

## Collection of local Kyrgyzstan Melon genotypes and determination of morphological relationships between some Anatolian Melons

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**Abstract:** Collection, characterization, and protection of genetic resources are among the high-priority issues of increasing importance throughout the world, especially for the breeding and release of novel cultivars. To understand and describe the characteristics of germplasm, the morphological status of genetic resources must accurately represent their agricultural applications. In this study, the genotypes of melon in Kyrgyzstan were collected by visiting several regions and contacting farmers. The genetic diversity of 35 Kyrgyz and 13 Turkish melon accessions was characterized based on the corresponding phenotypes. The morphological characterizations were largely based on the IPGR and, to some extent, UPOV standards. The genotypes from the collections of both countries were separated into three main clusters using the ward method. It was demonstrated that among the 40 morphological parameters, the fruit-related characteristics contributed most significantly to the separation of genotypes in the PCA analysis, and the results of the PCA analysis also validated the cluster analysis. According to the squared eigenvalues, the accessions Kg-G and C-09 were observed to be the closest related genotypes, whereas the accessions Kav-3 and YYU-13 were the most distantly related. Accessions YYÜ-22, C-02, and C-03 were observed to have the heaviest fruits, Manas-6 and Os-02 were observed to have the highest fruit flesh thickness, and C-08 was determined to have the highest SSC contents among all the accessions. It was observed that the characteristics of melon fruits from both countries differed significantly.

**Key words:** Germplasm comparison, local genotypes, melon, morphology, morphologic relatedness

### 1. Introduction

Melon (*Cucumis melo* L.), the most diverse crop in terms of fruit structure and quality in the genus *Cucumis* (Esteras et al., 2013; Hu et al., 2019), is economically and horticulturally an important open-pollinated vegetable crop that is broadly cultivated in the arid and semiarid regions of the world, including Turkey and Kyrgyzstan, also plays an important role in the horticulture industry, and it is considered one of the 10 most popular cultivated fruits in the world. To date, bioactive substances such as  $\beta$ -carotene, vitamin C, folic acid, and minerals, especially Mg and K, enrich the quality of melon fruits (Fundo et al., 2018; Kyriacou et al., 2018; Rolim et al., 2019) and these market demands and economic incentives cause melon cultivation growth rapidly (Karacan and Ceylan, 2020). Recently, melon, which has 12 pairs of chromosomes ( $2n = 2x = 24$ ), was classified into 19 botanical (horticultural) groups belonging to the subspecies *melo* and *agrestis* by Pitrat (2017). The subspecies *melo* is represented by large fruits that are widely distributed and mostly cultivated around the world, whereas the subspecies *agrestis* typically

consist of small, nonsweet or semisweet, thin-skinned fruits cultivated in Asia (Wang et al., 2018). The origin of melon has been subject to controversy in the scientific world, as some researchers argue that melon originated in Africa due to the similarity in chromosome numbers with the African species, while a part of the scientific community claim that it first emerged in Central Asia because of the close relation between *Cucumis picrocarpus* and *C. melo*, which is the most likely ancestor of the Asian species *Cucumis trigonus* and *Cucumis callosus* (Dhillon et al., 2007; Endl et al., 2018; John et al., 2013). Endl et al. (2018), who merged these two views into a common hypothesis, proposed that melons are separately domesticated in both Asia and Africa.

Regarding the morphology of melon, some melon-cultivating regions show a low genetic variability among the cultivars that have been bred and domesticated as a result of long-term selection. The major reason for this situation is that only the desired characteristics are selected in a population during cultivation over a long period (Sanseverino et al., 2015). Recently, a majority of the studies

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have focused on single nucleotide polymorphisms (SNPs) to investigate the genetic variability at the whole genome scale in various types of plants (Lin et al., 2014). However, genomes consist of several types of variations apart from SNPs, and these multiple sequence modifications are responsible for the dynamism and genetic variability associated with the evolution of the plant genome. Structural variations (SV) such as copy number variation (CNV) and presence/absence based variations (PAV) are commonly observed types of variation in plant species and are also one of the major sources of morphological diversity in melon genotypes (Saxena et al., 2014). Due to their capability of mobilizing gene sequences within the genome, transposons could generate the basis fraction causing CNV and PAV-like structural variations (Morgante et al., 2007). Transposons are regarded as a rich source of new gene and regulatory sequences, and also play a major role in the evolution of the plant genome (Lisch, 2013). (Garcia-Mas et al., 2012) sequenced 375 million base pairs from the melon genome and associated 27.427 sequences with functional genes. Apart from the functional association, they also revealed that 19.7% of the melon sequence consisted of transportable elements (TE). Sanseverino et al. (2015) stated that TE within the melon genome could reach up to 40%. In case of melon, several intermediate forms have frequently emerged due to the cross-pollination between cultural and wild-types, and some genotypes that shift from the cultural type to one similar to the wild-type (Pitrat, 2012). Therefore, the process of domestication of melon is quite complex in terms of its genome, and this dynamic development continues today through genetic variations with local populations (Roy et al., 2012; Omari et al., 2018).

The genetic resources of melon have an impressive and wide variety of morphological differences, particularly regarding fruit characteristics (such as netting, shape, size, color, etc.) and disease resistance (resistance or susceptibility of genotypes due to the quantitative inheritance nature) (Burger et al., 2006; Monforte, 2017). The dynamic gene exchange between genotypes, cultivars, native populations, and wild forms via cross-pollination makes the situation even more complicated. Therefore, the high morphological diversity in a melon can be explained by the fact that it still simply depends on the changing/evolving dynamic genome structure as a natural result of genetic exchange via cross-pollination. The most economically valuable traits in melon are generally expressed by more than one gene or are inherited quantitatively. The selections of these economically important features, as well as cross-breeding between cultivars and wild collections, still ensure the sustenance of the above-mentioned morphological diversity in melon.

Stoilova et al. (2013) reported that genetic resources in any vegetable species should be characterized

agronomically and morphologically to be effectively used by breeders. The characterization of germplasms provides breeders with the following advantages: it allows the breeder to measure and reconstruct the relative diversity within the germplasm and prevents the duplication of any genotypes (Bode et al., 2013; Sudré et al., 2005). Ahlawat et al. (2018) published a similar characterization study, which revealed the importance of the identification and protection of melon germplasm from India. Some other similar studies related to the morphological characterization of melon have been published in various parts of the world, such as those on Iranian (Maleki et al., 2018), Middle East snake melon genotypes (Pech-Kú et al., 2018), Azerbaijan (Guliyev et al., 2018), Spanish (Lázaro et al., 2017), Turkish (Dal et al., 2017), Tunisian (Trimech et al., 2013), and Hungarian melon genotypes (Szamosi et al., 2010). Since Kyrgyzstan is close to the Central Asian geography (a melon diversification center like India), and no such work has been done before in Kyrgyzstan, the aim of our study is to collect the genetic resources of melons cultivated in Kyrgyzstan and to make their morphological characterization by comparing some other collections (revealing their morphological relationships with Anatolian melon genotypes using morphological characterization) and also make them available to researchers.

## 2. Materials and methods

### 2.1. Genetic material

The genetic material used in the research included the melon collection of Prof. Dr. Önder Türkmen, which was mostly collected from east and southeast parts of Turkey and represented the Turkish melon genetic resources. Kyrgyzstan local melon genotypes were also collected from various locations of the country (Table 1 and Supplementary material 1). The genotypes entitled 'Kav' were provided by Prof. Dr. Nebahat SARI from Çukurova University, Department of Horticulture (Sarı and Solmaz, 2018). The genetic resources of the Kyrgyz melons were collected from the Osh, Celal Abad, Batken, and Bishkek (Chui region) regions, where the cultivation was carried out during the 2018 growing season by farmers, agricultural research institutes/stations, and places where genetic resources were frequently encountered (local markets). Thus, we collected as many different melon genotypes as possible from previously described regions and used them as genetic resources for morphological evaluation.

The detailed information of the 35 Kyrgyzstan-originating genotypes and 13 Turkish genotypes is summarized in Table 1.

### 2.2. Plant growth and cultural application

The plant material included was grown at the Sarıcalar Research and Application Farm under the Faculty of

**Table 1.** Description of melon genotypes included in this study.

Kyrgyzstan genotypes	Region	Turkish genotypes	Region
A	Unknown	Kav 1	Diyarbakir
K	Unknown	Kav 3	Mardin
Kırgız A	Chui	Kav 4	Sanliurfa
Kırgız C	Chui	Kav 6	Diyarbakir
Kırgız D	Chui	Kav 252	Ankara
Kırgız E	Chui	Kav 256	Konya
Kırgız F	Chui	YYÜ 6	Van
Kırgız G	Chui	YYÜ 19	Van
Kırgız H	Chui	YYÜ 13	Van
Kırgız İ	Chui	YYÜ 22	Van
Manas 1	Unknown	YYÜ 25	Van
Manas 2	Unknown	YYÜ 30	Van
Manas 3	Unknown	İğdir	İğdir
Manas 4	Unknown		
Manas 5	Unknown		
Manas 6	Unknown		
Manas 7	Unknown		
Manas 8	Unknown		
Ç 01	Chui		
Ç 02	Chui		
Ç 03	Chui		
Ç 04	Chui		
Ç 05	Chui		
Ç 06	Chui		
Ç 07	Chui		
Ç 08	Chui		
Ç Son	Chui		
Ç09	Chui		
J 01	Jalal-Abad		
J 02	Jalal-Abad		
Oş 01	Osh		
Oş 02	Osh		
Oş 03	Osh		
Oş 04	Osh		
Oş 05	Osh		

Agriculture of Selçuk University during the vegetation period of 2019. DAP (diammonium phosphate) (150 kg/ha) fertilizer was applied as the base fertilizer, based on the results of the soil analysis (Table 2) during the first tillage on the experimental site.

The melon genotypes were planted on 10.04.2019 as seeds 2 m apart in rows in the field, with the rows spaced 0.8 m apart. Fifteen plants were sown in the experimental

area from each genotype. Morphological observations were obtained from at least ten different plants belonging to each genotype. Fertilizers such as 10 L per hectare Synergy (12% humic acid, %2-3 fulvic acid w/w), 20 L per hectare Evergreen Soil (NPK: 5%, 10%, and 5% respectively w/w), and 20 L per hectare Nitrosol (nitrogen source: nitrate (NO<sub>3</sub> - N) 12% w/w) were applied using the drip irrigation system on June 10, 2019. The results of soil analysis in Table 2 were considered during the fertilization. When the main stem of melon seedlings begins to grow, maintenance and culture practice were carefully applied to each seedling (Vural et al., 2000). To protect the melon genotypes from powdery mildew and Fusarium wilt, a plant protection chemical (Cebir for fusarium and Topas for mildew) was applied either by using a drip irrigation system or spraying directly on the plants.

### 2.3. Morphological characterization

From the moment homogeneous growth was observed in the plants, morphological measurements and observations were made at the various stages during the vegetation periods of the grown melon genotypes. To record and evaluate the morphological characteristics of the melon genotypes, the melon descriptor developed and published by The International Plant Genetic Resource (IPGR) and UPOV organization was adapted and used in this study (IPGRI, 2003) (Supplementary material 2).

### 2.4. Statistical analyses

Using the measurements and observations related to morphological characters, all the data were subjected to cluster analysis to determine the relationship between genotypes using SPSS software. For the cluster analysis, the Ward method was used, which was present in the SPSS software. A squared Euclidean distance matrix was extracted from the morphological data and used for the construction of a dendrogram using the Ward method. Factor analysis (FA) and principal component analysis (PCA) were performed on the same data using the program JMP 19 (Scatter-plot using Minitab 16). Based on the Tukey post hoc test following one-way ANOVA, homogeneous groups of genotypes were determined and lettered accordingly. The Shannon-Weaver diversity index ( $H'$ ) for each qualitative and quantitative character was calculated using the following formula (Hutchenson, 1970):

$$H' = \sum_{i=1}^n (p_i \log_e p_i)$$

Equitability indices (E) for each qualitative and quantitative character were also calculated using the following formula (Sheldon, 1969):

$$E = \frac{H'}{H_{max}}$$

**Table 2.** Soil analysis report of trial land.

Soil sample (cm)	pH	N (ppm)	P (ppm)	Ca (ppm)	K (ppm)	Mg (ppm)	Na (ppm)	Cu (ppm)	Fe (ppm)	Mn (ppm)	Zn (ppm)	B (ppm)
0-30	7.44	29.01	9.40	7314.28	891.47	465.73	142.99	1.74	4.06	13.56	0.75	0.82
30-60	7.50	22.79	3.84	7374.92	425.41	429.07	157.50	1.72	5.17	10.28	0.26	0.93
60-90	7.47	37.30	5.07	7449.64	397.77	482.43	125.47	2.00	5.51	11.31	0.40	0.15

### 3. Results

#### 3.1. Quantitative measurements

To compare the melon genetic resources, 27 qualitative and 14 quantitative morphological parameters were observed or measured based on the melon descriptor (Supplementary material 2), and the data of quantitative characteristics (14 quantitative morphological characters) are summarized in Tables 3 and 4.

A wide diversity was observed in the length and width of leaves of melon genotypes collected from various regions of Turkey and Kyrgyzstan. The leaf length ranged between 7.38 and 16.27 cm, with the longest leaf (16.27 cm) being observed in the Ç-07 genotype from the Chui region of Kyrgyzstan, and the shortest leaf (7.38 cm) in the Kav-3 genotype from the Mardin region of Turkey (Table 3). The leaf width ranged between 9.34 and 22.92 cm. The two genotypes with the highest leaf width were YYÜ-13 (22.92 cm) and Ç-07 (20.10 cm). The two genotypes showing the lowest leaf width were Kg-E (9.34 cm) and Kg-C (10.25 cm). The longest leaf petiole was observed in Kg-İ (16.1 cm) and Ç-04 (14.46 cm). Both the genotypes that exhibited the longest leaf petiole belonged to the Kyrgyzstan melon germplasm. Fruit weight is an important agro-morphic parameter that represents yield in melons, and when the genotypes in this study were evaluated in terms of fruit weight, wide variation was observed. The heaviest fruits were observed in the Turkish melon genotypes YYÜ-22 (3790 g), Ç-02 (3730 g), and Ç-03 (3691 g). The Turkish accession YYÜ-30 (354 g) and the Kyrgyz accession Manas-4 (459 g) were recorded to have the lightest fruits among all the accessions.

Other important agro-morphic characteristics associated with melon yield are the fruit length and fruit diameter, which were separately measured in all the included accessions. The Kyrgyz accessions Ç-04 and Ç-05 exhibited the highest fruit length with 28.97 cm and 28.57 cm, respectively. Manas-4 and YYÜ-30 were observed to have the least fruit length with 10.48 and 9.4 cm, respectively (Table 3). The highest fruit diameter was observed in the Kyrgyz accessions Manas-6 and Kg-D with 19.24 and 18.70 cm, respectively, whereas YYÜ-30 and Mana-4 were observed to have the smallest fruits with diameter of 8.49 and 9.74 cm, respectively (Table 3). As all the fruit-related

features are important in melon genotypes, measurement of fruit rind thickness and flesh thickness are important agro-morphic characteristics and are frequently used in morphological characterization studies. The accessions Manas-6 and Oş-02 from Kyrgyzstan melon germplasm had fruits with the highest flesh thickness at 46.29 mm and 43.03 mm, respectively, whereas the YYÜ-30 melon accession showed the least flesh thickness (11.07 mm). Regarding the rind thickness of melon genotypes, fruits of Kav-4 had the thickest rind (12.22 mm), whereas Manas-4 showed the thinnest rind (3.77 mm) (Table 3).

Regarding the soluble solid content (SSC), the genotype Ç-08 was observed to have fruits with the highest SSC value (15.9%). The accessions C-05 and C-04 showed the best performance among all evaluated parameters, whereas YYÜ-13 and YYÜ-19 showed the worst performances (Table 4). The acidity (pH) of all accessions ranged narrowly, between 4.92 and 6.52. The seed weights of the Kyrgyz accessions Kg-H (69.33 mg) and J-01 (68.79 mg) were the highest compared to the others. As with several evaluated characteristics, the least seed weight was observed in the YYÜ-30 accession (25.02 mg). The accessions Kg-H and Ç-07 were observed to possess the longest seeds (14.31 and 14.21 mm, respectively), whereas the Manas-4 accession was observed to have the shortest seeds (8.63 mm). The quantitative measurements for comparing the accessions are presented in Table 4, and classified by using the Tukey post hoc test into the letters.

#### 3.2. Quantitative and qualitative measurements and cluster analysis

The dendrogram was drawn according to the Ward method using previously recorded and scored morphological measurements and observations including 14 quantitative and 27 qualitative characters, and the relationship among accessions is presented in Figure 1. While drawing the dendrogram, 41 measurements and observations were either recorded categorically or transformed from continuous to categorical variables (Supplementary material 2), which helped scoring them using the melon descriptor. Based on the cluster analysis, it was evident that the accessions were clustered into two major groups: Turkish and Kyrgyz genotypes. While most genotypes (29) included in this study were clustered in the first major

Table 3. Some quantitative leaf and fruit morphological characters in different melon genotypes.

Genotypes	Leaf length (cm)	Leaf diameter (cm)	Leaf petiole length (cm)	Fruit size (gr)	Fruit length (cm)	Fruit width (cm)	Fruit peduncle length (mm)
Kg-A	8.53 m-o	11.12 uv	8.60 o-s	1986 n-q	18.71 n-p	14.57 k-o	22.00 q-s
Kg-C	7.75 op	10.25 vw	9.53 j-p	1524 rs	14.53 vw	14.45 k-p	14.35 y
Kg-D	10.10	12.32 q-u	9.00 n-q	3320 b-d	17.37 q-t	18.70 ab	27.88 b-d
Kg-E	8.50 m-o	9.34 w	10.50 e-k	1556 q-s	13.36 w	15.06 h-m	15.69 xy
Kg-F	11.73 e-g	18.10 c-e	14.32 bc	1638 p-s	25.53 ef	11.45 v	24.11 h-n
Kg-G	11.08 f-j	15.13 i-m	10.63 e-1	2683 e-j	20.76 j-l	15.16 h-l	24.80 g-l
Kg-H	11.10 f-j	16.10 f-j	10.25 f-l	2241 k-o	16.22 tu	14.79 j-n	18.04 vw
Kg-İ	11.46 f-h	17.53 c-g	16.10 a	2441 h-m	26.02 d-f	13.06 r-u	26.26 d-g
K	11.83 d-g	15.46 h-l	10.80 e-h	2752 e-1	20.21 k-m	15.08 h-m	27.23 b-e
A	11.85 d-f	17.57 c-g	10.47 e-l	2491 g-l	17.52 q-s	15.94 e-1	19.92 t-u
Manas-1	10.97 g-k	14.00 l-q	13.70 bc	2806 e-h	23.47 h	13.62 o-s	23.82 i-p
Manas-2	8.14 m-p	13.83 l-q	9.15 m-q	2228 l-o	25.00 fg	13.00 r-u	28.62 b
Manas-3	8.70 mn	13.33 o-t	8.92 n-q	2673 f-k	17.64 p-s	17.29 cd	24.12 h-n
Manas-4	7.99 n-p	11.20 uv	9.45 l-p	459 t	10.48 y	9.74 w	23.22 k-q
Manas-5	8.18 m-p	14.61 j-p	10.24 f-l	1496 rs	19.40 m-o	12.00 uv	22.64 m-r
Manas-6	8.37 m-o	13.60 m-r	10.12 g-m	3463 a-c	19.42 m-o	19.24 a	26.69 c-f
Manas-7	11.33 f-1	14.77 j-o	11.90 d	2394 h-n	16.95 st	16.87 d-f	21.30 r-t
Manas-8	8.68 mn	15.06 i-n	10.56 e-j	2492 g-l	18.21 p-r	17.27 cd	22.21 o-s
Ç-01	8.64 mn	14.85 j-o	10.66 e-h	2776 e-1	27.42 bc	15.24 g-k	28.82 b
Ç-02	8.02 m-p	14.25 l-p	9.02 n-q	3730 ab	24.33 gh	18.04 bc	24.26 h-m
Ç-03	12.33 c-e	18.01 c-e	13.60 c	3691 ab	25.24 fg	11.32 v	26.83 c-f
Ç-04	12.71 c	18.93 bc	14.46 b	2742 e-1	28.97 a	13.76 n-s	25.31 f-1
Ç-05	12.33 c-e	17.50 c-g	11.24 d-f	2348 i-n	28.57 ab	13.42 p-t	27.57 b-d
Ç-06	8.44 m-o	14.62 j-p	8.11 q-t	2289 j-o	20.43 k-m	14.47 k-p	23.90 i-o
Ç-07	16.27 a	20.10 b	14.58 b	2900 d-g	20.21 k-m	16.83 d-f	15.93 xy
Ç-08	12.62 cd	16.56 e-1	9.02 n-q	2910 d-g	21.36 i-k	14.58 k-o	27.54 b-d
Ç-09	10.45 j-l	17.66 c-g	9.47 k-p	2051 m-p	21.81 ij	14.41 k-p	24.07 h-n
Ç-Son	11.51 e-h	16.92 d-h	9.64 j-p	1530 rs	16.63 s-u	13.98 m-r	22.12 p-s
J-01	8.86 m	13.95 l-q	9.61 i-o	3116 c-e	26.65 c-e	16.13 e-h	28.38 bc
J-02	11.60 e-h	17.77 c-f	11.45 de	3075 c-f	22.00 i	17.02 c-e	19.25 uv
Oş-01	8.52 m-o	16.00 g-k	11.32 de	1890 o-r	17.07 r-t	15.06 h-m	16.30 x
Oş-02	10.14 kl	14.86 i-o	9.90 h-n	2768 e-1	19.55 mn	16.32 d-g	25.32 f-1
Oş-03	8.60 m-o	13.55 m-r	10.20 g-m	2706 e-j	28.00 ab	14.26 k-q	25.26 f-j
Oş-04	10.45 j-l	14.37 k-p	10.14 g-m	3020 d-f	20.38 k-m	13.27 q-t	25.48 f-1
Oş-05	10.5 i-l	14.50 j-p	11.08 d-g	2962 d-f	26.73 cd	13.76 n-s	27.66 b-d
YYÜ-6	11.13 f-j	18.30 cd	9.00 n-q	1422 s	18.27 o-q	13.00 r-u	32.00 a
YYÜ-13	14.76 b	22.92 a	14.71 b	1248 s	14.50 vw	13.04 r-u	23.57 j-q
YYÜ-19	10.78 h-l	15.37 h-l	8.73 o-r	2269 j-o	21.36 i-k	14.96 i-m	23.13 l-q
YYÜ-22	8.70 mn	14.95 i-o	11.36 de	3790 a	25.31 fg	17.39 cd	32.87 a
YYÜ-25	7.76 op	13.00 p-t	8.66 o-s	2023 m-p	20.28 k-m	12.71 s-u	20.72 s-u
YYÜ-30	8.70 mn	13.98 l-q	6.53 u	354 t	9.40 y	8.49 x	17.35 wx
Iğdır	8.42 m-o	15.50 h-l	10.28 f-l	2230 l-o	19.67 l-n	15.19 h-l	25.75 e-h
Kav-1	10.85 h-l	13.43 n-s	8.56 p-s	1255 s	11.72 x	14.11 l-r	22.00 q-s
Kav-3	7.38 p	11.70 t-v	7.32 tu	1346 s	14.02 w	13.11 r-u	31.25 a
Kav-4	10.85 h-l	15.18 i-m	8.93 n-q	1474 rs	17.74 p-s	12.31 t-v	22.96 m-r
Kav-6	8.13 m-p	12.05 r-u	7.68 st	1205 s	14.11 w	12.80 s-u	22.45 n-r
Kav-256	8.15 m-p	12.05 r-u	7.79 r-t	1969 n-q	13.43 w	16.51 d-f	28.70 b
Kav-252	8.85 m	11.85 s-v	9.43 l-p	2143 l-o	15.63 uv	15.77 f-j	24.93 g-k

The letters within the table have 5% of the statistical significance level and indicate homogeneous groups due to Tukey's post hoc test after ANOVA.

Table 4. Some quantitative leaf and fruit morphological characters in different melon genotypes.

Genotypes	Fruit peduncle width (mm)	Blossom scar size (mm)	Rind thickness (mm)	Flesh thickness (mm)	SSC	pH	Seed weight (mg)	Seed length (mm)
Kg-A	9.65 a-e	9.88 m-p	6.39 g-p	36.63 cd	10.88 d-1	6.52 a	28.86 r-t	10.27 v-x
Kg-C	6.14 lm	9.29 n-q	5.6 l-r	30.70 g-o	10.40 d-j	6.16 a	46.23 h-l	11.00 q-v
Kg-D	8.84 a-g	52.63 a	10.41 ab	34.37 d-h	9.60 e-l	6.02 ab	46.06 h-l	10.40 u-w
Kg-E	6.49 k-m	13.3 j-o	4.31 qr	30.42 g-o	11.21 d-g	6.11 a	41.25 j-o	11.46 o-u
Kg-F	6.58 i-m	15.61 i-l	6.27 h-p	23.50 rs	7.20 m-r	5.75 ab	27.74 st	12.53 f-o
Kg-G	9.28 a-f	16.14 h-k	8.71 b-f	34.15 d-1	7.97 l-q	5.80 ab	38.31 n-p	12.90 c-k
Kg-H	10.13 a-c	36.97 c	8.22 c-g	29.41 i-p	8.71 j-p	5.92 ab	69.33 a	14.31 a
Kg-İ	6.70 h-m	21.61 fg	6.73 g-p	34.32 d-h	7.22 m-r	6.22 a	43.82 i-n	11.63 m-s
K	8.86 a-g	14.17 i-m	7.67 d-k	33.69 d-j	7.00 n-r	5.75 ab	42.66 i-n	13.58 a-f
A	6.53 j-m	27.47 de	6.73 g-p	32.00 d-n	12.00 b-d	6.03 ab	57.01 b-d	12.70 e-m
Manas-1	7.28 g-l	17.45 g-k	5.07 p-r	34.33 d-h	8.20 k-p	6.12 a	39.11 m-p	12.27 h-p
Manas-2	6.31 lm	27.18 de	6.03 i-q	29.20 j-p	7.30 m-r	6.04 ab	35.08 o-r	11.35 p-v
Manas-3	8.53 c-h	30.09 d	10.61 ab	36.68 cd	8.88 i-o	5.95 ab	45.79 h-m	10.58 r-w
Manas-4	6.46 k-m	30.75 d	3.77 r	20.68 s	6.96 n-r	6.14 a	32.56 p-s	8.63 y
Manas-5	8.43 c-j	12.85 k-o	6.47 g-p	24.83 p-s	7.92 l-q	5.95 ab	38.85 n-p	12.51 f-o
Manas-6	8.49 c-1	20.77 f-h	7.57 e-k	46.29 a	10.24 d-k	6.17 a	55.79 de	12.62 e-n
Manas-7	7.85 e-l	29.11 d	7.00 f-p	33.25 d-k	9.42 f-l	5.99 ab	52.00 d-h	12.57 f-o
Manas-8	9.03 a-g	29.25 d	10.13 bc	33.66 d-j	7.24 m-r	5.65 ab	48.35 f-1	13.73 a-e
Ç-01	9.63 a-e	7.81 pq	8.25 c-f	23.90 q-s	11.60 c-e	5.88 ab	48.39 f-1	11.04 q-v
Ç-02	8.52 c-h	13.94 i-m	7.05 f-o	36.63 cd	7.66 l-q	5.70 ab	63.75 ab	13.74 a-e
Ç-03	6.72 h-m	17.26 g-k	6.11 h-q	28.12 l-r	13.66 b	6.24 a	39.52 l-o	11.81 k-q
Ç-04	10.63 ab	21.30 fg	5.91 k-q	34.58 l-h	12.25 b-d	6.40 a	3565 o-q	11.76 k-q
Ç-05	7.89 e-l	17.72 g-j	6.29 g-p	32.70 d-m	8.83 j-p	6.20 a	43.58 i-n	11.61 m-t
Ç-06	10.72 a	15.26 i-l	6.96 f-p	30.32 g-o	8.43 j-p	5.70 ab	43.94 i-n	12.09 i-q
Ç-07	8.35 c-k	44.68 b	8.70 b-f	31.47 f-o	8.91 i-o	5.79 ab	63.18 a-c	14.21 ab
Ç-08	8.91 a-g	13.81 i-n	6.92 f-p	29.27 j-p	15.90 a	5.82 ab	49.20 e-1	10.98 q-v
Ç-09	10.58 ab	14.43 i-m	6.93 f-p	30.75 g-o	9.00 h-n	5.63 ab	47.10 g-j	11.92 j-q
Ç-Son	9.47 a-f	31.39 d	5.95 j-q	34.24 d-1	6.92 o-r	5.64 ab	53.34 d-g	13.29 a-h
J-01	7.70 f-l	11.37 l-p	9.51 b-d	33.89 d-j	7.89 l-q	5.52 ab	68.79 a	12.75 d-m
J-02	9.63 a-e	9.04 o-q	8.04 d-h	33.96 d-j	10.90 d-1	6.31 a	68.00 a	12.98 c-j
Oş-01	7.65 f-l	37.08 c	7.34 f-l	28.59 k-q	9.22 g-m	5.52 ab	56.49 cd	12.57 f-o
Oş-02	9.54 a-f	17.19 g-k	7.86 d-1	43.03 ab	5.55 rs	5.44 ab	48.79 f-1	13.86 a-d
Oş-03	9.41 a-f	10.57 m-p	6.90 f-p	35.73 d-f	7.82 l-q	5.98 ab	44.35 i-n	13.09 b-1
Oş-04	6.67 h-m	28.84 de	7.02 f-o	30.11 h-o	13.50 bc	6.19 a	39.53 l-o	11.95 i-q
Oş-05	8.82 a-g	20.33 f-h	7.03 f-o	34.50 d-h	9.55 f-l	6.17 a	38,80 n-p	11.86 j-q
YYÜ-6	6.44 k-m	7.77 pq	7.85 d-j	23.51 rs	7.31 m-r	5.85 ab	48.29 f-1	13.93 a-c
YYÜ-13	7.86 e-l	17.51 g-j	5.16 n-r	26.79 o-r	5.51 rs	5.68 ab	54.11 d-f	13.51 a-g
YYÜ-19	8.77 b-g	10.44 m-p	5.47 l-r	31.65 e-o	4.83 s	6.03 ab	54.56 d-f	12.83 c-l
YYÜ-22	7.32 g-l	18.27 g-1	9.45 b-e	34.60 d-h	7.7 l-q	5.66 ab	51.34 d-h	11.69 l-r
YYÜ-25	6.41 lm	7.90 pq	5.12 o-r	27.76 n-r	11.46 d-f	6.39 a	37.94 n-p	11.95 i-q
YYÜ-30	5.23 m	4.81 q	4.28 qr	11.07 t	6.15 q-s	4.92 b	25.02 t	9.57 w-y
İğdir	9.48 a-f	17.86 g-j	5.41 m-r	34.30 d-h	11.30 d-f	6.45 a	39.79 k-o	13.00 c-j
Kav-1	9.88 a-c	24.32 ef	6.53 g-p	35.04 d-g	8.51 j-p	6.12 a	30.17 q-t	9.72 w-y
Kav-3	9.84 a-d	17.60 g-j	7.87 d-1	30.28 g-o	11.90 b-d	6.48a	31.13 q-t	10.52 s-w
Kav-4	7.94 d-l	9.04 o-q	12.22 a	28.07 m-r	11.00 d-h	6.35 a	32.72 p-s	11.54 n-u
Kav-6	10.09 a-c	17.09 g-k	6.11 h-q	36.36 de	8.87 i-o	6.25 a	30.24 q-t	10.46 t-w
Kav-256	10.03 a-c	17.28 g-k	7.26 f-m	32.95 d-l	8.00 l-q	5.96 ab	46.31 h-k	12.38 g-p
Kav-252	10.48 ab	20.61 f-h	7.08 f-n	41.32 bc	6.80 p-s	5.82 ab	34,82 o-r	9.23 xy

The letters within the table have 5% of the statistical significance level and indicate homogeneous groups due to Tukey's post hoc test after ANOVA.

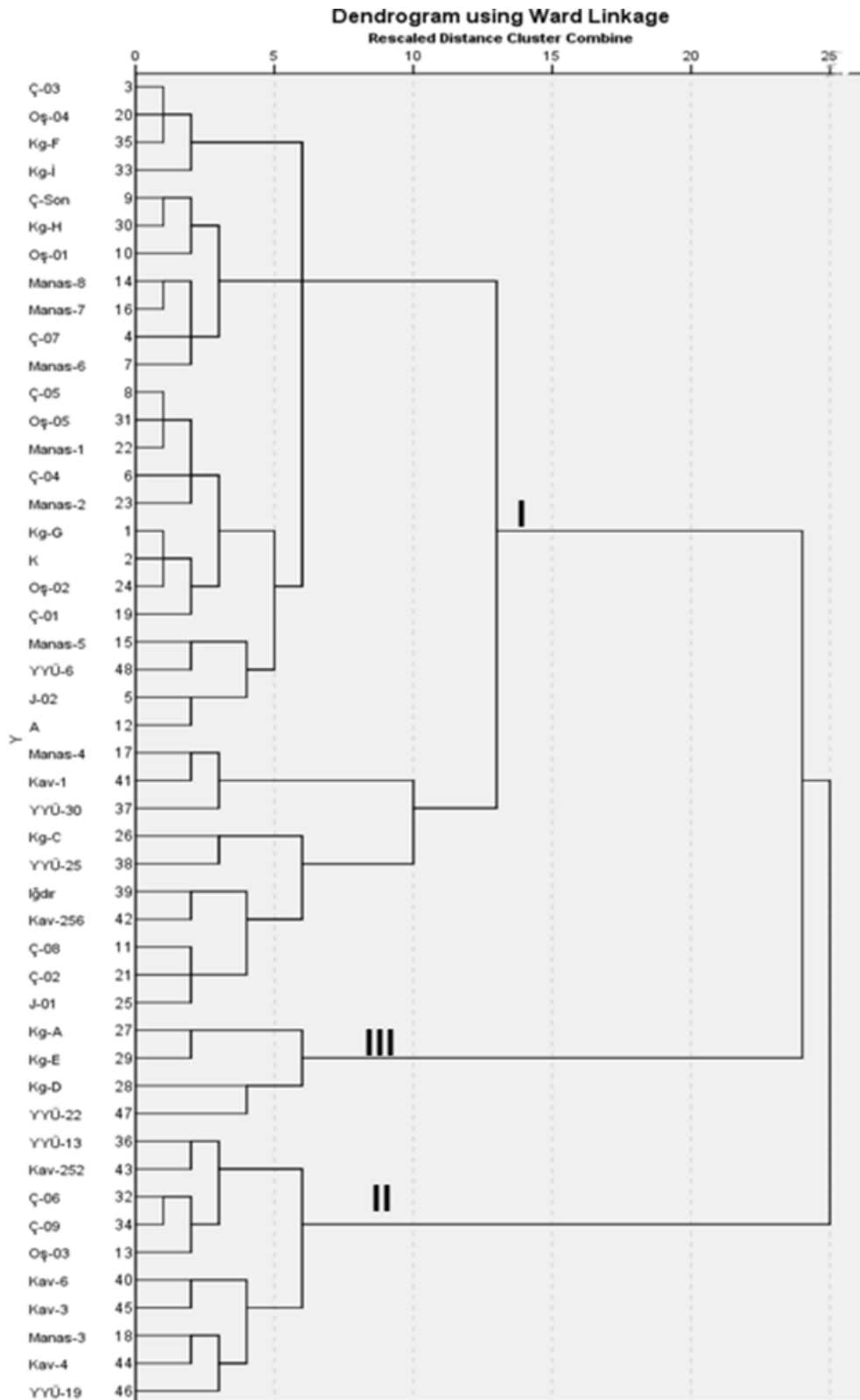


Figure 1. Cluster analysis results of melon genotypes.

group of the dendrogram, the remaining 19 genotypes were clustered in the second major group of the dendrogram. The first group consisted of genotypes collected only from Kyrgyzstan, except for YYÜ-6. These two major groups were further classified into four subgroups (Figure 1). The second major group had a more complex nature than the first major group, with seven Kyrgyz and 12 Turkish accessions being closely related in that group. In subgroup 1, Ç-03, Oş-04, Kg-F, and Kg-İ showed high similarity and were placed together. Figure 1 presents the relationship among the following Kyrgyz and Turkish genotypes in the second subgroup: J-02, J-01, Ç-08, Ç-01, Manas-8, Manas-7, Oş-02, Kg-H, Ç-02, K, Ç-07, Oş-fi01, A, Ç-Son, Manas-5, Ç-06, Ç-09, Oş-03, Ç-05, Oş-05, Kg-G, Manas-1, Ç-04, Manas-2, (Supplementary material 3) and the Turkish genotype named YYÜ-6. Subgroup 3 consisted of the Turkish accessions YYÜ-30, Kav-6, Kav-1, Kav-4, Kav-3, and YYÜ-13, and the Kyrgyz accession Manas-4. Subgroup 4, which belonged to the second major group, consisted of a mix of pairwise accessions from Kyrgyzstan and Turkey: Kg-A and Kg-E, YYÜ-25 and YYÜ-19, Iğdir and Kav-256, and Manas-3 and Kg-D. As shown in Figure 1, the scored data separated melon accessions based on their collection sites; for example, the first major group covers the Kyrgyz population and the second major group covers Kyrgyz-Turkish populations.

### 3.3. Principal component analysis (PCA)

This study evaluated the relatedness of 48 melon accessions collected from various sites in Kyrgyzstan and Turkey, based on 41 qualitative and quantitative characters

(Supplementary material 2). According to the PCA (Figure 2), the morphological characters that contributed to the genetic relatedness among genotypes were fruit length, fruit size, seed size, leaf petiole length, SSC, fruit shape, and leaf length for the Kyrgyz accessions, and flesh color, leaf width, leaf base shape, seed color, fruit diameter, and fruit size for the Turkish and some Kyrgyz accessions (Figure 3). The variations among melon accessions as explained by PCA were determined to be 51.65% in three components, with component 1 accounting for 22.8% of the variation, component 2 17.4%, and component 3 11.4% (Table 5). The first and second principal components of 48 melon accessions were scattered and revealed the relationship between the genetic resources. From Figure 2, it was evident that the melon accessions were located within three main clusters, and the first cluster appeared to consist of the same accessions represented by the dendrogram's first major group.

The second cluster was composed mainly of Turkish accessions, whereas the third cluster was composed mainly of Kyrgyz accessions (Figure 2). The detailed descriptions, variability, and lettering of melon genotypes, based on the Tukey post hoc test, are presented in Tables 3 and 4. The accession Kav-256 had some missing data related to some morphological characters, which resulted in its placement between the Turkish and Kyrgyz genotypes.

### 4. Discussion

*C. melo* var. *melo*, an economically important and widely cultivated (99 countries throughout the world) member

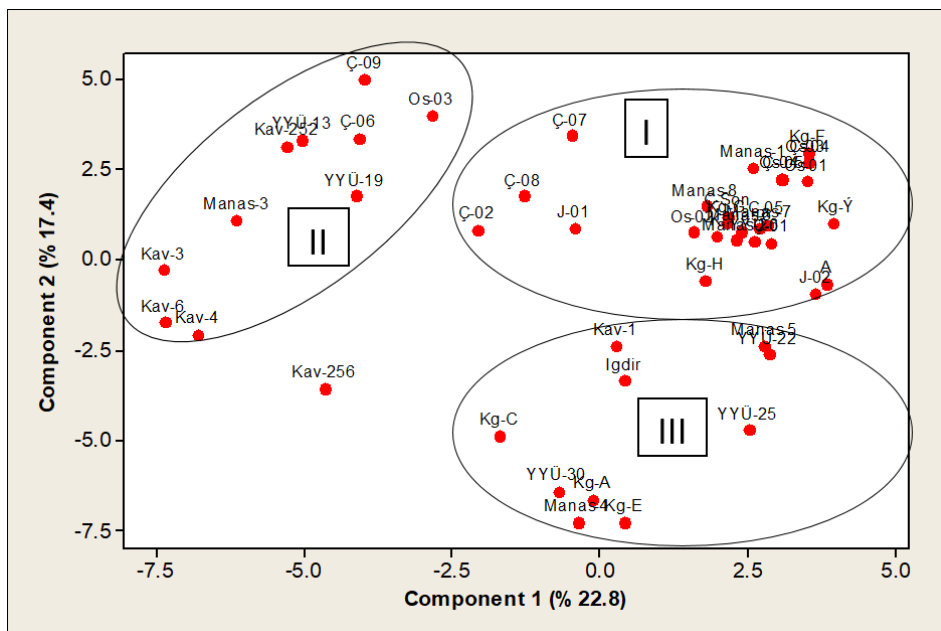
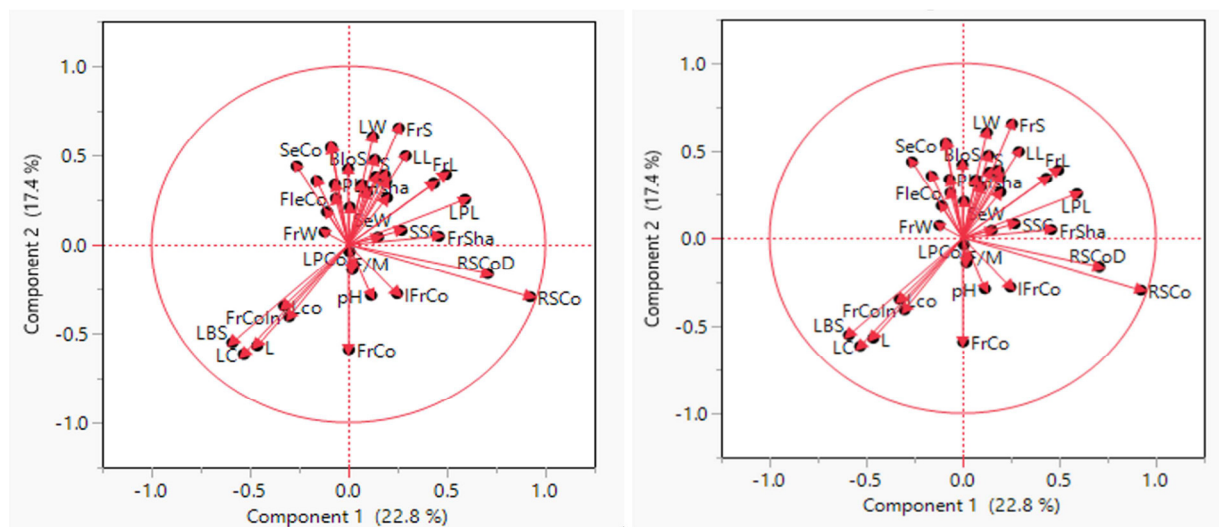


Figure 2. Principle component analysis results of melon genotypes.





**Figure 3.** Loading plot (on left) and biplot (on right) graphs of melon genotypes. All abbreviations within the Loading and Biplot graphs represent morphological characters based on the melon descriptor.

of the family Cucurbitaceae, is among the common and important vegetables consumed in Kyrgyzstan. Kyrgyzstan also has the potential to become a secondary center of diversity due to its direct or indirect connection with South Asia, which is among the primary diversity centers of melon (Monforte et al., 2014). Besides the agricultural cultivation of melon, due to commercial and agricultural business with countries such as China, Russia, Kazakhstan, Tajikistan, and Uzbekistan, Kyrgyzstan is home to a certain type of vegetables and fruits such as melon. Melon is a cross-pollinating species, and this feature requires a special effort to maintain the genetic stability regarding certain traits that are demanded by the local, national, or global consumers (Tzitzikas et al., 2009).

Genetic and morphological diversities in melon are important factors in developing new cultivars according to consumer demand. Repetitive selection performed by the farmer during melon cultivation could result in the fixation of certain different traits besides the already available ones (Ali-Shtayeh and Jamous, 2005). Selection by either the traditional or modern farmer is vital for local speciation (existence of landrace) and local adaptation. In Kyrgyzstan's case, long-term selection/cultivation was carried out by farmers, who assumed that the melon accessions, especially those of unknown origin, were landraces, which reshaped fruits toward a long and heavy fruit type. Monforte et al. (2014) have stated that melon fruits weighing less than 100 g are classified as very small, 100–400 g as small, 400 g up to 1 kg as medium, 1–5 kg as large, and more than 4 kg as very large. The assumption that Kyrgyz melon fruits were long and heavy is verified in Table 3 using the average value of fruit size (g), fruit length (cm), and fruit diameter (cm) in comparison to the Turkish

ones. Regarding the variability in fruit characteristics such as size and length/diameter, rind color, flesh content, and color considerable variation was observed among all accessions, which contributed significantly to the extraction of components (Table 5).

Due to the importance of leaf position, size, and shape in photosynthetic nutrient supply, gas exchange, distribution of photosynthetic nutrients, and water transfer, plants optimize these parameters to adapt to different habitats (Hasson et al., 2011; Tsukaya, 2006). Some studies on leaf lengths and widths were performed and published on melon accessions originating from Azerbaijan (leaf width and length ranged between 7.12–12.7 and 8.28–13.48 cm, respectively) and Hungary (the average leaf width and length were 9.9 and 13.7 cm, respectively) (Guliyev et al., 2018; Szamosi et al., 2010). The Kyrgyz genotypes were observed to show greater leaf length and width than the average values of Hungarian, Azerbaijan, and Turkish genotypes. On the other hand, the observed lengths of melon leaves were observed to be similar to leaves from Spanish genotypes (leaf length ranged between 15.46 and 21.09 cm). To obtain higher yield and quality in melon fruits, the rapid growth of leaf biomass is an important parameter, as it results in the production of a large amount of assimilates that transfer to and accumulate directly in the fruit throughout its growth and development (Castellanos et al., 2011). Therefore, the large fruit characteristic of Kyrgyzstan melon accessions could be a natural consequence of wider and longer leaf features compared to Turkish accessions as observed in this study. The following average weights of melon fruits have been previously reported from different countries: Hungarian melon accessions (1333 g), Turkish accessions (1017

**Table 5.** Contribution percentage and eigenvectors of characters associated with the three first principal components of melon genotypes (H': Shannon diversity index, E: equitability index).

	PC-1	PC-2	PC-3	H'	E
Explained variation	22.780	17.431	11.439	-	-
Cumulative variation	22.780	40.211	51.650	-	-
Traits	<b>Eigen vectors</b>				
LC	-0.266**	-0.352**	-0.182**	0.56	0.81
LBS	-0.075	-0.080	-0.041	0.58	0.84
L	-0.193**	-0.271**	-0.280**	0.63	0.58
Lco	-0.051	-0.061	0.051	0.77	0.70
LL	0.128	0.251**	-0.030	0.89	0.81
LW	0.037	0.206**	0.001	0.40	0.36
LPL	0.171**	0.083	0.028	0.69	-
LPCo	0.001	-0.011	-0.005	0.23	0.33
S	0.016	0.039	-0.035	0.33	0.48
F/M	0.000	-0.003	-0.021	0.23	0.33
Bsha	0.012	0.069	-0.028	0.96	0.87
BS	-0.034	0.247**	-0.171**	1.01	0.92
FS	-0.071	0.179**	-0.264**	1.03	0.93
Bha	0.043	0.014	-0.074	1.27	0.92
Osha	0.122	0.110	0.022	1.29	0.93
FrSha	0.230**	0.027	0.086	1.54	0.86
FrS	0.111	0.328**	0.308**	1.40	0.87
FrCo	0.001	-0.437**	0.630**	1.66	0.79
IFrCo	0.019	-0.025	0.002	0.28	0.41
FrL	0.112	0.101	0.088	0.94	0.86
FrW	-0.029	0.019	0.196**	1.07	0.97
FrSiz	0.029	0.092	0.142	1.03	0.94
FrCoIn	-0.073	-0.113	0.058	1.09	0.99
RSCo	0.793**	-0.289**	-0.155**	0.87	0.80
RSCoD	0.270**	-0.071	-0.176**	1.55	0.96
PL	-0.025	0.143**	0.154**	0.94	0.86
PW	-0.083	0.158**	0.060	0.70	0.63
BloS	-0.000	0.158**	-0.184**	0.84	0.76
FleT	-0.022	0.043	0.065	1.00	0.91
RinT	0.027	0.097	0.074	1.05	0.96
FleCo	-0.020	0.093	-0.114	1.34	0.83
SSC	0.103	0.035	-0.043	0.73	0.66
pH	0.043	-0.122	-0.175**	0.90	0.82
SeW	0.000	0.034	0.089	0.68	0.98
Hsha	0.015	0.024	0.049	0.28	0.41
SeCo	-0.023	0.162**	0.093	0.99	0.71
SeS	0.022	0.090	0.069	0.83	0.75
SeSha	0.003	-0.018	-0.054	0.72	0.65
SeNum	0.018	0.038	0.067	0.37	0.54

\*\* 0.01 statistical significance level. Traits are given in supplementary material 2.

g), and Spanish accessions (2610 g) (Lázaro et al., 2017; Szamosi et al., 2010). Our study revealed that the average weights of melon fruits of each accession were 2489 g for Kyrgyz accessions and 1864 g for Turkish accessions (Table 3). The average melon fruit weight of 1017 g in Turkish accessions reported by Szamosi et al. (2010) could be due to the inclusion of more Turkish accessions than our study. Nevertheless, the overall average weights of Turkish melon genotypes range between 1017 and 1864 g, and Kyrgyz genotypes generally have heavier melon fruits compared to Turkish, Hungarian, and Azeri melon genotypes.

Melon genotypes show an extraordinary variability in fruit size, shape, and morphology, and most of the diversiform varieties could be found in Central Asia together with the wild-types, and a cross between wild-type and cultivars (Dhillon et al., 2012; Roy et al., 2012). This extraordinary diversity in melon fruits could be explained by the diameter and length of the fruits, as well as the activity and quantitative inheritance of the genes that determine the sex and shape of the ovary (Monforte et al., 2004). In this study, we observed that the melon accessions belonging to the Kyrgyz germplasm had longer fruits (average length = 21.03 cm) than the Turkish ones (16.57 cm). Regarding fruit diameter, Kyrgyz melon fruits (14.83 cm) had a similar fruit diameter as the Turkish collection (13.79 cm). Although the fruit diameters of Kyrgyz melons were generally similar to the Turkish genotypes, a longer fruit formation compared to the Turkish collection might result in an elongated fruit shape in Kyrgyz melons. Results on melon fruit length and diameter were recorded and published from Spain (average fruit diameter 15.46 cm and length 22.83 cm), Azerbaijan (fruit diameter range 14.88–24.2 cm and fruit length range = 15.28–29.87 cm), and Tunisia (fruit diameter range = 10–20 cm and fruit length range = 10–26 cm) (Chikh-Rouhou et al., 2019; Guliyev et al., 2018; Lázaro et al., 2017). Kyrgyz melon genotypes exhibited similar melon fruit lengths and diameters as Spanish and Tunisian accessions, whereas the fruit diameter of Azeri accessions was greater than Kyrgyz melon accessions. Pouyesh et al. (2017) published a report on the weights of cantalupensis-type Iranian melon, which ranged between 1200 and 1700 g. Comparing our results with those of relevant studies published in various countries, Kyrgyzstan melons may be categorized to range between large and very large sizes, with some exceptions.

The morphological traits in this study exhibited great variation between Turkish and Kyrgyzstan melon accessions. The first component accounted for 51% of the variation among accessions, and morphological traits such as fruit size, fruit length, fruit shape, rind color, fruit color, and bud size contributed more to the variation among melon accessions than other morphological traits (Table 5). The eigenvector values of morphological traits such

as fruit size, fruit color, and rind skin color were higher than other characteristics for differentiating the melon accessions. Pitrat (2017) classified the melon genetic resources using their fruit weights (size), fruit shape, fruit rind color, seed size, texture, and aroma. Based on the PCA analysis performed in that study, similar traits, as observed in our study, were observed to be more prominent to reveal the relationship between genotypes. PCA analysis was also used to reveal the genetic relatedness of various melon genotypes from different parts of the world. The study by Ali-Shtayeh et al. (2017) on snake melon genotypes explained 66.9% of the total variation in the first two components; that by Yildiz et al. (2014) on Turkish melon accessions explained 44% of the variation in the first three components; Szamosi et al., (2010) on Turkish and Hungarian melon accessions, explained 64% of the variation in first three components; Soltani et al., (2010) on Iranian melons, explained 39.4% of the variation in the first three components; Liu et al., (2004) on 72 melon accessions, explained 50% of the variation in the first three components; and the study by Escribano and Lázaro (2009) on Spanish melon landraces explained 38.74% of the variation in the first three components. As demonstrated by Ali-Shtayeh et al. (2017), Pitrat (2017), and some other studies, the morphological data, particularly the pomological traits of the given study, showed enough capability of differentiating the melon genotypes.

In the dendrogram derived from the morphological data, the accessions showed a tendency to cluster based on their regions or countries of origin/collection. An in-depth evaluation of the dendrogram showed some pairs of accessions with lower squared Euclidean distance, such as Os-04 and C-03 with a squared Euclidean distance value of 0, indicating that the accessions were the same; Os-04 and Kg-F with a squared Euclidean distance value of 6.00, indicating that the accessions were quite closely related; and Os-05 and C-05 with a squared Euclidean distance value of 9.00. Apart from these pairs of accessions, Manas-1 and Os-05, Kg-G and Os-02, and Os-02 and K were also observed to be quite close to each other, indicating that the Manas-1 and Kg-G genotypes were possibly taken from growers in the Osh or Chui region. Kyrgyz melon growers possibly saved these seeds and adapted those accessions to the local conditions by sharing them with regional growers. A similar study was published on Palestinian snake melon genotypes, which were morphologically studied and adapted to different regions by the preservation of the seeds by the regional farmers (Ali-Shtayeh et al., 2017). This situation could most likely be attributed to the exchange of seeds between farmers. Kav-3 and YY-22 were observed to be the genetically most diverse genotypes in the Turkish collection based on the squared Euclidean distance, while the most diverse Kyrgyz accessions were observed to be

Kg-E and C-09. The dendrogram revealed that subgroup-3 included the most diverse accessions.

Regarding the cultivation of melon and other vegetables, the selection of a cultivar/genotype merely depends on yield-related traits and the capacity to adapt to a specific area of cultivation. The variety to be grown in a specific region is decided by considering its adaptation and yield. Cultivation/adaptation capacity can be enhanced or threatened by climatic conditions (Shaffril et al., 2018). Rad et al. (2017) argued that the selection of fruit related-traits such as fruit weight, fruit diameter, and flesh diameter might contribute much more to yield than the other traits. In the case of Kyrgyzstan, growers most probably saved/shared melon seeds by selecting the resistant genotypes against common diseases and selecting heavier fruits (long and large ones considering the consumer's preference). In our study, most of the morphological traits used in determining genetic relationships between genotypes were associated with the mentioned parameters of yield, and the relationship between genotypes was successfully established. The fact that scientific studies on melon breeding in Kyrgyzstan are scarce and the maintenance of seeds is carried out by farmers, or predominantly Russian commercial seeds are used, has caused a decrease in the Kyrgyz melon genetic diversity. Formerly, Russian cultivars may have well-adapted and changed due to cross-pollination as a result of seed exchange between local growers. This situation can be validated by the resemblance of the grown melon genotypes with the torpedo melon genotype, which is a commercial variety from Russia and has adapted well to the region.

The overall analysis and evaluation of Kyrgyz melon genotypes indicate well-adapted regional genotypes, which include considerable variation within the melon collection. The germplasms of both countries are separated from each other based on morphological evaluation. Manas-6 and Os-02 were determined to be prominent for fruit flesh thickness, Ç-08 for soluble solid content, and YYÜ-22, C-02, and C-03 for fruit weight. Although it was observed that both countries had some morphologically similar genotypes, all these morphological parameters

were related to yield and yield components and could be integrated into various breeding programs. Highlighting the existing potential of genetic resources is very important for breeding purposes and improving available resources, which has been evaluated in Kyrgyzstan melon genetic resources in this study.

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#### Informed consent

Informed consent is not applicable.

#### Conflicts of interest

The authors have no financial or proprietary interests in any material discussed in this article. The authors have no conflicts of interest to declare that are relevant to the content of this article. The authors certify that they have no affiliations with or involvement in any organization or entity with any financial interest or nonfinancial interest in the subject matter or materials discussed in this manuscript.

#### Ethical approval

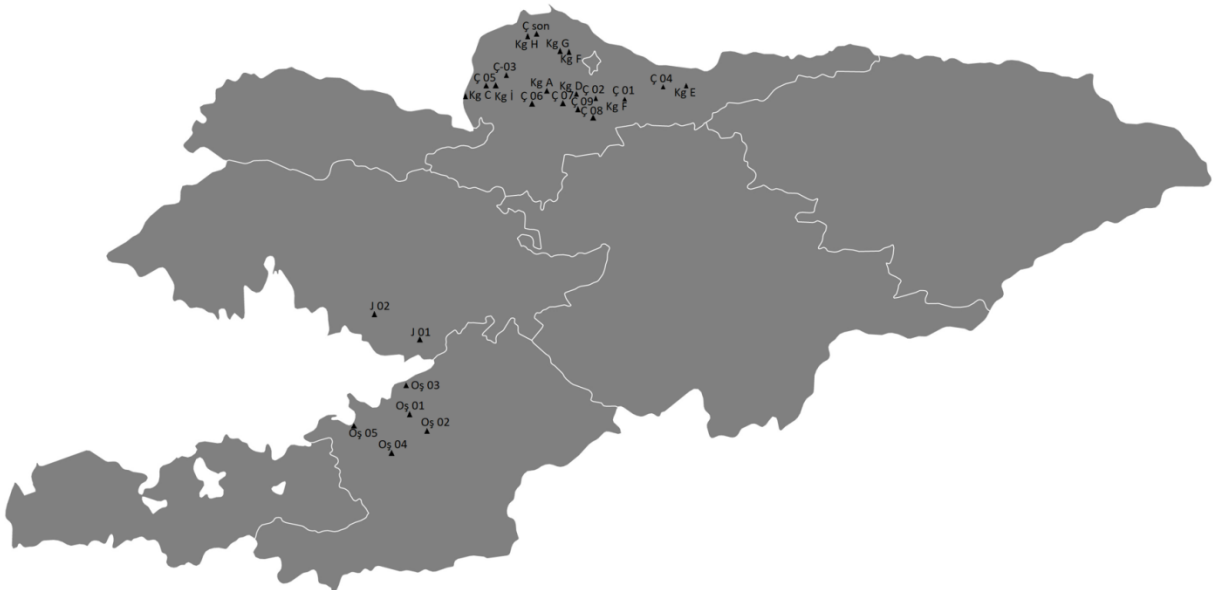
This article does not contain any studies with human participants performed by any of the authors

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Supplementary Material 1. Location of Kyrgyzstan melon genotypes.

**Supplementary Material 2.** Abbreviations of morphological traits included to the study and sources.

<b>Abbreviation</b>	<b>Morphological traits</b>	<b>Source</b>
LF	Leaf shape	IPGR
LBS	Leaf base shape	IPGR
L	Leaf lobe	IPGR
Lco	Leaf color	IPGR
LL	Leaf length	IPGR
LW	Leaf width	IPGR
LPL	Leaf petiole length	IPGR
LPCo	Leaf petiole color	IPGR
S	Sex type	IPGR
F/M	Ratio female/male flowers	IPGR
Bsha	Flower bud shape	IPGR
BS	Flower bud size	IPGR
FS	Flower size	IPGR
FC	Flower color	IPGR
Bha	Ovary pubescence length	IPGR
Osha	Ovary shape	IPGR
FrSha	Fruit shape	IPGR
FrS	Fruit size	IPGR
FrCo	Predominant fruit skin color	IPGR
IFrCo	Primary color of immature fruit	IPGR
FrL	Fruit length	UPOV
FrW	Fruit width/diameter	UPOV
FrSiz	Fruit size variability	IPGR
FrCoIn	Fruit intensity of ground color of skin	UPOV
RSCo	Secondary skin color pattern	IPGR
RSCoD	Fruit at over maturity: hue of color of skin	UPOV
PL	Length of peduncle	IPGR
PW	Diameter of peduncle	IPGR
BloS	Blossom scar size	IPGR
FleT	Flesh thickness	IPGR
RinT	Rind thickness	IPGR
FleCo	Main color of flesh	IPGR
SSC	SSC	IPGR
pH	Flesh acidity	IPGR
SeW	Seed weight	IPGR
Hsha	Seed shape at hilum end	IPGR
SeCo	Predominant seed coat colour	IPGR
SeS	Seed size	IPGR
SeSha	Seed length/seed weight	UPOV/IPGR
SeNum	Number of seeds per fruit	IPGR





**Supplementary Material 3.** Pictures belong to Kyrgyzstan melon genotypes.