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The phenotypic and genetic diversity test of several inbred lines on the 7th generation of melon (*Cucumis melo*)

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Abstract. *Kustanto H. 2023. The phenotypic and genetic diversity test of several inbred lines on the 7th generation of melon (*Cucumis melo*). Biodiversitas 24: 2623-2629.* The needs for melon (*Cucumis melo* L.) keep increasing year by year. Some efforts to increase the quality of melon have been carried out to obtain better quality and quantity through plant breeding programs. Providing new melon inbred lines with different phenotypic and genotypic traits is very important in assembling melon hybrid varieties with new genetic characteristics, potentially production superior melon varieties. The study's objective was to find out the genetic diversity of the tested melon genotypes and to obtain inbred lines of melon, which are the potential to be developed as superior hybrid varieties. The inbred lines of melons showed that the diversity coefficient values of morphological traits ranged from 0.57 to 1.0. There are 3 Groups, namely Group I, II, and III. Group I comprises two genotypes: MJ 34 and HHX 015. Group II is divided into 2, Group A and B. Gaboup A comprises three genotypes: MJ 25, Amanda variety as the standard of comparison, and MO 29, while Group B has one genotype: HHA 02. Group III comprises three genotypes: MSO 12, MSP 13, and HHAL 01. The traits are as follows: leaf length, leaf width, fruit length, fruit diameter, and the fruit flesh thickness have closely related to yield per plant.

Keywords: Genetic, inbred, lines, melon, morphological, phenotypic

INTRODUCTION

The need for melon (*Cucumis melo* L.) for consumption keeps increasing along with standard of living. The increase in living is accompanied by the increase in fulfilling the need for foods that are good and delicious and contain good nutrients. Melon is very popular because it tastes good, is easily cultivated, and has high economic value. Melon contains vitamins and minerals that benefit human health (Manchali et al. 2021). Melon contains vitamins A, B, B6 potassium, folic acid, and niacin. Some minerals contained in melon include potassium, calcium, iron, magnesium, phosphor, sodium, and zinc. Orange melon contains carotenoid which benefits heart health and the immune system, while green melon contains vitamin B6 for maintaining strong bones and teeth (Vanoli 2015; Setiawan 2018; Sánchez et al. 2021).

Increasing production in breeding melon requires superior varieties such as high production and resistance to pests and diseases (Cao et al. 2022). A breeding program of melon is carried out in several steps to obtain superior hybrid varieties. The first step is making genetic diversity (Chikh-Rouhou et al. 2021; Saputra et al. 2022). The second step is making inbred lines through inbreeding. Self-pollination (autogamy) on heterozygous plants may cause segregation and decrease the vigor (Castro et al. 2020). The vigor may decrease in each generation of self-pollination and form a homozygote inbred. In the first generation of self-pollination, the vigor decreased to about half of the total decrease in vigor, and would become half in the next generation. Traits of the plants, which have decreased in vigor due to self-pollination, show some deficiencies: the plants grow shorter, tend to fall over easily, are sensitive to disease, and other unwanted traits will appear. Such a phenomenon is the so-called inbreeding depression (Poehlman 1983; Ali et al. 2019). The third step is a determination of the best crossing combination. The fourth step is the initial testing of production, resistance to pests and diseases, and so on, following the purpose of plant breeding. The fifth step is adaptation testing and multi-location of the obtained hybrids (Nhi et al. 2010; Amzeri et al. 2021).

Genetic diversity in melon is found in various biomass components and yield traits, such as fruit size, fruit shape, fruit flesh (pulp) color, and fruit sweetness level. Genetic diversity is affected by gene composition differences in chromosome (Chomicki et al. 2020; Cao et al. 2022). Diversity formation in a breeding melon can be carried out by hybridization between genotypes from the accession of the germplasm or varieties bred by the farmers (Cui et al. 2022). A plant population's phenotypic diversity is affected by genetic diversity, environment varieties, and diversity in genetic x environment interaction. Therefore, information about variance components and heritability of traits could increase the selection process effectiveness in the breeding process of melon. Heritability is a measure of genetic influence on phenotypic traits of the plant. Heritability values range from 0-1. The higher the heritability value, the greater the genetic influence of a genotype compared to the influence of the environment where the plants grow (Ritonga et al. 2018).

The availability of inbred lines with high diversity is the

most important for making a hybrid variety of melon with superiorities: high production, thick fruit flesh (pulp), sweetness, and high productivity of melon. Unfortunately, the availability of the inbred lines of melon is very limited due to the long process of making it that takes a long time from some generations of melon, and the lining yield in the form of lines, such as perishable seeds and could not be stored for a long time. Therefore, providing new melon inbred lines with different phenotypic and genotypic traits is crucial in assembling melon hybrid varieties than compete in the market. Furthermore, the new genetic characteristics contained in each inbred line have the potential to produce melon varieties that have better and superior characters than existing melons if they are released to the market. Therefore, the study's objectives were to find out the genetic diversity of tested genotypes of melon and to obtain inbred lines of melon that are a highly potential to be developed as superior hybrid varieties of melon.

MATERIALS AND METHODS

Study area

This research used a Completely randomized block design (RCBD) with three replications. The number of plants per replication was 50 plants, and the number of plants selected per replication for recording observation was ten samples. The research materials were eight inbred lines of melon on the 7th generation (S_7) and one commercial hybrid variety, Amanda (PT. Bisi International), as the standard of comparison. The eight lines were MJ 34, MJ 25, MSO 12, MSP 13, HHAL 01, HHA 02, HHX 015, and MO 29 as sib-mating on the seventh-generation (S_7) that has been developed by CV. Hakako Seed. Amanda Hybrid Variety, used as the standard of comparison, is a commercial hybrid variety (F_1) of melon that people like very much today. Other materials included fertilizers of nitrogen-phosphate-potassium (NPK), phosphate (P), Potassium (P), plastic mulch, small polybags, stakes (sticks), markers, and pesticides. The experiment was conducted at Ngarum Village, Ngrampal Subdistrict, Sragen Regency, Central Java Province, Indonesia, from August to November 2022.

Land preparation was conducted by tillage, clearing the land from the crop remains and weeds, making the seedbed, and applying the plastic mulch. Before planting, basic fertilizer was applied using organic fertilizer at 15 tons/ha dose and inorganic fertilizers such as: urea 150 kg/ha, SP-36 250 kg/ha, and KCl 50 kg/ha. The seedbed dimensions were 1 m x 0.4 m x 6 m (width x height x length). The seedbeds were covered with plastic mulch, and the dibbles were made with a spacing of 0.7 x 0.6 m. Before planting, the seeds were germinated in small polybags, and by the age of one week, the plants were transferred while the plant had three leaves. The plants were maintained by applying supplement fertilizer, weeding, installing the stake (stick), pruning the lateral branches, irrigation and pest and disease control. The first supplement fertilizer was applied seven days after planting (DAP) using NPK by 100 kg/ha dose. The second supplement fertilizer was applied 14 DAP using NPK 30 kg/ha and boron 4.0 kg/ha dose. The third supplement fertilizer was applied at 21 DAP using NPK by 40 kg/ha dose. The fourth supplement fertilizer was applied at 28 DAP using NPK by 35 kg/ha dose. The fifth supplement fertilizer was applied at 42 DAP using NPK 40 kg/ha, phosphate by 100 kg/ha and potassium by 25 kh/ha dose. The sixth supplement fertilizer was applied at 49 DAP using NPK 40 kg/ha and by 40 kg/ha and potassium by 30 kg/ha dose. Manual weeding was carried out by hand and a hoe. Lateral branches were pruned at 35 DAP. Irrigation is done every day until 7 DAP, after that, it is done every two days. Pest control and spraying were carried out using pesticides with active ingredients of abamectin at a dose of 2,0 ml/L, hexaconazole at 1.5 ml/L, and azoxystrobin at 1 ml/L, while there were signs of pest attacked. The observed traits are: (i) stem diameter (cm) was measured at the midpoint between stem and blossom end, (ii) the number of stems (pcs) was counted from the beginning of the emergence of branches until before harvesting, (iii) the number of leaves (pcs) was counted from first stem segment to tip plant, (iv) leaf length (cm) was measured from base to tip of leaves using rules, (v) Leaf width was measured from left side to right side of leaves using rules, (vi) fruit length (cm) was measured from stem to blossom end, (vii) fruit diameter (cm) was measured from midpoint between stem and blossom end, (viii) skin thickness (cm) was measured from the top, bottom, and left/right sides skin of the fruit sliced, (ix) fruit flesh thickness (cm) was measured from the top, bottom and left/right sides of the fruit sliced (x) fructose level (brix) was used refractometer, and (xi) fruit weight per plant was balanced using scales.

Data analysis

F-test was carried out to see the genotypic influence. If the genotype shows a significant difference, it will be followed by an LSD test. LSD = $t_{\alpha/2}$ $(2s^2/r)^{½}$, in which: $t_{\alpha/2}$ = t value at level-α, s^2 = value for mean squared error (MSe), r = the number of replications (Esteras et al. 2020; Kustanto 2022). The statistical software of DSAASTAT is used for data analysis. However, variances between genotypes can be found out using the genotypic equation. However, variances between genotypes can be found using the genotypic equation. Coefficient of variations (GCV) as follows: GCV = √(genetic variance/x) x 100%, in which: X = mean of the population, genetic variance = σ2g, σ2g = (MS_g-MS_e)/r, σ2g = σ2f- σ2e, in which: σ2f = phenotypic variance, σ2e = environmental variance/error. Moreover, variances in genotypes are obtained using the equation as follows: Coefficient of Variance (CV) = (Standard deviation/mean) x 100%, high or low values for GCV criteria are as follows: 0-25% (very low); 25-50% (rather low); 50-75% (high enough); 75-100% (high). The percentage of the genetic role that affects the phenotypic appearance is assumed with broad heritability (H_2), by the equation: H_2 = (σ2g/σ2f) = σ2g/(σ2f+σ2e). Classification of the heritability is as follows: <25% (low): 25-50% (rather low); 50-75% (rather high); >75% (high) (Pantalone et al. 1996; Ali et al. 2019). The relationship of inbred lines on the tested melon was determined through genetic similarity

analysis. The inbred lines were grouped following the genetic similarity matrix through Unweighted Pair Group Method using Arithmetic Average (UPGMA). Dendrogram was constructed using Euclidian Coefficient. The distance between the matrix and dendrogram was formed using NTSYSpc (Numerical Taxonomic System) program version 2.0 A Correlation analyzed the relationship between variables of observation. The formulas for correlation coefficients between the two traits are $\sigma 2f_{xy} = Cov\ (x.y)/\sqrt{\sigma^2(x).\ \sigma^2(y)}$ in which: $\sigma 2f_{xy}$ = phenotypic correlation coefficient between x and y, Cov (*x,y = trait covariance* x and n y), $\sigma^2(x)$ = traits variance x and $\sigma^2(y)$ = trait variance y (Hastini et al. 2019; Kustanto 2022). Calculations for the correlation values are: (a) not strong (0.1-0.2), (b) rather strong (0.2-0.4), (c) strong enough (0.4-0.6), (d) strong (0.6-0.8) and (e) very strong (0.8-1.0).

RESULTS AND DISCUSSION

Results of the F-test on traits of stem diameter, leaf length, and leaf width showed a very significant influence. The number of stems showed insignificant influence, and the number of leaves/plants showed significant influence based on F-test. The MJ 34 genotype has the highest stem diameter, while the Amanda variety has the lowest. The average number of stems of the whole tested genotypes ranged from 2.93-3.75/plant and were not significantly different based on F-test. The highest number of leaves were found on MJ 34 genotype, and the lowest ones were found on MO 29. The highest leaf length was found on MJ 25 and the lowest on MO 29, while the highest leaf width was found on MJ 25 and the lowes on MO 29, and it was not significantly different from HHA 02 (Table 1). The phenotypic trait appearances of agronomic components are presented in Table 1. The leaf shape of each genotype shows differences in the shape, indentation, and surface of the leaf blade. The leaf appearances are presented in Figure 1.

Results of the F-test on traits of fruit length, skin thickness, fruit flesh (pulp) thickness, and fruit weight/plant showed a significant influence between the tested genotypes. Fruit diameter showed a significantly different influence between the tested genotypes and F-test. The highest fruit length was found on HHX 015, and the lowest was found on MJ 34 and was not significantly different from MO 29, MJ 25, and HHA 02. The highest fruit diameter was found on Amanda as the standard of comparison variety, and the whole tested genotypes showed lower fruit diameter. The highest skin thickness was found on MSO 12 and MSO 13, while the lowest was on MJ 34, MJ 25, HHA 02, and MO 29. The highest fruit flesh thickness was found on the Amanda variety, while the lowest was found on MJ 34 and MSO 12. The highest fructose level was found on the Amanda variety and was not significantly different from MJ 25, MSO 12, MSP 13, HHA 01, and MO 29, while the lowest was found on HHX 015. The highest fruit weight/plant was found on the Amanda variety as the standard of comparison, and the lowest were found on MJ 34 and MO 29 (Table 2). The shape of the melon fruit in each tested genotype showed differences in fruit shape, fruit skin color, and web pattern (Figure 2). The melon flesh of each genotype tested showed differences in the color and softness of the flesh (Figure 3).

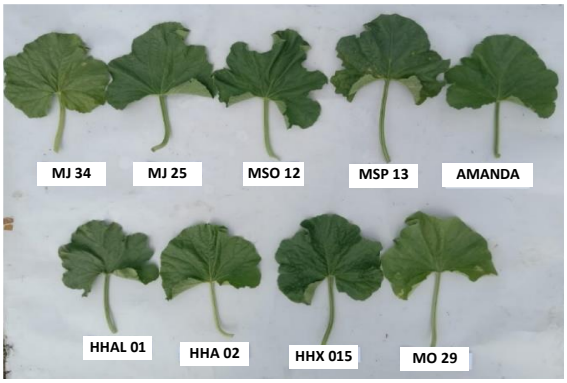

Figure 1. Morphological traits of leaf on the tested genotypes

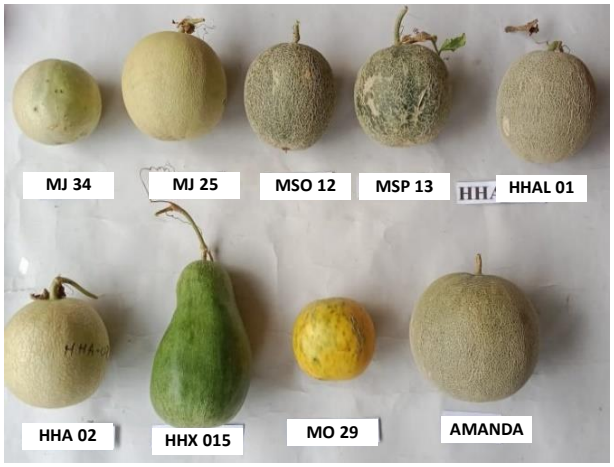

Figure 2. Morphological traits of the fruit on the tested genotypes

Figure 3. Morphological traits of the fruit flesh (pulp) on the tested genotypes

Table 1. Phenotypic traits and agronomic traits of different inbred lines of melons

Genotype	SD (cm)	NS (pcs)	NL (cm)	LL (cm)	LW (cm)
MJ 34	1.52 a	3.27	21.17 a	15.34 b	11.92 bc
MJ 25	1.21 bc	3.75	18.77 ab	18.34 a	14.97 a
MSO 12	1.28 b	3.25	19.67 ab	17.94 ab	12.03 b
MSP 13	1.2 bc	3.68	19.57 ab	16.28 ab	10.41 bc
HHAL 01	1.21 bc	2.93	16.72 bc	15.78 b	11.19 bc
HHA 02	1.23 bc	2.93	18.72 ab	16.00 ab	10.35 c
HHX 015	1.26 b	3.21	19.22 ab	17.20 ab	13.60 ab
MO 29	1.28 b	3.51	15.22 c	12.32 c	10.15 c
Amanda	1.04 c	3.19	18.21 b	16.99 ab	10.90 bc
Mean	1.25	3.3	18.58	16.24	11.72
p	**	ns	*	**	**
LSD (p<0.05)	0.13	-	2.81	2.45	1.59
CV (%)	6.04	14.05	8.75	8.71	7.83

Notes: SD: Stem diameter, NS: Number of the stem, NL: Number of leaves, LL: Leaf length, LW: Leaf width, **Significant level of 1%, *Significant level of 5%; ns: not significant, CV: Coefficient of Variance, p: Significance. LSD: A least significant difference. The mean value followed by different letters in the same column showed a significantly different between genotypes base on LSD (p=0.05)

Table 2. Morphological appearance of some traits on yield components of different inbred lines of melons

Genotype	FL (cm)	FD (cm)	ST (mm)	TFF (cm)	FL (brix)	FWP (kg)
MJ 34	10.06 c	9.39 b	2.01 d	2.82 c	8.65 b	0.53 e
MJ 25	12.11 bc	11.22 b	2.02 d	3.52 b	11.18 a	1.76 b
MSO 12	12.23 b	10.51 b	5.03 a	2.82 c	12.37 a	0.87 d
MSP 13	11.21 bc	11.22 b	5.08 a	3.01 bc	11.07 a	0.91 d
HHAL 01	14.22 b	11.07 b	4.03 b	3.00 bc	12.84 a	1.05 d
HHA 02	12.22 bc	11.22 b	2.02 d	3.01 bc	10.72 ab	0.98 d
HHX 015	21.23 a	11.02 b	3.02 c	3.04 bc	6.20 c	1.33 c
MO 29	9.49 c	9.45 b	1.97 d	3.06 bc	11.14 a	0.57 e
Amanda	14.23 b	13.69 a	3.02 c	5.08 a	13.02 a	2.10 a
Mean	13.00	10.98	3.13	3.26	10.79	1.12
p	**	*	**	**	**	**
LSD (p<0.05)	3.26	2.29	0.32	0.49	2.32	0.17
CV (%)	14.51	12.03	5.95	8.62	7.41	8.94

Notes: FL: Fruit length, FD: Fruit diameter, ST: Skin thickness, TFF: Thickness of the fruit flesh, FL: Fructose level, FWP: Fruit weight/plant, CV: Coefficient of Variance, p: Significance. LSD: A least significant difference. The mean value followed by different letters in the same column showed a significantly different between genotypes base on LSD (p=0.05)

The grouping based on morphological traits with a dendrogram shows that the similarity coefficient values ranged from 0.0 to 0.43 or the morphological trait diversities ranged from 0.57 to 1.0. As presented in Figure 4, there are 3 Groups, Group I, II, and III. Group I comprises 2 genotypes: MJ 34 and HHX 015. Group II is divided into 2, Group A and B, Group A comprises 3 genotypes: MJ 25, Amanda variety as the standard of comparison, and MO 29, while Group B has 1 genotype: HHA 02. Finally, Group III comprises 3 genotypes: MSO 12, MSP 13, and HHAL 01 (Figure 4).

The value of genetic variance, phenotypic variance, genetic coefficient of variation, phenotypic coefficient of variations, and heritability of the tested plant traits showed diverse values. Values of genetic variance ranged from 0.02-16.39, values of phenotype variance raged from 0.24-19.95, values of genetic coefficient of variation (GCV) ranged from 4.38-56.80%, values of phenotypic coefficient of variations ranged from13.04-50.72%, and values of heritability ranged from 8.85-98.62% on traits of the tested plants (Table 3).

The traits of leaf length, leaf width, fruit length, fruit diameter, and fruit flesh thickness (flesh) have a strong and significant relationship with fruit yield per plant. Leaf length has a significant relationship between fruit weight per plant 0.61. Leaf width has a significant relationship between fruit weight per plant 0.42. Fruit diameter has a significant relationship with fruit weight per plant 0.87. Thickness of fruit flesh has a significant relationship with fruit weight per plant, which is 0.83 (Table 4).

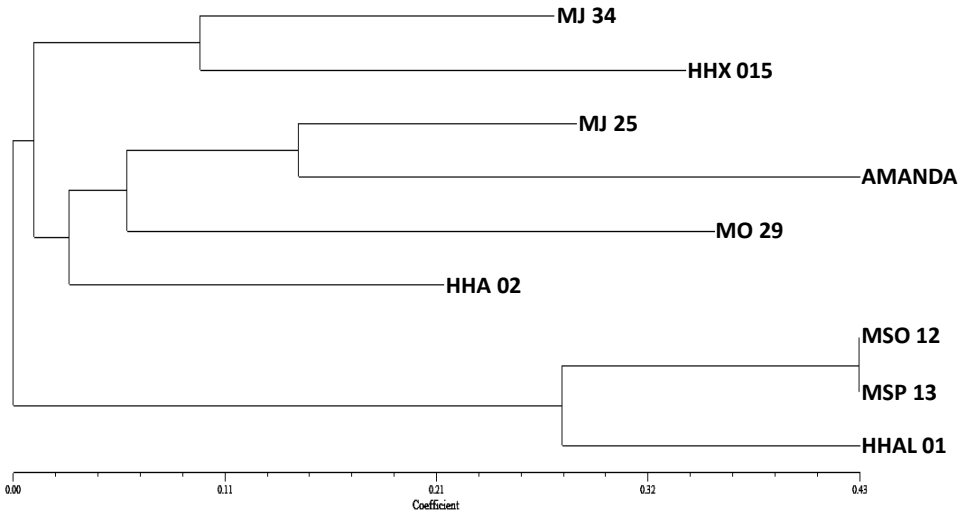

Figure 4. Dendrogram on the relationship between the tested genotypes based on morphological traits

Table 4. Correlations among the observed traits using the averages of replications

	SD	NS	NL	LL	LW	FL	FD	ST	TFF	FRL	FWP
SD	1										
NS	0.02^{ns}	1									
NL	0.41^{*}	0.06^{ns}	1								
LL	-0.29^{ns}	0.04^{ns}	0.57^{*}	1							
LW	0.12^{ns}	0.33^{ns}	0.34^{ns}	0.64^{*}	1						
FL	-0.28^{ns}	-0.33^{ns}	0.07^{ns}	0.43^{*}	0.42*	1					
FD	-0.87^{**}	-0.15^{ns}	-0.02^{ns}	0.51^{*}	-0.01^{ns}	0.38^{ns}	1				
ST	-0.25^{ns}	0.01^{ns}	0.16^{ns}	0.34^{ns}	-0.18^{ns}	0.12^{ns}	0.18^{ns}	1			
TFF	-0.71^{**}	0.02^{ns}	-0.15^{ns}	0.23^{ns}	-0.02^{ns}	0.15^{ns}	0.84^{**}	-0.14^{ns}	1		
FRL	-0.52^{*}	-0.04^{ns}	-0.41^{*}	0.01^{ns}	-0.39^{ns}	-0.49^{*}	0.38^{ns}	0.32^{ns}	0.38^{ns}	1	
FWP	-0.75^{**}	0.07^{ns}	-0.02^{ns}	0.61^{*}	0.42^{*}	0.45^{*}	0.87^{**}	,-0.06^{ns}	0.83^{**}	0.21^{ns}	1

Note: SD: Stem diameter, NS: Number of the stem, NL: Number of leaves, LL: Leaf length, LW: Leaf width, FL: Fruit length, FD: Fruit diameter, ST: Skin thickness, TFF: The thickness of fruit flesh, FRL: Fructose level and FWP: Fruit weight per plant, **Significant in p=0.01, *Significant in p=0.05, ns: non-significant

Table 3. Values for genetic variance, phenotypic variance, genetic coefficient of variance, phenotypic coefficient of variations, and heritability

Traits	σ2g	σ2f	GCV	PCV	H_2
LW	3.73	5.73	11.89	14.74	65.03
FL	3.55	4.40	16.46	18.31	80.79
NL	3.22	5.87	9.66	13.04	54.93
NS	0.02	0.24	4.38	14.72	8.85
SD	0.02	0.03	11.64	13.13	78.56
LL	16.39	19.95	31.17	34.38	82.16
FD	1.50	3.24	11.15	16.41	46.18
FWP	0.40	0.41	56.80	57.51	97.56
ST	2.49	2.52	50.37	50.72	98.62
TFF	0.72	0.80	26.03	27.42	90.11
FL	6.74	7.38	24.06	25.17	91.32

Note: SD: Stem diameter, NS: Number of stems, NL: Number of leaves, LL: Leaf length, LW: Leaf width, FL: Fruit length, FD: Fruit diameter, ST: Skin thickness, TFF: The thickness of fruit flesh, FL: Fructose level, FWP: Fruit weight per plant, σ2g: genetic variance, σ2f: phenotypic variance, PCV: phenotypic coefficient of variations, GCV: genetic coefficient of variations

Discussion

Variabilities on inbred lines of melon over the morphological traits indicate different traits between the tested lines. The differences between the homozygote inbred lines of melon were not noticeable compared to the hybrid variety (F_1), Amanda, which was more heterozygote (Table 1). Such growth variation was caused by diverse gene composition in each tested genotype. Growth is an irreversible volume, size, or weight increasing, including cell division phase, elongation, and differentiation. The decreased growth of the plant could be caused by limited cell division, cell enlargement due to the loss of turgor and inhibition of various growth metabolisms, and a decrease in photosynthesis (Barzegar et al. 2018). Different growth will affect the melon's agronomic traits and yield traits (Nhi et al. 2010; Ilahy et al. 2020). Variabilities of melon are mostly found in the morphological traits of the fruit, such as the size and shape of the fruit as well as skin color and the fruit flesh (Ilahy et al. 2020). Genetic control on phenotypic traits in melon is still poorly understood, for instance, fruit size and no bitter taste. The phenotypic traits

are controlled by major and minor genes, which cause dominant or recessive genetic traits, The recessive genetic traits relate to non-functional proteins due to point mutation, stop codons, and transposon insertion. The genetic structures of melons are different among them based on traits analysis and molecular polymorphism (Duong et al. 2021). The decreased ethylene concentration in the flower bud causes the emergence of the stamen. In comparison, the decline of hormonal levels in fruit will produce bigger fruits due to the number of cells or the cell size increase (Pitrat 2013). Besides genetic factors, environmental factors also create variabilities in the tested genotypes of melon. The productivity and quality of melon are affected by environmental factors, such as good watering, which will increase the harvest yield without any negative effect of decreasing fruit quality (Fernando et al. 2018; Pengli et al. 2020).

The similarity coefficient indicated that the tested genotypes showed high genetic variance based on the morphological traits. Each group shows genetic differences which can be seen from the genetic distance. The grouping conformed to the relationship used to assess the variations in melon′s genetic resource and was useful in the selection process. This information can be used for genetic resources development and management, including breeding, to deal with rapid climatic change. The greater the genetic distance, the greater the opportunity of obtaining heterosis and better melon hybrid values when crossed (Chikh-Rouhou et al. 2021; Silveira et al. 2022).

GCV values reflect the extent of genetic variation, so the traits of fruit weight and thickness of the fruit skin have high genetic variability. On the other hand, the traits of fruit length and thickness of the fruit flesh have rather low genetic variability. However, the genetic coefficients of variation for other characters are low. Without such genetic variance, improving the plant traits in the breeding program would be difficult (Amzeri et al. 2021). Germplasm and genetic resources of melon are the valuable genetic reservoir in the breeding program. A melon genotype's morphological characteristics and organoleptic can be used to assemble superior commercial varieties and have high commercialization value (Chikh-Rouhou et al. 2021). Genetic variability is affected by qualitative and quantitative traits. A single gene controls the qualitative trait, so predicting segregation patterns between generations (offspring) is easier. On the other hand, many genes control quantitative traits, and each gene influences certain traits differently. Genetic variability in inbred melon is required to assemble a variety with good yield stability in fluctuating climatic conditions (Daryono et al. 2019).

The inbred melon lines tested showed that the characteristics of fruit weight per plant, leaf length, fruit lesh thickness, and fructose level had a high phenotypic coefficient of variation (PCV). The diversity of inbred lines in phenotypic appearance was high. That shows the new inbred lines have different characteristics from existing melons. The growing environment of melon plants influences phenotypic characteristics expressed through qualitative and quantitative characteristics (Wahyuni et al. 2022). Processes such as the protection of plant varieties and intellectual property rights require an accurate recording of phenotypic characteristics that can reflect the genotypic properties contained in the genotype (Bostyn 2021; Yu et al. 2021). Some traits observed in the tested inbred lines showed low to high heritability values. Traits of leaf length, stem diameter, fruit length, fruit weight, fruit skin thickness, fruit flesh (pulp) thickness, and fruit content showed high heritability. Heritability is the percentage of the ratio between genetic variance and phenotypic variance. Heritability estimation is used to measure genetic and environmental factors on phenotypes. High heritability indicates that the genetic factor is more influential than the environmental factor, and the selection can be carried out following the traits. High heritability is used to increase the selection effectiveness of plant breeding (Bekele and Rao 2014; Yani et al. 2018).

Traits inheritance of fruit weight, fruit shape, the thickness of fruit flesh, density of the fruit flesh and the fructose content can be used as selection criteria because those traits are controlled by major genes and polygenes with dominant and additive effects (Dantas et al. 2023). Melon traits are controlled by quantitative inheritance with dominant and additive effects. Therefore, Quantitative trait loci (QTL) mapping of the traits is required to identify all genes, which control traits of the fruit in the improved variety of melon (Sakulphrom et al. 2018). The traits of leaf length, leaf width, fruit length, fruit diameter, and thickness of fruit flesh (pulp) have strong dan significant relationship with the fruit yield per plant. Therefore, these traits can be used as criteria for selection. Furthermore, Success in the plant breeding process is mostly determined by good selection. Information about the relative contribution from each trait, agronomy, and yield components, can be used to determine the selection criteria, directly and indirectly. Correlation between the observed traits could describe the relationship between the traits phenotypically, so the selection activity will be more appropriate and directed (Yani et al. 2018; Can and Turkmen 2022).

The inbred lines of melons showed that the diversity coefficient values of morphological traits ranged from 0.57 to 1.0. There are 3 Groups, namely Group I, II, and III. Group I comprises of 2 genotypes: MJ 34 and HHX 015. Group II is divided into 2, Group A and B. Group A comprises 3 genotypes: MJ 25, Amanda variety as the standard of comparison, and MO 29, while Group B has 1 genotype: HHA 02. Finally, group III comprises of 3 genotypes: MSO 12, MSP 13, and HHAL 01. Based on the relationship study approach on agronomic traits and yield components, they showed that the tested genotypes indicate high genetic diversities. The traits are as follows: leaf length, leaf width, fruit length, fruit diameter, and thickness of the fruit flesh (pulp) have closely related to the fruit yield per plant.

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