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Research Paper

Evaluation of Quantitative Floral Traits in Eleven Melon (Cucumis melo L.) Genotypes

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Abstract

Floral trait evaluations in melon are still limited, despite their importance in breeding programs. This study aimed to evaluate the performance of melon genotypes and to identify their clustering patterns based on floral traits. The experiment was conducted from June to August 2025 in a greenhouse at the Wedomartani Experimental Station, UPN Veteran Yogyakarta, using eleven melon genotypes arranged in a randomized complete block design (RCBD) with three replications. Significant differences were detected for hermaphrodite flower petal length (HFPL) and hermaphrodite flower petal width (HFPW). Genotypes G11 (3.3 cm and 2.3 cm) and G9 (3.2 cm and 2.2 cm) exhibited the highest HFPL and HFPW values, respectively. Based on the traits of HFPL and HFPW, genotypes G9 and G11 were selected as sources of genetic material to be continued in the next planting season. Cluster analysis using Ward's method grouped the genotypes into three major clusters. The first cluster consisted of genotypes G1 and G3. The second cluster consisted of genotypes G2, G7, G14, G10, G13, and G15. The third cluster consisted of genotypes G5, G9, and G11. The first group consisted of genotypes derived from the offspring of the Makuwa group. The genotypes in the second group were mainly from the Cantalupensis melon group, while those in the third group belonged to the Inodorus melon group. This indicates that the clustering analysis effectively distinguished the genotypes according to their group. The relationships among the eleven genotypes based on floral traits provide valuable insights for melon breeding and the development of improved cultivars.

Keywords *cluster analysis, diversity floral traits, melon*

INTRODUCTION

Melon is a horticultural commodity with high economic value. Melon is a species of the *Cucurbitaceae* family that has large genetic diversity (Robinson & Decker-Walters, 1999). Consumers highly value melons for their nutritional composition, which includes vitamin C, provitamin A, folic acid, phenolic phytochemicals, dietary fiber, minerals, and cucurbitacin. Musk melons are particularly rich in provitamin A (β-carotene). In contrast, both musk melons and honeydew melons serve as good sources of potassium and vitamin C, with the added benefit of being low in fat, sodium, and calories (Lija & Beevy, 2021). Phenotypic variants of melon based on plant types such as leaves, flowers, and fruit. The size of the melon fruit is round, 30-50g (wild type melon), while the cultivated melon is reported to reach a weight of 35kg. Wild melons are low in sugar and even have a bitter taste, while cultivated melons generally do not (Pitrat, 2016). Melon fruits may exhibit either climacteric or non-climacteric ripening behavior. Accordingly, fruits may either remain attached to the stem or develop an abscission layer that enables natural detachment at maturity (Nuñez-Palenius et al., 2008).

Cultivated melons are wild types that have undergone domestication and selection for particular or combinations of traits, such as fruit size, sugar content, texture, and leaf size. There are also differences in sex expression between wild and cultivated melons. Wild melons are a monoecious type, while cultivated melons are generally andromonoecious (Pitrat, 2016; Shivapriya et al., 2021). There are differences in the number of petals in male and hermaphrodite flowers of

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the *reticulatus* (5-5.4 and 5-5.2 petals), *inodorus* (4-5 and 5 petals), and *makuwa* group (5-8 and 5-6 petals) (Saputra et al., 2024).

Diversity identification has advanced rapidly with the development of molecular markers for assessing variation at the DNA level. Biochemical analyses, including measurements of pH, total soluble solids, ascorbic acid content, and titratable acidity, have also been widely employed to characterize melon diversity. Nevertheless, morphological characterization, particularly of floral and fruit traits, remains extensively used and continues to provide valuable information for plant breeders. Floral biology is crucial information in breeding programs. Floral traits, such as sex expression, play a role in the crossbreeding or combination of melon genotypes. Other floral traits, such as petal numbers, petal size, sepal size, ovary size, flower size, and the ratio of male to female/hermaphrodite flowers, provide information on melon diversity.

Furthermore, the variation in floral traits was analyzed to support the determination of marker characters and to distinguish subspecies under their respective botanical varieties and cultivars (Pandey et al., 2021). Information on floral traits is rarely observed. This study aimed to evaluate the performance of melon genotypes and determine clustering among genotypes based on floral traits.

LITERATURE REVIEW

Morphological Diversity of Melon

Melon exhibits a wide range of diversity, particularly in fruit-related traits such as fruit shape, rind color, flesh color, texture, aroma, and sugar content. According to Pitrat (2016), melons are classified into 19 groups: A*grestis, Kachiri, Chito, Tibish, Acidulus, Momordica, Conomon, Makuwa, Chinensis, Flexuosus, Chate, Dudaim, Chandalak, Indicus, Ameri, Cassaba, Ibericus, Inodorus,* and *Cantalupensis.* This high genetic variability provides significant advantages for breeders in developing superior cultivars, as it offers a wide selection of desirable traits during the breeding process.

Previous studies have reported that the *Makuwa* group exhibits resistance to several pathogens, including viruses and *Fusarium* wilt. This group is further classified into several subgroups, namely *Ogon*, *Nashi-uri*, *Yuki*, *Kanro*, *Ginmakuwa*, and *Seikan*. The makuwa group exhibits an andromonoecious sex expression, although some accessions have been reported to be hermaphroditic, possessing short appressed hairs on the ovary. The fruits of this group are generally medium to small in size, with relatively small seeds. Morphologically, the plants are characterized by dark green leaves and stems bearing stiff hairs (Pitrat, 2016).

Melon varieties cultivated in Indonesia exhibit variation in fruit shape, skin color, flesh color, and sweetness. Based on the surface characteristics of the fruit, melons are classified into two types: netted melons and winter melons. Netted melons are distinguished by a hard, rough, veined, and net-like rind, whereas winter melons have a smooth, shiny surface without netting (Hidzroh et al., 2021).

Melon Breeding Program and Floral Traits

The first step in breeding programs, following the definition of breeding objectives, is the collection of germplasm. High genetic diversity facilitates subsequent genotype selection, whereas low variability requires breeders to broaden the genetic base through hybridization or genotype combination. At each stage, from germplasm collection to selection—comprehensive characterization and evaluation of traits at the plant, flower, and fruit levels are essential. This information enables breeders to understand the genetic potential of each genotype and to monitor progress across breeding generations (Maghfiroh et al., 2023; Saputra et al., 2022).

Comprehensive information on melon traits is valuable for plant breeders. Detailed studies on fruit traits of melon are common, whereas floral traits remain underexplored. The brief flowering-to-fruit set phase in melon likely explains the limited information on floral traits. A comprehensive understanding of floral biology is essential for determining the most suitable selection methods and variety types, including pure lines, open-pollinated cultivars, and hybrids. Diversity in floral morphology can serve as a crucial reference point for identifying marker traits in melon improvement. Floral traits information provides valuable insights into the performance of specific genotypes, while also serving as a basis for analyzing genetic relationships among them (Kalyan et al., 2023; Pandey et al., 2021; Saputra et al., 2022).

RESEARCH METHOD

Genetic Material and Experimental Design

Eleven melon genotypes consisted of G1 (CHAMOE-0-1), G2 (CHAMOE-0-6), G3 (CHAMOE-0-8), G5 (SWEET NET-0-5), G7 (SWEET NET-0-C), G9 (NEW GOLDEN-0-1-2), G10 (ALISHA-0-2), G11 (ALISHA-0-3), G13 (HAMI-0-7), G14 (HAMI-0-8), and G15 (HAMI-0-1-1). The trial was conducted from June to August 2025 in a greenhouse at the UPN Veteran Yogyakarta Experimental Station, Yogyakarta. The trial was arranged in a Randomized Complete Block Design (RCBD) with three replications. Based on the number of genotypes and replications, a total of 33 experimental units were established, with three plants per sample included in each experimental unit.

Melon cultivation began with soaking seeds in warm water for 5 hours, followed by draining and incubation in moist tissue for 36 hours, until germination occurred. Cocopeat was used as the growing medium in seedling trays, and seedlings were maintained for 10 d until the appearance of true leaves. Transplanting was conducted in the afternoon to minimize heat stress. Crop management included pest control with chemical pesticides, monitoring of AB mix nutrient solution, pruning of side branches, pollination, fruit thinning, topping of the main stem, and harvesting. Side branches at nodes 1–7 were pruned, while those at nodes 8–14 were retained. Female or hermaphroditic flowers at these nodes were manually pollinated to induce fruit set. Fruit thinning was performed to retain a single fruit per plant. Fruits were harvested at 60–70 days after sowing. Harvest maturity was determined by external characteristics: non-netted melons exhibited a bright rind color, whereas netted melons showed a clearly developed net pattern.

Observation and Data Analysis

Flower traits observed include male flower petal length (MFPL), male flower petal width (MFPW), number of male flower petals (NMFP), male flower sepal length (MFSL), hermaphrodite flower petal length (HFPL), hermaphrodite flower petal width (HFPW), number of hermaphrodite flowers (NHFP), hermaphrodite flower diameter (HFD), male flower diameter (MFD), hermaphrodite flower sepal length (HFSL). The flower traits observed refer to the descriptors for melon *Cucumis melo* L (IPGRI, 2003), with modifications. Analysis of variance was calculated using SAS OnDemand for Academics (2025) software (https://welcome.oda.sas.com). Cluster analysis was performed using PBSTAT (2025) (https://apps.pbstat.com) based on the Average Linkage dissimilarity method and Ward clustering method.

FINDINGS AND DISCUSSION

Analysis of variance showed that only the hermaphrodite flower petal length (HFPL) and hermaphrodite flower petal width (HFPW) traits showed significant differences among genotypes (Table 1). Other floral traits, such as male flower petal length, male flower petal width, number of male flower petals, male flower sepal length, number of hermaphrodite flowers, hermaphrodite flower diameter, male flower diameter, and hermaphrodite flower sepal length, were not

significantly different. The most excellent hermaphrodite flower petal length was observed in genotype G11 (3.3 cm), although it was not significantly different from genotype G9 (3.2 cm). Genotype G11 exhibited the widest hermaphrodite flower petals (2.3 cm), although this was not significantly different from genotype G9 (2.2 cm). The smallest hermaphrodite flower petal width was observed in genotype G2 (1.1 cm). The petal length of hermaphrodite flowers in genotype G2 (1.5 cm) did not differ significantly from that of genotypes G10, G15, G13, G3, G1, and G14. Variation in floral structures indicates differences in reproductive mechanisms. Comprehensive information on the diversity of floral traits is essential in plant breeding, particularly in facilitating effective crossbreeding programs.

The coefficient of variation (CV) for the traits showed <20% except for the hermaphrodite flower sepal length trait (Table 1). The coefficient of variation serves as an indicator of experimental precision, with higher coefficient of variation values reflecting lower accuracy and lower coefficient of variation values reflecting higher accuracy (Gomez & Gomez, 1984; Huda & Suwarno, 2023). The male flower petal width was positively correlated with petal length ($r = 0.86$, $p \leq 0.05$) and internode length ($r = 0.55$, $p \leq 0.05$). In addition, male flower petal length showed a positive correlation with internode length ($r = 0.66$, $p \leq 0.05$) (Maghfiroh et al., 2023).

Table 1. Means of Flower Traits

Genotype	MFPL	MFPW	NMFP	MFSL	HFPL	HFPW	NHFP	HFD	MFD	HFSL
G1	2.0a	1.5a	5a	0.9a	1.9^{cd}	1.5^{c}	5a	2.9a	3.9a	1.1a
G2	1.4a	1.1a	5a	0.4a	1.5^{d}	1.1^{e}	5a	2.9a	2.7a	0.8a
G3	2.1a	1.3a	6a	0.8a	1.8^{cd}	1.2^{de}	5a	3.7a	4.1a	0.8a
G5	1.7a	1.4a	5a	0.4a	2.6^{b}	1.9^{b}	5a	4.6a	3.2a	0.4a
G7	1.8a	1.6a	5a	0.4a	2.0^{c}	1.6^{c}	5a	3.2a	3.9a	0.6a
G9	2.0a	1.3a	5a	0.5a	3.2^{a}	2.2^{a}	5a	5.5a	3.5a	0.7a
G10	1.7a	1.4a	5a	0.6a	1.6^{cd}	1.4^{cd}	5a	3.4a	3.4a	0.4a
G11	1.9a	1.5a	5a	0.4a	3.3^{a}	2.3^{a}	5a	5.3a	3.3a	0.8a
G13	1.7a	1.5a	5a	0.5a	1.8^{cd}	1.4^{cd}	5a	3.4a	3.4a	0.6a
G14	2.2a	1.8a	5a	0.6a	1.9^{cd}	1.5^{c}	5a	3.6a	4.0a	0.7a
G15	1.7a	1.5a	5a	0.4a	1.7^{cd}	1.2^{de}	5a	3.2a	3.3a	0.4a
p-value	ns	ns	ns	ns	*	**	ns	ns	ns	ns
CV (%)	14.3	15.3	3.3	27.3	8.5	5.7	2.4	25.7	13.0	40.6

Note: numbers followed by the same letter in the same column are not significantly different based on the Duncan Multiple Range Test at the 5% level, CV: coefficient of variation, MFPL: male flower petal length (cm), MFPW: male flower petal width (cm), NMFP: number of male flower petals, MFSL: male flower sepal length (cm), HFPL: hermaphrodite flower petal length (cm), HFPW: hermaphrodite flower petal width (cm), NHFP: number of hermaphrodite flower, HFD: hermaphrodite flower diameter (cm), MFD: male flower diameter (cm), HFSL: hermaphrodite flower sepal length (cm), **: significant at $\alpha = 0.01$, ns: not significant

Based on quantitative floral traits, cluster analysis separated the eleven genotypes into three major clusters (Figure 1). The first cluster consisted of G3 and G1 genotypes, the second cluster of genotypes G2, G7, G14, G10, G13, and G15, and the third cluster of genotypes G5, G9, and G11. Grouping provides breeders with an overview of the existing genetic diversity among genotypes, serving as a basis for determining suitable parental combinations in hybridization programs aimed at increasing genetic variability. Both G3 and G1 are progenies of the *Chamoe* F1 hybrid variety, classified within the *makuwa* Makino group. *Chamoe* flowers are presented in Figure 2. Based on

the length of the ovary pubescence trait, *Cucumis melo* L. is classified into Subsp sp. *melo* and Sub sp. *agrestis*. The *Makuwa* Makino variety belongs to Subsp. *agrestis*, characterized by spreading ovary pubescence with long hairs (Lija & Beevy, 2021). The variety *Cucumis melo*var. *makuwa* has been cultivated in Korea and South China. The *makuwa* group is known to exhibit resistance to diseases such as viruses and Fusarium wilt. Morphologically, it is characterized by flowers with large sepals, medium-sized fruits with small seeds, early maturity, and short postharvest shelf life. The stems are distinguished by the presence of stiff hairs (Pitrat, 2016).

Genotypes G1 and G3 display a monoecious flowering habit, producing both male and female flowers on the same plant. The male flowers exhibit larger diameters (3.9 and 4.1 cm) compared to the female flowers (2.9 and 3.7 cm). In the study by Kustanto (2023), cluster analysis revealed that the observed genetic diversity was primarily associated with agronomic traits and yield components. Monoecious flowering genotypes initiated female flowers on the basal nodes and were characterized by longer fruit development (Soltani et al., 2022). The second group consisted mainly of genotypes derived from the HAMI variety (G13, G14, and G15), which belong to the *Cantalupensis* group. The third group primarily comprised genotypes originating from the *Inodorus* group.

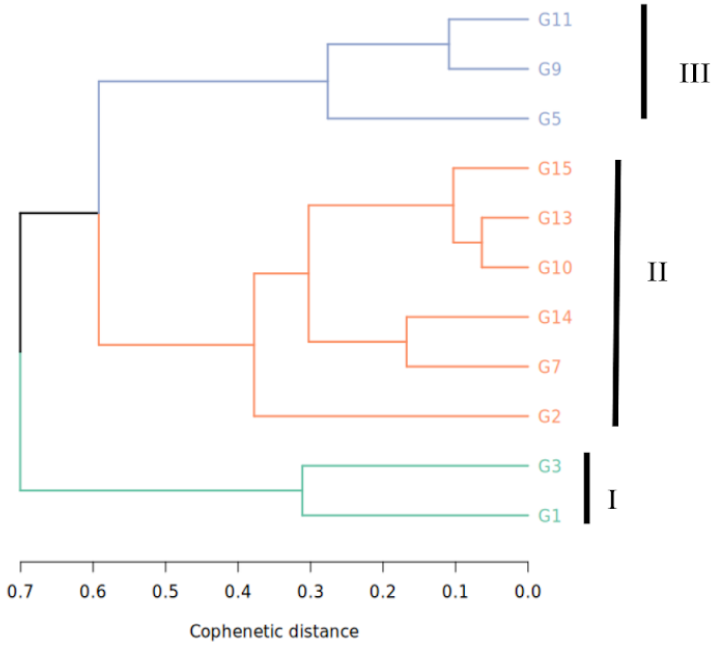

Figure 1. Ward Clustering of Eleven Melon Genotypes Based on Ten Flower Quantitative Traits

Figure 2. A: *makuwa* hermaphrodite flower, B: *makuwa* male flower

CONCLUSIONS

Significant differences were observed among genotypes for hermaphrodite flower petal length (HFPL) and hermaphrodite flower petal width (HFPW). Genotypes G11 and G9 exhibited the largest values for hermaphrodite flower petal length and hermaphrodite flower petal width, respectively. Based on the traits of the hermaphrodite flower petal length and the hermaphrodite flower petal width, genotypes G9 and G11 were selected as sources of genetic material to be continued in the next planting season. Cluster analysis grouped the eleven genotypes into three major clusters. Group 1 consists of genotypes G1 and G3, the second cluster of genotypes G2, G7, G14, G10, G13, and G15, and the third cluster of genotypes G5, G9, and G11. Genotypes G1 and G3 belong to the Makuwa melon group. The genotypes in the second group were mostly from the Cantalupensis melon group, while those in the third group belonged to the Inodorus melon group. This indicates that the clustering analysis effectively distinguished the genotypes according to their group. Based on the quantitative floral traits, cluster analysis successfully classified the melon genotypes according to their similarities. The diversity of melon genotypes based on floral traits provides valuable information for the development of improved melon varieties.

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