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Diversity and similarity of melon (*Cucumis melo* L.) groups and determination of distinguishing morphological characters

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Abstract. *Saputra HE, Syukur M, Suwarno WB, Sobir. 2022. Diversity and similarity of melon (*Cucumis melo *L.) groups and determination of distinguishing morphological characters. Biodiversitas 23: 6254-6261.* Characterization is an important activity for the study of genotype diversity and similarity. The study was aiming at obtaining information about the diversity and similarity of melon groups and to determine morphological characters as differentiators between melon groups. The genotypes tested were IPB240, IPB283, IPBM21, IPBM23, IPBME5, IPBMETA9, UME20, UME38, UME39, UME90, UME91, UME98, UME99, UME100, UME101. Characterization was based on UPOV and IPGRI guidelines for qualitative and quantitative characters. Two qualitative characters showed no variation in all tested genotypes, namely sex expression (EK) and secondary skin color outside the groove (WKSDA). Qualitative characters that have high diversity were groove color (WA), maximum width between grooves (LMAA), groove color intensity (IWA), and flower stalk thickness (KTBN). The UME98 genotype had the most different color appearance from the other genotypes on the heatmap. The color and depth of fruit grooves are distinguishing characteristics of all genotypes. There were genotype differences in the inodorus and reticulatus types. Unlike the IPBMETA9 genotype, UME100, UME101, and UME38 formed the same clusters with the characteristics of the makuwa group. Melon group makuwa had different characteristics with the inodorus and reticulatus groups. The distinguishing characters for the makuwa type were groove depth, ratio length to diameter, the diameter of hermaphrodite flower stalks, fruit diameter, and fruit skin thickness. Melon groups in the inodorus and reticulatus groups had high similarities, making it difficult to find specific characters in all melon genotypes observed.

Keywords: Diversity, genotype, melon, qualitative, quantitative

INTRODUCTION

Melon (*Cucumis melo* L.) is one of the important and diverse vegetable crops in the Cucurbitaceae family and is classified into two subspecies, *C. melo* ssp. agrestis and *C. melo* spp. melo. The origin of the melon remains controversial, with many studies reaching different conclusions. The old hypothesis stated that *C. melo* originated in Africa because of the large number of wild relatives present. Furthermore, another theory concludes that Asia is the center of origin (origin), with abundant melon diversity throughout India and East Asia (Wang et al. 2021). However, a recent analysis of diverse collections of *C. melo* accessions from Asia, Australia, and Africa, focused on two melon domestication sites, one in Africa and the other in Asia (Endl et al. 2018). Additionally, a recent study based on large-scale genome sequencing data showed three independent domestication events in melons, two in India and one in Africa (Zhao et al. 2019), consistent with the abundant melon diversity found across India and Africa; Africa is also the center of melon diversity. Another study on the genetic characterization of melon accessions and germplasm construction showed the analysis of population structure and genetic diversity of *C. melo* ssp. The melo was first introduced from its center of origin, India, and Pakistan, to Central and West Asia and later to Europe and America. *C. melo* ssp. melo from East Asia most likely originated from *C. melo* ssp. aggressive in India and Pakistan, and shows a different genetic background compared to other subspecies (Wang et al. 2021).

The first step in assembling superior varieties is to have high genetic diversity by collecting various genotypes in the country (exploration) and introductions from abroad. Furthermore, the collected genotypes must be characterized to obtain character information for each. For example, the melon characterization was aimed at obtaining genetic similarity from a collection of melon population (Vella et al. 2019; Esteras et al. 2020; Merheb et al. 2020; Wibowo et al. 2020; Salamah et al. 2021). After collecting several genotypes, it is necessary to select the genotypes that can be used as parents to produce high-quality new varieties that meet the community's needs (Ewing et al. 2019; Zaidi et al. 2019).

Many genetic diversity studies have been carried out on several groups of cultivated and wild melons (Guliyev et al. 2018; Chikh-Rouhou et al. 2021; Pandey et al. 2021; Yusuf et al. 2022). Melons produce several types of flower

structures, such as hermaphrodite or perfect flowers (bisexual), andromonoecious (staminate and perfect flowers), gynomonoecious (pistillate and perfect flowers), monoecious (staminate and pistillate) and gynoecious (pistillate), but andromonoecious is the most dominant (Revanasidda and Belavadi 2019). The high diversity of melons is found in the character of the fruit (Soltani et al. 2022). The characterization of the fruit skin color has six colors: orange, creamy white, yellow, green-yellow, red-green, and light green (Singh et al. 2020). Important components of external quality that determine consumers' preferences on fruit morphology are fruit shape (fruit length/diameter ratio), fruit weight, skin color, and flesh color (Monforte 2017). Pourranjbari et al. (2018) subdivided melon species into eight groups: agrestist (wild melon), flexuous (snake melon), conomon (pickling melon), cantalupensis (cantaloupe or musk melon), inodorous (winter melon, honeydew, casaba), chito (mango melon), and momordica (phoot or snap-melon). Choi et al. (2012) stated that one type of melon that exists is the makuwa group. Information on plant genetic diversity and similarity is useful for both identification of different accessions and the formation of core collections in gene banks, as well as the use of genotypes in breeding programs (Guliyev et al. 2018) so that studies of melon similarity and diversity and determination of distinguishing characters are important in the plant breeding program. The study aimed to obtain information about the diversity and similarity of melon groups and to determine morphological characters as differentiators between melon groups.

MATERIALS AND METHODS

Study area

The research was conducted in Bengkulu City, Indonesia, from June to September 2022. Fifteen melon genotypes were tested in the present study. The melon genotype is a collection of the Tropical Horticultural Study Center of IPB, Lab. Genetics and Plant Breeding Department of Agronomy and Horticulture IPB, Indonesia and Agronomy Lab. of University of Bengkulu, Indonesia.

Procedures

The melon genotypes tested were IPB240, IPB283, IPBM21, IPBM23, IPBME5, IPBMETA9, UME20, UME38, UME39, UME90, UME91, UME98, UME99, UME100, UME101. Melon planting was done in a greenhouse using a drip irrigation system. Seed germination was done by soaking the seeds in warm water for 5 hours. Seeds were ripened using damp opaque paper until germination, approximately 36 hours, depending on genotype. Seeds that germinated were immediately sown in nursery media. Melon seeds of 14 days old after the seedlings are ready to be planted. Embroidery or replacement of dead plants was carried out every day for 7 days after planting. The growing medium used was cocopeat. The polybag used was 40 cm x 40 cm.

The nutrient solution was an AB mix melon solution with a TDS of 700-1000 ppm, depending on the plant growth phase with a drip irrigation system. In the vegetative phase, the nutrient solution given was 700 ppm. Furthermore, 1000 ppm of the nutrient solution was given in the generative phase. The drip irrigation application was given 5 times a day for 5 minutes for each application. First, melon plant stems were wrapped around the rope. Then, pruning of melon plant shoots was carried out on each lateral shoot that appeared on the 1st to 8th segment. Meanwhile, shoots that appear on the 9th segment and above were maintained for fruiting. Pruning was done by cutting the growing lateral shoots with scissors that have been sterilized with mancozeb 70%. Melon harvest was done when the fruit has entered the physiological ripe phase characterized by the presence of an abscission layer on the fruit stalk and the flag leaf has withered; the bottom of the fruit, when pressed, is slightly soft and emits an aroma.

Melon characterization was carried out on qualitative and quantitative characters. Melon characterization with qualitative characters followed UPOV (2006) and IPGRI (2003) methods. Quantitative characters observed included leaf, stem, flower, and fruit organs. Characters in leaf organs are leaf length, leaf width, petiole length, and leaf stalk diameter. The stem organs observed were stem diameter and internode length. The flower characters observed were the number of male flower petals, the number of female flower petals, the length of the male flower stalk, the length of the female flower stalk, the diameter of the male flower stalk, the diameter of the female flower stalk, the diameter of the male flower and the diameter of the female flower. The fruit organs characterized included the fruit length, diameter, diameter ratio, cavity thickness, fruit flesh thickness, fruit skin thickness, fruit weight, and total dissolved solids.

Data analysis

Principal component and cluster analysis were performed by grouping genotypes based on the calculated coefficient of dissimilarity. The principal component and cluster analysis method used was the single linkage with a Ward dissimilarity coefficient matrix. Furthermore, the determination of the distinguishing character was determined from the heatmap. All analyzes were performed using R i386 4.2.1 software.

RESULTS AND DISCUSSION

Qualitative character

The qualitative characters observed were 33 characters of the leaf, flower, and fruit organs. Observational characters are reduced to principal components. The number of principal components used to explain variation in characters was based on the cumulative proportion of total diversity. The number of components for the qualitative characters observed with a diversity of 100% is 14. The grouping of qualitative characters based on the principal component 1 and principal component 2 with a cumulative proportion of 47.1% is presented in Figure 1. Characters close to the center point show that the diversity of these characters is very low for the tested genotypes.

On the other hand, the characters located far from the center showed high diversity in the tested genotypes. Two qualitative characters had no diversity in all tested genotypes, namely sex expression (EK) and secondary skin color outside the groove (WKSDA). The characters farthest from the center point are groove color (WA), maximum width between grooves (LMAA), groove color intensity (IWA), and flower stalk thickness (KTBN).

Genotypes with the same color in the grouping based on principal component 1 and principal component 2 have high similarity. For example, UME100, UME101, IPBMETA9, and UME38 genotypes were grouped into group 1. The UME98 genotype was a genotype with very low similarity to other genotypes. UME20 is the genotype closest to the center point (Figure 2).

The grouping of 15 genotypes based on the observed qualitative characters formed four clusters (Figure 3). The genotypes clustered in Cluster I were UME20, UME91, IPB240, UME90, IPB283, IPBME5, UME39, and UME99. Cluster 2 consisted of two genotypes, namely IPBM21 and IPBM23. Cluster 3 has only one genotype, namely UME98. The other four genotypes; UME100, UME101, IPBMETA9, and UME38, were grouped into cluster 4.

The position of the point between the genotype and the qualitative character is presented in Figure 4. The proximity of the character point to the genotype on the biplot shows a close and specific relationship between the characteristics of the genotype. UME98 genotype is adjacent to groove color (WA). UME100 and UME101 genotypes were close to the groove depth (KA) character.

The mapping of the same characters in the melon group is presented in Figure 5. Based on the heatmap, the qualitative characters are divided into 4 groups. Group 1 consists of UME100, UME101, IPBMETA9, and UME38. Group 2 has only one genotype, namely UME98. Group 3 consisted of IPB240, UME91, UME20, UME90, IPB283, IPBM23 and IPBM21. Group 4 consists of UME99, IPBME5, and UME39. UME98 genotype has the most different color appearance from other genotypes. The darkest color was found in the character of the fruit groove color. Groups 1 and group 2 had similarities in the characters of groove depth, groove color, maximum width between grooves, groove color intensity, groove width, and fruit grooves. On the other hand, group 3 and group 4 also have similarities for these six characters.

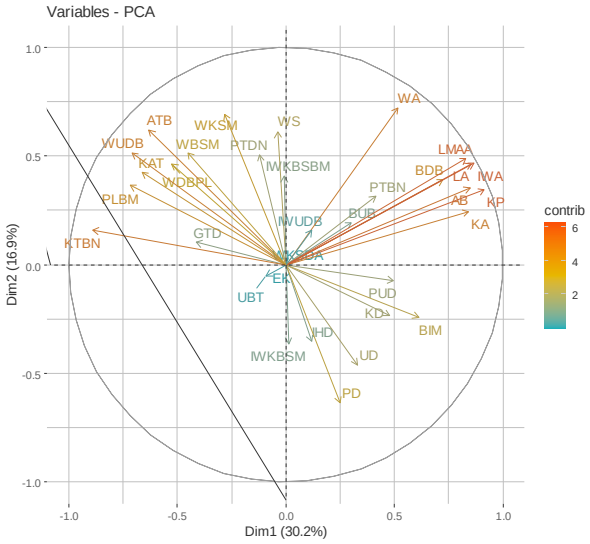

Figure 1. Grouping of qualitative characters based on principal component 1 and principal component 2

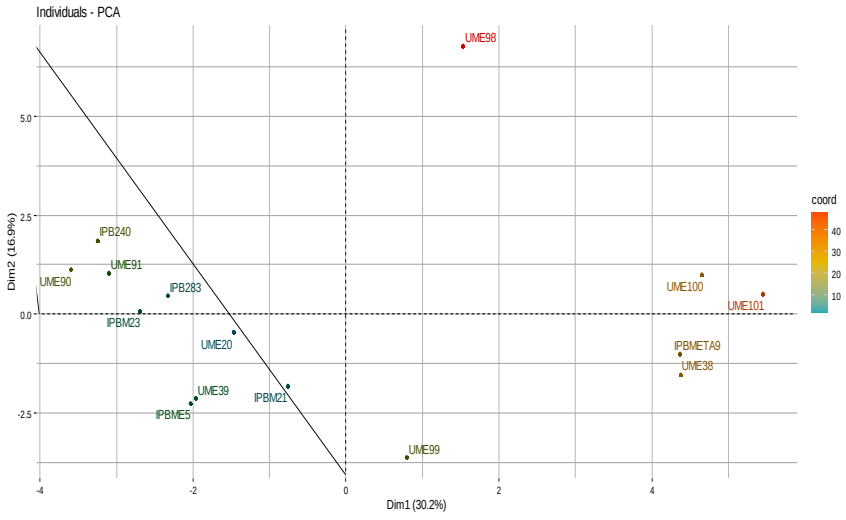

Figure 2. Grouping of genotypes based on principal component 1 and principal component 2 for qualitative character

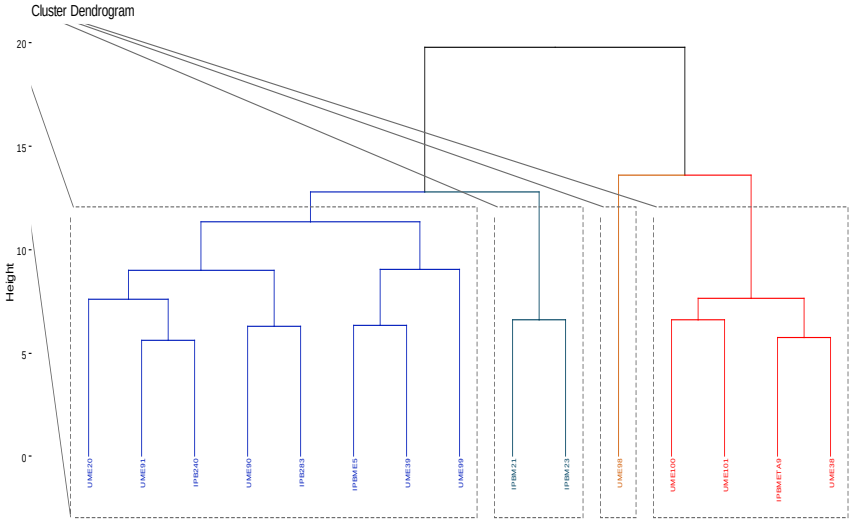

Figure 3. Grouping between genotypes based on Euclidean distance on qualitative characters

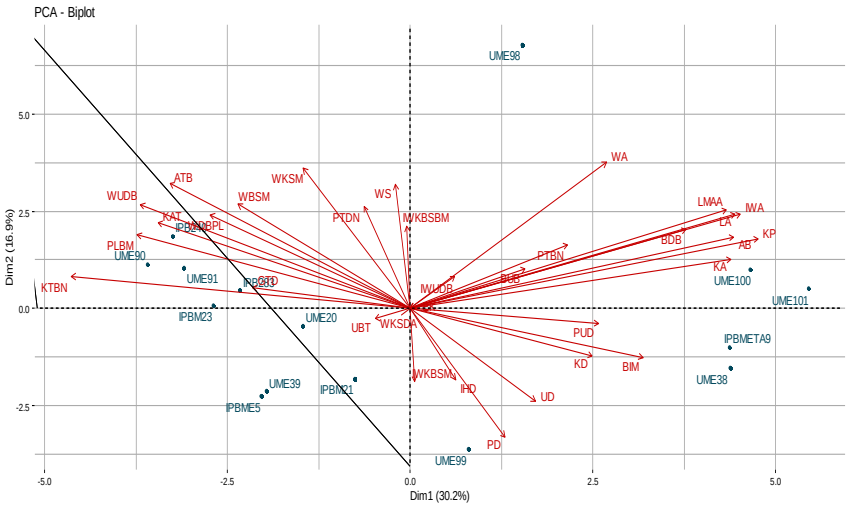

Figure 4. Grouping of genotypes and qualitative characters based on principal component 1 and principal component 2

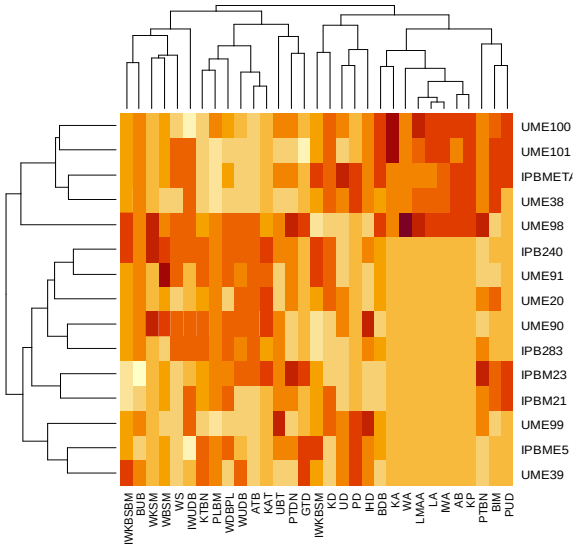

Figure 5. Heatmap of qualitative character traits in the melon group

Quantitative character

The quantitative characters observed included 22 characters of the leaves, flowers, and fruit organs. Observed characters were reduced to principal components. The number of principal components used to explain variation in characters is based on the cumulative proportion of total diversity. The number of components in the quantitative characters responsible for 100% observed diversity was 14. The grouping of quantitative characters based on the principal component I and principal component 2 with a cumulative proportion of 47.1% is presented in Figure 6. Characters close to the center point show that the diversity of these characters is very low for the tested genotypes. On the other hand, the characters located far from the center showed high diversity in the tested genotypes. For example, one quantitative character with low diversity in all tested genotypes was fruit cavity thickness (trb). The character farthest from the center point is the thickness of the flesh (tdb).

Genotypes with the same color in the grouping based on principal component 1 and principal component 2 have high similarity. UME99 and UME20 genotypes are the genotypes that are farthest from the center point (Figure 7). UME99 genotype is a genotype that has a very low level of similarity with other genotypes. IPBM23 and UME39 genotypes are the genotypes closest to the center point.

The grouping of 15 genotypes based on the observed quantitative characters formed four clusters (Figure 8). The genotypes clustered in Cluster I were IPB240, UME90, UME39, IPB283, UME91, IPBM21, IPBM23, and IPBME5. Cluster 2 consisted of two genotypes, namely UME20 and UME98. Cluster 3 has only one genotype, namely UME99. Cluster 4 consisted of four other genotypes, namely IPBMETA9, UME100, UME101, and UME38.

The position of the point between the genotype and the quantitative character is presented in Figure 9. The proximity of the character point to the genotype on the biplot shows a close and specific relationship between the characteristics of the genotype. For example, the UME20 genotype was close to the stem internode length (prb). UME101 and UME38 genotypes were close to the character of the ratio of length to diameter (rpd) and female flower stalk diameter (dtbb).

Based on the quantitative character heatmap, the UME99 genotype has the darkest color appearance compared to other genotypes for the number of female petals, the number of male petals, and petiole diameter (Figure 10). UME101 genotype has the characteristic of the highest ratio of length to diameter. The UME20 genotype has different characteristics from other genotypes for stem internode length, male flower stalk length, female flower stalk length, leaf stalk length, fruit diameter, and total dissolved solids. The IPBME5 genotype has the characteristic of having the largest fruit weight among all genotypes.

Discussion

The diversity and similarity of melons can be seen from the qualitative and quantitative characters. Qualitative characters less influenced by the environment and controlled by major genes have an important role in distinguishing characters between melon plants. In addition, quantitative characters are highly influenced by the environment and controlled by minor genes, so the growing environment will affect the diversity and similarity of melons. Thirty-three qualitative and 22 quantitative characteristics of melons, including the characters of leaf, stem, and fruit organs, were observed in 15 melon genotypes (Figure 1 and Figure 6).

Characters with the same vector direction and form an angle of less than 90° have a positive correlation. Otherwise, if the vector direction of the characters is different and forms an angle of more than 90°, then the characters are negatively correlated. Non-correlated characters are indicated by the direction of the vector, forming an angle of 90°. Based on the 15 genotypes observed, the characters of sex expression and secondary skin color outside the plot were qualitative characters with low diversity; thus, all tested genotypes have the same characteristics based on these characters. The groove color, the maximum width between the grooves, the color intensity of the grooves, the surface wrinkles, the fruit grooves, and the width of the grooves are characters that have high diversity. Each of these characters was negatively correlated with the thickness of the flower stalk, the color of the main flesh of the fruit, the abscission of the fruit stalk, and the strength of the abscission of the stalk so that they became distinguishing characters between genotypes (Figure 1). Different results were obtained by Yusuf et al. (2021) that the distinguishing characters in the melon genotype for qualitative characters are the shape, skin color, and flesh color of the fruit. The differences in the distinguishing characters are presumably due to the different genetic backgrounds of melons and even different melon botanical groups. Therefore, the distinguishing character for differentiating between genotypes depends on the melon botanical group.

Quantitative characters with high diversity were flesh thickness, and this character was negatively correlated with leaf length, leaf width, number of male flower petals, and number of hermaphrodite flower petals (Figure 6). The fruit cavity thickness character is a quantitative character with high similarity among the 15 melon genotypes observed and is not correlated with fruit diameter. The thickness of the fruit cavity was negatively correlated with the diameter of the hermaphrodite flower stalk, the diameter of the male flower stalk, fruit length, and the length ratio to diameter for the observed melon genotype population. Boitshepo et al. (2020) reported that the fruit length and diameter, pericarp thickness, number of fruits per plant, and number of fruits positively correlated with melon yields according to market needs. Other studies also reported that fruit diameter, fruit cavity width, and skin thickness had positive correlations and direct effect on fruit yield and fruit flesh thickness (Reddy et al. 2017), indicating that the correlation between characters depended on the genetic background of each population, thus the information is important for the improvement of the characters in the population tested with this information.

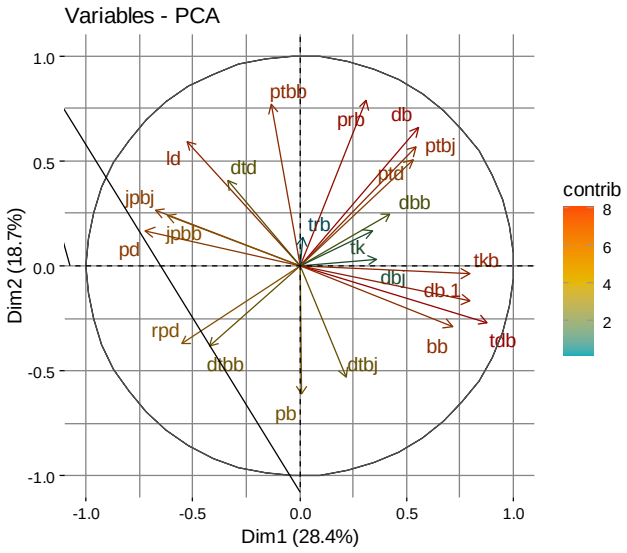

Figure 6. Grouping of quantitative characters based on principal component 1 and principal component 2

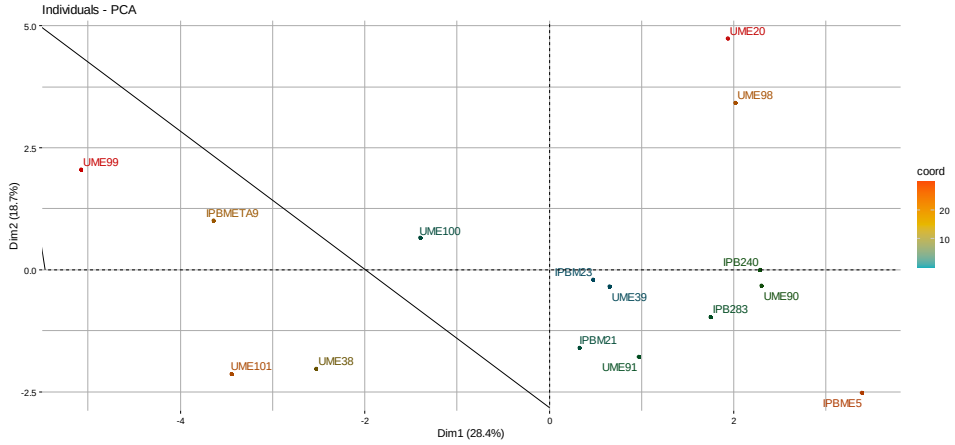

Figure 7. Grouping of genotypes based on principal component 1 and principal component 2 for quantitative characters

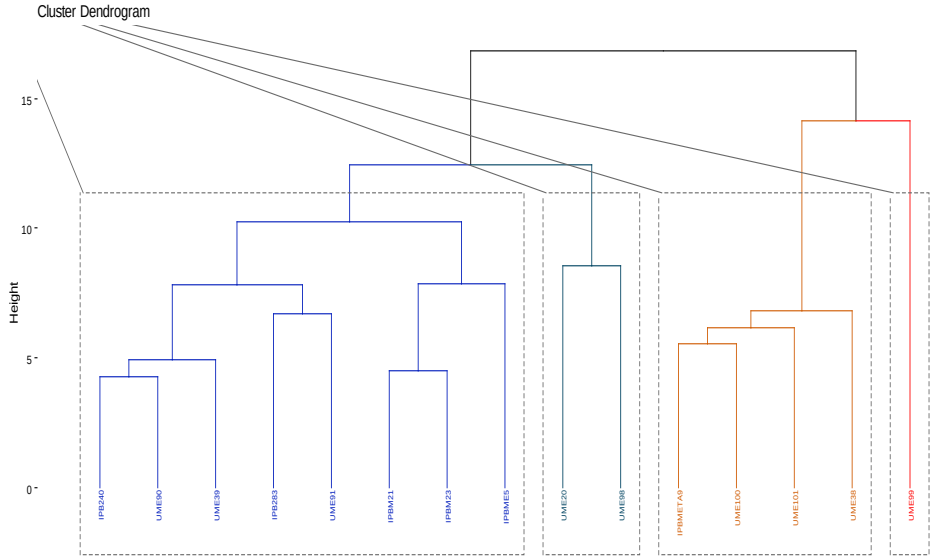

Figure 8. Grouping between genotypes based on Euclidean distance on quantitative characters

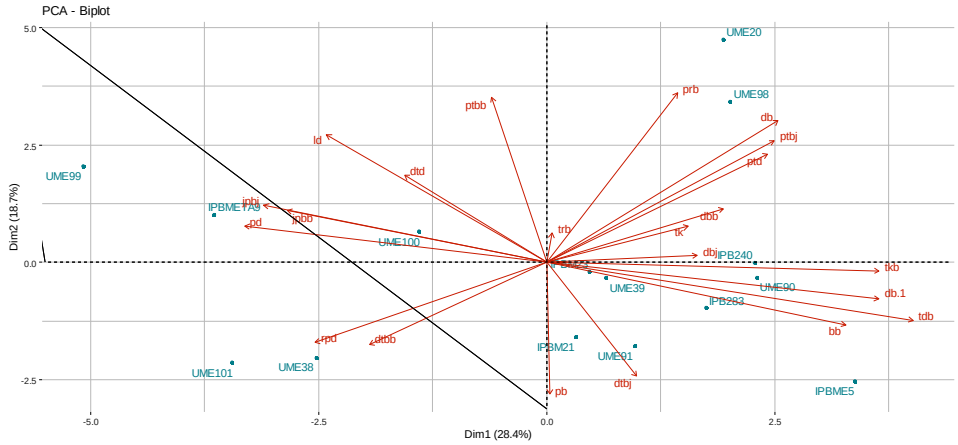

Figure 9. Grouping of genotypes and quantitative characters based on principal component 1 and principal component 2

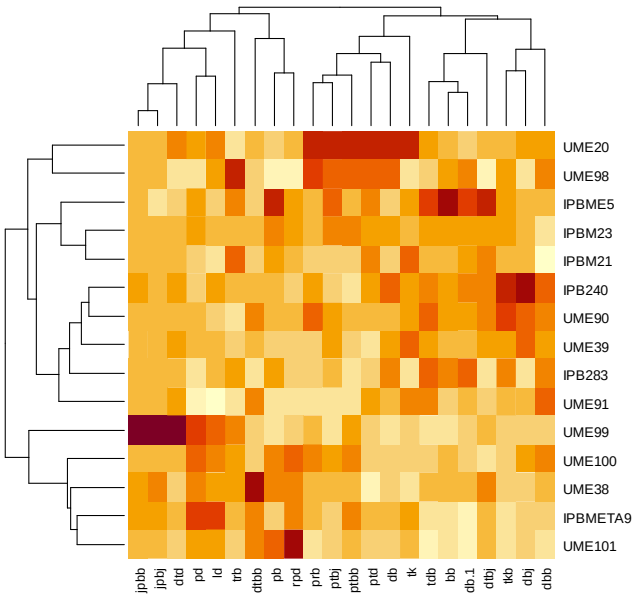

Figure 10. Heatmap of quantitative character traits in the melon group

Principal Component Analysis (PCA) and cluster analysis have been used to identify the most relevant characters and differentiate relationships between species (Saputro et al. 2020; Yusuf et al. 2021). In recent years, many genetic studies have focused on melon fruit traits, including flesh color (Galpaz et al. 2018) and fruit size and shape (Liu et al. 2019). Based on tests on qualitative and quantitative characters, only the same genotypes IPBMETA9, UME100, UME101, and UME38 formed clusters (Figure 3 and Figure 8). The distinguishing characters for this Cluster were groove depth, length ratio to diameter, the diameter of the hermaphrodite flower stalk, fruit diameter, and fruit skin thickness (Figure 5 and Figure 10). This mob-like characteristic is the makuwa group. In clusters, UME99 has proximity to cluster 4, namely the makuwa type. In addition, UME99 has specific characteristics, namely the number of male flower petals and the number of hermaphrodite flower petals, which are more than the genotypes in cluster 4 (Figure 10). Makuwa melons usually have thin skin, high sugar and juice content, and a slight odor. However, thin mesocarp, small fruit size, and short postharvest shelf life affect the commercial value of oriental melon (Wang et al. 2015).

The other clusters, namely clusters 1, 2, and 3, are groupings for the inodorus and reticulatus types. Nunez-Palenius et al. (2008) stated that the inodorus type has the characteristics of a smooth or netted surface, the color of the fruit flesh is generally white, green, or orange, and does not have a characteristic aroma. These fruits usually ripen more slowly and are stored longer due to reduced or no ethylene production compared to reticulatus. Another characteristic of the reticulatus type is the fruit of medium size and net, flesh color from green and white to red-orange, generally have a sweet taste and an aroma. In the 15 melon genotypes, the inodorus and reticulatus types were not clearly differentiated based on the specific characteristics of the melon population tested. This shows a high similarity between the inodorus type and the reticulatus type. A similar result was shown by Maleki et al. (2018) that even though there is a significant difference between var. cantalupensis and inodorus in morphology and physiology but the molecular resolution between them is scanty. Therefore, the relatively small number of genes may be responsible for the differences between the groups (Maleki et al. 2018).

The traditional approach to identifying a species based on morphological characters remains important and provides an accurate picture of the distinctive character of a variety. Accuracy in selecting the appropriate parent to improve melons' quality is necessary. The study of morphological and agronomic characters that can be used as parent selection characters is a problem that must be solved to obtain potential genotypes as parents for the assemble of superior melon varieties with good fruit quality (sweet taste, crunchy, long shelf life, aromatic). Each melon group has a specific character that shows superiority. The diversity of melons between groups is botanically an opportunity to carry out plant breeding activities, especially in combining the superior characters in each group. Melon group makuwa has different characteristics from the inodorus and reticulatus groups. The inodorus and reticulatus melon groups have high similarity, so it is difficult to find specific characters in all the melon genotypes observed. The character of the fruit plot (color and depth) is the distinguishing character of all genotypes.

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