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Morphological Characterization of Some Local Watermelon (*Citrullus lanatus* L.) Genotypes of Turkey

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ABSTRACT

The scope of this study, some of the local Turkish watermelon genotypes were evaluated morphologically. A total of 20 local genotypes and three commercial varieties were assessed regarding their cotyledon, leaf, fruit, and seed phenotypes. An extensive morphological analysis was performed on a diverse set of genotypes. Traits such as cotyledon shape and color intensity, leaf size and lobing, and fruit size, shape, and color were measured and compared. Hierarchical clustering analysis, correlation matrices, and principal component analysis were employed to interpret the data. The study revealed significant morphological variability among the watermelon genotypes. Cotyledons ranged from narrow to broad, with a predominance of large sizes and dark green coloration. Leaf characteristics varied widely, with a notable distribution across different sizes and degrees of lobing. Fruit analysis showed a broad spectrum of shapes, sizes, and colors, indicating a rich genetic diversity. Two main genotype clusters were identified, suggesting a clear distinction based on morphological traits.

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Introduction

Due to its diverse geographical layout and varying ecological conditions in different regions, Türkiye is situated at a significant intersection of global gene centres and origins[1]. The significance of 3,708 out of the total 10,754 taxon present in its flora is heightened by the fact that they are exclusive to this particular region[2]. Despite not being a genetic centre for watermelon, Türkiye has benefited from its favourable geographical location, diverse climate, and historical presence on trade routes. As a result, a wide range of watermelon genotypes have been introduced, and their diversity has further expanded due to the fact that watermelon is a non-self-fertilized plant[1].

Currently, there is a greater understanding of the inheritance of the physical characteristics of watermelon, and many of these characteristics have been identified in the genome[3-14]. This accumulation of knowledge facilitates the utilization and assessment of local watermelon varieties in the breeding research[15].

Numerous investigations have been conducted to identify local varieties[14, 16-32]. Those local varieties could play a crucial role in new cultivars' development and genetic variation[33]. This is due to their ability to adapt to the specific ecological conditions of the region and their potential to provide resistance against prevalent diseases or pests in the area[34]. The genetic base of cultivated watermelon is rather limited[35]. Hence, the identification and conservation of plant genetic resources holds a significant research topic[15].

South Africa is a significant hub for the genetic resources of *C. lanatus*, serving as a key genetic centre[17, 22, 36]. The endeavours to collect, categorize, and safeguard resources in this region have commenced belatedly in comparison to other regions worldwide, and until recently, have not been accorded the requisite significance McGregor [15]. The South African Plant Genetic Resources Centre has preserved a combined total of 179 genetic samples of watermelon from Namibia, Botswana, and South Africa. The Namibian National Institute of Botanical Research has conserved 89 genetic sources, while the National Centre for Plant Genetical Resources and the Zambian Institute of Agricultural Research have preserved 89 and 75 genotypes, respectively. However, there is a scarcity of information regarding these resources, and it remains uncertain whether any conflicts exist among the institutions concerning genetic resources[15]. In their study, Maggs-Kölling and Christiansen [36]conducted a comparison between local varieties of Namibia and commonly cultivated varieties (Congo, Sweet Princess, and Crimson Sweet) in order to assess their morphological characteristics. The researchers discovered that local varieties can serve as significant sources of plant vigour,

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durability, and seed characteristics. In his 2007 study, Goda [17] analyzed the morphological traits of 30 accessions collected from various locations of Sudan, including the western, northern, and central areas. The researcher grouped the accessions under study into various morphotypes. According to Hakimi and Madidi [37] research on the physical traits of indigenous Moroccan variations, the degree of diversity among these varieties ranged from 17% to 43% across different features.

India and East Asia are recognized as secondary genetic centres for the watermelon species[18, 19, 38, 39]. Research conducted in these places, such as Anatolia, has revealed a significant level of morphological variation among the researched indigenous watermelon species[18, 19, 28, 30, 38-40].

Türkiye is located in an area abundant in genetic resources for watermelon. Previous studies in the country have conducted morphological characterizations of numerous local watermelon genotypes[1, 23, 31, 41-49]. In the scope of this study, some of the local Turkish watermelon genotypes were evaluated morphologically to understand morphological features and diversities. A total of 20 local genotypes and three commercial varieties were assessed regarding their cotyledon, leaf, and fruit phenotypes.

Material and Methods

Genetic materials, were evaluated before the aspect of their seed characteristics[50], supplied from different sources were evaluated in this study. Three commercial standard varieties are used as a control provided from the local seed market; seventeen of them were provided by Dr. Polat’s personal collection, and three of them which are originally from Türkiye were supplied by United States Department of Agriculture (USDA) (Table 1).

Table 1 Origin information of genetic materials

Accession No/Cultivar	Provience/Country	Donor
Washington	-	Standard variety
Galaxy	-	Standard variety
Crimson Sweet	-	Standard variety
94004	Çanakkale/Türkiye	Dr. Polat/T. Namık Kemal University
94005	Mersin/Türkiye	Dr. Polat/T. Namık Kemal University
94006	Sakarya/Türkiye	Dr. Polat/T. Namık Kemal University
94017	Uşak/Türkiye	Dr. Polat/T. Namık Kemal University
94027	Unknown/Türkiye	Dr. Polat/T. Namık Kemal University
94047	Unknown /Türkiye	Dr. Polat/T. Namık Kemal University
94051	Unknown /Türkiye	Dr. Polat/T. Namık Kemal University
94054	Sakarya/Türkiye	Dr. Polat/T. Namık Kemal University
94058	Tekirdağ/Türkiye	Dr. Polat/T. Namık Kemal University
94064	Tekirdağ/Türkiye	Dr. Polat/T. Namık Kemal University
94081	Unknown /Türkiye	Dr. Polat/T. Namık Kemal University
94100	Rize/Türkiye	Dr. Polat/T. Namık Kemal University
94120	Unknown /Türkiye	Dr. Polat/T. Namık Kemal University
94123	Unknown /Türkiye	Dr. Polat/T. Namık Kemal University
94127	Unknown /Türkiye	Dr. Polat/T. Namık Kemal University
94128	Unknown /Türkiye	Dr. Polat/T. Namık Kemal University
94131	Unknown /Türkiye	Dr. Polat/T. Namık Kemal University
PI169240 / cv. Kaymakam	Istanbul/Türkiye	USDA
PI169264 / cv. Yenidunya	Bursa/Türkiye	USDA
PI169294 / cv. Cinilikiz	Manisa/Türkiye	USDA

The experiment was designed according to a randomized plot experimental design with 20 plants on each plot. Plants were planted in a high tunnel, 1.5 x 2 m within and between rows. Cultural practices applied during the vegetation period according to[51]. Morphological observations were conducted according to the International Union for the Protection of New Varieties of Plants’ (UPOV) TG/142/5 (proj.1) document[52]. For cotyledons three parameters (size, shape, and intensity of green color), for leaves six parameters (leaf length, leaf width, leaf blade size, leaf blade ratio length/width, color, degree of lobing, blistering, color of veins), for fruits eighteen parameters (fruit weight, fruit shape in longitudinal section, depression at base, shape of apical part, depression at apex, ground color of skin, conspicuousness of veining, pattern of stripes, width of stripes, main color of stripes, conspicuousness of stripes, margin of stripes, size of insertion of peduncle, size of pistil scar, grooving, waxy layer, thickness of pericarp, main color of flesh) were investigated in the study. Collected data were evaluated by R statistical environment for correlation, principal component (PCA), and hierarchical clustering analyses[53].

Results and Discussion

Cotyledons

Evaluated genotypes regarding cotyledon shapes were 21.73% narrow, 52.17% elliptical, and 26.08% broad characteristics. Cotyledon sizes of the genotypes were observed as 8.70% small, 21.73% medium, and 69.56% large. The intensity of green color on cotyledons varied among the genotypes, as 43.47% had medium intensity and 55.52% was dark.

In their studies on Distinctiveness, Uniformity, and Stability testing in watermelon, Choudhary, Pandey [38]also examined the differences in cotyledon shapes during the seedling stage. They have reported that the Sugar Baby and Charleston Grey varieties exhibit narrow elliptical cotyledons, the African-origin Arka Manik variety has medium elliptical cotyledons, and the Japanese-origin Asahi Yamato and African-origin Thar Manak varieties have broad elliptical cotyledons.Sarı, Solmaz [1], in their studies conducting the morphological characterization of Turkish-origin accessions, also examined criteria such as cotyledon shape, size, and the intensity of the green color in cotyledons. In the study, 54% of the examined accessions had elliptical cotyledons, 46% had broad cotyledons, and no narrow elliptical cotyledon structure was observed among them. Our study observed that 21.73% of the genotypes examined according to cotyledon shapes had narrow, 52.17% had elliptical, and 26.08% had broad structures. Although the studies of Solmaz [54] cover the Southeastern Anatolia, Aegean, Marmara-Thrace, Central Anatolia, and Mediterranean Regions, they predominantly contain samples from the Southeastern Anatolia and Aegean Regions. However, the differences between the two studies may also stem from being conducted in completely different ecologies.

In the studies conducted bySolmaz, Sarı [55], the cotyledon size of the examined accessions was observed as 4% small, 44% medium, and 52% large. They have reported that the intensity of the green color in the cotyledons was medium in all accessions. In our study, however, it was observed that 8.70% of the parents examined according to cotyledon size had small, 21.73% had medium, and 69.56% had large structures, and concerning the intensity of the green color in cotyledons, 43.47% of the examined parents had medium intensity, and 55.52% had dark intensity. The distributions of these two characters reviewed in our study also support the positive relationship in the factor analysis. Still, the findings of Solmaz, Sarı [55] were not the sameSzamosi, Solmaz [31], in their comparative study examining Hungarian and Turkish origin accessions, reported that only 2% of the Hungarian accessions were narrow and 98% were elliptical.

Leaves

In the study, it has been observed that leaf widths range between 28.23 cm and 19.96 cm, leaf lengths between 27.13 cm and 19.7 cm, and petiole lengths between 13.53 cm and 8 cm. Alimari, Zaid and Fadda [16]examined leaf width, length, and petiole length in their study investigating the genetic diversity among Palestinian local varieties. Their results indicated leaf widths ranged from 14.8 cm to 11.3 cm, leaf lengths from 15.3 cm to 12.1 cm, and petiole lengths from 8.5 cm to 5.4 cm. Choudhary, Pandey [38]classified leaves as large if they were longer than 14 cm, wider than 12 cm, and had a petiole length over 9 cm. In their findings, the Charleston Grey variety was described as having long, broad leaves with long petioles. According to this classification, most local varieties examined in our study were classified into the large leaf category according to Choudhary, Pandey [38], but most local varieties examined in our study were classified as medium-sized.

According to leaf size, it was observed that 26.08% of the examined lines and standard varieties are small, 47.82% are medium, and 26.08% are large. When examined according to the leaf length/width ratio, 4.34% were broad, 56.52% medium, and 39.13% narrow. Regarding leaf colors, 8.69% were yellowish-green, 39.13% green, and 52.17% were grayish-green. No bluish-green leaf type was observed among the lines and standard varieties examined in the study. Based on the degree of leaf lobing, 4.34% were observed to be very weak, 17.39% weak, 8.69% between weak and medium, 65.21% medium, and 4.34% strong. No examples of very strong leaf lobing degrees were encountered in the study.

When local varieties were examined for leaf curliness, 30.43% were weak, 56.52% medium, and 13.04% strongly curled. The vein color characteristic was green in all genotypes, without variation.

Solmaz, Sarı [55]reported in their studies on Turkish-origin genotypes that 39% had a wide leaf length/width ratio, 60% medium, and 1% narrow. Regarding leaf color, no yellowish-green or bluish-green colors were encountered among the genotypes; 28% had green leaves, and 72% had grayish-green leaves. Regarding the degree of leaf lobing, 12% of the genotypes were weak, 51% medium, and 49% strong. As for leaf curliness, 42% were weak, 47% medium, and 11% strong.

Fruits

In the research by Soltani, Ebadi [30] on Iranian watermelons, the study of plant growth form, leaf, and fruit characteristics concluded that fruit morphological characters are useful indicators for determining genetic variation and selection. Additionally, Gichimu, Owuor [20 and Dida 2009]found in their study on Kenyan genotypes and commercial varieties that commercial varieties exhibit less genetic diversity than non-commercially bred accessions and varieties. In our study, according to fruit sizes, genotypes showed a distribution of 21.73% small, 21.73% between small to medium, 39.13% medium, 13.04% between medium to large, and 4.34% large. Based on the fruit shape in the longitudinal section, 52.17% of the local genotypes and standard varieties had a circular shape, 43.47% were broad elliptical, and 4.34% were medium elliptical. When examining the characteristics of the depression at the fruit base, 47.82% had no or very superficial base depression, 26.08% had superficial base depression, and 26.08% had medium base depression.

Among the genotypes examined within the scope of our study, high variation in fruit characteristics was observed. According to the shape of the apical part of the fruit, 47.82% of the genotypes exhibited a truncate shape, 8.69% between truncate to round, and 43.47% round. In terms of the depression at the apex, 17.39% of the genotypes showed absent or very shallow, 43.47% had shallow, and 39.13% had medium depression at the apex. The ground color of the skin varied from very light green to very dark green. The genotypes were 34.78% very light green, 26.08% light green, 8.69% from light green to green, 13.04% green, 4.34% dark green, 4.34% from dark green to very dark green, and 8.69% very dark green.

Strong fruit grooving was not observed among the genotypes; 86.95% had no or indistinct grooving, 8.69% had weak grooving, and 4.34% had medium grooving. The genotypes included in the study also exhibited a wide variety in terms of stripe pattern. The genotypes were 27.8% only one color, 8.3% one colored and veins, 5.6% one color, veins and marbled, 8.3% one color and marbled, 8.3% two colors, veins and marbled, and 41.7% veins only. The conspicuousness of the veins was inconspicuous or very weakly conspicuous in 56.52% of the genotypes, weak in 8.69%, medium in 17.39%, and strong in 17.39%.

The pattern of the stripes among the genotypes was 26.08% one color, 8.69% one color with veins, 8.69% one color with veins and marbled, 8.69% one color and marbled, 8.69% two colors with veins and marbled, and 39.13% veins only. When examining the stripe width, 52.17% had very narrow, 8.69% narrow, 13.04% medium, 8.69% wide, and 17.39% very wide. The main stripe color distribution was 8.69% yellow, 13.04% very light green, 4.34% light green, 39.13% green, 26.08% dark green, and 8.69% very dark green. The conspicuousness of stripes varied among the genotypes, with 34.78% having inconspicuous or very weakly conspicuous stripes, 4.34% weak, 39.13% medium, 17.39% strong, and 4.34% very strong. In the samples examined, the margin of stripes was observed as 58.3% diffuse, 25% medium, and 16.7% sharp. Regarding the size of the insertion of the peduncle, it was found that 17.39% of the samples had a small insertion, 13.04% had a medium insertion, and 69.56% had a large insertion. The size of the pistil scar was small in 34.78% of the samples, medium in 34.78%, and large in 30.43%. A waxy layer was either not observed or was very weak in 56.52% of the samples, medium in 4.34%, and very strong in 39.13%. Regarding pericarp thickness, 13.04% of the fruit samples were thin, 4.34% were between thin and medium, 26.08% were medium, 4.34% were between medium and thick, 43.47% were thick, and 8.69% were very thick. In genotypes, the fruit flesh color was observed as 8.69% white, 17.39% yellow, 17.39% pink, 30.43% pinkish-red, 21.73% red, and 4.34% dark red.

Correlation between morphological traits

The heatmap showed on Figure 1 is a correlation matrix that illustrates the relationships between different characteristics of cotyledons, leaves, and fruits. Size, shape, and intensity of green color of the cotyledons may have correlations with each other. For instance, larger cotyledons might also tend to be a darker green, which could be indicated by a red square where CSI and CCI intersect.

Length and width of the leaves are likely correlated (larger leaves are both longer and wider), which would appear as a red square at the intersection of LL and LW. The ratio of length to width (LL/W) would have a strong positive correlation with length (LL) and a strong negative correlation with width (LW), showing as a red square with LL and a blue/purple square with LW. Leaf color (LC) and degree of lobing (LDoL) or blistering (LB) might not be directly related to the size of the leaves but may show correlation with each other if certain leaf colors are associated with specific morphologies.

Fruit weight (FW) is likely correlated with the dimensions of the fruit (such as length and width), and this would show as red squares where FW intersects with size-related variables. The shape in longitudinal section (FLS), depression at base (FDB), and shape of apical part (FAS) may show correlations with each other, indicating that certain shapes are commonly associated with specific features at the fruit's base or apex. Ground color of the skin (FGC) and main color of the flesh (FC) may or may not be correlated depending on whether there's a common pigmentation pattern in the species studied. The degree of grooving (FG), conspicuousness of veining (FVC), and pattern of stripes (FPS) might be related to one another if they are features that tend to occur together in certain varieties. The color characteristics like the main color of stripes (FMSC), conspicuousness of stripes (FSC), and margin of stripes (FMS) are likely to show correlations, as these are all coloration patterns on the fruit's skin.

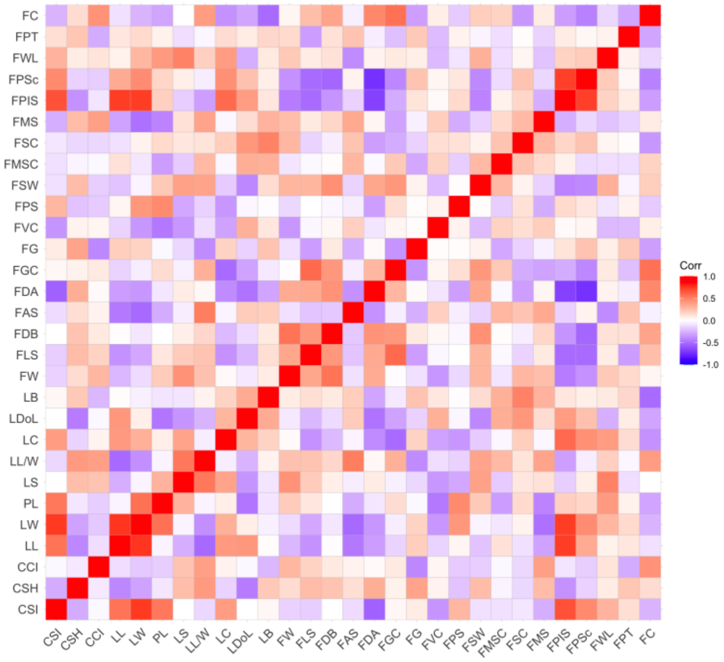

Fig 1 Correlation between the evaluated characters

CSI; Cotyledon: Size, CSH; Cotyledon: Shape, CCI; Cotyledon: Intensity of Green Color, LL; Leaf: Length, LW; Leaf: Width, PL; Leaf: Peduncule Length, LS; Leaf: Size, LL/W; Leaf: Blade Ratio Length/Width, LC; Leaf: Color, LDoL; Leaf: Degree of Lobing, LB; Leaf: Degree of Blistering, FW; Fruit: Weight, FLS; Fruit: Shape in Longitudinal Section, FDB; Fruit: Depression at Base, FAS; Fruit: Shape of Apical Part, FDA; Fruit: Depression at Apex, FGC; Fruit: Ground Color of Skin, FG; Fruit: Grooving, FVC; Fruit: Conspicuousness of Veining, FPS; Fruit: Pattern of Stripes, FSW; Fruit: Width of Stripes, FMSC; Fruit: Main Color of Stripes, FSC; Fruit: Conspicuousness of Stripes, FMS; Fruit: Margin of Stripes, FPIS; Fruit: Size of Insertion of Peduncle, FPSc; Fruit: Size of Pistil Scar, FWL; Fruit: Waxy Layer, FPT; Fruit: Thickness of Pericarp, FC; Fruit: Main Color of Flesh [14.07 cm (H) X 15.01 cm (W)]

There may also be interesting correlations between categories, such as whether certain leaf characteristics correlate with fruit characteristics. For example, the intensity of green color in cotyledons (CCI) might correlate with the main color of flesh in fruits (FC) if a deeper green in early plant development is an indicator of certain fruit pigmentation.

Principal components and hierarchical cluster analyses

There is vector map of PC analysis of variables in Figure 2. The first main component (Dim1), accounting for 48% of the variance, is likely indicative of a distinction between size-related characteristics and other morphological traits, as it exhibits the highest variability across the axes. The second main component (Dim2) captures additional variance (18.1%) that is perpendicular to the first component, potentially expressing other independent changes in traits such as color or texture.

The color scheme applied to the vectors depicting the squared cosine of the variable indicates the degree to which each variable is accurately represented in the principal components. The presence of darker hues on vectors indicates that those variables are accurately depicted by the two shown components.

The vectors of CSI, CSH, and CCI align in the same direction, it suggests that these traits tend to change together within the samples and may form a cluster. From this perspective, it is suggested that larger cotyledons may have a certain form and higher color intensity.

LL, LW, PL, LS, and LL/W are all parameters that pertain to the dimensions and proportions of the leaves. The vectors of these traits were aligned, they exhibit correlation. LC, LDoL, and LB exhibit contrasting patterns compared to the size-related features, it indicates that color and texture are not influenced by leaf size and shape. The association between LC, LDoL, and LB with the size-related characteristics does not necessarily indicate that color and texture are unrelated to leaf size and shape, as there may still be other variables influencing these qualities. The weight of the fruit and traits linked to its size, such as FLS, FDB, and FAS, may exhibit a correlation if they indicate similar tendencies.

The surface properties of the fruit are described with FDA, FGC, FG, FVC, and FPS. If these vectors exhibit proximity, it is probable that these qualities exhibit co-variation. There is a possibility that there is no correlation between fruit weight and size-related qualities such as FLS, FDB, and FAS. This could be due to the presence of other factors that independently influence these features. Conversely, the surface attributes of the fruit, as defined by FDA, FGC, FG, FVC, and FPS, may not always exhibit similar variations simply because their vectors are in close proximity. Additionally, the color trait FC is not directly related to structural features.

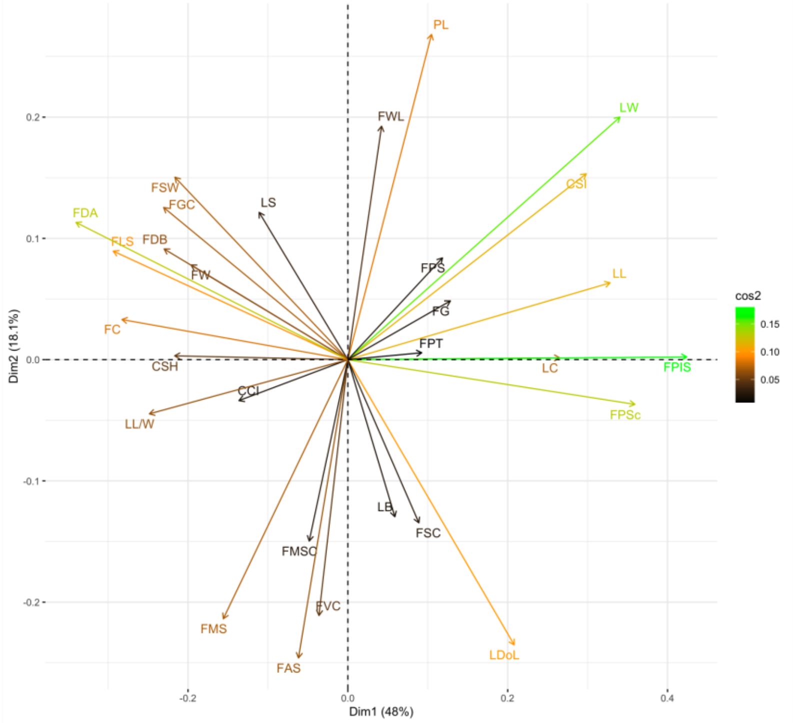

Fig 2 Principal component analysis of variables

CSI; Cotyledon: Size, CSH; Cotyledon: Shape, CCI; Cotyledon: Intensity of Green Color, LL; Leaf: Length, LW; Leaf: Width, PL; Leaf: Peduncule Length, LS; Leaf: Size, LL/W; Leaf: Blade Ratio Length/Width, LC; Leaf: Color, LDoL; Leaf: Degree of Lobing, LB; Leaf: Degree of Blistering, FW; Fruit: Weight, FLS; Fruit: Shape in Longitudinal Section, FDB; Fruit: Depression at Base, FAS; Fruit: Shape of Apical Part, FDA; Fruit: Depression at Apex, FGC; Fruit: Ground Color of Skin, FG; Fruit: Grooving, FVC; Fruit: Conspicuousness of Veining, FPS; Fruit: Pattern of Stripes, FSW; Fruit: Width of Stripes, FMSC; Fruit: Main Color of Stripes, FSC; Fruit: Conspicuousness of Stripes, FMS; Fruit: Margin of Stripes, FPIS; Fruit: Size of Insertion of Peduncle, FPSc; Fruit: Size of Pistil Scar, FWL; Fruit: Waxy Layer, FPT; Fruit: Thickness of Pericarp, FC; Fruit: Main Color of Flesh [13.69 cm (H) x 15.01 cm]

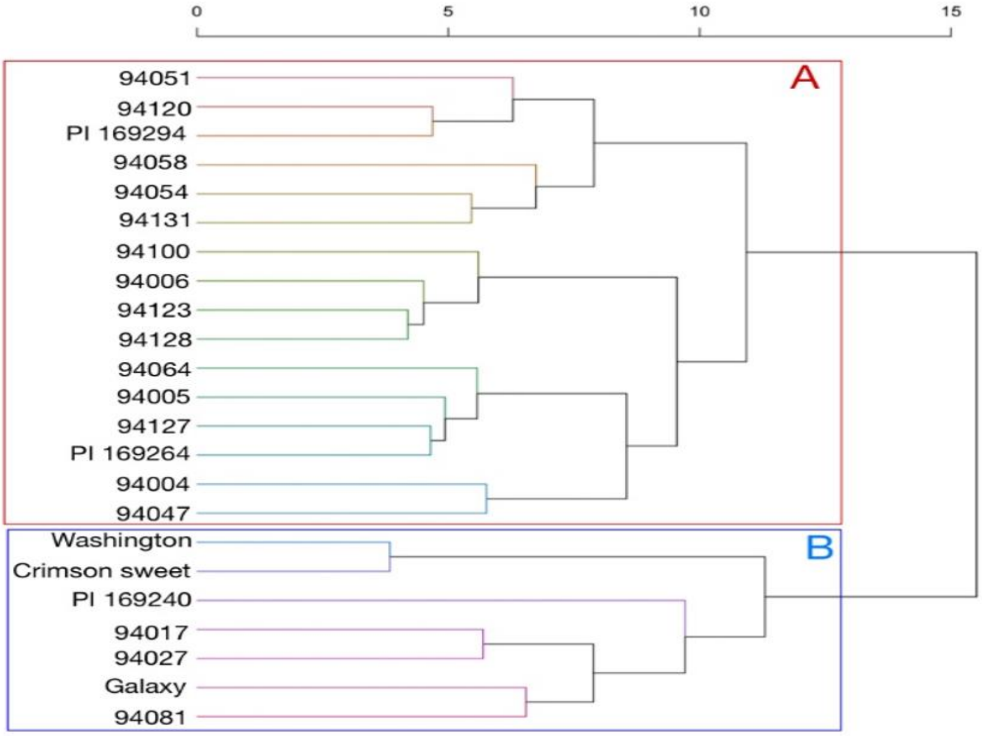

Fig 3 Hierarchical cluster analysis dendrogram of genotypes

Regarding to hierarchical clustering analysis there were two main clusters (A, B) (Figure 3). According to this segregation in the first main cluster (A) there are 16 genotypes and in the second cluster (B) 7 genotypes.

PI 169294, PI169264, 94051, 94120, 94058, 94054, 94131, 94100, 94006, 94123, 94128, 94064, 94005, 94127, 94004, and 94047 genotypes were placed in the first main cluster. All of three commercial varieties placed at cluster B and PI 169240, 94017, 94027, and 94081 were placed together at cluster B.

This study provides a comprehensive analysis of the morphological characteristics of watermelon genotypes, particularly focusing on cotyledons, leaves, and fruits. Our findings suggest a diverse range of shapes, sizes, and colors within these characteristics, which contribute significantly to the distinctiveness and identification of varieties. The cotyledon characteristics observed in our study closely align with the findings of Choudhary, Pandey [38] and contrast withSolmaz, Sarı [55], highlighting the influence of different ecological conditions on morphological traits.

In comparison with previous studies, our research noted a greater prevalence of larger cotyledon and leaf sizes and a wider variation in the intensity of green color. These differences may stem from the varied geographic sampling of genotypes or the inherent genetic diversity within our study group. Similarly, leaf characteristics such as size, color, and degree of lobing showed notable variability, which may serve as additional descriptors for genotype identification and classification.

Our analysis of fruit characteristics revealed a high degree of variation, particularly in size, shape, and color traits, suggesting a rich genetic diversity within the examined genotypes. This diversity is crucial for breeding programs aimed at improving specific traits, as it provides a larger pool of characteristics from which to select. The findings also support previous research by Soltani, Ebadi [30] and Gichimu, Owuor [20] on the importance of morphological characteristics in assessing genetic variation and selection within watermelon genotypes.

The correlation matrix and principal component analysis provided in Figures 1 and 2 illustrate the relationships between different characteristics, suggesting that certain traits may have a tendency to cluster together. These patterns are essential for understanding the morphological structure of watermelon genotypes and for the potential prediction of other traits based on observed correlations.

Hierarchical clustering analysis identified two main clusters, suggesting a clear differentiation among the genotypes based on the measured morphological characteristics. The distribution of commercial varieties in a separate cluster from local varieties could indicate distinct selective breeding practices that have influenced their morphological traits.

Conclusion

Despite the lack of genetic diversity in watermelon breeding lines because of the narrow genetic base, there are many opportunity aspects of biotechnology tools for crop improvement. Underutilized crops, like local varieties or local genotypes, could be answer for lack of genetic diversity. Using biotechnology tools with those valuable underutilized crops also leads crop improvement studies one step further for the resistance of biotic and abiotic stress vectors. Overall, our study underscores the complexity of morphological characteristics in watermelon genotypes and provides valuable insights for breeding and conservation efforts. The observed variability and correlations between traits offer a resource for future research aiming to understand the underlying genetic basis of these morphological differences and their potential exploitation in the development of new varieties with desired characteristics. Since we present detailed morphological background information for those local genotypes, our further goal is to understand their resistance to biotic/abiotic stressors and combining abilities for gene pyramiding studies.

Abbreviations

CSI; Cotyledon: Size, CSH; Cotyledon: Shape, CCI; Cotyledon: Intensity of Green Color, LL; Leaf: Length, LW; Leaf: Width, PL; Leaf: Peduncule Length, LS; Leaf: Size, LL/W; Leaf: Blade Ratio Length/Width, LC; Leaf: Color, LDoL; Leaf: Degree of Lobing, LB; Leaf: Degree of Blistering, FW; Fruit: Weight, FLS; Fruit: Shape in Longitudinal Section, FDB; Fruit: Depression at Base, FAS; Fruit: Shape of Apical Part, FDA; Fruit: Depression at Apex, FGC; Fruit: Ground Color of Skin, FG; Fruit: Grooving, FVC; Fruit: Conspicuousness of Veining, FPS; Fruit: Pattern of Stripes, FSW; Fruit: Width of Stripes, FMSC; Fruit: Main Color of Stripes, FSC; Fruit: Conspicuousness of Stripes, FMS; Fruit: Margin of Stripes, FPIS; Fruit: Size of Insertion of Peduncle, FPSc; Fruit: Size of Pistil Scar, FWL; Fruit: Waxy Layer, FPT; Fruit: Thickness of Pericarp, FC; Fruit: Main Color of Flesh

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Data Availability statement

The author confirms that the data supporting this study are cited in the article.

Compliance with ethical standards

Conflict of interest

The authors declare no conflict of interest.

Ethical standards

The study is proper with ethical standards.

Authors' contributions

All authors contributed equally to the study.

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