a mutation at the active site of *CmACS7*. This study confirmed that the amplification of *CmACS7* in F_1 progeny produced specific 330 and 180 bp DNA amplicons in monoecious genotypes. This result is similar to the findings of Boualem et al. (2008) and Duong et al. (2021).

Genetic variation was also observed in the fruit shape of the F_1 population. The F_1 progenies with andromonoecious phenotypes produced round fruit shapes, whereas those with monoecious phenotypes produced oval fruit shapes (Figure 2). In addition, all the F_1 progenies showed uniform orange flesh color. These research breeding goals are to develop a newly improved cultivar with a round fruit shape, high TSS content, good fruit firmness (fruit flesh with a crunchy texture), orange flesh color, and good peel color. Researchers employed the pedigree method and selected a specific individual from the F_1 population, namely, the IG-10 genotype, and self-pollinated it to establish the F_2 population for inbred line production. This genotype had a good round fruit shape, orange flesh color, netted peel, yellow flesh (Figure 2e–2f), high TSSs (14% Brix), high PT (3.8 cm), the proportional FL and width of 12.0 and 12.3 cm, respectively, good FW (1.042 kg), and a very crunchy fruit flesh texture. The IG-10 genotype had a homozygous allele related to sex expression (*aaGG*). The homozygous andromonoecious genotype *aaGG* was exhibited by all individuals in the F_2 population derived from the self-pollinated IG-10 genotype. This population showed uniform sex expression traits, i.e., andromonoecious. This result suggests that andromonoecious traits may be fixed in the F_2 generation and will be inherited by the advanced generation without any segregation.

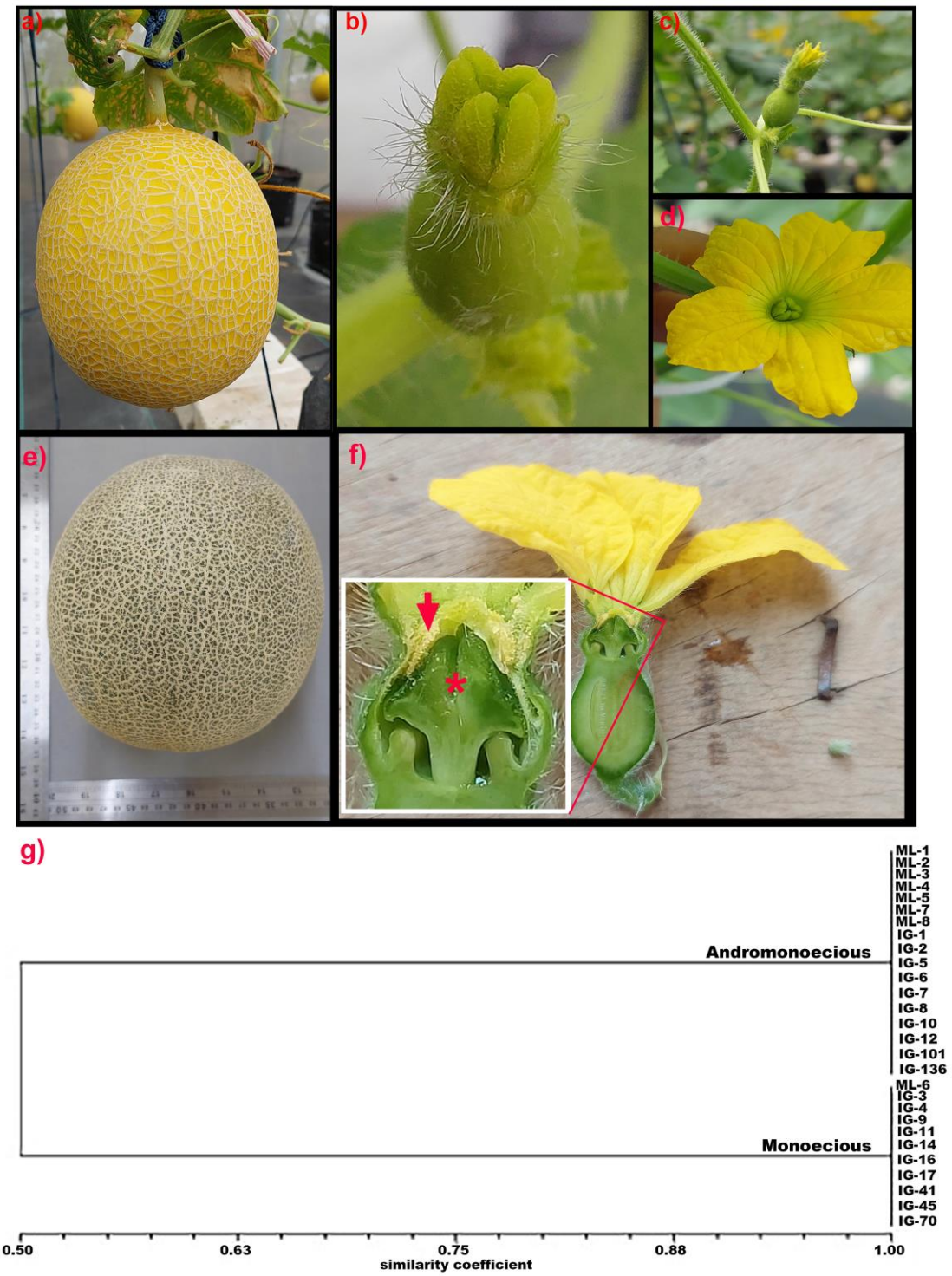

Figure 1. The parental lines, 'Inthanon RZ' F_1 hybrid (a–d) and 'Glamour Sakata' F_1 hybrid (e–f), used to develop the F_1 population, exhibited distinct sex expressions on axillary branches (c–d): 'Inthanon RZ' produced female flowers (b), whereas 'Glamour Sakata' produced hermaphrodite flowers (f). The inset image in Figure f shows the positions of the anthers (red arrow) and stigma (red arrowhead) in the hermaphrodite flower of 'Glamour Sakata'. Dendrogram of F_1 progenies with the parental lines and other melon genotypes based on the *CmACS7* marker (c)

Note: ML-1 = GM-03, ML-2 = GM-98, ML-3 = GM-107, ML-4 = MF-032, ML-5 = 'Action 434', ML-6 = 'Inthanon RZ', ML-7 = 'Prince', ML-8 = 'Glamour', IG series = Individual number of F_1 population

Noguera et al. (2005) and Sakata et al. (2013) reported that sex expression in melons is associated with fruit shape. This study revealed that the monoecious and andromonoecious genotypes had distinct fruit shapes. Andromonoecious lines, such as IG-1, IG-2, IG-10, IG-103, IG-84, and IG-39, exhibited round fruit shapes, whereas monoecious lines, such as IG-98, IG-69, IG-127, IG-90, IG-117, and IG-134, had oval fruit shapes. The monoecious lines had elongated fruit because *CmACS7*-mediated ethylene synthesis in carpel primordia promotes cell expansion and suppresses cell division (Boualem et al., 2022). All individuals in the F_1 population had an orange flesh color (Figure 2). In melon, flesh color is an essential trait that influences not only customer preferences but also the content of nutrients related to carotenoid accumulation (Tzuri et al., 2015; Xu et al., 2022). The female parent ('Inthanon RZ') had green flesh, whereas the male parent ('Glamour Sakata') had orange flesh. Orange, white, and green are the principal flesh colors in commercial melon cultivars and are mostly controlled by two key genes: white flesh (*wf*) and green flesh (*gf*). *Gf* determines orange flesh and is dominant over *gf* (Xu et al., 2022). Therefore, all individuals in the F_1 population exhibited an orange flesh color.

Agronomic performance of F_1 and F_2 melon populations

This study showed that the FL, FWd, PT, and TSSs of the F_2 population were higher than those of the F_1 population (Table 1), indicating that the F_2 population had potential segregants with good quality for producing premium melon. The mean PT and TSSs of the segregated F_2 population showed higher improvement than those of the F_1 population. High TSSs and PT are two important traits of premium melon in Indonesia that describe consumer preferences. The F_1 and F_2 populations had similar average FWs. The FL and width (14.17 and 14.72 cm) of the F_2 population were higher than those of the F_1 population (13.09 and 12.36 cm), suggesting that the F_2 population produced larger fruit than the F_1 population. The

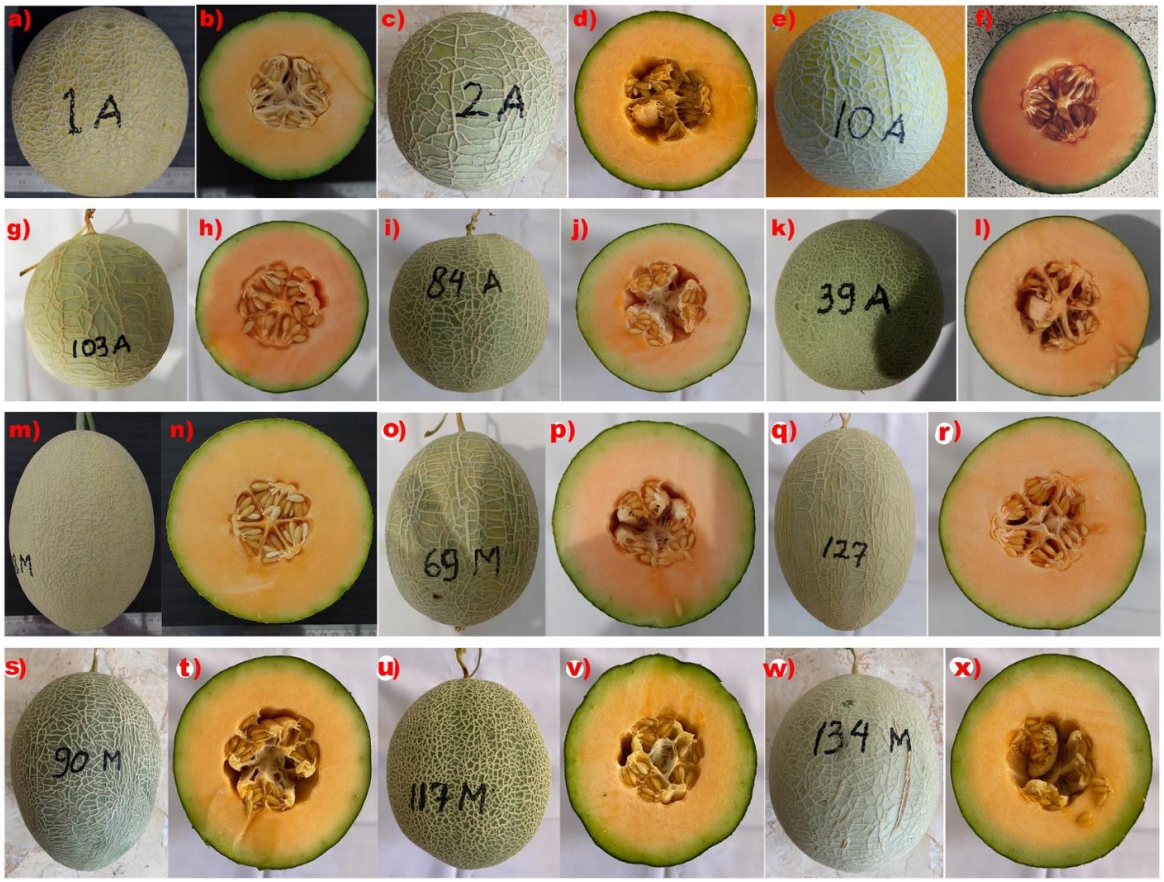

Figure 2. Fruit shape and flesh color of the F_1 population. Andromonoecious lines exhibited round fruit shape: IG-1 (a–b), IG-2 (c–d), IG-10 (e–f), IG-103 (g–h), IG-84 (i–j), and IG-39 (k–l). Monoecious lines exhibited oval fruit shape: IG-98 (m–n), IG-69 (o–p), IG-127 (q–r), IG-90 (s–t), IG-117 (u–v), and IG-134 (w–x)

LWR showed that the F_2 population produced fruit with a better and rounder shape than the F_1 population.

Specific traits that can be used for indirect selection were identified based on the correlation between phenotypic traits. The correlation coefficients of phenotypic traits in the F_2 population are listed in Table 2. Correlation analysis showed that FL had a significant and positive correlation with LWR (0.688), implying that FL influences fruit shape. FW and PT also had a significant and positive correlation coefficient (0.253), suggesting that PT increases melon FW. A significant and negative correlation was observed between FWd and LWR (-0.657), as well as between PT and TSSs (-0.515). These results indicate that high TSSs and FWd negatively influenced PT and LWR, respectively.

The breeding objectives of this research are to develop a newly improved cultivar with a round fruit shape, high TSSs, good fruit firmness (fruit flesh with a crunchy texture) and peel color, and orange flesh. Given the presence of genetic and phenotypic variation in this population, selection was performed on the early F_1 generation. Selection in early generations is usually effective when applied to populations descended from phenotypically diverse parents (Alahmad et al., 2018). Applying selection in early generations of segregating populations is favorable because it permits the population to be enriched with the desired alleles (Hickey et al., 2011, 2012; Richard et al., 2018). A pedigree selection approach was employed to develop inbred lines from superior genotypes that possessed desirable traits. Pedigree selection is effective for developing inbred lines because it considers phenotype and genotype, making it an excellent strategy for selecting superior lines from segregating populations (Acquaah, 2012). Pedigree selection has been applied in the development of inbred lines tolerant of melon vine disease (Fita et al., 2009). The andromonoecious IG10 was selected from F_1 progenies and self-pollinated to generate an F_2 population. This genotype had a good round fruit shape, orange flesh color, netted peel, yellow (Figure 2e–2f), high TSSs (14% Brix), high PT (3.8 cm), good FL and width of 12.0 and 12.3 cm, respectively, good FW (1.042 kg), and very crunchy fruit flesh. The F_2 population derived from the self-pollinated line IG10 exhibited uniform sex expression, i.e., it was andromonoecious. This result demonstrates that IG10 is homozygous (*aaGG*) and that this trait may be fixed in the F_2 generation and inherited without segregating in the advanced generation.

The phenotypic trait–related yield and fruit quality of melon in the F_1 population were lower than those in the F_2 population, implying that the F_2 generation had potential segregants with good quality for producing premium melon. The F_2 population may have superior genotypes with more desirable traits than their parental lines (Sintia et al., 2023). The mean TSSs and PT of the

Table 1. Mean and SD of the phenotypic traits of F_1 and F_2 melon populations

Traits	F_1	F_2
FW (kg)	0.97±0.27[a]	0.97±0.30[a]
FL (cm)	13.09±2.26[b]	14.17±2.46[a]
FWd (cm)	12.36±2.65[b]	14.72±3.06[a]
LWR	1.08±0.19[a]	1.00±0.24[b]
PT (cm)	3.14±0.43[a]	3.23±1.29[a]
TSS (% Brix)	9.96±1.75[b]	14.14±2.16[a]

Note: The mean values of each trait followed by the same letter are not significantly different at $\alpha = 0.05$. FW = Fruit weight, FL = Fruit length, FWd = Fruit width, LWR = Length-to-width ratio, PT = Pericarp thickness, TSS = Total soluble solid

Table 2. Correlation coefficients of phenotypic traits in the F_2 melon population

Traits	FW	FL	FWd	LWR	PT
FL	0.090				
FWd	0.082	0.033			
LWR	0.028	0.688*	-0.657*		
PT	0.253*	-0.022	-0.032	0.008	
TSSs	0.126	0.010	0.008	0.003	-0.515*

Note: *significantly different at $\alpha = 0.05$. FW = Fruit weight, FL = Fruit length, FWd = Fruit width, LWR = Length-to-width ratio, PT = Pericarp thickness, TSS = Total soluble solid

Table 3. Variance components, PVC, GVC, and h^2_{bs} of the F_2 population

Traits	σ^2_p	σ^2_e	σ^2_g	PCV (%)	Category	GCV (%)	Category	h^2_{bs} (%)	Category
FW	0.09	0.07	0.02	30.02	High	13.63	Moderate	22.22	Low
FL	6.07	5.10	0.97	17.38	Moderate	6.94	Low	15.98	Low
FWd	9.37	7.02	2.35	20.80	High	10.43	Moderate	25.08	Low
LWR	0.06	0.04	0.02	24.05	High	13.22	Moderate	33.33	Moderate
PT	1.66	0.18	1.48	16.01	Moderate	9.14	Low	89.15	High
TSS	4.66	3.06	1.60	15.27	Moderate	8.95	Low	34.33	Moderate

Note: FW = Fruit weight, FL = Fruit length, FWd = Fruit width, LWR = Length-to-width ratio, PT = Pericarp thickness, TSS = Total soluble solid, σ^2_p = Phenotypic variance; σ^2_e = Environmental variance; σ^2_g = Genetic variance; PCV = Phenotypic coefficient of variation; GCV = Genotypic coefficient of variation; H^2 = Broad-sense heritability

F_2 population were higher (14.14% Brix and 3.23 cm) than those of the F_1 population (9.96% Brix and 3.14 cm). High contents of TSSs determine the sugar content in melon fruit, and an increase in PT increases the edible portion of melon fruit. Sugar content is an important trait that determines fruit quality and consumer preferences and a primary concern in melon improvement (Argyris et al., 2017; Xu et al., 2022). Chikh-Rouhou et al. (2024) reported that sugar content is a reliable indicator of melon fruit quality, as it correlates with flavor, aroma, flesh texture, and TSSs. The mean FL and width of the F_2 population had highly improved compared with those of the F_1 population. Fruit shape is not only determined based on sex expression through *CmACS7*-mediated ethylene synthesis in carpel primordia (Boualem et al., 2022) but also by the ratio between fruit length and width (Chaim et al., 2003; Pereira et al., 2015).

Indirect selection was evaluated based on correlations among phenotypic traits. Indonesian consumers prefer melon fruit with high TSSs and PT. TSSs are not only important for nutrient content, but they also affect fruit flavor (Wang et al., 2023). Correlation analysis revealed that these two traits had a significantly negative correlation, in which the increase in TSSs decreased PT. A similar study reported that TSSs have a strong negative correlation with fruit load and flesh development (Wang et al., 2023). Therefore, progeny selection for these two traits must be carefully conducted by considering other parameters, such as PCV, GCV, heritability, selection index, and predicted response selection.

Variance components and h^2_{bs} of the F_2 melon population

Variance components, PCV, GCV, and h^2_{bs} were estimated (Table 3). PCV ranged from 15.27 to 30.45%, whereas GCV ranged from 6.94 to 13.63%. The highest PCV (30.45%) was obtained for FW, followed by that for LWR (24.05%) and FWd (20.80%). The highest value of GCV (13.63%) was obtained for FW, followed by that for FL:FW ratio (13.22%) and FWd (10.43%). For all observed traits, PCV was higher than GCV, implying that environmental factors had a greater influence on trait expression than genetic factors.

Heritability can be used to estimate the variation degree of a trait in a particular population. The estimated values of h^2_{bs} ranged from 15.98 to 89.15% (Table 3). PT had the highest h^2_{bs} (89.15%). Two traits, i.e., LWR (33.33%) and TSSs (34.33%), had a moderate h^2_{bs}

value, whereas FW (22.22%), FL (15.98%), and FWd (25.08%) had a low h^2_{bs} value. A high heritability value indicates that the variation in a particular trait is affected by genetic factors rather than environmental factors.

Plant breeding relies on trait variation and inheritance to introduce new desirable phenotypic expression by modifying the genetic constitution of plants (Holme et al., 2019; Swarup et al., 2021). PCV and GCV provide information about the degree of variation in a particular trait. All observed traits had higher PCV than GCV (Table 3), suggesting that environmental factors had a greater influence on trait expression than genetic factors. Terfa and Gurmu (2020), Magar et al. (2021), and Adedugba et al. (2023) reported similar results. In addition, PT and TSSs showed high and moderate h^2_{bs}, signifying the increased probability of successful selection for these traits for character improvement. By contrast, the other traits had low h^2_{bs}. Low heritability indicates that traits are controlled by nonadditive gene action; thus, direct selection is difficult because trait variations are mainly affected by environmental factor (Terfa and Gurmu, 2020). Although PT and TSSs had high and moderate heritability, their h^2_{bs} relied only on total genetic variance, including additive, dominant, and epistatic. Thus, genetic advances may increase selection effectiveness. Estimating heritability in conjunction with high genetic advances is reliable and efficient for selecting desirable traits (Prakash et al., 2019).

Selection index and predicted selection response of the F_2 melon population

The weighted selection index was used for multiple-trait selection based on PT and TSSs as priority traits in the researchers' melon breeding program. Researchers increased the weights of PT and TSSs by 5-fold because they are important traits that are desired by the market. Four genotypes with a high selection index were selected for comparison with their progenitor line IG10 (Table 4). The selection index of the four genotypes ranged from 12.68 to 27.61, whereas that of the progenitor line IG10 was 19.62. The genotype IG10-124 had the highest selection index compared with the F_2 genotypes and progenitor line. In addition, the four selected genotypes of this F_2 population had distinct peel and flesh colors, fruit shapes, net density, high PT, high TSSs, and crunchy fruit flesh (Table 4 and Figure 3). The IG10-80 genotype had green flesh (Figure 3e–3f), demonstrating that the progenitor line IG10 possessed a heterozygote allele controlling this trait because similar to the progenitor line, the other genotypes had orange flesh color. The IG10-44 genotype exhibited yellow peel, orange flesh color, and moderate net density (Figure 3a–3b). The IG10-76 genotype had a slightly yellow peel, orange flesh color, and high net density (Figure 3c–3d). Furthermore, the IG10-124 genotype had a green peel, orange flesh color, and high net density (Figure 3g–3h).

Table 4. Weighted selection indices of four genotypes of the F_2 melon population and progenitor line

Genotypes	Mean of traits		Standardized mean of the traits		Selection index
	PT	TSSs	PT	TSSs	
IG10-44	3.80	17.10	1.10	1.76	14.30
IG10-76	3.51	17.50	0.54	1.99	12.68
IG10-80	3.94	17.60	1.37	2.05	17.14
IG10-124	4.90	18.00	3.23	2.29	27.61
IG10 (F1)	3.80	14.10	1.56	2.37	19.62

Note: PT = Pericarp thickness, TSSs = Total soluble solids

Table 5. Selection response based on the weighted selection index of the F_2 melon population

Traits	μ_0	μ_s	S	ΔG
FW	0.97	1.26	0.29	0.058
FL	14.17	14.98	0.81	0.129
FWd	14.72	14.87	0.15	0.038
LWR	1.00	1.08	0.08	0.024
PT	3.23	4.19	0.96	0.856
TSSs	14.14	17.06	2.92	1.001

Note: μ_0 = Mean population before selection; μ_s = Mean selected population; S = Differential selection; ΔG = Predicted selection response, FW = Fruit weight, FL = Fruit length, FWd = Fruit width, LWR = Length-to-width ratio, PT = Pericarp thickness, TSSs = Total soluble solids

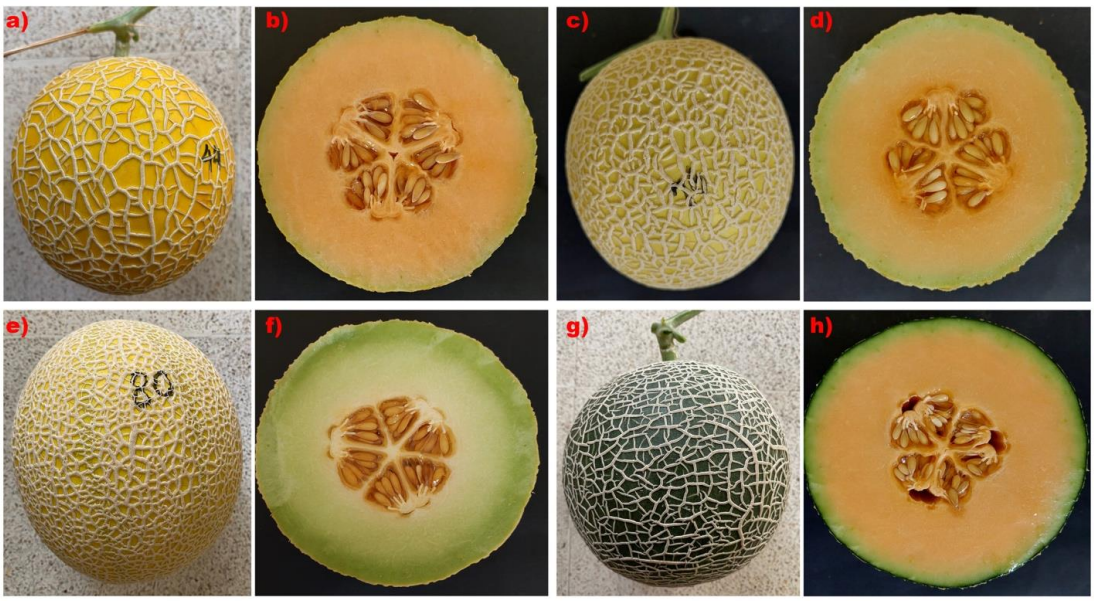

Figure 3. Selected genotypes of the F_2 population exhibited andromonoecious sex expression as well as distinct fruit shapes and peel and flesh colors. IG 10-44 (a–b), IG 10-76 (c–d), IG 10-80 (e–f), and IG 10-124 (g–h)

A selection intensity of 3% was applied to 237 F_2 individuals, generating seven genotypes with the highest selection index. These genotypes were then used to estimate differential selection and determine the predicted selection response (Table 5). This study showed that the selected genotypes of the F_2 population have high potential production and fruit quality because their selection response showed an increase in FW followed by an increase in PT and TSSs (Table 5). High TSS levels, especially in four genotypes with top selection indices (Table 4), were likely inherited from the female parent 'Inthanon RZ,' which is known for elevated TSS content (Hai and Thao, 2021). Nguyen et al. (2024) similarly reported that melon sweetness is predominantly influenced by the maternal parent. FL, FWd, and LWR also showed increasing mean values. Among methods, the selection index method is the most efficient for selecting superior genotypes and is based on the simultaneous selection of several traits (Rahimi and Debnath, 2023).

Among the selected genotypes, IG10-124 had the highest selection index (Table 4). Although IG10-44, IG10-80, and IG10-76 had slightly lower selection indices than their progenitor (IG10), they had higher PT and TSSs than their progenitor line. Selection indices have also been applied to select superior lines of millet (Sintia et al., 2023), rice (Sabouri et al., 2022; Sarwendah et al., 2022), barley (Eshghi et al., 2011), and melon (Gomes et al., 2021) based on the simultaneous selection of several traits. In addition, the predicted selection response based on PT and TSSs indicates that the mean value of these traits will increase. IG10-44, IG10-80, IG10-76, and IG10-124 had distinct traits and good fruit quality (Figure 3). These four genotypes had crunchy flesh, showing that superior fruit firmness leads to an extended fruit shelf life. In addition, they possessed good peel and flesh color and high TSSs. These traits suggest that these genotypes meet Indonesian consumer preferences. Therefore, these four genotypes are highly promising for selection and advancement to the next generation.

CONCLUSIONS

The F_2 melon population showed high genetic variability and moderate-to-high heritability for pericarp thickness and sugar content, indicating significant potential for genetic improvement. The uniform andromonoecious trait (*aaGG*) confirmed stable inheritance linked to desirable round fruit shape. Four genotypes, particularly IG10-124, exhibited preferred market traits such as high sugar content, thick pericarp, and crunchy texture. Future melon breeding programs should prioritize these promising genotypes and further investigate molecular markers associated with fruit quality traits. This approach will support breeders and farmers in developing sustainable melon production systems suitable for greenhouse cultivation, particularly in developing countries such as Indonesia.

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