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DETERMINATION OF SOME LEAF FEATURES OF SOME MELON GENOTYPES COLLECTED FROM AFGHANISTAN

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Abstract
The significance of plant genetic resources increases day by day. In order to adapt to the novel conditions brought about by environmental issues and climate change and to combat the emergence of new diseases and pests, plant genetic resources will be the primary resource utilised to meet future needs, in line with emerging lifestyles, regardless of the methods used. Melon (Cucumis melo L.*) is a prime example of this and is an important agricultural product on a global scale. The species under consideration is distributed throughout the world, with one of its distribution areas being Afghanistan. The present study was conducted for the morphological characterisation of 36 local melon accessions collected from diverse regions of Afghanistan using a range of leaf features. Ten leaf traits such as number of nodes on main stem, leaf blade size, green colour of leaf blade, development of lobes, length of terminal lobe, dentation of leaf margin, undulation of margin, blistering of leaf blade, attitude of petiole (at 3 leaf stage) and length of petiole were examined and significant variations were observed. The findings obtained may contribute to future breeding programmes to be conducted for melon production regions both in Afghanistan and worldwide.*

Keywords: *Melon, genetic resources, Afghanistan*

1. INTRODUCTION

Melon (*Cucumis melo* L.) is an economically improtant vegetable that is cultivated extensively around the world, including Turkey, Ozbekistan and Afghanistan. According to FAO Statistics (FAOSTAT) global melon production reached 29.54 million metric tons anually across 100 coutries in 2023, with Asian countries contributting the highest production share of 75.54%. It is a member of the diverse Cucurbitaceae familly. According to Rolnik and Olas (2020), this familly includes around 130 genera, and 800 species. Melon (*Cucumis melo* L.) is a diploid species, with a chromosome number of 24 (Tadmor *et al*., 2007; Dogimont & Sari, 2022; Ezura & Fukino, 2009). Systematically, the melon (*Cucumis Melo* L.) is a diploid species belonging to the genus *Cucumis* within the subfamily Cucurbitioideae, family Cucurbitaceae, and order Cucurbitales (Robinson and Decker-Wlaters, 1997; Pitrat *et al*.1998).

The origin of melon is reported to be Central Asia, including the Caucasus, Iran, Afghanistan, India, Turkmenistan, Tajikistan and Uzbekistan (Renner *et al*. 2007). Howeover, according to Bezirganoglu (2018) and Mavlyanova *et al*. (2020), Türkiye, Afghanistan, Iran, and India, are recognized as secondery center of origion and diversity of melons.

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The importance of genetic diversity in plant breeding is clear. Selection of high-yielding and disease and pest resistant genotypes based on genetic diversity from populations is one of the most important issues being studied by the plant breeders (Gepts, 2006). On the other hand, third world countries where many centers of genetic diversity are located face significant treat to the conservation of their wild and endemic varieties due to harsh climatic and soil conditions (Frankel, 1970; Plucknett *et al*., 1983).

Plants constitute the raw material of plant and animal products and play a vital role in human nutrition. In addition to this, they are the most important elements that can direct agriculture and humanity with the possibility that the genetic codes they carry until today have the potential to adress the problems that may arise in the future. Plant genetic resources hold an important place in food and agriculture, as they contain genetic codes that have survived to the present day. These resources are thought to carry agriculture forward by standing against environmental and climatic factors and adapting to the environment in which they have been cultivated for years. The convservation and utlization of Plant genetic resources under changing environmental conditions will be essential for agriculture resilinece (Hodgkin & Bordoni, 2012). Agricultural structures and crop production are constantly changing under various social, economic, industrial and environmental influences. This change is predicted to be more rapid in the future. Plant genetic resources will be the most important issue that can be utilized to adapt to the conditions created by environmental factors and rapidly changing climatic characteristics, to show resistance to novel diseases and pests, and to solve new problems and needs that are expected to develop accordingly with new lifestyles that are thought to emerge in the future (Yılmaz *et al*. 2012).

Plant diversity is decreasing and disappearing due to reasons such as agriculture intensification, ever-increasing land clearing, substitution of improved uniform varieties for local varieties in population form, natural disasters such as fire and erosion, construction of dams etc (Tan, 1992; Singh *et al*., 2017). National development priorities, urbanization and zoning practices, changes in agricultural systems and pest and diseases management practices, continuous consumption by removing from nature without production. Recognizing this treat, many countries have initiated efforts to identify, conserve and preserve plant resources. Subsequently, the collection and characterization of genetic resources became a priority, especially cultivated species with high economic value.

Due to their vital role in plant breeding and development of new plant varieties, it is of great importance to characterize local populations and breeding lines of target plant species at both morphological and molecular levels. Determination of the degree of relatedness is valuable, paricularly for the developing hybrid varieties. Afghanistan is rich in local melon genetic resources and most of them are commercially produced and consumed regionally and have export potential. However, some melon genotypes have suffered losses in productivity and quality over time due to the fact that producers have obtained their own seeds from open-pollinated production areas for many years and continued production this manner.

Plant genetic resources are divided into two groups: the oldest existing local varieties and their wild relatives. Local cultivars and landraces are valuable resources due to their adaptability to local climate and soil conditions. In addition, these genetic resources can show better resistance/tolerance to some diseases and pests and have many other desirable characteristics.Moreover, local melon genotypes often supass commercial hybrids in quality parameters such β-Carotene content, antioxidant activity, and vitamin C levels (Chikh-Rouhou *et al*., 2019). Determination of morphological and molecular characteristics of traditional local cultivars and landraces will enable

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the development of new varieties with resistance and/or tolerance to pests, diseases, salinity, drought and other environmental stresses. Therefore, evaluating the diversity of local genetic resources is very important for breeding of new varieties (Yılmaz *et al*., 2012; Solmaz *et al*., 2016; Dal *et al*., 2017).

In this study, we evaluated certian leaf features of melon genotypes collected from different regions of Afghanistan. We identified notable morphological diversity within the local Afghan melon germplasm resources. Our results provide valuable data for future melon breeding programs and the conservation of Afghanistan's local melon germplasm resources.

2. MATERIALS AND METHODS

In the present study, 36 local melon genotypes collected from diffrent regions of Afghanistan were used for characterisation. For morphological characterization, 9 leaf traits and 1 flower traits were examined (Table 1 and Table 2). Morphological characterization was carried out using 3 plants from teach genotype and 3 fully developed leaves on each plant. In morphological characterization, the criteria selected from the descriptors for melon (*Cucumis melo* L.).determined from International Plant Genetic Resources Institute (IPGRI) (2003) were used. The data obtained as a results of morphological analyses were evaluated and NTSYS (Numerical Taxonomy Multivariate Analysis System) 2.1 Computer Package Program was used for the analysis of the data obtained, the level of genetic relationship was determined by UPGMA (Unweigted Pair Group Method Arithmetic Average) grouping of the similarity matrix obtained according to Rohlf method (Rohlf, 1998). Similarity indices were calculated according to Dice (Dice, 1945).

Table 1. Leaf characteristics of the genotypes used in the study

No	characteristics
1	Plant : Number of nodes on main stem (up to and including 1 st tendril)
2	Leaf blade : Size
3	Leaf blade : Green color
4	Leaf blade : Development of lobes
5	Leaf blade : Length of terminal lobe
6	Leaf blade : Dentation of margin
7	Leaf blade : Undulation of margin
8	Leaf blade : Blistering
9	Petiole : Attitude (at 3 leaf stage)
10	Inflorescence : Sex expression

3. RESULTS AND DISCUSSIONS

Morphological characteristics of 36 local melon genotypes of Afghanistan are presented in Table 2. Among them, 26 genotypes had many nodes on main stem, while 2 genotypes had few. Majority of genotypes (22 genotypes) had medium size leaf blades, followed by large leaves (11 genotpes) and small size leaf blades (3 genotypes). Leaf color was medium green in 15 genotypes, followed by light green (13 genotypes) and dark green (8 genotypes). Lobe development was varied, ranging from weak in 13 genotypes to moderate in 17 genotypes and strong in 6 genotypes.

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Margin dentation was strong in 22 genotypes, while in 10 genotypes medium & in 4 genotypes weak leaf margin dentation was observed. Short leaf magin undulation was predominante (18 genotypes), while 16 genotypes showed medium undulation and 2 genotypes with long undulation. Leaf blistering was medium in 16 genotypes, whereas 18 genotypes showed strong blistering and only 2 genotypes had weak leaf blistering.

In most of the genotypes (20 genotypes) long terminal lobes were observed, followed medium (10 genotypes) and short (6 genotpes). Furthurmore, in 16 of out of 36 genotypes semi erect form of petiole was observed, followed by erect (18 genotypes) and horizonal (2 genotypes). Among the genotypes, 15 genotypes exhibited medium petiole length, while in 14 genotypes long and 8 genotypes short petioles were observed.

The dendogram obtained as a result of the characterization study performed on 36 Afgan melon genotypes with 10 plant features is given in Figure 1. According to the dendogram obtained, 2 main groups were formed and Afgan melon genotypes AF18, AF15, AF12 and AF38 were in the 1st main group, while the control and other Afgan melon genotypes were in the 2nd main group. On the other hand, while genetic similarity was determined between 0.33-1.00 in dendrogram, genotypes AF4 and AF23 were determined to be similar to each other (Figure 1).

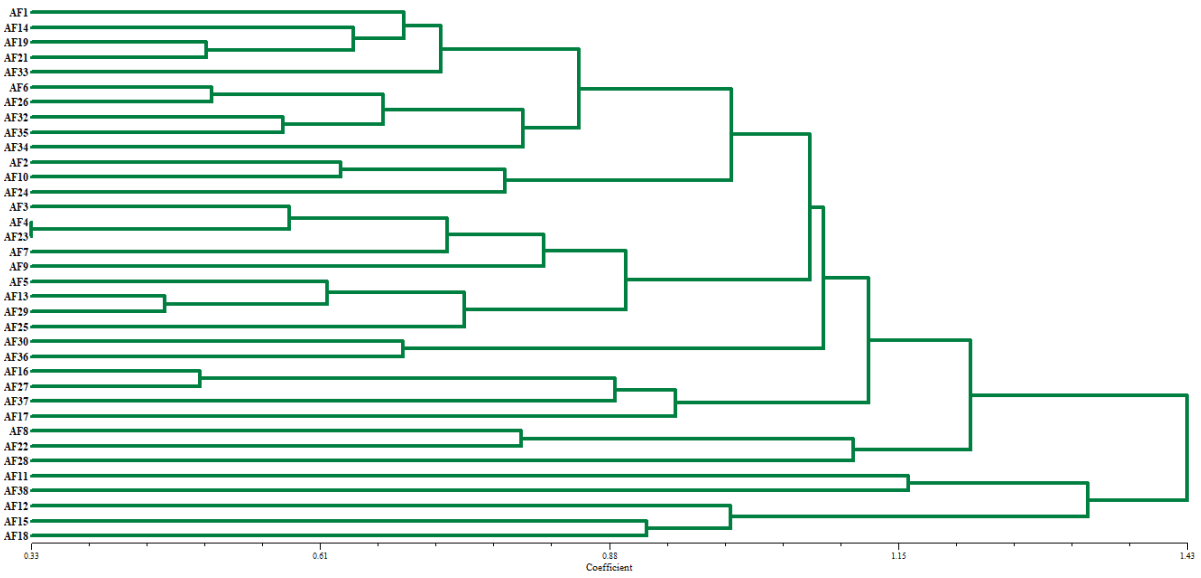


Figure 1. Dendogram obtained from plant features for characterization of Afgan melon genotypes

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Table 1. Leaf Morphological Traits of 36 local melon genotypes collected Afghanistan

Genotype	No. of nodes on main stem	Size of leaf blade	Green color of leaf blade	Development of lobes	Length of terminal lobe	Dentation of margin	Undulation of margin	Blistering of leaf blade	Attitude of Petiole	Petiole length
AF1	Many	Medium	Medium	Medium	Medium	Strong	Short	Strong	Semi-erect	Long
AF2	Many	Large	Medium	Medium	Medium	Medium	Short	Medium	Semi-erect	Medium
AF3	Many	Medium	Medium	Weak	Medium	Strong	Medium	Strong	Semi-erect	Short
AF4	Many	Medium	Medium	Weak	Long	Strong	Short	Strong	Semi-erect	Short
AF5	Medium	Medium	Light	Weak	Long	Strong	Medium	Strong	Erect	Medium
AF6	Many	Large	Medium	Medium	Long	Strong	Short	Strong	Erect	Medium
AF7	Many	Small	Medium	Weak	Long	Medium	Medium	Strong	Semi-erect	Short
AF8	Medium	Medium	Light	Strong	Medium	Medium	Short	Medium	Semi-erect	Medium
AF9	Medium	Medium	Dark	Weak	Long	Strong	Medium	Strong	Semi-erect	Medium
AF10	Many	Large	Medium	Strong	Long	Medium	Short	Medium	Semi-erect	Medium
AF11	Many	Medium	Medium	Strong	Medium	Weak	Long	Medium	Semi-erect	Medium
AF12	Medium	Large	Dark	Medium	Long	Medium	Medium	Medium	Semi-erect	Long
AF13	Many	Medium	Light	Medium	Long	Strong	Medium	Strong	Semi-erect	Medium
AF14	Medium	Large	Light	Medium	Medium	Strong	Short	Strong	Erect	Long
AF15	A few	Medium	Dark	Weak	Short	Medium	Medium	Medium	Erect	Long
AF16	Many	Medium	Dark	Weak	Short	Medium	Medium	Strong	Erect	Medium
AF17	Many	Small	Light	Weak	Short	Medium	Medium	Medium	Erect	Medium
AF18	Medium	Large	Medium	Weak	Short	Weak	Medium	Medium	Semi-erect	Long
AF19	Many	Medium	Light	Medium	Medium	Strong	Short	Medium	Erect	Long
AF21	Many	Medium	Light	Medium	Medium	Strong	Medium	Strong	Erect	Long
AF22	A few	Medium	Light	Strong	Long	Strong	Short	Medium	Semi-erect	Short
AF23	Many	Large	Medium	Weak	Long	Strong	Short	Strong	Semi-erect	Short
AF24	Many	Large	Light	Medium	Long	Weak	Short	Strong	Erect	Medium
AF25	Many	Medium	Light	Medium	Long	Strong	Medium	Medium	Semi-erect	Short
AF26	Many	Medium	Medium	Medium	Long	Strong	Short	Medium	Erect	Medium
AF27	Many	Medium	Dark	Weak	Short	Strong	Medium	Strong	Erect	Short
AF28	Many	Medium	Light	Medium	Medium	Medium	Short	Medium	Horizontal	Long
AF29	Many	Medium	Light	Medium	Long	Strong	Short	Strong	Erect	Medium
AF30	Many	Medium	Medium	Weak	Long	Strong	Medium	Weak	Erect	Medium
AF32	Many	Medium	Medium	Strong	Long	Strong	Short	Medium	Erect	Long
AF33	Many	Large	Medium	Strong	Short	Strong	Short	Strong	Erect	Long
AF34	Medium	Large	Dark	Medium	Long	Strong	Short	Strong	Erect	Long
AF35	Many	Medium	Medium	Medium	Long	Strong	Short	Medium	Semi-erect	Long
AF36	Many	Small	Light	Weak	Long	Medium	Medium	Weak	Erect	Long
AF37	Many	Large	Dark	Medium	Long	Strong	Long	Strong	Erect	Long
AF38	Medium	Medium	Dark	Medium	Medium	Weak	Medium	Medium	Horizontal	Medium

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Plant architecture has a key role in light reception, photosynthesis, and nutrient distribution which influences plant productivity, quality and cultivation practices (Shahwar & Park, 2023). Hence, morphological characterization of melons genotypes uncovers diversity and breeding potential. Several studies have examined various traits including plant morphology, fruit characteristics, and genetic relationships in the past (Bagheriyan *et al*., 2015; Solmaz *et al*., 2010; Can & Türkmen, 2022; Saputra *et al*., 2022). Solmaz *et al*. (2010) identified significant diversity in 68 morphological traits, except for cotyledon color, petiole attitude, and petal color, in 78 melon genotypes collected from Eastern and Central Anatolia. Kayak *et al*. (2020) evaluated some morphological and agronomic characters of 83 melon lines using UPOV parameters and found differences and in leaves, flowers, fruits and seeds. Şahin (2024) evaluated 20 local Turkish watermelon genotypes and three commercial varieties, observing wide variation in leaf size and lobing.

In current study, a wide variation was observed in the characterization of local melon genotypes of Afghanistan. The source of this variation may be due to the fact that the melons underwent both open pollination and self-pollination. According to the data obtained in this study, quite wide variation was observed as a result of morphological characterization in some local Afghanistan melon cultivars. From this point of view, the similarities and differences between these genotypes suggest opportunities for melon breeding. Genotypes with appropriate characteristics can be improved in future breeding programs. When compared with previous studies, morphological similarities and differences were observed both among the genotypes themselves and with different species and cultivars. These differences can be attributed to some factors such as open pollination, the production of their own seeds by the villagers and gardeners, and adaptation to the ecological structure of the area.

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