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Genetic Variability and Trait Correlations of Melon (*Cucumis melo* L.) Genotypes

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Abstract

Melon (*Cucumis melo* L.) is an important horticultural crop. Melon breeding programs require comprehensive information on genetic variability and selection-related traits. Genetic variability and correlations among plant characters are essential parameters for effective selection in the S_2 Population. This study aimed to evaluate the genetic variability of several melon genotypes and to analyze correlations among plant characters as a basis for selection. The experiment was conducted using fourteen melon genotypes derived from selfed populations at the S_2 generation. The study employed a randomized complete block design with a single factor, consisting of 14 S_2 melon genotypes and four replications. The experimental unit is one individual plant in a polybag. The Observations of qualitative traits indicated the presence of variation within the genotypes for fruit rind color and fruit flesh color. Genotypes G2 exhibited the greatest fruit length (13.47 cm) and fruit diameter (11.95 cm). Genotypes G15 showed the highest total soluble solids content (15^0 Brix), while genotypes G7 had the thickest fruit flesh (3.25 cm). Broad-sense heritability estimates of the observed traits ranged from low to moderate. The traits of fruit length, fruit diameter, and fruit weight exhibited moderate broad-sense heritability (>45%). They were positively and significantly correlated with fruit weight, indicating that these traits can be used as selection criteria for fruit weight in subsequent plant breeding programs.

Keywords: correlation; heritability; melon breeding

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Introduction

Melon (*Cucumis melo* L.) is a leading horticultural crop and an important economic commodity with continuously increasing market demand. Data from Statistics Indonesia (1) indicate that melon production increased from 117,794 tons in 2023 to 125,384 tons in 2024. The observed increase in melon production reflects a rising demand in both domestic and export markets. Enhancing melon productivity can be achieved through plant breeding programs aimed at developing superior varieties with high yield potential, tolerance to major pests and diseases, and improved nutritional quality to support human health.

Increasing public awareness of healthy and nutritious food has driven efforts to improve melon fruit quality and has become a significant priority in melon variety development programs. Melon varieties possessing a sweet flavor, high nutritional content, and smaller fruit size are considered to have higher consumer preference. (2) reported that melon fruit contains β-carotene, with orange-fleshed melon exhibiting a β-carotene content of 2.05 mg per 100 g of fresh flesh, which is higher than that of green-fleshed melon. Furthermore, (3) reported that melon fruit is a good dietary source of provitamin A and vitamin C, which are beneficial for human health.

Improvement in fruit quality and productivity of melon can be achieved through plant breeding programs focused on the development of superior melon varieties with high yield potential, desirable fruit quality, and tolerance to biotic and abiotic stresses. (4) reported that high-yielding melon varieties with thick flesh and high sweetness levels constitute essential criteria for superior melon cultivars. Melon breeding activities have been conducted at the Tropical Fruit Research Center, IPB University, resulting in the release of several

melon varieties, including ‘Sunrise Meta’ and ‘Orange Meta’.

The second-generation selfed population (S_2) represents an early generation in which the frequency of heterozygous alleles begins to decrease while homozygosity increases, resulting in genotypes that exhibit more stable allele combinations and traits that can be consistently inherited in subsequent generations. The S_2 population still retains sufficient genetic variation to allow the identification of segregants with desirable trait combinations, while also beginning to display inheritance patterns that can be utilized for more accurate phenotypic selection. This is particularly relevant for the development of inbred lines in melon (5). Therefore, the S_2 population constitutes a critical stage in conventional breeding schemes for estimating genetic parameters such as heritability and trait correlations, and serves as a basis for selecting genotypes in subsequent plant breeding programs.

Plant breeding activities aimed at developing superior varieties involve several stages, including selection. The selection process is conducted based on specific breeding objectives by considering plant genetic variability, heritability, and correlations among traits, thereby improving the efficiency of selection (6). Both genetic and environmental variance components influence phenotypic variation in plants. Heritability represents the proportion of phenotypic variation that is attributable to genetic factors (7)(8). This study aimed to evaluate the genetic variability of several melon genotypes and to analyze correlations among plant traits as a basis for selection, in order to identify superior genetic materials for melon breeding programs.

Material and Methods

This research was conducted in a greenhouse at the Cikabayan Experimental Farm, Department of Agronomy and Horticulture, Bogor Agricultural University, at an altitude of approximately 250 m above sea level, with air temperatures ranging from 25 to 38 °C. This study employed fourteen melon genotypes derived from selfed populations at the S_2 generation. Fourteen melon genotypes were developed from crosses among five cultivars, namely ‘Honey Dew’, ‘Honey Blonde’, ‘Brilliant’, ‘Athena’, and ‘Serenade’, followed by self-pollination up to the S_2 generation. The experiment was conducted using a randomized complete block design (RCBD) with a single factor, consisting of fourteen S_2 melon genotypes and four replications. The experimental unit is one individual plant in a polybag. The instruments used in this study included a refractometer, ruler, weighing scale, and vernier caliper.

The study commenced with the preparation of the growing medium for melon seed germination, consisting of compost, rice husk charcoal, and soil in a 1:1:1 ratio. Melon seedlings aged 10 days were subsequently transplanted into polybags measuring 40 × 40 cm filled with the same growing medium. Pruning was performed on the primary branches from the first to the seventh node. Plant maintenance involved the application of AB mix nutrient fertilizer at a rate of 5 mL of solution A and 5 mL of solution B diluted in 1 L of water, with 200 mL of the solution applied to each plant. Irrigation was conducted manually according to the condition of the growing medium and the plant growth and development stages. Harvesting was carried out when the melon fruits exhibited physiological maturity indicators.

Observations were conducted on both qualitative and quantitative traits. Qualitative traits included fruit aroma, fruit shape, netting intensity (scale 1 = no netting; 2 = very sparse; 3 = moderate; 4 = fairly dense; 5 = very dense), netting distribution, fruit surface color, flesh color, and flesh texture. The assessment of qualitative traits was performed based on the *Descriptors for Melon (Cucumis melo L.)* published by IPGRI (9). Quantitative traits observed included stem diameter, petiole length, leaf length, leaf width, days to harvest, fruit length, fruit diameter, flesh thickness, rind thickness, fruit weight, and total soluble solids content. Days to harvest were calculated from the time seedlings were transplanted from the nursery into larger polybags until the fruits reached harvest maturity. Total soluble solids content was measured using a refractometer.

Analysis of variance (ANOVA) was performed using the F-test at a 5% significance level. When treatment effects were significant, mean comparisons among genotypes were conducted using Tukey’s honestly significant difference (HSD) test to identify differences between genotypes. Pearson’s phenotypic correlation coefficients (r) were calculated to determine the relationships among the observed traits.

All statistical analyses were performed using R-Studio software. Heritability analysis was conducted to assess the contribution of genetic factors to phenotypic expression, with heritability values calculated according to the method described by (7).

Results and Discussion

Qualitative traits

The results of the qualitative trait evaluation indicated the presence of variation among the observed traits (Table 1). Observations of fruit aroma revealed that genotypes G14, G16, and G21 exhibited internal fruit aroma, whereas the remaining genotypes did not show this characteristic. Genotypes G10, G11, G14, G16, G20, G21, and G6 displayed a flattened fruit shape. Genotypes G15, G17, and G19 exhibited an oblate fruit shape, while genotypes G7 and G8 showed an elliptical fruit shape. Variability was also observed among genotypes for netting intensity and netting distribution. Qualitative traits in plants are generally controlled by simple genetic mechanisms involving one or a few genes, with minimal influence from environmental factors (10)(11).

According to (7), qualitative traits are generally controlled by simple genes with major effects on plant characteristics and are relatively stable against environmental influences. Therefore, selection based on qualitative traits is more efficient and enables the identification of target genotypes in early populations. Observations of fruit surface color and flesh color revealed the presence of variation within plant genotypes. Genotypes G10, G11, G14, G15, G16, G17, G20, G21, G6, G7, G8, and G2 exhibited intra-genotypic variability in fruit rind color. In addition, genotypes G15, G16, G17, G20, G21, G6, G7, and G8 showed intra-genotypic variability in fruit flesh color. (Table 1). The observed within-genotype variation may be attributed to the genetic materials used in the breeding program, as these genotypes represent early-stage selection materials in the process of line development. (7) reported that self-pollination in plant genotypes increases the frequency of homozygous gene pairs, resulting in greater uniformity within genotypes and increased variability among genotypes.

Table 1. Qualitative traits of 14 melon genotypes

Genotype	Internal fruit aroma	Fruit shape	Netting density	Netting distribution	Fruit surface color	Flesh color	Flesh texture
G10	Absent	*Flattened*	2	Distributed on one side	yellow orange, orange	white	crisp
G11	Absent	*Flattened*	2	Distributed on one side	yellow green, yellow orange	white	crisp
G14	Present	*Flattened*	1	absent	white, white green	orange	soft
G15	Absent	*Oblate*	1	absent	white, white yellow	orange, yellow orange	crisp
G16	Present	*Flattened*	3	Partially distributed	white, yellow orange	green, white orange	soft
G17	Absent	*Oblate*	3	Partially distributed	yellow, yellow green	orange, white orange	soft
G19	Absent	*Oblate*	1	Absent	yellow	yellow	crisp
G20	Absent	*Flattened*	1	Absent	white, yellow orange	white, white green	crisp
G21	Present	*Flattened*	1	Absent	white, green	white, white orange	crisp
G22	Absent	*Elliptical*	1	Absent	white	white orange	crisp
G6	Absent	*Flattened*	1	Absent	white, yellow orange	orange, yellow orange	crisp
G7	Absent	*Elliptical*	2	Distributed on one side	orange, yellow orange	white, orange	crisp
G8	Absent	*Elliptical*	2	Distributed on one side	orange, yellow orange	orange, yellow orange	crisp
G2	Absent	*Elliptical*	1	Absent	white, white yellow	white	crisp

Notes: Netting intensity score: 1 = no netting (0%); 2 = very sparse (10–25%); 3 = moderate (26–50%); 4 = fairly dense (50–75%); 5 = very dense (76–100%).

Quantitative traits

The results of the study indicated that genotype effects were significant for several traits, except for stem diameter, fruit weight, and total soluble solids content (Table 2). Quantitative characteristics are generally controlled by multiple genes (polygenic inheritance) and are strongly influenced by environmental factors (7). The coefficient of variation (CV) plays a vital role in determining the direction of plant breeding programs. The observed traits exhibited CV values ranging from 4.6% to 35.64% (Table 2). Low CV values indicate relatively uniform trait expression, suggesting that self-pollination can be effectively applied to develop pure lines. (12) reported that the coefficient of variation reflects the level of variability within a plant population, where lower CV values indicate greater uniformity of plant traits.

Table 2. Summary analysis of variance

Characters	MS Genotypes	MS Replication	CV (%)
Stem diameter	0.85^{ns}	0.89^{ns}	11.19
Petiole length	$9{,}39^{**}$	$6{,}98^{ns}$	12.92
Leaf length	$18{,}45^{**}$	$13{,}46^{*}$	11.6
Leaf width	$21{,}42^{**}$	$16{,}12^{ns}$	12.7
Days to harvest	$24{,}09^{*}$	$12{,}64^{ns}$	4.6
Fruit length	$12{,}96^{**}$	$0{,}90^{ns}$	12.97
Fruit diameter	$6{,}99^{**}$	$1{,}33^{ns}$	11.52
Flesh thickness;	$0{,}63^{**}$	$0{,}05^{ns}$	16.05
Rind thickness	$0{,}04^{*}$	$0{,}01^{ns}$	35.64
Fruit weight	$543{,}33^{ns}$	$944{,}9^{ns}$	28.5
Total soluble solids	$16{,}68^{**}$	$4{,}78^{ns}$	20.76

Notes: MS = mean square; CV = coefficient of variation; * significant at the 5% level; ** significant at the 1% level; ns = not significant.

Variation in fruit length and fruit diameter indicated that genotype G2 exhibited the largest fruit size, with a fruit length of 13.47 cm and a fruit diameter of 11.95 cm. In contrast, genotype G19 showed the smallest fruit size, with a fruit length of 7.28 cm and a fruit diameter of 7.05 cm. Variation in flesh thickness revealed that genotype G7 had the greatest flesh thickness (3.25 cm), whereas genotype G19 exhibited the smallest flesh thickness (1.82 cm). For rind thickness, genotypes G21 displayed the thickest rind (0.60 cm), while genotypes G10 had the thinnest rind (0.22 cm). Total soluble solids content varied among genotypes. Genotypes G15 recorded the highest total soluble solids content (15.57 °Brix), whereas genotypes G20 and G22 showed the lowest values (7.75 °Brix) (Table 3). Total soluble solids content is an essential trait in the selection process, as consumer preference tends to favor melon varieties with higher soluble solids content.

Table 3. Mean values of fruit length, fruit diameter, flesh thickness, rind thickness, and total soluble solids content in melon genotype

Genotype	FL (cm)	FD (cm)	FT (cm)	RT (cm)	TSS(°Brix)
G2	13.47a	11.95a	2.50abc	0.35ab	11.25ab
G6	13.27a	11.47a	1.92bc	0.47ab	9.50b
G7	12.90a	11.87a	3.25a	0.30ab	11.00ab
G8	13.15a	11.52a	2.67abc	0.40ab	11.25ab
G10	10.53abc	10.35a	2.85ab	0.22b	11.00ab
G11	11.05ab	9.87ab	2.20bc	0.42ab	10.50ab
G14	12.27ab	11.37a	2.17bc	0.37ab	11.75ab
G15	9.00bc	9.07ab	2.02bc	0.32ab	15.75a
G16	10.93abc	11.35a	2.75abc	0.25b	12.50ab
G17	10.93abc	11.12a	2.62abc	0.30ab	10.00b
G19	7.28c	7.05a	1.82c	0.52ab	7.75b
G20	11.77ab	11.25a	2.25bc	0.32ab	8.75b
G21	11.20ab	10.85a	2.17bc	0.60a	10.00b
G22	13.43a	11.30a	2.30abc	0.42ab	7.75b

Notes: Values followed by the same letter are not significantly different according to Tukey–Kramer's test at the 5% significance level. FL = fruit length; FD = fruit diameter; FT = flesh thickness; RT = rind thickness; FW = fruit weight; TSS = total soluble solids.

The observation of days to harvest indicated that genotype G7 exhibited the earliest maturity, reaching harvest at 67 days after transplanting. In contrast, genotype G6 required a longer period to reach harvest, at 77 days after transplanting. For petiole length, genotype G8 showed longer petioles compared to the other genotypes. Genotypes G7 exhibited greater leaf length and leaf width than the remaining genotypes. In contrast, genotype G20 had the smallest leaf size, with a leaf length of 14.0 cm and a leaf width of 15.5 cm, compared to the other genotypes (Table 4).

Table 4. Mean values of petiole length, leaf Length, leaf width, and days to harvest in Melon Genotypes

Genotype	PL (cm)	LL (cm)	LW (cm)	DH (days)
G2	14.50ab	18.25ab	18.62abc	74.00ab
G6	13.12ab	18.87ab	20.25abc	77.00a
G7	15.25ab	21.25a	23.50a	67.50b
G8	16.00ab	19.25ab	21.12abc	74.50ab
G10	17.12a	17.25ab	19.25abc	70.50ab
G11	13.37ab	18.00ab	19.00abc	73.25ab
G14	12.37b	16.75ab	18.25abc	73.50ab
G15	13.75ab	20.00a	20.25abc	74.25ab
G16	13.25ab	20.12a	22.00ab	71.50ab
G17	14.00ab	20.25a	20.87abc	69.75ab
G19	11.87b	14.62b	15.62c	74.00ab
G20	13.50ab	14.00b	15.50c	73.25ab
G21	15.50ab	18.75ab	20.62abc	70.00ab
G22	12.12b	16.125ab	16.87bc	71.75ab

Notes: Values followed by the same letter are not significantly different according to Tukey–Kramer's test at the 5% significance level; PL = petiole length; LL = leaf length; LW = leaf width; DH = days to harvest

Estimation of Variance Components and Broad-Sense Heritability

The results indicated that stem diameter and fruit weight exhibited low heritability estimates (Table 5). Low heritability values suggest that environmental variance plays a significant role in influencing these plant traits. Selection based on traits with low heritability is considered inefficient for genetic improvement, as ecological factors rather than genetic effects largely govern phenotypic variation. (13) reported that stem diameter heritability falls within the low to moderate range, indicating a greater influence of environmental variance compared to genetic variance. Traits with low heritability reflect a substantial environmental contribution to phenotypic variation in plants (14).

Moderate heritability estimates were obtained for petiole length, leaf length, leaf width, days to harvest, fruit diameter, flesh thickness, and total soluble solids content. Fruit length exhibited a high heritability value (Table 5). The high heritability of fruit length indicates that phenotypic variation in this trait is more strongly influenced by genetic variance than by environmental variance. (15) explained that traits with high heritability values ($h^2\_bs \geq 50\%$) reflect a greater contribution of genetic variability compared to ecological variability in determining phenotypic variation. Therefore, fruit length, which exhibited high heritability, can be effectively utilized as a selection criterion. (16) also stated that plant traits with high heritability indicate a strong genetic influence relative to environmental effects, making them suitable as selection traits in plant breeding programs.

Table 5. Estimated variance components and broad-sense heritability values

Characters	VG	VE	VP	h^2_{bs} (%)
Stem diameter	0.04	0.69	0.73	5
Petiole length	1.53	3.27	4.799	32
Leaf length	3.51	4.43	7.94	44
Leaf width	3.84	6.07	9.91	38
Days to harvest	3.22	11.2	14.42	22
Fruit length	2.68	2.23	4.91	55
Fruit diameter	1.36	1.53	2.89	47
Flesh thickness	0.12	0.18	0.30	45
Rind thickness	0.0065	0.018	0.028	26
Fruit weight	30.86	419.88	450.74	6
Total soluble solids	2.95	4.87	7.82	38

Notes: VG = genetic variance; VE = environmental variance; VP = phenotypic variance; h^2_{bs} = broad-sense heritability.

Correlation among plant traits

According to (15), when traits exhibit low heritability, the selection process can be optimized by utilizing other characteristics that show strong associations with the primary target trait. Correlation analysis has positive or negative values, indicating the strength and direction of relationships among traits. Positive correlations suggest that selection for correlated characteristics will result in simultaneous improvement of the target trait, whereas negative correlations indicate an inverse relationship between traits. In plant breeding programs, correlation coefficients can be used as indicators for indirect selection of target traits (17).

The results showed that fruit weight exhibited positive and significant correlations with peduncle length ($r = 0.35$, $P < 0.01$), leaf length ($r = 0.47$, $P < 0.01$), leaf width ($r = 0.50$, $P < 0.01$), fruit length ($r = 0.76$, $P < 0.01$), fruit diameter ($r = 0.78$, $P < 0.01$), and flesh thickness ($r = 0.65$, $P < 0.05$) (Table 6). (18) also reported that fruit weight is positively correlated with fruit length, fruit diameter, and flesh thickness.

Total soluble solids content showed positive and significant correlations with leaf length ($r = 0.33$, $P < 0.05$) and leaf width ($r = 0.31$, $P < 0.05$). Flesh thickness exhibited a negative and significant correlation with rind thickness ($r = -0.39$, $P < 0.05$) (Table 6). A negative and significant correlation indicates an inverse relationship between traits. (17) reported that traits with negative correlations exhibit opposing linear relationships, in which an increase in one trait is accompanied by a decrease in another, and vice versa. According to (19), traits showing non-significant correlations indicate that selection for these traits can be conducted independently and simultaneously.

Table 6. Linear correlation coefficients among melon plant traits

	DB	PTD	PD	LD	UP	PB	DB	TDB	TKB	BB
PTD	0.07^{ns}									
PD	0.21^{ns}	0.49**								
LD	0.21^{ns}	0.50**	0.92**							
UP	-0.23^{ns}	-0.14^{ns}	-0.16^{ns}	-0.23^{ns}						
PB	0.13^{ns}	0.29*	0.28*	0.34*	-0.02^{ns}					
DB	0.13^{ns}	0.29*	0.43**	0.48**	-0.15^{ns}	0.85**				
TDB	0.21^{ns}	0.46**	0.47**	0.54**	-0.44*	0.45**	0.54**			
TKB	0.02^{ns}	-0.16^{ns}	-0.12^{ns}	-0.05^{ns}	0.05^{ns}	0.04^{ns}	-0.01^{ns}	-0.39*		
BB	0.20^{ns}	0.35*	0.47**	0.50**	-0.22^{ns}	0.76**	0.78**	0.65*	-0.02^{ns}	
PTT	0.06^{ns}	0.08^{ns}	0.33*	0.31*	0.09^{ns}	-0.10^{ns}	0.08^{ns}	0.12^{ns}	-0.11^{ns}	-0.05^{ns}

Notes: *significant correlation at the 5% level based on Pearson's method; **considerable correlation at the 1% level; ns = not significant; SD = stem diameter; PL = petiole length; LL = leaf length; LW = leaf width; DH = days to harvest; FL = fruit length; FD = fruit diameter; FT = flesh thickness; RT = rind thickness; FW = fruit weight; TSS = total soluble solids.

Conclusion

The evaluated melon genotypes exhibited variability in both qualitative and quantitative traits. Genotypes G2 showed the greatest fruit length and fruit diameter. Genotype G15 recorded the highest total soluble solids content, while genotype G7 exhibited the most significant flesh thickness. Broad-sense heritability estimates of the evaluated traits ranged from low to moderate. Fruit weight showed positive and significant correlations with peduncle length, leaf length, leaf width, fruit length, fruit diameter, and flesh thickness. The traits of fruit length, fruit diameter, and fruit weight exhibited moderate broad-sense heritability, showed positive and significant correlations with fruit weight, indicating that these traits can be used as selection criteria for genotypes in subsequent plant breeding programs.

Conflict of Interest

All authors declare no conflicts of interest.

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