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Diversity and morphological characteristics of flowers in reticulatus, inodorus, and makuwa group melon (*Cucumis melo*)

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Abstract. *Saputra HE, Syukur M, Suwarno WB, Sobir. 2024. Diversity and morphological characteristics of flowers in reticulatus, inodorus, and makuwa group melon (*Cucumis melo*). Biodiversitas 25: 3130-3137.* Characterization of melon (*Cucumis melo* L.) flowers is useful for crossing. This research aimed to obtain information about the diversity and morphological characteristics of melon flowers in the reticulatus, inodorus, and makuwa groups. Fifteen genotypes from 3 groups (5 genotypes each) were tested. There were 8 flower characters observed. Principal component and cluster analysis have been used to calculate similarity coefficients. Grouping based on flower characters was divided into 4 groups with a diversity of 52.7%. There are no morphological characteristics of flowers to characterize each group of melons. The reticulatus group has flower characteristics as follows: NMFP of 5-5.4 petals, NHFP of 5-5.2 petals, SLMF of 0.95-2.9 cm, SLHF of 0.36-1.98 cm, DMFS of 1.01-1.34 mm, DHFS of 2.57- 3.15 mm, DMF of 3.12-4.99 cm, and DHF of 8.03-8.61 cm. The inodorus group has flower characteristics as follows: NMFP of 4-5 petals, NHFP of 5 petals, SLMF of 1.34-3.18 cm, SLHF of 0.7-2.46 cm, DMFS of 1.16-1.61 mm, DHFS of 2.72-2.94 mm, DMF of 3.47-4.34 cm, and DHF of 6.56-8.15 cm. The makuwa group has flower characteristics as follows: NMFP of 5-8 petals, NHFP of 5-6 petals, SLMF of 1.32-1.98 cm, SLHF of 1.04-1.74 cm, DMFS of 1.07-1.36 mm, DHFS of 2.67- 3.86 mm, DMF of 3.31-3.85 cm, and DHF of 7.16-8.35 cm.

Keywords: Characterization, *Cucumis melo*, diversity, flowers, genotype, melon

INTRODUCTION

Melon (*Cucumis melo* L.) belongs to the family Cucurbitaceae with a diverse range of flowering traits. According to Endl et al. (2018), Zhao et al. (2019), and Wang et al. (2021), Asia and Africa are the regions with the greatest origins and diversity of melon. It produces a variety of flower structures, including monoecious (staminate and pistillate), andromonoecious (staminate and hermaphrodite flowers), gynomonoecious (pistillate and hermaphrodite flowers), and gynoecious (pistillate), but andromonoecious is the most prevalent (Revanasidda and Belavadi 2019; Ye et al. 2020). In the beginning, flower primordia are bisexual and sex is determined by stopping the growth of the stamens or the carpel whorl, resulting in unisexual blooms. Male, female, and hermaphrodite flowers are all developed under the regulation of genes particularly expressed in stamen primordia or carpels (Zhang et al. 2015; Li et al. 2019).

The genetic diversity of multiple melon groups has an impact on plant breeding success (Monforte 2017; Guliyev et al. 2018; Pourranjbari et al. 2018; Chikh-Rouhou et al. 2021; Pandey et al. 2021; Soltani et al. 2022; Yusuf et al. 2022). The melon characterization is commonly aimed to identify genetic similarities among the population of melon samples (Vella et al. 2019; Esteras et al. 2020; Merheb et al. 2020; Singh et al. 2020; Wibowo et al. 2020; Saputra et al. 2022). Flower variety aids in the classification of melon groupings (Pandey et al. 2021).

Bell-shaped and yellow melon blooms can be monoecious or andromonoecious (one plant produces male and hermaphrodite flowers) compared to the monoceous form, the andromonoceous type is more prevalent. Ovaries are located under the flower crowns of female flowers. The female melon flowers typically develop from the formation of lateral shoots on the axils of the first and second deep leaves on each main stem. If pollination is not achieved, they will fall 2-3 days after blossoming. Therefore, to achieve a 6-19:1 balance between male and hermaphrodite blooms, male flowers continuously form in groups and are located in each leaf axil (Tschoeke et al. 2015). After flowering, male flowers will fall 1-2 days. On the main stem node, male flowers will alternately occur one, two, or more times (Abdelmohsin et al. 2015; Kiill et al. 2016; Revanasidda and Belavadi 2019). Anthesis occurs in the morning between 5.30 and 6.30 am and the pollen is viable until 2:00 pm. If the main stem has grown to a length of 60 cm and is present in the first or second segment of the primary branch, hermaphrodite flowers will bloom individually and fall if they are not pollinated within 2-3 days.

Reticulatus, inodorus, and makuwa are a group of melons that are often cultivated in Indonesia. These three groups of melons have a variety of flower morphologies.

One of the indicators for the melon group is flower features (Pandey et al. 2021). Male and hermaphrodite blooms grow on the same plant in the melons' reticulatus, inodorus, and makuwa groups. Numerous genetic studies have been conducted recently on the characteristics of melon fruit, such as sweetness (Thakur et al. 2019), flesh color (Galpaz et al. 2018), and fruit shape and size (Liu et al. 2019).

Melon blossom traits are still very infrequently observed. In addition, melon crossbreeding for plant breeding is easier because of the characteristics of melon blooms. The ultimate stage of plant breeding comes next to articles for the development of new varieties of high quality that meet societal needs (Ewing et al. 2019; Zaidi et al. 2019). This research aimed to obtain information on melon flowers' diversity and morphological characteristics in the reticulatus, inodorus, and makuwa groups.

MATERIALS AND METHODS

Study area

The research was conducted at the Greenhouse Universitas Bengkulu in Kandang Limun, Bengkulu City, Indonesia. The research period was from May to August 2023.

Plant materials

There were 15 melon genotypes tested, namely 6 genotypes from the collection of the Center for Tropical Horticulture Studies, Laboratory of Genetics and Plant Breeding, Department of Agronomy and Horticulture, Institut Pertanian Bogor, Bogor, Indonesia (IPB240, IPB283, IPBM21, IPBM23, IPBME5, IPBMETA9) and 9 genotypes from the Laboratory Agronomy, Universitas Bengkulu (UME20, UME38, UME39, UME90, UME91, UME98, UME99, UME100, UME101). For each genotype, 5 plants were observed. Genotypes tested i.e. the reticulatus group (IPBM240, IPB283, UME90, UME91, and UME98), the inodorus group (IPBM21, IPBM23, IPBME5, UME20, and UME39) and the makuwa group (UME38, UME99, UME100, UME101, and IPBMeta9).

Procedures

Melon cultivation

Preparing plant materials, seeding, planting, and caring for melon plants are all parts of the study process. The planting medium is cocopeat and the used polybag is 40×40 cm in size. The seeds were soaked in warm water for 6 hours before sowing. The seeds are then germinated through the paper-to-paper technique. Next, the seeds are sown in seedling trays for 7-10 days after germination. In the afternoon, seed polybags that are ready to be planted contain 1 plant each. Deceased plants are replaced or replanted for 7 Days After Planting (DAP).

A drip irrigation system has been used to plant melons in a greenhouse. The seeds were soaked in warm water for 6 hours, causing them to germinate. Depending on the seed genotype, it takes roughly 36 hours to germinate after being covered in damp, opaque paper. Immediately after germination, seeds are sown in nursery media. After the seedlings are ready for planting, melon seeds ready to be observed are 14 days old. Dead plants must be replaced or replanted for 7 DAP.

Plant maintenance includes nutrition by fertigation (drip irrigation), pruning shoots, and controlling plant pest organisms. Fertigation nutrition is given as AB mix melon solution with a TDS of 700-1,000 ppm, depending on the plant growth phase. The fertilizer solution used throughout the vegetative period is 700 ppm. The generative phase then receives 1,000 ppm of nutrient solution. Drip irrigation applications are conducted 5 times daily for 5 minutes each. Next, melon plant stems are stabbed by winding them around a stake rope and each lateral shoot that emerges on the 1st to 8th node of melon plants must be pruned (Saputra et al. 2022). Then, to observe male and hermaphrodite flowers, the shoots that develop on the 9th to 15th nodes are kept alive for a period of 21-30 DAP (Yoshioka et al. 2018; Ye et al. 2020). Pruning is carried out by cutting the developing lateral branches with scissors that have been sterilized with 70% mancozeb.

Parameters observed

The 8 flower characters were observed during research, namely Number of Male Flower Petals (NMFP), Number of Hermaphrodite Flower Petals (NHFP), Stalk Length of Male Flower (SLMF-cm), Stalk Length of Hermaphrodite Flower (SLHF-cm), Diameter of Male Flower Stalk (DMFS-mm), Diameter of Hermaphrodite Flower Stalk (DHFS-mm), Diameter of Male Flower (DMF-cm), and Diameter of Hermaphrodite Flower (DHF-cm).

Data analysis

The principal component and cluster analysis were conducted to calculate similarity coefficients. These analysis methods are the average linkage with a Gower similarity coefficient matrix. Furthermore, the determination of the distinguishing character is determined from the heatmap. The flower characters obtained were analyzed by analysis of variance. If the genotype effect was significant, a Tukey HSD test at a 5% level was performed. The analyses were performed with R i386 4.2.1 and PBSTAT-CL software (www.pbstat.com).

RESULTS AND DISCUSSION

Flower diversity

Eight different melon blossom characters are distilled into their essential traits. The overall diversity of 52.7% comprises principal component 1 and principal component 2 cumulatively (Figure 1). Their placement in the biplot also hints at the variety of flower personalities. Characteristic diversity is extremely low for characters close to the center. Compared to other characteristics, the Diameter of the Hermaphrodite Flower (DHF) character has the least diversity. The 4 flower features that are furthest from the biplot's center are the Number of Male Flower Petals (NMFP), Number of Hermaphrodite Flower Petals (NHFP), Stalk Length of Male Flower (SLMF), and Stalk Length of Hermaphrodite Flower (SLHF) (Figure 1).

Table 1. Similarities in flower characters of the 15 melon genotypes studied

	IPB 240	IPB 283	IPB M21	IPB M23	IPB ME5	IPB Meta9	UME 100	UME 101	UME 20	UME 38	UME 39	UME 90	UME 91	UME 98	UME 99
IPB240	1														
IPB283	0.747	1													
IPBM21	0.734	0.771	1												
IPBM23	0.669	0.752	0.850	1											
IPBME5	0.667	0.730	0.771	0.806	1										
IPBMeta9	0.689	0.746	0.742	0.824	0.687	1									
UME100	0.719	0.837	0.727	0.819	0.734	0.773	1								
UME101	0.665	0.788	0.830	0.852	0.728	0.894	0.749	1							
UME20	0.627	0.700	0.644	0.773	0.711	0.698	0.829	0.673	1						
UME38	0.674	0.681	0.711	0.714	0.691	0.833	0.649	0.778	0.574	1					
UME39	0.816	0.803	0.781	0.819	0.787	0.748	0.834	0.789	0.783	0.703	1				
UME90	0.820	0.762	0.762	0.782	0.770	0.752	0.816	0.793	0.738	0.736	0.944	1			
UME91	0.754	0.841	0.732	0.716	0.681	0.781	0.766	0.841	0.662	0.695	0.792	0.807	1		
UME98	0.597	0.832	0.636	0.778	0.723	0.717	0.879	0.691	0.826	0.600	0.735	0.708	0.689	1	
UME99	0.557	0.605	0.613	0.648	0.559	0.713	0.578	0.676	0.498	0.652	0.589	0.550	0.581	0.527	1

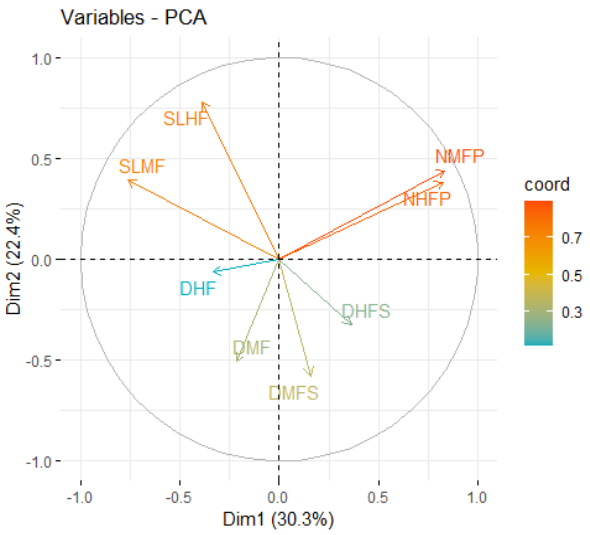

Figure 1. Grouping of flower characters based on principal component 1 and principal component 2

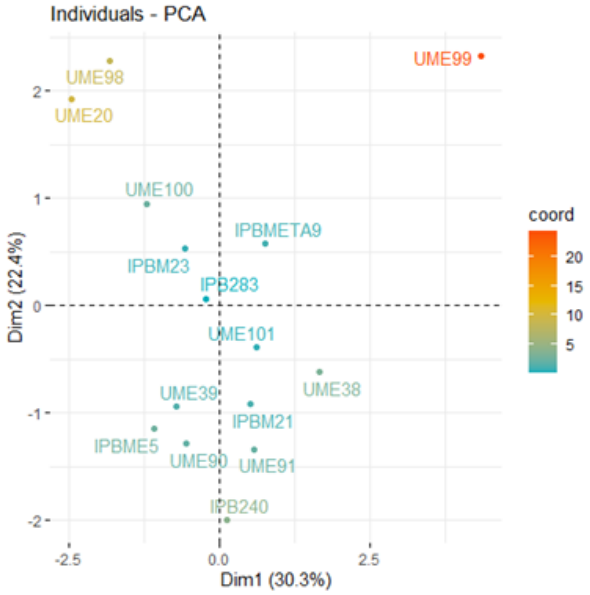

Figure 2. Grouping of genotypes based on principal component 1 and principal component 2

Principal component 1 and principal component 2 with the same color were used to group the flower features of 15 melon genotypes and they showed a high degree of similarity (Figure 2). For example, genotypes that have a high similarity value such as 0.826 also have the same color, namely UME98 and UME20. The genotypes with different colors, namely UME98 and UME38 have a low similarity of 0.600 (Table 1). The position of the genotypes near one another reveals a high degree of similarity among the genotypes. The UME99 genotype with the most distinct in terms of color is also the most rare.

Three clusters were produced when 15 genotypes were grouped based on the Gower distance between floral features (Figure 3). IPB240, UME39, UME90, IPB283, UME91, IPBM21, IPBM23, IPBMeta9, UME101, UME38, and IPBME5 were the genotypes that clustered in Cluster 1. Cluster 2 contains the genotypes UME100, UME98, and UME20. UME99, the rare genotype, belonged to Cluster 3.

The location of the intersection point between the genotype and the flower character is shown in Figure 4. The biplot's character point's proximity to the genotype reveals the genotype's closeness and specific characteristics. The NMFP (Number of Male Flower Petals) and NHFP (Number of Hermaphrodite Flower Petals) traits are closely associated with the UME99 genotype. It is near the Stalk Length of Hermaphrodite Flower (SLHF) characteristics are the UME20 and UME98 genotypes. The DMF genotype borders the UME90 genotype. The DMFS characteristics are close to the UME91 genotype. The DHFS characteristics are close to the IPBM21 genotype.

The heatmap shows how flower genotypes and character mapping are displayed (Figure 5). Characteristics and genotypes of flowers were grouped into 4 clusters based on the heatmap. UME99 is a member of Cluster 1. Cluster 2 is contained in the UME20, UME100, and UME98 genotypes. Cluster 3 contains the genotypes

UME38, IPBMeta9, and UME101. The remaining eight genotypes, meanwhile, are part of cluster 4. The NMFP and NHFP features set the UME99 genotype apart from other genotypes and are distinct flower traits. A special trait for IPBME5 is the DMFS character. The flower character DHFS is unique to the UME38 genotype. Specific characters that UME20 possesses are SLMF and SLHF. The IPB240 genotype has a specific flower character, namely DMF. The DHF character also has a low level of variability, making it less specific for the genotype examined.

Flower characteristics

All of the tested genotypes of melons belonged to 1 of 3 groups, namely reticulatus, inodorus, or makuwa. Melon reticulatus has IPB240, IPB283, UME90, UME91, and UME98 genotypes. Inodorus melon genotypes include IPBM21, IPBM23, IPBME5, UME20, and UME39. The genotypes of the makuwa melon include IPBMeta9, UME38, UME99, UME100, and UME101.

All genotypes examined exhibited NMFPs between 5.00 and 7.85 petals. The UME99 genotype shows the most male flower petals compared to other genotypes. Genotype UME38 has more male flower petals than the other 11 genotypes, but less than UME99. The genotypes IPB283, IPBM21, IPBM23, IPBME5, UME100, UME101, UME20, UME39, UME90, UME91, and UME98 contain the same number of male flower petals (Figure 6.A). Furthermore, comparing all of the genotypes studied, UME99 genotype had the most hermaphrodite flower petals with 6 petals (Figure 6.B). The average number of hermaphrodite flower petals in all genotypes was between 5 and 6.

The melon genotype tested had a stalk length of the male flower of 1.1-3.1 cm (Figure 6.C). The genotype with the smallest stalk length of the male flower is UME91, while the genotype with the largest male flower is UME20. Based on the boxplot, the diversity of stalk length of male flowers in the UME98, IPBME5, IPBM23, and IPBM21, IPB240 genotypes is greater than the other genotypes (Figure 6.C). All genotypes tested had a stalk length of hermaphrodite flower of 0.39-2.46 cm (Figure 6.D). Compared to all other genotypes, the UME20 genotype has the longest stalk length of the hermaphrodite flower. The genotype that has the smallest stalk length of hermaphrodite flower was UME91.

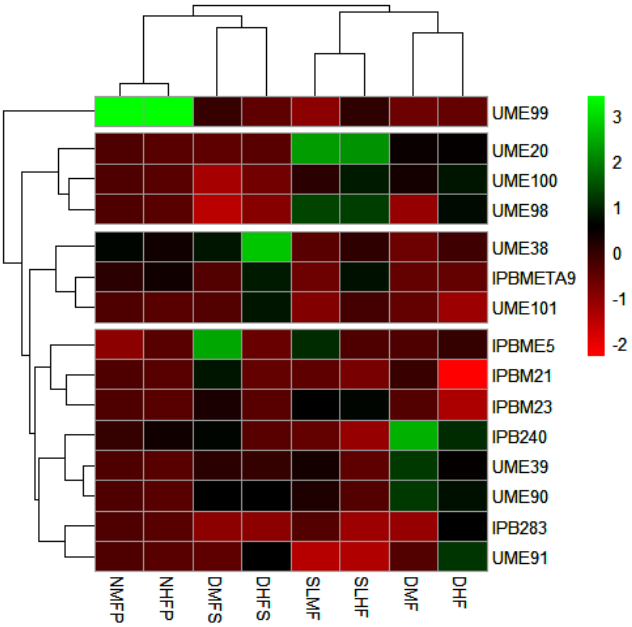

Figure 5. Heatmap of flower characters and melon genotypes

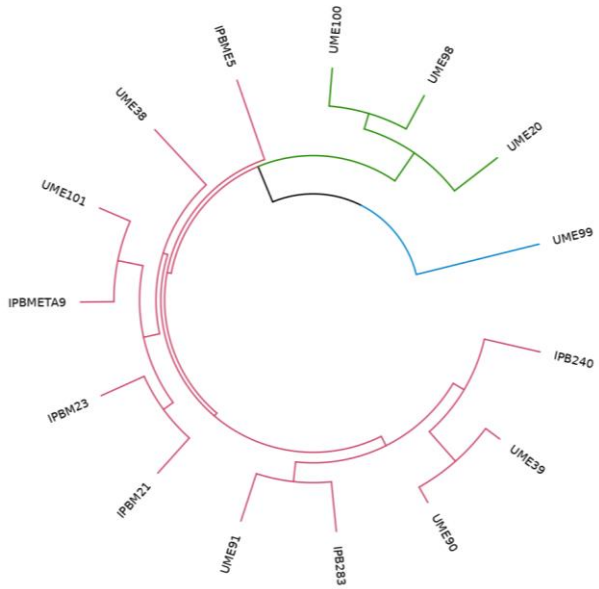

Figure 3. Grouping between genotypes based on Gower distance on flower characters

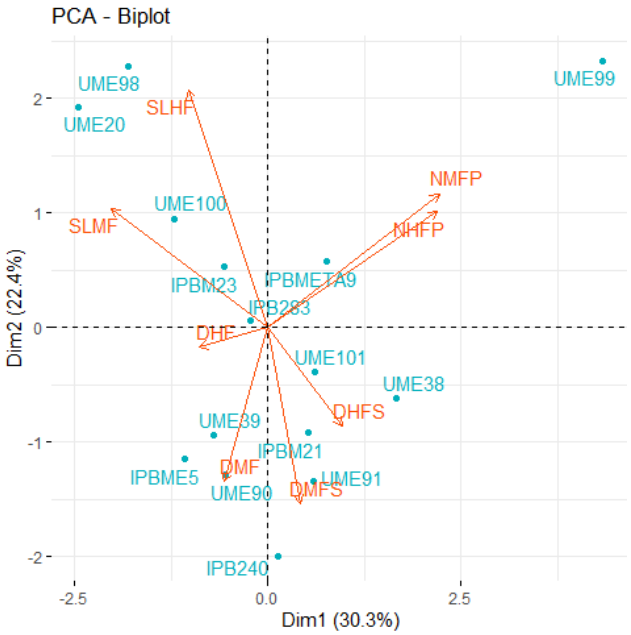

Figure 4. Grouping of genotypes and flower characters based on principal component 1 and principal component 2

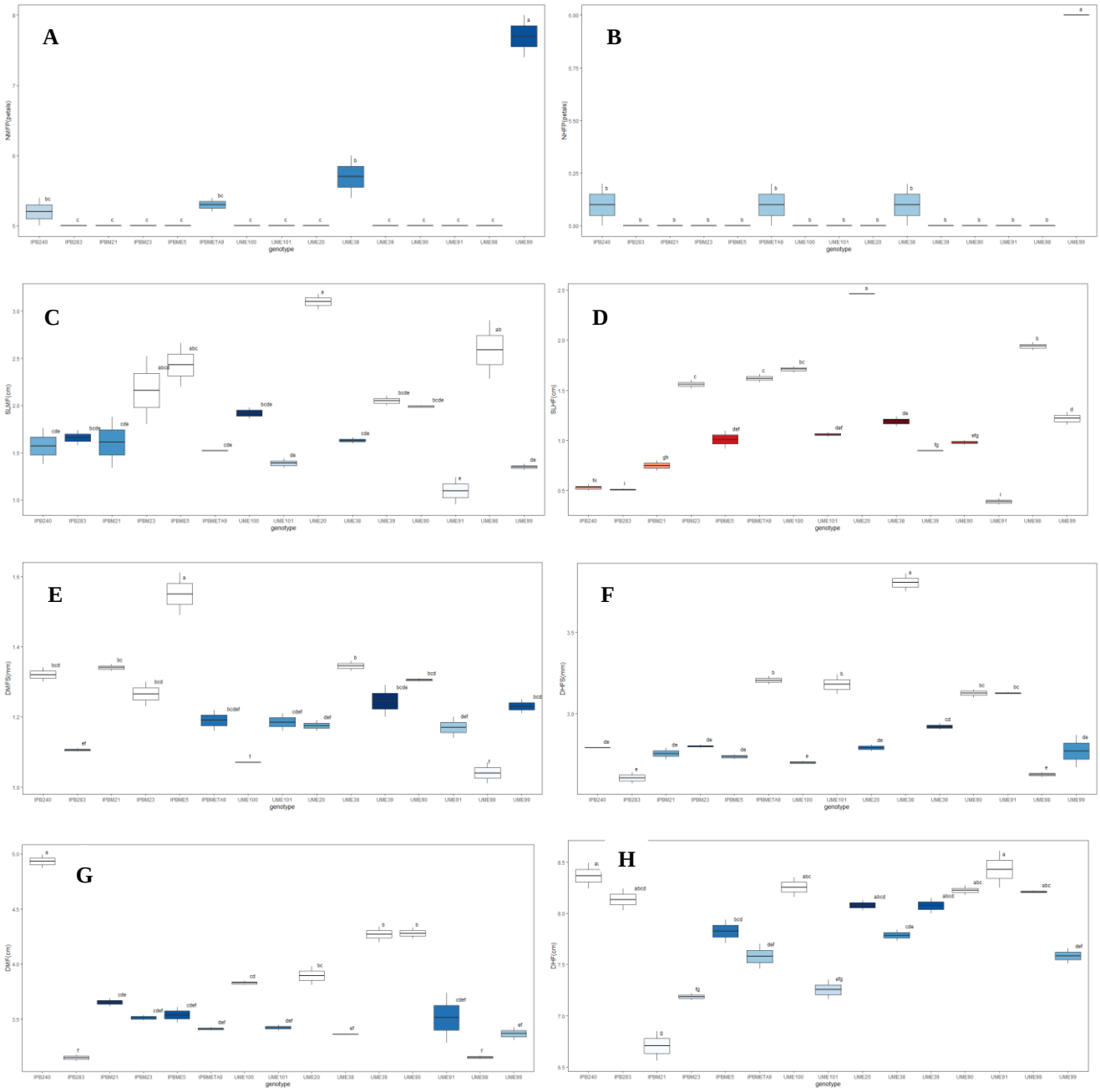

Figure 6. Performance of 15 melon genotypes for 8 flower characters: A. NMFP; B. NHFP; C. SLMF; D. SLHF; E. DMFS, F. DHFS, G. DMF; H. DHF. At a 5% level, the Tukey test finds no difference between boxplots with the same letter indication

The diameters of male flower stalks for the genotypes studied ranged from 1.04 to 1.55 mm (Figure 6.E). The genotype with the biggest diameters of male flower stalk was IPBME5, whereas the genotype with the shortest male flower stalk was UME98. The genotype with a large variety of diameters of male flower stalks, as indicated by wide boxplots, was IPBME5. The UME38 genotype had the diameter of the hermaphrodite flower stalk with the biggest, measuring 3.80 mm (Figure 6.F).

The diameter of the hermaphrodite flower stalk of the IPB283 genotype was the smallest at 2.60 mm. The diameter of the hermaphrodite flower stalk ranged from 2.60 to 3.80 mm for all genotypes examined. Among other genotypes, the UME99 genotype exhibits different diameters of hermaphrodite flower stalks.

The diameter of the male flower for all genotypes studied ranged from 3.15 to 4.93 cm (Figure 6.G). IPB240 is the genotype with the greatest diameter of the male flowers. IPB283 and UME98 are the genotypes with male flowers that are the shortest in diameter. The diameter of the male flower is more variable in the UME91 genotype than in other genotypes. All genotypes show hermaphrodite floral features with a diameter between 6.70 and 8.43 cm (Figure 6.H). The diameter of hermaphrodite flower of the

genotypes UME91, IPB240, UME100, UME90, UME98, IPB283, UME20, and UME39 was greater than 8 cm. The hermaphrodite flower's lowest diameter belongs to the genotype IPBM21.

Discussion

Studies on melon flower characteristics are still limited and focus more on gender expression and arrangement rather than flower architecture and its relationship to other fruit characteristics. Therefore, it is important to study the morphological characteristics and diversity of flowers. Principal Component Analysis (PCA) and cluster analysis are employed in diversity and grouping analyses to distinguish correlations between characters (Saputro et al. 2020; Yusuf and Daryono 2021). However, examining variety and grouping concerning melon flower traits is still uncommon. Characterizing flowers helps with one aspect of plant breeding, namely crossing, by providing gene recommendations. Therefore, to increase the number of crosses produced, flower structuring would make crossing operations easier. With a total cumulative proportion of 52.7%, the 8 floral characters in the reticulatus, inodorus, and makuwa groups are diverse.

The diameter of hermaphrodite flower is the character with the lowest diversity (Figure 1). The relationship between melon characters can be determined based on the vector direction in the biplot of principal component 1 and principal component 2. Characters that have the same vector direction and form an angle between vectors of less than 90° indicate that the characters are positively correlated (Saputra et al. 2022). The NMFP and NHFP characters have the same vector direction and form an angle of less than 90°, so the 2 characters are positively correlated. This result shows that an increase in NMFP will also be followed by NHFP so that this character can become a specific characteristic in the genotype that will be used for plant breeding activities. The same is true for the characters SLHF and SLMF, DHFS and DMFS, and DMF and DHF. The difference is in the character of NMFP and SLHF as well as NHFP and SLHF with the direction of the vector forming an angle of 90°. Characters with vector directions form a 90° angle, indicating that the two characters do not correlate. This is also the same as genotype characters that have NMFP and SLHF. The genotype that has the highest NMFP is not followed by high SLHF, such as UME99 has the highest NMFP while SLHF is not the highest. Characters like the NHFP and SLMF, whose vector directions diverge and form an angle greater than 90°, correlate negatively. Different only from the two previous characters, the UME99 genotype has the highest NHFP but the lowest SLMF. Genotypes that have long SLHF and SLMF characters are advantageous because they make it easier for pollinators so that more fruit can be formed (Kalyan et al. 2023). Flowers' diversity and structural characteristics suggest different mechanisms involved in melon plants' reproduction and distribution of variability. Information on flower structure diversity is useful for an easy hybridization between groups and for choosing the best time for crossing (Sanabria-Verón et al. 2019).

The position of each genotype on the PCA cluster analysis can be used to discover differences among genotypes (Figure 2). Compared to other genotypes, UME99 exhibits substantially diverse flower features; the distance between UME99 and other genotypes also demonstrates this. Three clusters are formed by grouping 15 genotypes based on gower distance. Cluster 1 contains 11 genotypes, cluster 2 has 3 genotypes, whereas cluster 3 has only 1 genotype (Figure 3). The more dominant genotypes in cluster 1 are reticulatus (IPBM240, IPB283, UME90, UME91 and UME98) and inodorus (IPBM21, IPBM23, IPBME5, UME20 and UME39). This result shows that the reticulatus and inodorus are very close, as the differences between the groups may be due to a small number of genes (Maleki et al. 2018). Principal component and cluster analysis produced the same grouping of the 15 genotypes tested (Figures 2 and 3). This shows the consistency of the grouping of genotypes so that the characters that characterize each genotype can be used as characteristics of that genotype. These characters are presented in a heatmap. The plant genotypes and traits are grouped to provide information on the distinctive properties of each genotype. It shows that UME99 is distinguished by the NMFP and NHFP traits (Figures 4 and 5); the green characters on the heatmap indicate the properties of a genotype. Regarding flower stalk diameter features, IPBME5 and UME38 genotypes had the most diversified variances from the other genotypes. The UME20 genotype is distinguished by the stalk length of male flower (SLMF) and the stalk length of hermaphrodite flower (SLHF). The IPB240 genotype has a unique trait of male flower diameter form (Figure 5). One other flower characteristic, the diameter of hermaphroditic flowers, cannot be used as a distinguishing feature in the 15 genotypes studied. All genotypes have a similar phenotype and limited diversity (Figure 5).

Melon plants are cross pollination plants, thus researching the morphology and structure of flowers is vital, particularly in assisting crossings to produce ideal fruit. The pollinator, such as bee, naturally aids in the crossing of the melons (Kiill et al. 2016; Pandey et al. 2021; Kalyan et al. 2023). The UME99 genotype has the highest number of male flower petals and several hermaphrodite flower petals (Figures 6.A and 6.B). The number of petal characteristics generally has 5 petals, so there are genotypes with more than 5 petals, providing new information regarding the number of petal characters. Both male and hermaphrodite flowers of all the genotypes contained 5 petals (polypetalous) without variation (Pandey et al. 2021). The UME99 genotype contains makuwa group traits, which have many petals. There was a positive link between petal size and seed set because flowers with larger petals attract more pollinators or are more successfully pollinated, resulting in more ovules being fertilized and growing into seeds. The characteristics of the stalk length of the male flower vary more than the stalk length of the hermaphrodite flower (Figures 6.C and 6.D). This is indicated by the boxplot size of the male flower's stalk length, which is greater than the stalk length of the hermaphrodite flower. The long stalk length of the male

flower makes pollination easier; thus, the ideal genotype with a long stalk length of the male flower. The genotypes IPBM23 and UME98 have the greatest diversity in the stalk length of male flowers. In contrast to the stalk length of the hermaphrodite flower, all genotypes tested had nearly the same diversity; hence, the boxplot size was relatively the same.

The same phenomena may be seen in the diameters of male flower stalks and hermaphrodite flower stalks. Figures 6.E and 6.F show a large boxplot of male flower stalks vs. diameters of hermaphrodite flower stalks. However, the genotype with a large boxplot size for the diameters of male flower stalks differs from the genotype with a long boxplot size for the stalk length of male flowers. The size of both male and female flowers varied significantly across genotypes, showing that these genotypes had evolved. Flower length and diameter variations may be due to genetic differences across genotypes. The IPBME5 and UME39 genotypes had larger diameters of male flower stalks than the other genotypes, resulting in a larger boxplot size. Unlike with stalk length of the hermaphrodite flower, one genotype, UME99, has a boxplot size character with a large diameter of the hermaphrodite flower stalk. The high boxplot size shows that the individual genotypes are more diverse than the small boxplot size.

In contrast to the length of the stalks of male flowers and the diameter of male flower stalks, which have a big boxplot size, the length of stalks of hermaphrodite flowers and the diameter of hermaphrodite flower stalks have a small boxplot size. For some genotypes, the diameter of hermaphrodite flowers has a greater boxplot size than that of male flowers (Figures 6.G-6.H). Kiill et al. (2016) reported that flowers of the hybrids Piel de Sapo and Cantaloupe had larger corolla diameters, larger nectar chamber dimensions, and a greater supply of foraging resources, which could explain why bees visited their flowers more frequently in the tested areas. Therefore, genotypes that have large flowering diameters become selected and can be developed as a genetic source in crop breeding. Kalyan et al. (2023) reported that the flower morphology was developed to assist both the plant and the pollinator. Compared to other genotypes, the UME91 genotype exhibited the biggest diameter of the hermaphrodite flower boxplot, indicating that its variability was larger. Despite being botanically distinct groupings, the flowering features of reticulatus and inodorus melons are strikingly similar. This is owing to the low molecular resolution and the relatively modest number of genes (Maleki et al. 2018). The flower traits of makuwa melons differ from those of the inodorus and reticulatus groups, particularly the number of male flower petals and the number of hermaphrodite flower petals. The UME20 genotype can be prioritized to facilitate crossbreeding because the stalk length of the male flower and the stalk length of the hermaphrodite flower is longer than the other genotypes. In addition to the stalk length of the flower, the diameter of hermaphrodite flowers is an important characteristic for pollination. A larger bloom diameter could be more attractive to pollinators since it provides a larger area for landing, resulting in effective pollination. Pollinators are drawn to flowers based on their size, shape, and color, all of which impact crop reproduction success (Kiill et al. 2016; Pandey et al. 2021). Genotypes UME91, IPB240, UME100, UME90, UME98, IPB283, UME20, and UME39 had larger hermaphrodite flower diameters than the other genotypes.

In conclusion, based on flower characters, 15 melon genotypes within reticulatus, inodorus, and makuwa group were divided into 4 groups. Group 1 consists of UME99. The genotypes UME20, UME100, and UME98 are included in group 2. Three genotypes, namely UME38, IPBMeta9, and UME101, are included in group 3. Meanwhile, the other eight genotypes are included in group 4. There are no morphological characteristics of flowers as a characteristic of each group of melons. However, there are characteristics of each genotype. The reticulatus group has flower characteristics as follows: NMFP of 5-5.4 petals, NHFP of 5-5.2 petals, SLMF of 0.95-2.9 cm, SLHF of 0.36-1.98 cm, DMFS of 1.01-1.34 mm, DHFS of 2.57-3.15 mm, DMF of 3.12-4.99 cm, and DHF of 8.03-8.61 cm. The inodorus group has flower characteristics as follows: NMFP of 4-5 petals, NHFP of 5 petals, SLMF of 1.34-3.18 cm, SLHF of 0.7-2.46 cm, DMFS of 1.16-1.61 mm, DHFS of 2.72-2.94 mm, DMF of 3.47-4.34 cm, and DHF of 6.56-8.15 cm. The makuwa group has flower characteristics as follows: NMFP of 5-8 petals, NHFP of 5-6 petals, SLMF of 1.32-1.98 cm, SLHF of 1.04-1.74 cm, DMFS of 1.07-1.36 mm, DHFS of 2.67- 3.86 mm, DMF of 3.31-3.85 cm, and DHF of 7.16-8.35 cm). These results may provide insights into the utilization of the test genotypes for crossbreeding.

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