

**T.C.
AKDENİZ ÜNİVERSİTESİ**



**SELECTION, EVALUATION, MORPHOLOGICAL AND MOLECULAR
ANALYSIS OF GENETIC DIVERSITY IN MELON (*Cucumis melo* L.) FROM
CENTRAL ASIA (KYRGYZSTAN, UZBEKISTAN)**

Aidai MURATBEK KYZY

GRADUATE SCHOOL OF NATURAL AND APPLIED SCIENCES

BIOTECHNOLOGY

DEPARTMENT

DOCTORAL THESIS

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Prof. Dr. Faik KANTAR

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Assist. Prof. Dr. Nihat YILMAZ

ÖZET

SELECTION, EVALUATION, MORPHOLOGICAL AND MOLECULAR ANALYSIS OF GENETIC DIVERSITY IN MELON (*Cucumis melo* L.) FROM CENTRAL ASIA (KYRGYZSTAN, UZBEKISTAN)

Aidai MURATBEK KYZY

Doktora Tezi, Biyoteknoloji Anabilim Dalı

Danışman: Prof. Dr. Nedim MUTLU

Eş Danışman: Doç. Dr. Hasan PINAR

Mart 2024; 131 sayfa

Bu çalışmada, sera ve açık tarla koşullarında yetiştirilen 31 Kırgız, 16 Özbek yerel genotipi ve 1 yabani tip olmak üzere toplam 48 kavunun morfolojik ve moleküler biyoçeşitliliği araştırılmıştır. Genotipler arasındaki ilişkileri anlamak için tohum, yaprak ve meyve özelliklerini kapsayan 79 morfolojik ve biyokimyasal özellik detaylı olarak analiz edilmiştir. Farklı genotipler ve yetiştirme koşullarında tohum büyüklüğü ve şekli, yaprak morfolojisi ve meyve özellikleri bakımından önemli varyasyonlar gözlemlenmiştir. SRAP belirteçleri kullanılarak yapılan moleküler analiz, ortalama %83 polimorfizm ile önemli bir genetik çeşitlilik olduğunu ortaya koymuştur.

Verileri yorumlamak için başlıca bileşen analizi (PCA), tanımlayıcı istatistik, UPGMA dendrogramı ve strüktür analizi gibi istatistiksel teknikler kullanılmıştır. Genotipler, yapısal analize dayalı olarak dört ana gruba ayrılmıştır. Küme analizi, ilk iki bileşenin morfolojik özelliklerdeki genel varyasyonun %22'sini oluşturduğunu, Temel Koordinat Analizi (PCoA) ise ilk üç eksenin toplam moleküler varyansın %25,48'ini oluşturduğunu göstermiştir. AMOVA analizi, üç popülasyon arasında önemli genetik farklılaşmayı (%11,6) ortaya koymuştur. Strüktür analizi, örnekler içinde dört farklı genetik küme tanımlamış; Küme 2 en büyük heterozigotluğu göstermiştir.

Çalışmada kavun genotipleri arasındaki hastalık direnci de incelenmiştir. Fusarium solgunluğu için Kırgız genotiplerinin %70'i ve bazı Özbek genotipleri Fom1'e karşı tam direnç gösterirken, Fom2'ye karşı direnç daha az yaygın olmasına rağmen her iki bölgeden de önemli genotipler içermektedir. Özellikle, bazı genotipler hem Fom1 hem de Fom2'ye karşı direnç göstermiştir ve bu da onları Fusarium solgunluğuna dayanıklı kavun çeşitlerinin geliştirilmesini amaçlayan ıslah programları için umut verici adaylar haline getirmiştir. Antraknoz ve küllemeye karşı duyarlılık genotipler arasında farklılık göstermiştir. KGZ-13, KGZ-14, KGZ-15 ve UZB-12 gibi bazı genotipler düşük duyarlılık göstererek hastalığa dirençli çeşitler geliştirme potansiyellerini ortaya koymuştur.

Bu araştırma, kavun gen havuzundaki genetik çeşitliliğin önemini vurgulayarak ve hastalık direnci ile gelişmiş tarımsal özellikler için önemli genotipleri belirleyerek ıslah çalışmaları ve koruma çabaları için değerli bilgiler sağlamıştır.

ANAHTAR KELİMELER: Biyoçeşitlilik, *Cucumis melo* L., Gen havuzu, Kavun, Karakterizasyon, Kırgızistan, Moleküler, Morfolojik, Orta Asya, Özbekistan

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ABSTRACT

SELECTION, EVALUATION, MORPHOLOGICAL AND MOLECULAR ANALYSIS OF GENETIC DIVERSITY IN MELON (*Cucumis melo* L.) FROM CENTRAL ASIA (KYRGYZSTAN, UZBEKISTAN)

Aidai MURATBEK KYZY

Doctoral Thesis, Department of Biotechnology

Supervisor: Prof. Dr. Nedim MUTLU

Co-supervisor: Assoc. Prof. Dr. Hasan PINAR

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This study investigated the morphological and molecular biodiversity of 48 melon accessions, including 31 Kyrgyz, 16 Uzbek local genotypes, and 1 wild type, grown under greenhouse and open field conditions. Detailed analysis of 79 morphological and biochemical attributes, including seed, leaf, and fruit characteristics, was conducted to understand the relationship between genotypes. Significant variations were observed in seed size and shape, leaf morphology, and fruit attributes across different genotypes and growth conditions. Molecular analysis utilizing SRAP markers revealed significant genetic diversity, with an average polymorphism of 83%.

Statistical techniques, including principal component analysis (PCA), descriptive statistics, UPGMA dendrogram, and structural analysis, were employed to interpret the data. The genotypes were categorized into four primary groups based on structural analysis. Cluster analysis indicated that the first two components accounted for 22% of the overall variation in morphological traits, while Principal Coordinates Analysis (PCoA) revealed that the top three axes accounted for 25.48% of the total molecular variance. AMOVA analysis highlighted significant genetic differentiation (11.6%) among the three populations. STRUCTURE analysis identified four distinct genetic clusters within the samples, with Cluster 2 showing the greatest heterozygosity.

The study also assessed disease resistance among the melon genotypes. For Fusarium wilt, 70% of Kyrgyz genotypes and several Uzbek accessions demonstrated complete resistance to Fom1, while resistance to Fom2 was less common but included key accessions from both regions. Notably, some genotypes exhibited resistance to both Fom1 and Fom2, making them promising candidates for breeding programs aimed at developing Fusarium wilt-resistant melon cultivars. Susceptibility to anthracnose and powdery mildew varied among the genotypes, with some accessions like KGZ-13, KGZ-14, KGZ-15, and UZB-12 showing low susceptibility, highlighting their potential for breeding disease-resistant cultivars.

This research provides valuable knowledge for breeding and conservation efforts, emphasizing the importance of genetic diversity in melon germplasm and identifying key genotypes for disease resistance and improved agronomic traits.

KEYWORDS: Central Asia, *Cucumis melo* L., Diversity, Gene pool, Kyrgyzstan, Melon, Molecular, Morphological, Uzbekistan

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PREFACE

I would like to express my sincere gratitude for all of the people who have helped me along the way as I begin this academic adventure. Their advice and encouragement have been invaluable in helping me shape and finish this thesis.

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This scientific work is dedicated to myself and all the brave girls who chase their dreams without giving up and following their own values. Your determination and strength are truly inspiring!!!

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DECLARATION

I state that this doctoral thesis “Selection, Evaluation, Morphological and Molecular Analysis of Genetic Diversity in Melon (*Cucumis melo* L.) from Central Asia (Kyrgyzstan, Uzbekistan)”, was written under academic rules and ethical values, and I declare that I have indicated the source of all information that does not belong to me in this thesis.

20/03/2024

Aidai MURATBEK KYZY



SYMBOLS AND ABBREVIATIONS

Symbols

° : degree

', min : minute

", sec : second

bp : base pair

cm : centimetre

h : hour

hz : frequency

kg : kilogram

m : meter

min : minute

ml : milliliter

µl : microliter

mm : millimetre

rpm : rotations per minute

t° : temperature

t : ton

Abbreviations

AU : Akdeniz University

CA : Central Asia

CV : Coefficient Variation

CTAB : Cetyltrimethylammonium Bromide

EDTA : Ethylenediamine Tetraacetic Acid

DNA : Deoxyribonucleic Acid
HCL : Hydrochloric Acid
ISSR : Inter Simple Sequence Repeats
KGZ : Kyrgyzstan
Max : Maximum
Min : Mnimum
NaCL : Sodium Chloride
PCR : Polymerase Chain Reaction
PIC : Polymorphic Information Content
pH : Potential of Hydrogen
RFLP : Restriction Fragment Length Polymorphism
SD : Standard Deviation
SSR : Simple Sequence Repeats
SRAP : Sequence - Related Amplified Polymorphism
TA : Titratable Acidity
TRIS : Tris(hydroxymethyl)aminomethane
TSSC : Total Soluble Solids Content
UPOV : The International Union for the Protection of New Varieties of Plants
UZB : Uzbekistan

A dot (.) is used as a decimal separator. For example 12.91

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1. INTRODUCTION

Melons, scientifically known as *Cucumis melo* L., represent a significant annual diploid plant within the Cucurbitaceae family with rich history of domestication and diversification. Despite their botanical classification, melons are commonly referred to by various names such as muskmelon, cantaloupe, nutmeg melon, and others, leading to confusion due to the wide range of shapes, colors, and cultivar types they encompass. This diversity manifests in fruits displaying reticulate netting or smooth rinds, varying sizes, and hues of green, white, and yellow, sometimes with distinctive stripes, contributing to the complexity of identifying specific melon varieties (Wehner et al. 2020).

Melon is a member of the genus *Cucumis*, subtribe *Cucumerinae*, tribe *Melothrieae*, subfamily *Cucurbitoideae*, and family *Cucurbitaceae*. Melon is one of the most important agricultural economic Cucurbitaceae species due to its high consumption and worldwide commercial value (McCreight et al. 1993).

With increasing of world population, negative effects of plant diseases and pests have revealed nutritional problems and encouraged people to different plant breeding programs. One of the most commonly used conventional breeding programs is resistance breeding.

Geographic data and morphological characters are used (Ford-Loyd 2001) in breeding programs, but last decade more molecular markers are used extensively for this purpose. Morphological characterization, which is one of the first procedures to be used in the evaluation of genetic resources, is extremely important in terms of ensuring the accurate identification of genotypes within collections (Escribano and Lazaro 2009). There are many studies on the morphological characterization of melons (Sarı and Solmaz 2007; Şensoy et al. 2007; Lotti et al. 2008; Escribano and Lazáro 2009; Szamosi et al. 2010).

In recent years, in addition to morphological characterization based on morphology, cross compatibility or physiology, molecular markers have also been used for studying genetic diversity and phylogenetic relationships in melon (Tanaka et al. 2006). Genetic diversity in melon has been analyzed using different molecular markers, ranging from phenotypic (Escribano and Lázaró 2009; Szamosi et al. 2010) and isozymic (McCreight et al., 2004) to molecular DNA markers, including random amplification of polymorphic DNA (Sensoy et al. 2007; Soltani et al. 2010), amplified fragment length polymorphism (Frary et al. 2013; Shamasbi et al. 2014), simple sequence repeat primers (SSR) (Monforte et al. 2003; Tzitzikas et al. 2009; Kaçar et al. 2016), inter-simple sequence repeat (ISSR) primers (Parvathaneni et al. 2011; Sestili et al. 2011), and other DNA markers.

Central Asia, encompassing regions like Kyrgyzstan and Uzbekistan, is considered a potential center of melon origin and diversity due to its favorable environmental conditions and long history of melon cultivation. In a book on Uzbekistan's melons from 1985, Kuchkarov stated, "For the development of industrial melon farming, it is first and foremost necessary to deepen and expand scientific research on the preservation and study of the gene pool of local varieties as the foundation of modern

melon growing. This includes selective improvement of local varieties to enhance their resistance to powdery mildew and Fusarium wilting in specific zones, as well as studying the transportability and shelf life of industrial varieties in these zones. Additionally, there is a need to develop a zonal seed production system, primarily focusing on industrial varieties. The goal is to broaden the range of melons cultivated in the Republic for local consumption by promoting low-transportable local varieties".

For many years, the aim of systematic research in the melon-growing area has been the collection and preservation of local varieties. Based on the study of their biological and varietal characteristics, the goal is to restore production varieties that meet modern requirements for melon cultivation. Additionally, the objective is to develop methods for improving the quality of melon seeds, focusing on enhancing biological adaptability to cultivation conditions and increasing the productivity and quality of fruits.

Currently, among the many varieties included in the State Register of Kyrgyzstan, only a few varieties fully meet the basic requirements of vegetable growers. In addition, in this main zone of industrial vegetable growing, there are very few varieties of universal type for the use of fruits, and hybrids, except for introduced ones, are completely absent for open and protected areas. As with other plant species, local varieties are gradually being withdrawn by the introduction of F1 hybrid varieties in melon. The main reason for this is the low productivity of local varieties, but the resistance to some diseases and pests are either lower or not existent. The other reason is that non-uniform fruit colors and fruitshape are confronted as producers try to produce their seeds in an inappropriate way. This reduces the amount of marketable product. It also affects the quality negatively.

The aim of this study will be to select and characterize the genotypes of melons cultivated in Kyrgyzstan and Uzbekistan. Characterization will be conducted in two ways: morphological and molecular. Additionally, standard melon varieties that are widely produced will be used as controls. Thus, the proposed study is expected to serve the purpose of characterizing the genotypes that can be used in open and protected production in Kyrgyzstan and elsewhere.

This study will contribute to the conservation and utilization of melon diversity in Central Asia, while also exploring potential disease resistance within the germplasm. The study will focus on melon accessions from Kyrgyzstan and Uzbekistan, employing a multi-pronged approach that integrates morphological and molecular analyses, along with disease resistance observations. The rationale behind the chosen methodologies will be outlined, including selection criteria for melon accessions, methods for morphological evaluation with a focus on disease-relevant traits, and the specific morphological characteristics targeted for analysis. Additionally, the study will elaborate on the chosen molecular markers used to assess genetic diversity and their advantages in uncovering population structure and genetic relationships within the melon germplasm. Disease resistance observations for Fusarium wilt, anthracnose, and powdery mildew will be incorporated into the analysis to identify potential sources of resistance within the germplasm collection.

By combining these selection, evaluation, and analysis methods, the study aims to achieve the following objectives:

The study will comprehensively characterize the genetic variation present within the melon accessions from Kyrgyzstan and Uzbekistan.

The morphological evaluation will focus on key phenotypic characteristics, including those potentially associated with resistance to Fusarium wilt, anthracnose, and powdery mildew. This information can be instrumental in future breeding programs for improved melon varieties.

This study will provide valuable insights into the genetic makeup and disease resistance potential of melon germplasm in Central Asia, aiding in the development of effective conservation strategies for this precious genetic resource.



2. LITERATURE REVIEW

2.1. Melon

Melons are a globally important vegetable crop. They are widely grown across various climates. Melon, an annual creeping herbaceous plant, produces an edible fruit known for its sweet taste and varying color tones. Its robust stems branch from the base, extending up to 3 meters in length and approximately 2 to 3 centimeters in thickness. The entire stem system, including lashings, can span 20 to 25 meters. The large leaves, with serrated edges, range from 14 to 18 centimeters in length and 20 to 22 centimeters in width, depending on soil fertility and agricultural practices. A single plant typically bears 200 to 400 leaves with thick, erect petioles measuring 12 to 18 centimeters. Melon plants display diverse floral structures, exhibiting monoecious or dioecious characteristics, occasionally with dioecious hermaphroditic flowers. These flowers, positioned in leaf axils, include one or two female flowers alongside cymose inflorescences of 5 to 7 or more male flowers. Yellow corollas with five petals, each possessing 5 stamens and two-lobed anthers, define these flowers. The inferior ovary yields a multi-seeded false berry, with fruit weights ranging from 0.5 to 40 kilograms. Seeds, along with placenta, occupy the fruit's central part. Ripe melons display a range of colors—white, greenish, yellowish, lemon, orange, brown, yellow-green, green, dark green, or orange, often with patterned areas in various hues. Fruit sizes, categorized as large, medium, or small, vary due to different varietal traits and growth conditions, such as soil-climate and agricultural practices (Ermokhin 1974).

Melons exhibit a robust root system characterized by a primary taproot and extensive lateral branches that diverge in various directions, displaying a high degree of branching. The development and vigor of the primary root vary based on factors like growing conditions, soil texture, moisture levels, and varietal traits. Typically, the primary root tends to be less developed compared to its lateral counterparts. At the end of the growing season, the root collar near the soil surface measures approximately 5-6 centimeters in diameter. At a depth of 7-10 centimeters, the root diameter nearly halves, reducing to about 0.4 centimeters at a depth of 1 meter (Bel-Kuznetsova 1937; Ermokhin 1974).

Melons grows in warm climates. Optimal seed germination occurs in moist conditions at temperatures between 15-18°C, with the most favorable range being 25-30°C. Seeds sown in cold soil delay germination until the soil warms up, and in prolonged cold spells, they may decay. Observations from 1957-1961 in various soil and climatic conditions of Uzbekistan revealed that earlier sowing leads to a longer seedling emergence period compared to later sowing. Delaying sowing until the soil warms up and stable warm weather prevails results in rapid seedling emergence. During the growth and ripening phases, melons demand substantial heat, with optimal temperatures between 30-35°C. At these temperatures, metabolic processes intensify, showing greater resistance to high temperatures than low ones (Ermokhin 1974). According to Khlebnikova (1932), leaf protein coagulation occurs at 64°C, and the increase in dry matter per leaf surface unit at 40°C is 2 to 2.5 times greater than at 20°C.

2.1.2. Phylogeny and taxonomy of *Cucumis melo* L.

Cucumis melo var. *cantalupensis* belongs to the family Cucurbitaceae and is a subspecies of the species *Cucumis melo*. It is a part of the plant kingdom, characterized under the class Magnoliopsida and order Cucurbitales (Anonymous 8).

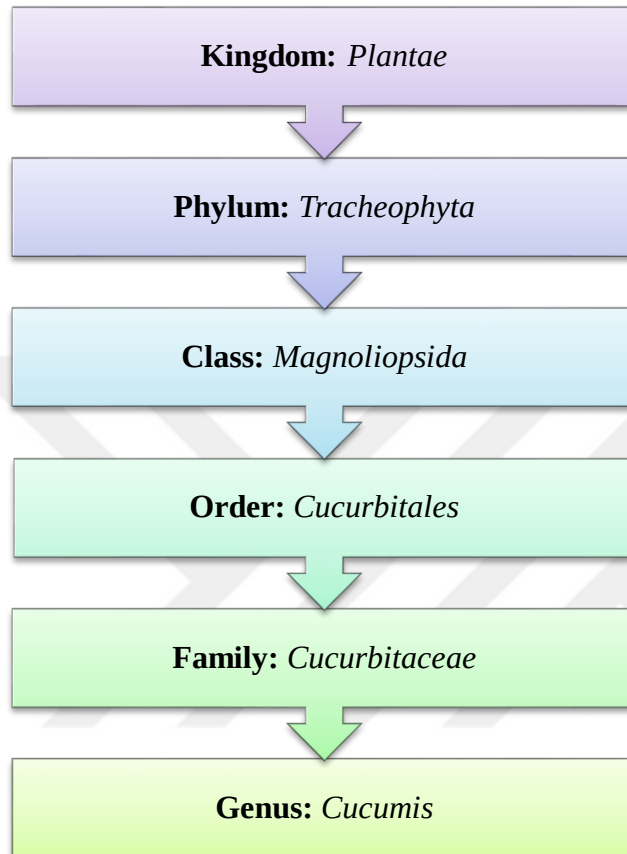


Figure 2.1. Systematic classification of *Cucumis* genus

2.1.3. Origin of melon

Melon, belonging to the *Cucumis melo* species of the *Cucumis* genus within the Cucurbitaceae family of the Cucurbitales order, is a significant vegetable both nationally and globally. Melon cultivation is generally classified into three botanical varieties: *Cucumis melo* var. *cantalupensis*, *Cucumis melo* var. *inodorus*, and *Cucumis melo* var. *reticulatus* (Robinson and Decker-Walters 1997).

When considering melon types worldwide in terms of consumption, distinct varieties are identified; cantaloupe or scented melons are popular in North America, characterized by a reticulated type with orange-colored flesh. Casaba (with white flesh) and honeydew (with green flesh) melons are important in Asia, North Africa, America, and Europe. Galia type melons are popular in Europe and the Middle East. Japanese type melons are cultivated and consumed in Japan. Pineapple Type Melons are native to the Middle East. French (Charentais) type melons are originating from France, preferred in parts of Europe. Spanish type melons are originating from Spain, favored in South

America and Brazil. Turkish type melons including varieties such as Yuva and Kırkağaç (Munger and Robinson 1991; Ünlü 2008). While the exact origin of melon is debated, it is widely believed to have originated in Southeast Africa. The Cantaloupe, the most consumed type worldwide, is said to have originated in the Van region of Turkey and was later introduced to Italy in the 1400s by missionaries (Vural et al. 2000).

2.1.4. Benefits of melon

The benefits of melon extend far beyond its delightful taste and juicy texture. Comprising nearly 90% water, this fruit also packs a punch in its nutritional profile. While low in protein and fat, melon is rich in carbohydrates, specifically fiber, and boasts an array of micronutrients that contribute to overall health (Anonymous 6).

Vitamins play a significant role in melon's nutritional value. With approximately 20 mg of vitamin C per 100 g, it provides a quarter of the Recommended Dietary Allowance (RDA) and serves as a vital supporter of immunity and various biochemical reactions, including collagen synthesis (Carr and Maggini 2017). Vitamin C's antioxidant properties safeguard against cell damage and are especially recommended for pregnant and lactating women, smokers, and individuals exposed to hazardous environments (Padayatty and Levine 2016, Pullar et al. 2017, Shin et al. 2013). Melon is also a source of vitamin A and beta-carotene, essential for cell renewal, supporting vision, immunity, cardiovascular and reproductive functions, kidney and lung health, and regulating antioxidant processes. The fruit contains vitamin K, which is crucial for synthesizing proteins that maintain normal blood clotting levels (Zeb 2016). Lutein and zeaxanthin in melon are recognized carotenoids that contribute to maintaining eye health and decelerating age-related vision loss (Sommerburg 1998).

In terms of minerals, melon stands out for its silicon content, providing 82 mg per 100 g. Silicon aids in calcium absorption, is essential for bone and tooth development, and fortifies blood vessel walls, cartilage tissue, ligaments, and skin structure. Potassium, at 120 mg per 100 g, regulates cellular water levels, alleviates allergic reactions, and supports kidney function. Phosphorus and calcium, at 12 mg and 16 mg, respectively, are integral for bone health, cell division, and growth, while also balancing acidity and gastrointestinal tract functionality (Fratoni and Brandi 2015). Magnesium, a crucial participant in numerous biochemical processes, contributes to energy production, nucleic acid and protein synthesis, ion transport, blood sugar stabilization, and blood pressure regulation. Moreover, melon offers 20% of the daily cobalt requirement, a key element in DNA synthesis and hemoglobin production within red blood cells (Orchard et al. 2014).

Furthermore, a 200-gram serving of melon provides a snapshot of its nutritional profile, including 64 calories, 16 grams of carbohydrates, 1.4 grams of fiber, 1 gram of protein, and no fat. This nutrient-packed fruit has been associated with strengthening bones, enhancing skin health, bolstering the immune system, and potentially aiding in regulating blood pressure and blood sugar levels. Melon contains a high amount of fiber, which helps in delaying the absorption of sugar into the bloodstream, supports regular digestion, and encourages the development of healthy intestinal bacteria (Fuller et al. 2016, Holscher 2017). Its rich composition, filled with vitamins, minerals, and beneficial compounds, supports various bodily functions, making melon a delightful addition to a nutritious diet (Du et al. 2017).

2.1.5. Melon production statistics

In Figure 2.1, presented a visual representation of melon production by country for the year 2021, using a color-coded map to highlight the variations in production levels between different countries. The chosen colors serve as an effective way to express the variations in melon production on a global scale. The countries shaded in yellow, representing the lowest production category ($\leq 1,112.31$), denote those with the most lowest contributions to the worldwide melon output. Moving up the scale, the light orange category ($\leq 14,230.0$) signifies countries with a moderate level of melon production, contributing a significant, though not dominating, share. Meanwhile, the dark orange shade ($\leq 69,170$) indicates those nations with substantial melon production, significantly impacting the global market. Countries in the red category ($\leq 979,580.97$) are among the leading worldwide melon producers, making an important contribution, while those marked in burgundy ($> 979,580.97$) represent a select group of highest melon producers, playing a pivotal role in shaping the global melon production landscape for the year 2021 (Anonymous 4).

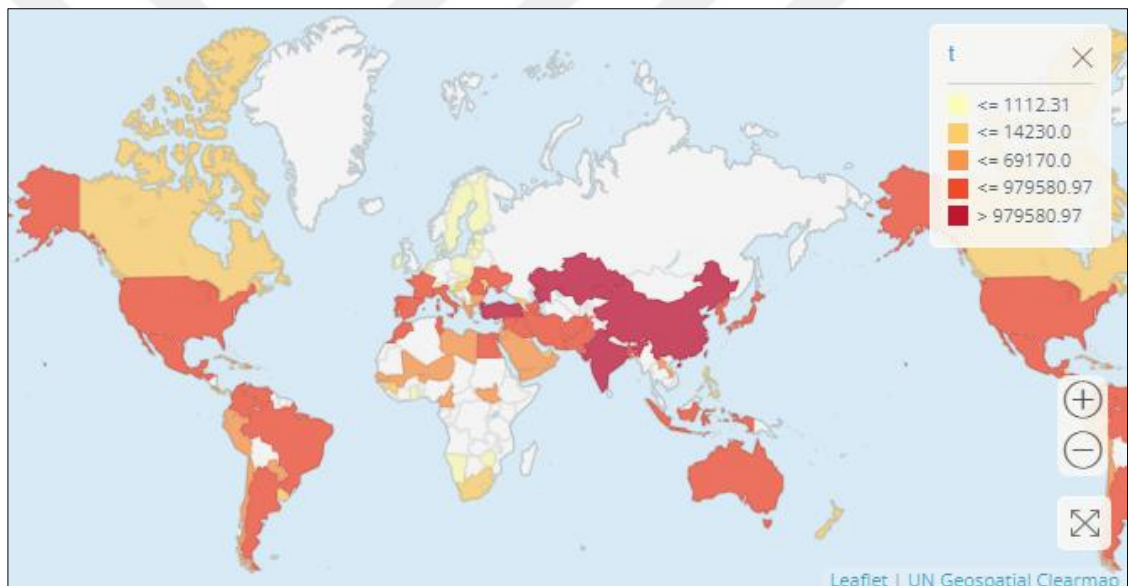


Figure 2.2. Cantaloupe and other melons produced worldwide on average of 2021

A detailed summary of cantaloupe and other melon varieties' global production and yield quantities from 1994 to 2021 is shown in Figure 2.2. This graph is a crucial visual help for recognizing changes in melon production and cultivation around the world over the past thirty years. The world's total area harvested for melon cultivation was 1,077,369 hectares in 2021, the most recent year for which data is available. The impressive global production of around 28,617,598.39 t was reached. These figures demonstrate the huge global scope of melon growing and underline the crop's current significance in agriculture and as a valuable crop for people all around the world (Anonymous 4).

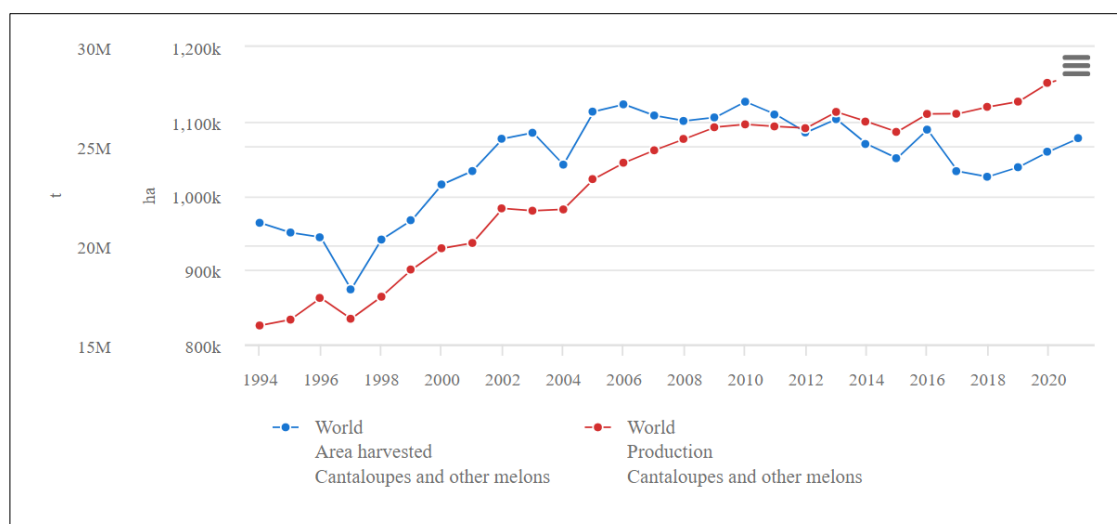


Figure 2.3. World + (Total) Cantaloupe and Other Melon Production/Yield Quantities, 1994–2021

The world's production of cantaloupes and other melon varieties was divided across different regions in 2021 (Figure 2.3). Africa contributed 3.9% to the global production of melon, indicating its role as a smaller but significant producer. The Americas, including North, Central, and South America, accounted for 11.5% of the world's melon production, reflecting the importance of melon farming in these regions. Asia emerged as the leading global producer, making a substantial contribution of 77%, underlining its important role in the global market. Europe represented 6.9% of the total production share, showing the presence of melon cultivation in European countries. Lastly, Oceania had the smallest production share at 0.7%, signifying the relatively limited scale of melon cultivation in the Oceania region (Anonymous 4).

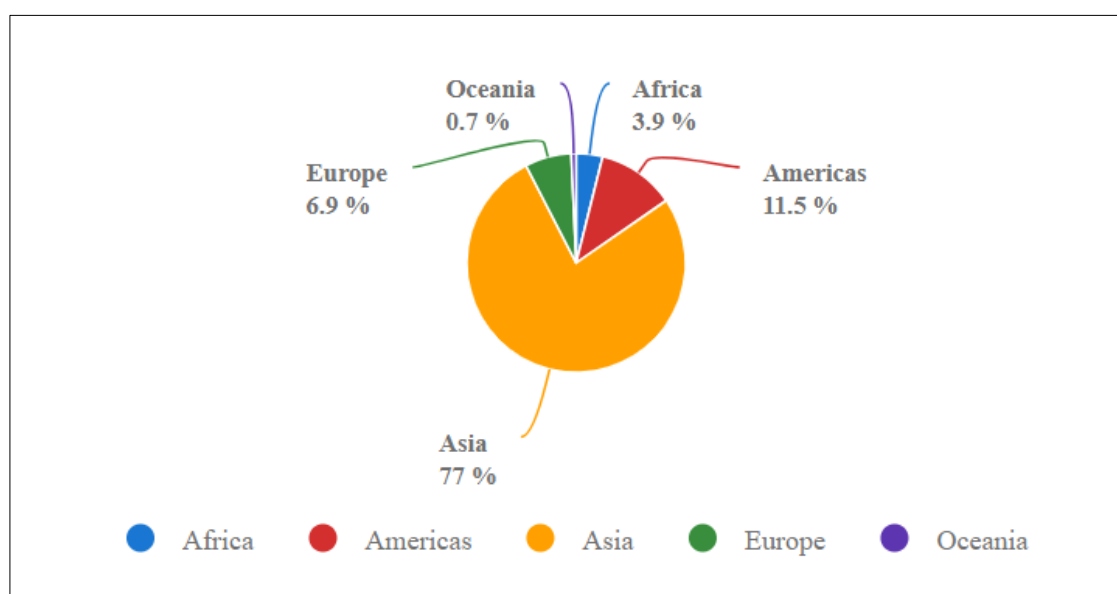


Figure 2.4. Cantaloupe and other melons produced by region in 2021

As Figure 2.4 illustrates, the top ten countries controlled the production of cantaloupes and other melons in 2021. China was in the lead with an outstanding production of about 14,013,294.28 t. With a significant production of 1,638,638 t, Türkiye (Turkey) placed in second, closely followed by India with 1,478,000 t. Significant contributions to the world's melon production came from Kazakhstan (1,395,170.92 t) and Afghanistan (979,580.97 t), respectively. The top 10 melon producers were completed by Guatemala, Iran (Islamic Republic of), Spain, Italy, and Brazil further down the list (Anonymous 4).

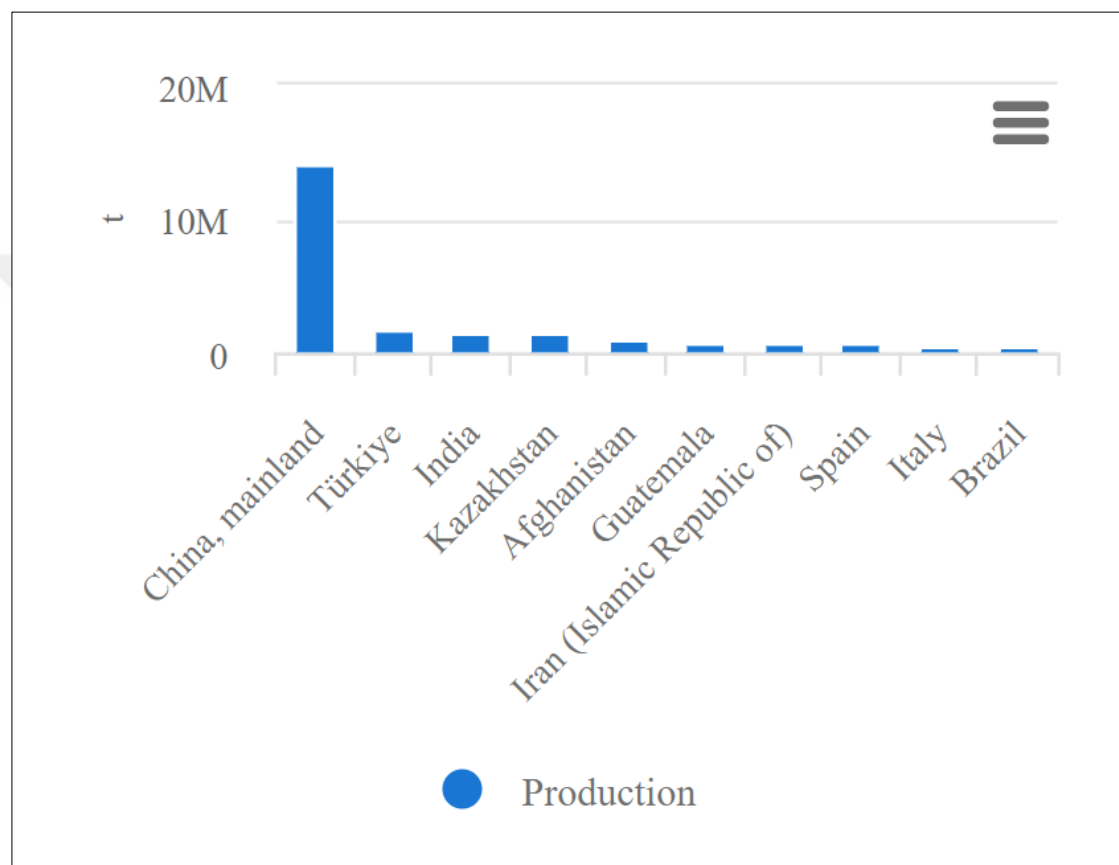


Figure 2.5. Top ten countries producing melon in 2021

Many worldwide important species, such as fruit and nut trees, have their origins and diversity in Central Asia.

Between January and June 2023, Uzbekistan exported 79.9 thousand tons of melons valued at \$16.7 million to 11 countries, marking an increase of 16.8 thousand tons from the same period in 2022. The primary destinations for Uzbekistan's melon exports during this period were Kazakhstan, receiving 35.7 thousand tons, followed by Russia with 29.3 thousand tons, Kyrgyzstan with 12.6 thousand tons, Belarus with 1.3 thousand tons, Tajikistan with 664 tons, and Mongolia with 143 tons (Anonymous 6).

2.2. Literature review

2.2.1. Genetic diversity of melon

Genetic diversity in melon (*Cucumis melo* L.) is essential for enhancing traits such as disease resistance, fruit quality, and adaptability to various environmental conditions. Significant genetic variation exists within and between different melon cultivars and wild types, which provides a valuable resource for breeding programs. This diversity enables the development of new cultivars that can meet specific agricultural needs, such as improved yield, better flavor, and increased resistance to pests and diseases. Molecular tools, such as DNA markers, have been effectively used to assess and manage this genetic diversity, aiding in the identification of desirable traits and the creation of superior melon varieties. Preserving this genetic diversity is crucial for the continued progress and sustainability of melon cultivation, ensuring that melons can thrive in changing climates and diverse growing conditions.

2.2.2. Genetic diversity of melon in Central Asia

The cultivation of melons in Uzbekistan has a rich history, spanning over 2000 years. Archaeological findings of melon seeds from the 3rd century AD, discovered near Berunii, reflect the ancient roots of melon cultivation. Renowned figures such as Ak-Saolibii, Ibn Batutta, and Sakheriddin Mukhamed Babur documented the exquisite taste of 'Khorezm melons' in the 14th and 15th centuries. Central Asian melons gained international recognition, with exports to China in the 2nd century BC and Iraq in the 9th–10th centuries (Mavlyanova et al. 2005). Dating back to the 2nd century BC, Uzbek delicacies were even exported to China. Skara-Azyam's medical work, written in Farsi in the 4th century BC, not only highlights the healing properties of melons but also provides recipes for using them against various diseases. Seeds of cultivated melons from the 3rd century BC were discovered by S.P. Tolstov during excavations in the ancient settlement of Khorezm.

Fragmentary information about the cultivation of melons can be found in written sources from the early Middle Ages. In Russian geographical and natural science literature, discussions about Central Asian melons began in the first half of the 19th century, coinciding with the exploration of Turkestan. In 1834, N.V. Khanykov mentioned the remarkable qualities of Bukhara melons and that the regions of Gijduvan and Kyzyltepe boast about 30 varieties of this crop, categorized into two groups - early (pagoi) and late (begoi).

Many Russian researchers who visited Central Asia in the second half of the 19th century wrote about the exceptional advantages of Uzbek melons (Krauzev 1837; Middendorf 1882; Burankov 1899; Osipov 1899; Sivarsky 1899 and others).

Russian researchers who focused on melon cultivation in Central Asia during the pre-revolutionary years gave particular attention to the agricultural practices related to this crop. They provided descriptions of varieties and organized them systematically (Moiseev 1803; Shakhnazarov 1908; Kichunov 1912 and others). A.F. Middendorf (1882), after exploring the Fergana Valley, categorized them as early (Khandalyak), middle, and late, a classification also acknowledged by the botanist Kortinsky (1896).

Shevchenko (1913, 1915), discussing the expertise related to Bukhara melons, offered detailed descriptions of their varieties. He classified them based on origin, including Chardzhou, Khiva, Samarkand, Ashgabat, Tashkent, Kokand, Bukhara, and more. Additionally, he further grouped them into varietal categories such as Khandalyaki, summer, autumn, winter, and cassabs.

A.P. Kuznetsov (1915) and N. Shavrov (1916) conducted detailed studies on the Chardzhou melon varieties and the methods of cultivating them in areas with nearby groundwater. Consequently, by the onset of the revolutionary agricultural reorganization in the USSR, there was considerable knowledge about Central Asian melons. However, a comprehensive and thorough examination of Central Asian melons commenced during Soviet rule. The initial experiments were initiated under the guidance of K.P. Pangalo at the Turkestan vegetable and seed station established in 1920 near Tashkent. The Khorezm experimental station, established in the early twenties, significantly contributed to the exploration of Khorezm melon cultivation. Notably, A.P. Yakhtenfeld (1928) and A.P. Filentsev (1930), in addition to describing local melon varieties, conducted the first-ever biochemical analysis.

Since 1923, the Central Asian experimental station of the All-Union Institute of Plant Growing started its operations in Uzbekistan. The findings from this station are consolidated in the works of Pangalo (1925, 1928, 1933, 1938, 1947, 1950, 1958); Belkuznetsova and Zhiteneva (1937); Borodai (1948); Donskoy (1949); Filov (1933, 1958, 1960).

Research activities conducted under the title of the Central Asian station "VIR" have been ongoing since 1933 at the Uzbek Vegetable and Potato Experimental Station, now known as the Uzbek Research Institute of Vegetables, Melons, and Potatoes. In the field of breeding, efforts have been made to investigate the local assortment of melons. Simultaneously, studies on mineral nutrition, plant placement, irrigation, crop rotation, and other relevant aspects have been undertaken. A comprehensive survey of the primary melon cultivation areas was carried out between the Central Asian experimental station "Vir" and the Uzbek Vegetable and Potato Experimental Station to identify and collect the best local varieties of traditional selection.

Research conducted by K.I. Pangalo (1930, 1931, 1934), A.I. Filov (1939), and others during the pre-war period addressed issues related to the biology, selection, and seed production of various melon varieties. Additionally, within the "Vir" system, alongside melon crop selection, a study was conducted on the chemical composition of the fruits of several melon varieties (Kudryavtseva 1930, Arasimovich 1938, 1939). Petrovsky and Sixtel's work (1935) revealed different water requirements for various melon varieties.

While investigating melon cultivation in Central Asia, Vavilov (1936) discovered that the so-called Chardzhou melons were not actually cultivated near Chardzhou but were brought from the lower reaches of the Amu Darya River, specifically the Khorezm oasis. In Turkmenistan, Vavilov identified melon cultivation areas such as Tashauz, Chardzhou, Merv-Tyadzen. Turkmenistan made a significant contribution to the study through the Turkmen Experimental Station for Botanical Cultivation. Its director, Kobytsev (1948, 1950, 1959), conducted several interesting works on the selection of local

melons in the Chardzhou oasis and the mechanization of their cultivation. Numerous works have addressed the challenges of combating Fusarium wilt disease in Central Asia.

Melons were stored until the next year in specialized rooms called 'kaunkhona.' However, during invasions in the Middle Ages, melon cultivation declined, leading to the loss of some valuable local varieties. Fortunately, many were preserved, serving as foundational material for modern varieties.

Wild melon species, believed to be the ancestors of current varieties, still grow in Uzbekistan. Farmers, across generations, refined their cultivation practices, selecting seeds from the best fruits. The creative process of selection in melon cultivation centers led to diverse local varieties adapted to various soil-climatic conditions.

In the early 20th century, scientists explored melon cultivation areas, collecting diverse varieties. Notable Uzbek scientists like K.I. Pangalo, A.I. Philov, M.K. Goldgausen, V.F. Bel-Kuznetsova, P.V. Donskoy, A.K. Karimov, G.O. Zeman, P.N. Dudko, M.N. Kulakova, N.E. Zhiteneva, A.S. Khakimov, A.S. Shyukina, R.A. Khakimov, A. Aligavharov, U. Karimschaev, O. Todgiev, Sch. Muydinov made significant contributions to studying and improving melon diversity.

Melon varieties were named based on traits, origin, breeder, locality, and feelings. Varieties demonstrated diverse morphological traits, such as shape, coloration, pulp quality, and seed coloration. The naming reflected the characteristics of the melon varieties.

Central Asian melons, developed through prolonged breeding, can be grouped into varieties with uniform traits, those differing in traits but retaining names, and varieties with similar traits but different names. Some varieties have synonyms, while others spread under a common name.

The composition of melon varieties in fields continuously changes, with old and new varieties coexisting. Some varieties are grown in modest amounts, demonstrating the ongoing evolution and adaptation of melon cultivation.

One of the world's largest melon germplasm collections, with over 1330 accessions, is maintained in Uzbekistan. Numerous expeditions and exchanges, even in recent times, contribute to the collection of new varieties.

Ongoing expeditions across Central Asia continue to discover new varieties. Scientific studies focus on variability, inheritance of traits, classification, and the development of new varieties. Intensive cultivation and seed-growing technologies are actively developed to further advance melon cultivation in Uzbekistan. There are over 120 cultivated varieties of melons that differ in terms of ripening. The fruits of most late-ripening varieties are characterized by a high degree of keeping quality (Kuchkarov 1985). Melons have held, and continue to hold, a prominent place in the diet of the Uzbekistan population. Their nutritional value is determined by the high content of various sugars. According to Bel-Kuznetsova and Zhiteneva (1937), the sugar content of the fruits of the best melon varieties can reach 20%.

Preserving the germplasm of indigenous melon varieties in Central Asia holds significant importance for breeding, and safeguarding the melon gene pool is considered a national priority in this region. Scientists in the country are actively engaged in crucial efforts to meticulously conserve both existing and vanishing local melon varieties for the benefit of future generations. This undertaking involves organized collecting expeditions, preservation in research institutes, and extensive research endeavors. The focus of these scientific endeavors extends to enhancing the resilience of local melon varieties against powdery mildew and *Fusarium* wilt. Additionally, scientists are dedicated to the development of new melon varieties and hybrids. Emphasis is placed on environmentally friendly melon cultivation practices, promoting the utilization of melon diversity, and scaling up seed production. Efforts are directed towards cultivating early ripening varieties and hybrids in protected areas, advancing rain-fed melon cultivation techniques, and boosting the export of both fresh and dried melon products (Mavlyanova et al. 2005).

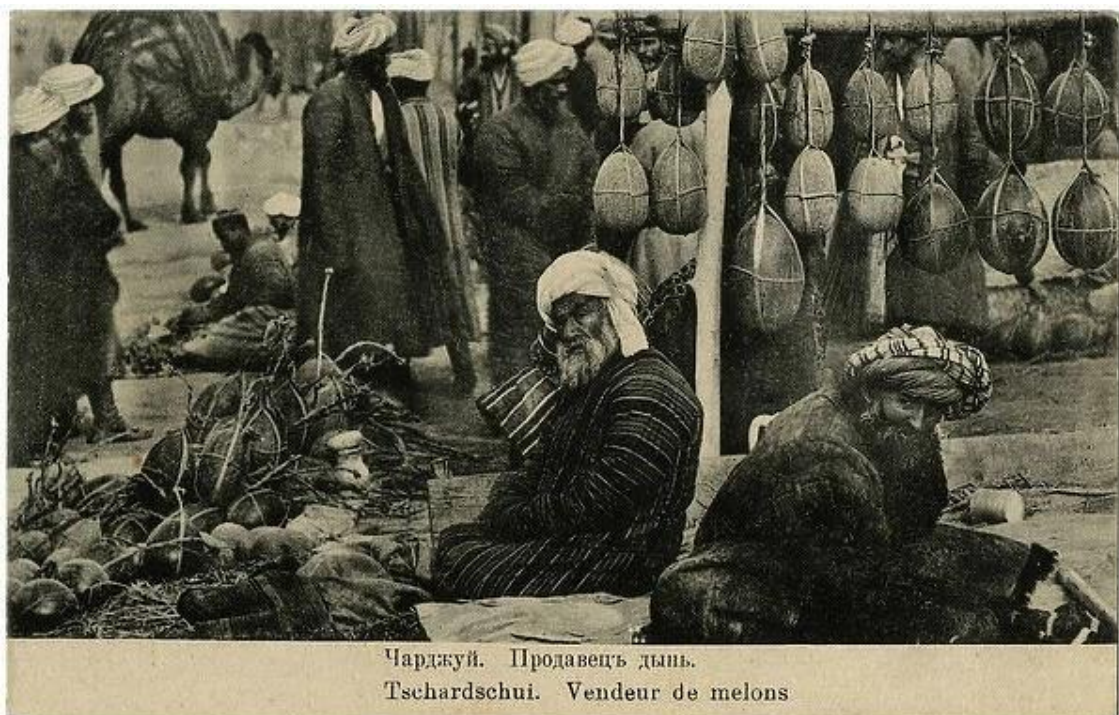


Figure 2.6. Uzbek melon sellers at the beginning of the 20th century

2.2.3. Importance of morphological characterisation

In study of Kaya (2020), a detailed morphological analysis was conducted on 32 melon genotypes, including 4 hybrids, 9 local varieties, and 19 genotypes collected from Northern Cyprus. These genotypes were evaluated for 52 morphological traits based on UPOV criteria. The resulting dendrogram revealed a similarity range between 15 and 120, categorizing the genotypes into two main groups.

Naroui Rad et al. (2018) explored the genetic diversity of melon species in Iran, a secondary center of origin. Morphological traits were studied, revealing significant differences among accessions. Principal component analysis and cluster analysis confirmed high variability, particularly between Semnan, Khorasan, and Sistan samples.

Ermiş and Aras (2017) performed morphological characterization of 64 melon varieties in Turkey, revealing significant differences and forming three main groups based on kinship degrees. The study highlighted clustering patterns among different melon species, emphasizing variations among 'Charantis' type, 'Piel de Sapo,' and 'Canary' type melons.

Solmaz et al. (2017) characterized orange-fleshed Altınbaş melon dihaploid lines developed in a breeding program. Morphological characterization, based on modified UPOV criteria and quantitative characters, exhibited diverse variation in fruit characteristics and β -carotene content among the dihaploid lines.

Dal et al. (2017) investigated the morphological diversity of 64 local melon genotypes collected from various regions of Turkey. Adhering to UPOV criteria, the study identified 20 features and emphasized the sufficiency of morphological diversity, suggesting the need for additional support through molecular studies.

Szamosi et al. (2010) compared morphological characterizations of 58 local genotypes, mainly Hungarian and Turkish melons. While general similarity between the melons of the two countries was lacking, a close relationship within the inodorus group was observed based on UPOV criteria.

Turkey prioritizes understanding the diversity of its cucurbit crops (melons, pumpkins, etc.) through morphological characterization. This involves detailed physical assessments of thousands of accessions across various institutions. These efforts help identify valuable traits, manage resources effectively, and ultimately improve future breeding programs for crops with better yield, disease resistance, and adaptation (Yetişir et al. 2008).

Köse (2008) conducted molecular and morphological characterization of 68 cucumber, 9 melon, and 1 cucumber genotypes from Turkey's local varieties and different gene banks. The study, utilizing UPOV criteria for morphological characterization and the RAPD method for molecular characterization, revealed four main groups based on quantitative characters and genetic relatedness.

Atalmış (2007) aimed to evaluate the morphological-agronomic characteristics of forty melon genotypes from National and American Gene Banks. Both morphological and molecular evaluations, using 56 ISSR markers, categorized the genotypes into four groups. Despite substantial morphological variation, the study indicated a close genetic relationship among melon genotypes.

2.2.4. Melon fungal diseases

Fungi, being the predominant plant pathogens, are accountable for a wide array of severe plant ailments, with most vegetable diseases attributed to fungal infections. These pathogens detrimentally impact plants by inducing cell death and causing physiological stress. Sources of fungal infections encompass infected seeds, soil, crop remnants, adjacent crops, and weeds. Spread occurs through wind dispersal, water splash, and transportation via contaminated soil, animals, machinery, and human activities, with

penetration into plants facilitated through natural openings like stomata or wounds incurred from pruning, harvesting, environmental factors, and mechanical damage.

A variety of fungi are associated with foliar diseases, with Downy mildews, Powdery mildews, and White blister being prevalent examples. Additionally, soilborne diseases such as Clubroot, Pythium, Fusarium, Rhizoctonia, Sclerotinia, and Sclerotium species are notable contributors to crop health challenges. While certain fungal diseases afflict a broad spectrum of vegetables, encompassing Anthracnose, Botrytis rots, Downy mildews, Fusarium rots, Powdery mildews, Rusts, Rhizoctonia rots, Sclerotinia rots, and Sclerotium rots, others exhibit specificity to particular crop groups. For instance, Clubroot (*Plasmodiophora brassicae*) is characteristic of brassicas, while Leaf blight (*Alternaria dauci*) affects carrots, and Red root complex is associated with beans (Anonymous 13).

Melon crops are susceptible to several fungal diseases that significantly impact yield and fruit quality. Cucurbit powdery mildew, caused by *Podosphaera xanthii* (Castagne) U. Braun & Shishkoff (previously *Sphaerotheca fuliginea*), primarily affects melon foliage (McGrath and Thomas 1996). Anthracnose, a disease caused by the fungal pathogen *Colletotrichum orbiculare*, infects melon leaves, stems, and fruits, directly reducing yield and marketability, particularly by damaging the fruit itself (Keinath 2016). These two fungal diseases, cucurbit powdery mildew and anthracnose, are widespread and have been documented to cause serious yield losses in melon crops (Jones et al. 2020).

2.2.4.1. Fusarium wilt

Fusarium wilt, caused by the fungus *Fusarium oxysporum* f. sp. *melonis* (Snyder and Hansen 1940), is a major threat to melon crops worldwide. This fungal disease has been reported on all continents, causing severe damage in melon-producing regions of America, Asia, Europe, and even Australia. Outbreaks can be highly destructive, leading to significant plant mortality and wiping out entire melon stems. Four races of the fungus have been identified using specific host plants: races 0, 1, 2, and 1-2 (previously known as race 3). Race 1-2 further divides into sub-races 1.2W (wilting) and 1.2Y (yellowing). Notably, race 1-2 has become predominant in many countries. While identifying the specific race can be helpful for some countries to choose resistant melon varieties and understand infection patterns, the key takeaway is that *Fusarium oxysporum* f. sp. *melonis* primarily targets melons, although it can also attack young plants of other cucurbits (Anonymous 12, Jain 2019).

In recent study conducted in Kumluca, Türkiye, the incidence and severity of root and stem rot diseases in melons grown under greenhouse conditions were evaluated across 72 melon greenhouses. Laboratory analysis of plant and soil samples revealed that *Fusarium oxysporum* and *Didymella bryoniae* were the most frequently isolated pathogens from plant samples, with other *Fusarium* species also present. Soil samples predominantly yielded *Fusarium* spp., *Rhizoctonia solani*, and *Macrophomina phaseolina*. Pathogenicity tests demonstrated that isolates of *F. oxysporum*, *F. solani*, *F. verticillioides*, *M. phaseolina*, and *R. solani* caused severe symptoms on melon seedlings. Additionally, the virulence of *F. oxysporum* isolates was tested on various cucurbit species, showing severe wilting on melon and watermelon seedlings, while squash and cucumber exhibited moderate to slight symptoms (Sarica and Karaca 2024).

In a study by Silva et al. (2023), *Fusarium falciforme* and *Fusarium suttonianum* were identified as the predominant fungal culprits responsible for root rot disease in northeastern Brazil's vital melon production region. This research represents the first documented instance of these specific *Fusarium* species causing root rot in Brazilian muskmelon. The findings underscore the critical need for continued monitoring of these emerging pathogens and the importance of incorporating disease resistance traits into melon breeding programs for effective disease management.

Li et al. (2020) identified a mobile pathogenicity chromosome in *Fusarium oxysporum* f. sp. *melonis* (Fom) that allows it to infect melons. This chromosome shares similarities with another chromosome found in *Fusarium oxysporum* f. sp. *radicis-cucumerinum* (Forc), which infects a wider range of cucurbit crops.

Sabahi et al. (2020) investigated the genetic diversity of *Fusarium oxysporum* f. sp. *melonis* (Fom), a major melon pathogen. By analyzing strains from Iran, a region with a long history of melon cultivation, the study identified nine distinct Fom lineages. The presence of similar genes in geographically distant lineages suggests horizontal gene transfer, a mechanism for spreading virulence factors. Notably, the study identified a new variant of a gene that allows the fungus to bypass a common melon resistance mechanism.

Lee et al. (2018) investigated the resistance of commercial melon cultivars to *Fusarium* wilt caused by *Fusarium oxysporum* f. sp. *melonis*. The study identified three races (0, 1, and 2) among seven fungal isolates but did not detect race 1.2, a particularly aggressive variant. Twenty-two commercial melon cultivars were tested for resistance against these isolates. All cultivars showed either high susceptibility or strong resistance, with no moderately resistant ones observed, 15 cultivars previously not reported as resistant displayed strong resistance to two races (0 and 1), suggesting they might harbor the Fom-2 resistance gene.

A study by Shokouhifar et al. (2016) explored the Fom2 gene in Iranian melon cultivars, hoping to find a connection between the gene and resistance to a specific race of fungal wilt disease. The researchers examined the Fom2 gene sequence in both resistant and susceptible cultivars. While they observed variations within the gene across different melons, these variations didn't clearly distinguish between those that could resist the wilt and those that couldn't. The study identified some mutations within a key region of the Fom2 gene, potentially linked to activating resistance mechanisms. These findings suggest that the Fom2 gene might play a role in disease resistance, but further investigation is needed to clarify how these specific mutations influence a melon's susceptibility to the fungal race.

Haegi et al. (2013) developed a reliable qPCR assay for detecting *Fusarium oxysporum*, a soilborne fungus that causes wilt disease in melons. This method can distinguish *F. oxysporum* from other *Fusarium* species. The study also investigated the effectiveness of grafting melon varieties to combat this disease. While grafting offers resistance against some *F. oxysporum* races, the qPCR assay revealed that fungal development is influenced by the specific melon genotype used as the rootstock and the time since infection. This suggests that grafting may not completely prevent colonization by all *F. oxysporum* races.

Chehri et al. (2011) investigated *Fusarium* species causing root and stem rot in cucurbits of Kermanshah province, Iran. Five species (*F. oxysporum*, *F. proliferatum*, *F. equiseti*, *F. semitectum*, and *F. solani*) were identified and tested for pathogenicity on cucumber and honeydew melon seedlings. *F. oxysporum* caused damping-off, while *F. solani* induced stem rot symptoms. PCR-ITS-RFLP analysis differentiated the species and revealed two RFLP types within the *F. solani* species complex. This study identified key *Fusarium* pathogens and a useful method for their differentiation.

Ekbic et al. (2010) employed molecular markers and dihaploidization to develop Turkish melon varieties resistant to *Fusarium* wilt. The Cum334 donor parent was used in a backcross program, and irradiated pollen from the BC3 population was used to generate haploid plants for faster breeding. Out of four embryo rescue methods tested, "inspecting seeds on the light" and "sowing seeds directly to nutrient media" proved most effective, yielding 122 haploid plants. These plants were screened for the *fom1* and *fom2* genes linked to resistance using various molecular markers. While some markers proved ineffective, others like the RAPD marker (OPG17) successfully distinguished resistant and susceptible plants for the *fom2* gene. Similarly, the SCAR marker (SB17) identified resistance in the *fom1* gene. Overall, 41% of the haploid plants displayed resistance to *Fusarium* wilt races 0 and 2, while 34% resisted races 0 and 1.

2.2.4.2. Anthracnose and powdery mildew

The study by Jiang et al. (2023) explored the cause of anthracnose in Katsura-uri melons, a prized Japanese pickling variety cultivated in Kyoto. In 2010, growers observed dark brown to black spots marring ripening Katsura-uri fruits after harvest. To investigate the culprit, researchers isolated four fungal strains (T1, K1, K2, and K3) from the lesions. Phylogenetic analysis revealed these strains belonged to four distinct *Colletotrichum* species: *C. orbiculare*, *C. fructicola*, *C. aenigma*, and *C. chlorophyti*. Interestingly, *C. orbiculare* (K3 isolate) specifically targeted Katsura-uri leaves, causing necrotic lesions. The remaining three species (*C. fructicola* K1, *C. aenigma* K2, and *C. chlorophyti* T1) exclusively infected the fruits, leaving leaves unharmed. Further experiments using ripe and immature Katsura-uri fruits suggested *C. chlorophyti* as the culprit behind a postharvest disease, as it only induced lesions on ripe fruits.

Takano et al. (2023) investigated the paradox of *Colletotrichum* fungi, which exhibited a broad host range despite the usual host specificity observed in plant pathogens. Plants typically possessed defenses against non-adapted fungi, but *Colletotrichum* seemed to possess mechanisms to overcome them. This study focused on the role of effector proteins, molecules secreted by fungi, in determining host specificity. While one effector (NIS1) interacted with plant defense systems, it was not critical for virulence. However, targeted gene knockout screening identified four other effectors (EPC1-4) essential for full virulence on cucurbit crops (cucumber, melon, etc.) but not on a distantly related plant species (*Nicotiana benthamiana*).

Matsuo (2022) investigated *Colletotrichum orbiculare*, a fungal culprit behind cucurbit anthracnose. The study in Japan identified three fungal races, including one that bypasses a key resistance gene in watermelon breeding. Notably, some strains breached the defenses of even the most resistant cucumber cultivar, highlighting the need for new resistance sources.

Maslennikova et al. (2022) studied complex resistance to anthracnose and powdery mildew in melons. These fungal diseases significantly reduce melon yield and quality. Researchers evaluated four melon hybrid combinations alongside a standard cultivar ('Osen') using artificial and natural infection methods. The hybrid combination 'Dune × Ponap (Japan) F1' emerged as the most promising, exhibiting complex resistance under both conditions.

Varivoda and Maslennikova (2019) investigated complex resistance in melons to powdery mildew and anthracnose, two fungal diseases causing substantial yield and quality losses globally. The study evaluated various melon varieties and F1 hybrids using artificial infection methods. Standardized disease ratings revealed significant susceptibility in the control melon cultivar ('Autumn'). Conversely, several promising hybrids exhibited superior complex resistance, with the hybrid 'Original x Autumn' demonstrating exceptional tolerance to both diseases. This hybrid also possessed commercially valuable traits like high productivity and dry matter content in the fruit juice.

2.3. Molecular markers

2.3.1. Markers

Molecular markers play a crucial role in understanding the natural history and evolution of species. By examining the molecular make up of organisms, scientists can trace evolutionary relationships, study genetic diversity, and unravel the processes that have shaped the biological world over time. Many molecular marker approaches have been developed and used globally in various systems over the past three decades. Only a small number of these methods - RFLPs, RAPDs, AFLPs, ISSRs, SSRs, and SNPs -have received global acceptance (Grover and Sharma 2016).

The development of DNA marker technology has given geneticists and plant breeders access to a variety of DNA markers and molecular breeding techniques, which have helped them overcome many of the challenges faced in traditional breeding (Kumar 1999).

Molecular markers are distinguishable and quantifiable characteristics or attributes at the molecular level, such as proteins, DNA sequences, or other molecules, that can be utilized to monitor a certain biological activity or to show the presence of a specific hereditary trait. In many scientific domains, including as genetics, genomics, medicine, and agriculture, these markers are essential.

The rapidly evolving field of genomics, also referred to as molecular biology, provides information on the identity, location, influence, and function of genes influencing these traits. In numerous higher plant species, researchers have identified, categorized, and mapped single gene markers (Jonah 2011).

2.3.2. Phylogenetics

The study of evolutionary relationships between species, known as phylogenetics, makes considerable use of molecular markers, particularly DNA sequences. Researchers

can create phylogenetic trees that show the evolutionary history and relatedness of various creatures by comparing DNA sequences.

2.3.3. Genetic Diversity

Molecular markers help assess genetic diversity within populations. By analyzing variations in DNA sequences or other molecular traits, scientists can understand the distribution of genetic diversity and identify factors influencing population structure.

2.3.4. Evolutionary Processes

Many evolutionary processes, including natural selection, genetic drift, and gene flow, can be better understood through the use of molecular markers. Researchers can figure out how various evolutionary processes have altered populations and species throughout time by examining patterns of genetic variation.

The use of molecular markers is essential in population genetics research. They contribute in the study of population bottlenecks, gene flow between populations, and population adaptation to environmental changes.

In order to distinguish the chromosome containing the mutant gene from the chromosome containing the normal gene based on the form of the marker it contains, markers must be polymorphic, meaning they must exist in several forms. There are three ways to identify polymorphism: morphological, biochemical, or molecular (Jonah 2011).

The ideal DNA marker should exhibit sufficient polymorphism to distinguish between individuals or populations. High polymorphism levels are particularly important for applications such as genetic mapping, population genetics, and marker-assisted selection in breeding programs.

However, an ideal DNA manufacturer should have the following characteristics, according to Joshi et al. (2011).

- 1) Highly polymorphism, defined as the co-occurrence of two or more discontinuous variations or genotypes of a characteristic at the same population.
- 2) Codominant inheritance: In order to distinguish between homozygote and heterozygote, a diploid organism needs to exhibit distinct markers.
- 3) Regular occurrence in the genome
- 4) Simple accessibility (available)
- 5) Simple and quick assay

Most molecular marker technologies can be categorized as hybridization-based on PCR systems depending on the method of detection.

Sequence – Related Amplified Polymorphism (SRAP)

The ISSR and SRAP marker techniques were employed to examine the genetic relationships among the melon genotypes. Out of the 19 ISSR and 16 SRAP primer combinations tested, 13 ISSR and 11 SRAP primers yielded results. The ISSR marker method achieved a 100% polymorphism rate with 120 out of 164 bands being

polymorphic. Similarly, the SRAP marker method also achieved a 100% polymorphism rate, with 56 out of 81 bands identified as polymorphic (Kaya 2020).

In 2001, SRAP was utilized for the first time to create a genomic map and tag genes in *Brassica oleracea* (Li and Quiros 2001). SRAP-PCR, is widely used marker technology that is easy to use, affordable, and efficient for creating genome-wide fragments with excellent repeatability and adaptability. SRAP markers are a type of DNA marker technique that combines aspects of polymerase chain reaction (PCR) and restriction fragment length polymorphism (RFLP) (Robarts and Wolfe 2014).

Using a single round of PCR, this molecular marker method can easily amplify many or even more than one hundred loci in a genome. Two random primers are included in the PCR mix reaction, allowing for the most possible flexibility in primer design and labeling. Additionally, there is no restriction on the number of primer combinations that can be made; one labelled primer is able to pair with any number of unlabelled primers (Li et al 2013).

SRAP technology has many uses, including cloning, gene tagging, genetic diversity study, and the creation of genomic maps. With SRAP, it is possible to quickly screen hundreds of loci and identify the genetic location that underlies a certain trait. SRAP is used to determine the chromosomal area of mapped genes in well-characterized genomes.

The majority of crops, tree species, ornamental and medicinal species, and many other plant species have had their genetic diversity analyzed using SRAP technology.

2.3.5. Application of SRAP Markers in Research

Various researchers have conducted genetic characterization studies on melons using different molecular markers, including RAPD, SRAP, SSR, and ISSR. Şensoy et al. (2007) compared 56 melon genotypes, revealing greater genetic diversity in Turkish genotypes compared to foreign ones. Iranian melons were also studied, confirming wide variation, and molecular data correlated with morphological findings (Kohpayegani and Behbahani, 2008).

The SRAP marker system, introduced by Li and Quiros (2001), proved reliable and cost-effective. Solmaz (2010) used SRAP and SSR markers, finding a 97.3% polymorphism rate with SRAP and clustering lanatus varieties closely. Yan and Zhang (2005) employed SRAP markers on hybrid watermelon varieties, resulting in 3 distinct groups. Staub et al. (2000) examined 46 melon varieties using RAPD and SSR markers, establishing a solid correlation and their utility in determining relatedness.

Daninig-Poleg et al. (2001) developed 61 SSR markers in Cucumis species, and Decker-Walters et al. (2002) used RAPD and SSR markers to study wild melons in North America. Daryono et al. (2019) evaluated a new Indonesian melon variety, 'Melonia,' using 27 morphological traits and 4 ISSR primers, confirming stability in phenotype and genotype.

Guliyev et al. (2018) explored genetic relationships in Azerbaijani melons, using 11 agromorphological traits and 10 ISSR primers. Genetic diversity and clusters were determined, highlighting the lack of significant correlation between agromorphological features and ISSR markers.

Maleki et al. (2018) applied ISSR markers to assess genetic diversity among Iranian *C. melo* landraces, revealing distinctions among different groups. Akash et al. (2019) used AFLP and ISSR markers on Jordanian blueberry landraces, successfully distinguishing genotypes and demonstrating moderate positive correlation between the markers.

Karaman et al. (2018) conducted a comprehensive study on 12 bitter melon genotypes, integrating morphological, molecular, and biochemical analyses. ISSR primers identified high genetic similarity among 'Melonia' populations. Yıldız et al. (2011) examined Turkish melon genetic resources using ISSR, SRAP, and RAPD markers, revealing genetic relationships and clustering patterns among different genotypes.

To explore the genotype-phenotype relationship and marker-trait associations in wheat, eight genotypes were analyzed using a set of 95 DNA-based SRAP molecular markers. The SRAP analysis revealed an average percentage of polymorphism (P%) of 62.59% and an average polymorphic information content (PIC) of 0.23. Additionally, the marker index (MI) averaged at 1.49. Notably, the ME1F-EM5R and ME9F-EM3R primer combinations exhibited particularly high levels of polymorphism, with rates of 88.89% and 90.91%, respectively. Through single-marker analysis (SMA), the ME-7F-EM-6R1250bp marker emerged as a potential candidate marker linked to 1000-grain weight. Furthermore, SRAP markers ME-7F-EM-5R900bp and ME-4F-EM-6R490bp were identified for the weight of grains per spike and the number of grains per spike, respectively. Cluster analysis, based on both SRAP markers and morphological data, revealed a range of similarity coefficient values, spanning from 57.40% to 80.40% for SRAP markers and from 90.61% to 98.81% for morphological traits. Although positive, the correlation between similarity matrices generated by SRAP markers and mean morphological traits was found to be non-significant ($r = 0.03$, $P > 0.05$). These findings provide valuable insights into the genetic diversity and trait associations in wheat genotypes, as elucidated by SRAP marker analysis (Khaled 2019).

Erdoğan et al. (2013) employed RAPD and ISSR markers to assess genetic diversity in melons from the Van region, detecting 96.19% polymorphism. The study emphasized the formation of clusters based on geographical regions.

SRAP markers have been employed in genetic studies to assess genetic diversity, population genetics, and other applications in various plant species, including melon (*Cucumis melo* L.). SRAP markers offer a cost-effective and relatively simple method for generating genetic fingerprints and identifying polymorphic loci in the melon genome.

They are employed in various types of analyses, including population genetics, phylogenetic analysis, comparative genomics, genetic diversity, and breeding. To assess the genetic diversity among several melon varieties, landraces, and wild relatives, SRAP markers have been employed. Researchers can learn more about the genetic links and

differences between various melon accessions by examining the SRAP banding patterns. In melon breeding programs, SRAP markers are used for marker-assisted selection (MAS). By employing markers associated with certain features, MAS enables breeders to more effectively identify individuals with desired traits. This may accelerate the process of creating new melon cultivars with enhanced qualities.

Melon SRAP data can be utilized to clarify the evolutionary relationships between various melon cultivars, varieties, or subspecies through phylogenetic reconstruction. This facilitates the categorization and comprehension of the genetic provenance of melon germplasm.

According to Zhang's (2012) research, SRAP markers were utilized to identify the hybrid seed purity of a melon cultivar and to analyze the genetic relationships between twelve different cultivars. This study offered data for melon cultivar identification of hybrid seed purity and genetic link analysis (Chen and Wang 2010).

Chen Y. (2010) identified the genetic diversity of a *Cucumis melo* L. germplasm collection using SRAP markers. A group of melon accessions' genetic linkages and classifications were examined in order to offer experimental evidence in favor of efficiently using genetic resources for breeding. A technique known as sequence-related amplified polymorphism was used to examine 61 melon accessions. Out of over forty-two primer combinations, sixteen were chosen for further analysis based on their distinct band pattern and polymorphism. 16 sets of SRAP primers were able to identify 452 loci. Of them, 265 had a polymorphism rate of 58.63%; on average, each set of primers amplified 28.56 loci and 16.56 polymorphic loci. These findings showed that the examined melon accessions exhibited a high degree of genetic diversity (Chen and Wang 2010).

Research by Liu (2010) showed that a race of *P. xanthii* is responsible for the inheritance of CPM resistance in Indian melon PI 134198, and a new SRAP marker was found to be connected to the dominant CPM resistance gene in this accession.

Another research conducted by Zhao (2010) employed the SRAP marker for the powdery mildew resistance gene in melon. The susceptible and resistant melon were used to create the mapping population. The SRAP approach was used to screen for powdery mildew resistance markers. The findings demonstrated that 6 of the 294 SRAP primers could identify the polymorphism between the susceptible and resistant pools. It was found that polygene recessive genes control melon resistance to powdery mildew.

3. MATERIAL AND METHODS

3.1. Plant material

Melon seed samples were collected from various regions of Kyrgyzstan and Uzbekistan during the 2019-2020 years, with an additional wild type genotype found in the campus of Akdeniz University. A total of 31 Kyrgyz, 16 Uzbek and 1 wild type genotypes were investigated in this research. Table 3.1, provides detailed information about genotypes, including their respective code, genotype names, collection regions, genetic types, and geographical coordinates. Kyrgyz landraces included a diverse range of locations, from Bishkek to Batken, and were predominantly categorized as local. The Uzbek landraces included regions like Samarkand, Bukhara, Termiz, Nurota, and were primarily classified as local too. The altitudes of Kyrgyz genotypes range from 310 meters (m) to 1280 m, while the altitudes of Uzbek genotypes vary between 229 m and 720 m above sea level, altitude of wild type is 50 m.



Figure 3.1. View of locations on the map where genotypes were collected (Anonymous 1)

In the following pages of the thesis, genotypes are given as: Kyrgyz genotypes - KGZ, Uzbek genotypes - UZB, and wild genotype is given as WT codes.

Table 3.1. Kyrgyz and Uzbek genotypes used in this research

No	Code*	Genotype name	Genetic type	Collection region	Latitude Longitude	Altitude
1	KGZ-1	Abunavat	rigidus var. bucharica	Kant	42.52599 74.85059	750
2	KGZ-2	Abunavat	rigidus var. bucharica	Talas	42.5228 72.2427	1280
3	KGZ-3	Abunavat	rigidus var. bucharica	Kemin	42.82800 75.3100	1125
4	KGZ-4	Altin	N/A	Sokuluk	42.8540 74.3025	730

Table 3.1. Continued

5	KGZ-5	Andelek	rigidus var. chandalak	Ivanovka	42.8877 75.0850	745
6	KGZ-6	Andelek	rigidus var. chandalak	Kemin	42.82800 75.3100	1125
7	KGZ-7	Efiopka	N/A	Chui	42.2959 74.2959	800
8	KGZ-8	Kitai 65	cantalupensis	Ivanovka	42.8877 75.0850	745
9	KGZ-9	Kitai 99	N/A	Kemin	42.82800 75.3100	1125
10	KGZ-10	Kolhoznitsa	N/A	Kant	42.52599 74.85059	750
11	KGZ-11	Korobka	N/A	Chui	42.2959 74.2959	800
12	KGZ-12	Lada	N/A	Chui	42.2959 74.2959	800
13	KGZ-13	Melba	N/A	Novopavlovka	42.88097 74.51053	740
14	KGZ-14	Mezim	N/A	Chui	42.2959 74.2959	800
15	KGZ-15	Mezin skorospelyj	N/A	Kant	42.52599 74.85059	750
16	KGZ-16	Mirzagul	N/A	Novopavlovka	42.88097 74.51053	740
17	KGZ-17	Noname	N/A	Tokmok	42.8333 75.2833	820
18	KGZ-18	Noname	N/A	Batken	40.0345 70.4909	1040
19	KGZ-19	Noname	N/A	Tokmok	42.8333 75.2833	820
20	KGZ-20	Noname	N/A	Tokmok	42.8333 75.2833	820
21	KGZ-21	Raduzhnaja	N/A	Ivanovka	42.8877 75.0850	745
22	KGZ-22	Rannij sort	N/A	Tokmok	42.8333 75.2833	820
23	KGZ-23	Rannjaja lubov	N/A	Kant	42.52599 74.85059	750
24	KGZ-24	Shar	N/A	Sokuluk	42.8540 74.3025	730
25	KGZ-25	Talas	N/A	Talas	42.5228 72.2427	1280
26	KGZ-26	Taman	N/A	Sokuluk	42.8540 74.3025	730
27	KGZ-27	Taman	N/A	Kemin	42.82800 75.3100	1125
28	KGZ-28	Tornado	reticulatus	Kemin	42.82800 75.3100	1125
29	KGZ-29	Torpedo	reticulatus	Kemin	42.82800 75.3100	1125

Table 3.1. Continued

30	KGZ-30	Torpedo	reticulatus	Chui	42.2959 74.2959	800
31	KGZ-31	Torpedo	reticulatus	Tokmok	42.8333 75.2833	820
32	UZB-1	Börü kalla	rigidus var. chandalak	Samarkand	39.6542 66.9597	720
33	UZB-2	Emir	N/A	Termiz	37.2242 67.2783	310
34	UZB-3	Kampir	N/A	Nurota, Navoyi	40.56500 65.68500	490
35	UZB-4	Kandelek	rigidus var. chandalak	Surkhandarya	38.089 67.252	535
36	UZB-5	Kandelek	rigidus var. chandalak	Samarkand	37.2242 67.2783	310
37	UZB-6	Kokcha	rigidus var. ameri	Termiz	37.2242 67.2783	310
38	UZB-7	Kokcha	rigidus var. ameri	Nurota, Navoyi	40.56500 65.98500	490
39	UZB-8	Kyrkma	N/A	Surkhandarya	40.56500 65.68500	490
40	UZB-9	Metrofka	N/A	Samarkand	39.7667 64.4333	229
41	UZB-10	Metrofka	N/A	Termiz	38.089 67.252	535
42	UZB-11	Noname	N/A	Nurota, Navoyi	39.7667 64.4333	229
43	UZB-12	Noname	N/A	Surkhandarya	38.089 67.252	535
44	UZB-13	Noname	N/A	Samarkand	39.6542 66.9597	720
45	UZB-14	Noname	N/A	Termiz	39.6542 66.9597	720
46	UZB-15	Shakar palak	rigidus var. ameri	Nurota, Navoyi	40.56500 65.68500	490
47	UZB-16	Zhizzak	N/A	Surkhandarya	39.6542 66.9597	720
48	WT-1	Wild	N/A	Antalya	36.5400 30.3913	50

*Genotypes code used in this research

N/A – not available

3.2. Methods

3.2.1. Morphological characterisation

Detailed morphological, biochemical characteristics that observed and measured for 79 characteristics of the plant is shown in the table 3.2. It has characteristics related to seeds, leaf blades, leaves, flowers, and fruits of the studied genotypes. Traits such as seed length, width, shape, and color are categorized numerically to classify the diverse range of observed variations. Similarly, leaf blade size, intensity of green color, lobe

development, margin dentation, and blistering are graded to understand the plant's leaf structure and characteristics. The table also includes measurements for leaf dimensions, petiole length, stem thickness, and other quantitative features critical in botanical studies. Furthermore, it shows details of flower sex type, fruit positioning, longitudinal and cross-sectional fruit shapes, surface creasing, and various measurements associated with fruit parameters like weight, length, width, seed pot diameter, shelf thickness, and flesh thickness. Additionally, it records chemical properties such as TSSC, pH, TA, and describes fruit skin and flesh color, providing a comprehensive guide for the comprehensive evaluation and characterization of the genotypes morphology.

Morphological characteristics were evaluated according to UPOV (Anonymous 3) and some of characteristic evaluations were combined with Descriptors for Melon (Anonymous 5).

Table 3.2. Characteristics of seeds, leafs and fruits that used in evaluation process

Seed	Length	(1) very short, (3) short, (5) medium, (7) long, (9) very long
	Width	(1) very narrow, (3) narrow, (5) medium, (7) broad, (9) very broad
	Shape	(1) not pine-nut shape, (2) pine-nut shape
	Color	(1) whitish, (2) cream yellow
Leaf blade	Size	(3) small, (5) medium, (7) large
	Development of lobes	(3) weak, (5) medium, (7) strong
	Length of terminal lobes	(3) short, (5) medium, (7) long
	Dentation of margin	(3) weak, (5) medium, (7) strong
	Blistering	(3) weak, (5) medium, (7) strong
Leaf	Shape	(1) entire, (2) trilobate, (3) pentalobate, (4) 3- palmately lobed, (5) 5-palmately lobed
	Length	cm
	Length from the end of	cm
	Width	cm
	Petiole length	cm
	Distance between 2 nodes	cm
	Stem thickness	mm
	Length of stem torn	mm
	Leaf color	L*a*b*
Petiole	Attitude	(1) erect, (3) semi-erect, (5) horizontal
	Length	(3) short, (5) medium, (7) long
Flower	Sex type	(1) monoecious, (2) andromonoecious
Young fruit	Density of dots	(1) absent or very sparse, (3) sparse, (5) medium, (7) dense, (9)
	Size of dots	(3) small, (5) medium, (7) large
	Contrast of dot color/ground color	(3) weak, (5) medium, (7) strong
	Conspicuousness of groove coloring	(1) absent or very weak, (3) weak, (5) medium, (7) strong, (9) very strong
	Intensity of groove coloring	(3) light, (5) medium, (7) dark

Table 3.2. Continued

	Thickness of peduncle 1 cm from fruit	(3) thin, (5) medium, (7) thick
	Extension of darker area	(1) absent or very small, (3) small, (5) medium, (7) large
Fruit	Position of maximum diameter	(1) toward stem end, (2) at middle, (3) toward blossom end
	Shape in longitudinal section	(1) ovate, (2) medium elliptic, (3) broad elliptic, (4) circular, (5) quadrangular, (6) oblate, (7) obovate, (8) elongated
	Ground color of skin	(1) white, (2) yellow, (3) green, (4) grey
	Intensity of ground color of skin	(3) light, (5) medium, (7) dark
	Hue of ground color of skin	(1) absent or very weak, (2) whitish, (3) yellowish, (4) orange, (5) ochre, (6) greenish, (7) greyish
	Density of dots	(1) absent or very sparse, (3) sparse, (5) medium, (7) dense, (9)
	Size of dots	(3) small, (5) medium, (7) large
	Color of dots	(1) white, (2) yellow, (3) green
	Intensity of color of dots	(3) light, (5) medium, (7) dark
	Density of patches	(1) absent or very sparse, (3) sparse, (5) medium, (7) dense, (9)
	Size of patches	(3) small, (5) medium, (7) large
	Warts	(1) absent, (9) present
	Strength of attachment of peduncle at maturity	(1) very weak, (3) weak, (5) medium, (7) strong, (9) very strong
	Shape of base	(1) pointed, (2) rounded, (3) truncate
	Shape of apex	(1) pointed, (2) rounded, (3) truncate
	Creasing of surface	(1) absent or very weak, (3) weak, (5) medium, (7) strong, (9) very strong
	Size of pistil scar	(3) small, (5) medium, (7) large
	Grooves	(1) absent or very weakly expressed, (2) weakly expressed, (3) strongly expressed
	Width of grooves	(3) narrow, (5) medium, (7) broad
	Depth of grooves	(1) very shallow, (3) shallow, (5) medium, (7) deep, (9) very deep
	Color of grooves	(1) white, (2) yellow, (3) green
	Creasing of surface	(1) absent or very weak, (3) weak, (5) medium, (7) strong, (9) very strong
	Cork formation	(1) absent, (9) present
	Thickness of cork layer	(1) very thin, (3) thin, (5) medium, (7) thick, (9) very thick
	Pattern of cork formation	(1) dots only, (2) dots and linear, (3) linear only, (4) linear and netted, (5) netted only
	Density of pattern of cork formation	(1) very sparse, (3) sparse, (5) medium, (7) dense, (9) very dense
	Firmness of flesh	(3) soft, (5) medium, (7) firm
	Weight	kg
	Length	cm
	Width	cm

Table 3.2. Continued

Fruit	Diameter of seed pot	cm
	Shelf thickness	mm
	Seconder shelf thickness	mm
	Fruit flesh thickness	cm
	TSSC	°Brix
	pH	

3.2.2. Seedling growing

Seeds were germinated in a seedling greenhouse facility operated by the private company United Genetics Turkey (UN), situated in Mustafakemalpasa, Bursa, a city located in the Marmara region of Turkey (39.95509, 28.51225).

3.2.3. Research area

A total of 48 genotypes were germinated, 31 from Kyrgyzstan, 16 from Uzbekistan, and 1 wild type sourced from Antalya. Once the seedlings reached the stage with 2-3 true leaves, they were transplanted to two different locations and planted at 80x40 cm planting distances, with 3 plants in each genotype:

- 1) to a greenhouse environment at Areo Tarim company, Antalya (36.90096, 30.69548), from April to July, positioned approximately 31 meters above sea level (Figure 3.2.).
- 2) another part of seedlings was cultivated in an open field environment at United Genetics field during the summer months, from May to August, situated at an approximate altitude of 16 meters above sea level (Figure 3.3.).

Throughout the growth period, routine maintenance operations such as watering, fertilization, and weed management were executed diligently by company staff, ensuring optimal care and support for the plant's growth.



Figure 3.2. View of melon genotypes in greenhouse



Figure 3.3. View of melon genotypes in open field

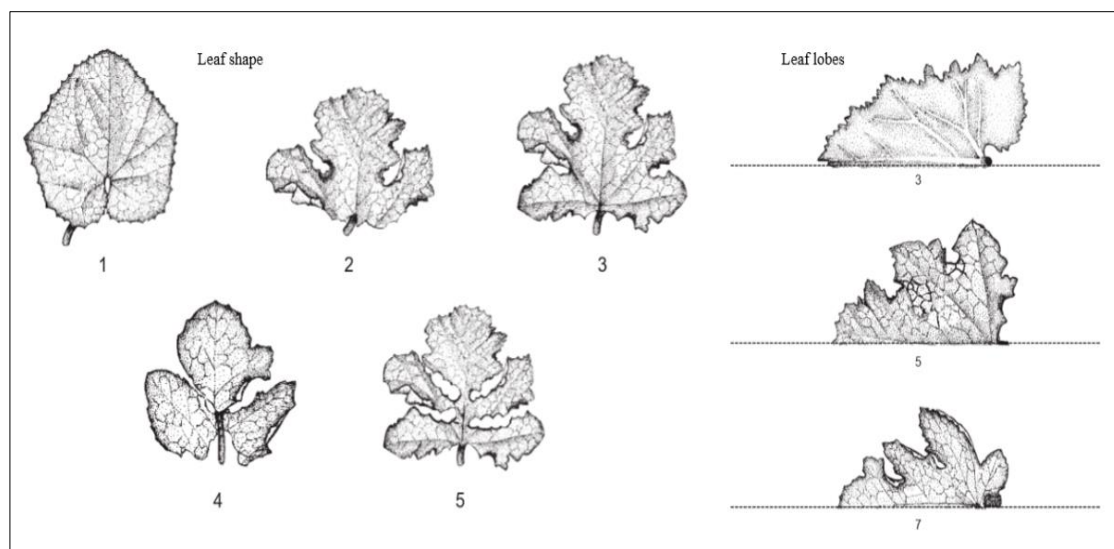


Figure 3.4. Leaf shape, leaf lobe types used in evaluation

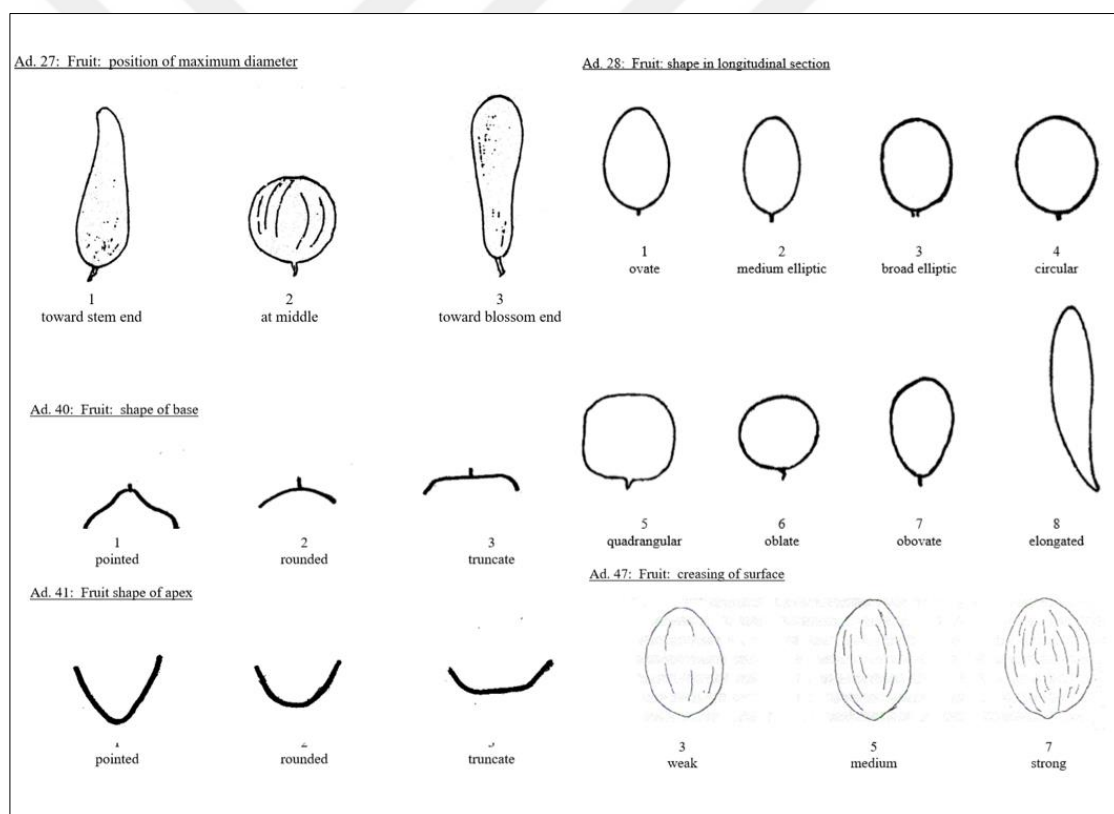


Figure 3.5. Fruit: osition of maximum diameter; shape in longitudinal section; shape of base, shape of apex, creasing surface.



Figure 3.6. Measurements of leaf blade length, length from the end of petiole till apix, stem thickness, length of stem torn



Figure 3.7. Some pictures from fruit measurement process and used devices (dual range counting and hand scales, tape ruler, electronic micrometer)

3.2.4. Biochemical analysis

The flesh of fruit was reduced to a pulp with blender and pH were measured. Total soluble solids content (TSSC) within the fruit flesh were measured with a hand refractometer (Hanna HI96801, Hanna Instruments, USA).

The fruit acidity (Titratable Acid, TA) was determined in 5 mL of juice by potentiometric titration with 0.01M NaOH to pH 8.1 (Figure 3.8); (Kurubas 2018, Petropoulos et al 2014).

Leaf color were determined by a Minolta CR-400 Chromatometer at three different points and taken as a mean (MINOLTA Camera Co, LTD Ramsey, NJ) specified in the CIE L*a*b* color space (Figure 3.9, 3.10) (Kurubas 2019).

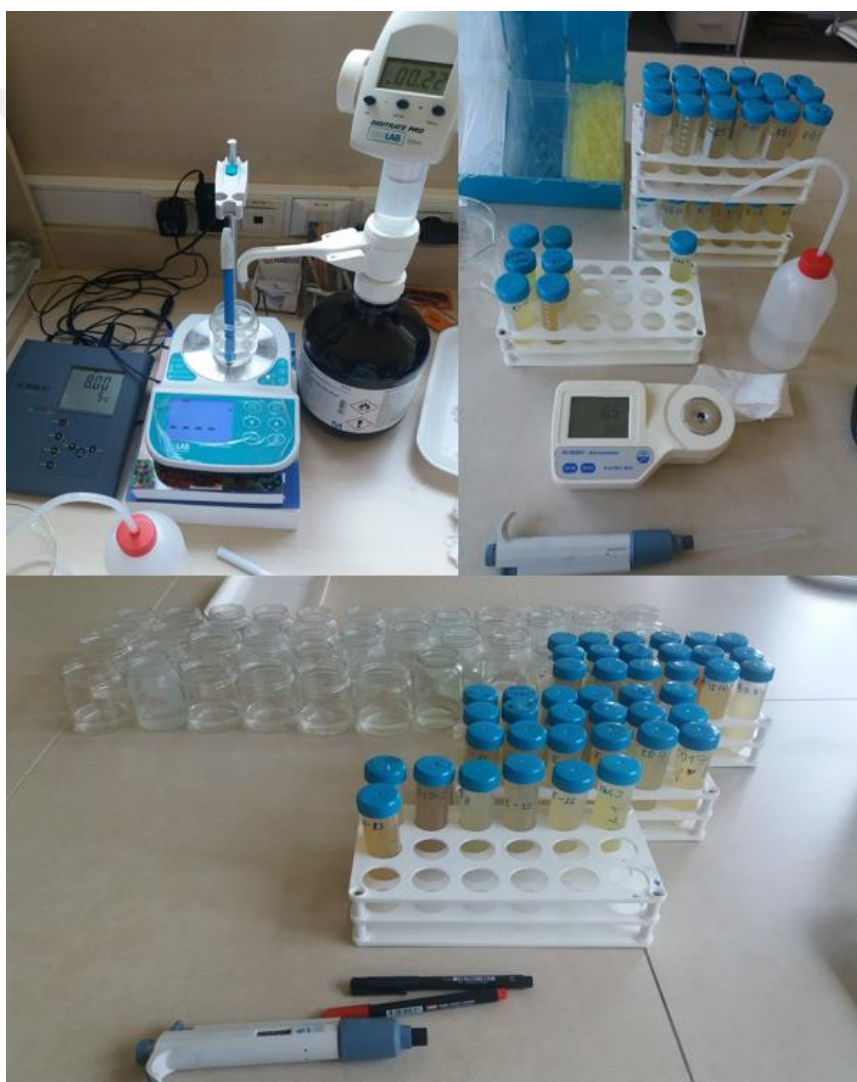


Figure 3.8. Measurement of pH, TA and TSSC

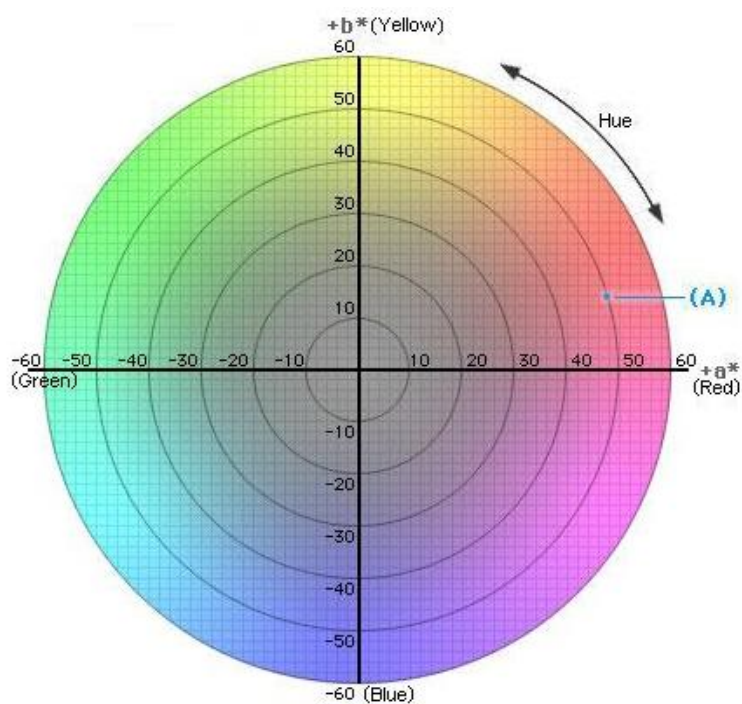


Figure 3.9. The $L^*a^*b^*$ color space (Anonymous 11)



Figure 3.10. Leaf color measurement with portable spectrophotometer

3.2.5. Molecular analysis

3.2.5.1. Dna Extraction

Genomic DNA was extracted from *in-vitro* seeds's cotyledonary leaves with CTAB method as described by Doyle and Doyle (1991), Pallotta (2000).

Plant material	Equipments	Chemicals
☐	☐	☐
☐ Fresh leaves	☐ 96 well plates	☐ 2% CTAB buffer
	☐ 1.5/2 mL tubes	☐ Chloroform : Isoamyl Alcohol (24:1)
	☐ Pipettes	☐ Isopropanol
	☐ Micropestle	☐ 70% Ethanol (ice cold)
	☐ Stainless steel beads	☐ Water (sterile)
	☐ Tissueliser	
	☐ Centrifuge mashine	
	☐ 65°C water bath	

Figure 3.11. Reagents and materials used for DNA extraction

CTAB buffer 2% /1 L

280 ml	5M NaCl
100 ml	1M Tris-HCl pH 8.0
40 ml	0.5M EDTA pH 8.0
20 gr	CTAB

Adjust to pH 5.0

Make up to 1 L by adding H₂O

10X TBE Buffer

108 gr	Tris
55 gr	Boric Acid

7.5 gr/40 ml EDTA

Make up to 1 L by adding H₂O

For a 0.5x working solution, make a 1:10 dilution of the concentrated stock.

1 M Tris pH 8.0

121.1 g of Tris base dissolve in 800 ml of H₂O.

By adding 42 ml of concentrated HCl adjust pH to 8.0. Cool and adjust volume to 1 L by adding H₂O.



Figure 3.12. Equipments used in DNA extraction

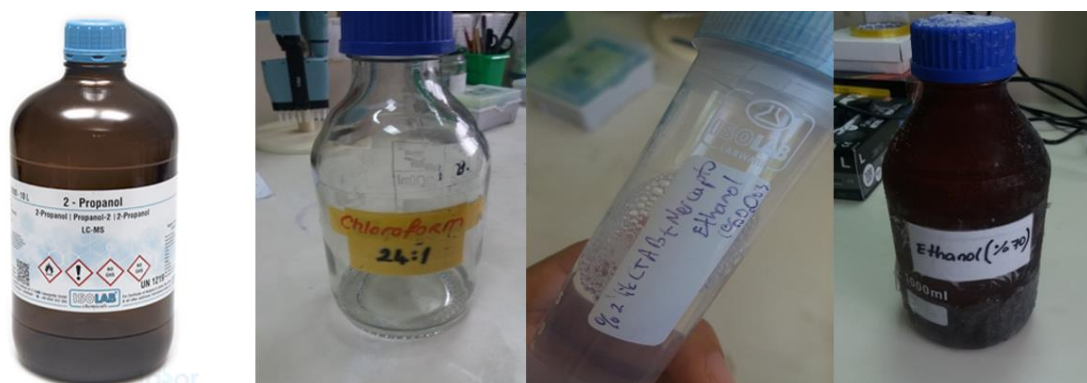


Figure 3.13. Chemicals used in DNA extraction

Young fresh leave material (200-400 mg) were carefully collected and arranged in 96-well plates or 1.5/2 mL Safe-Lock microtubes (depends on the numbers of samples) sourced from the greenhouse.

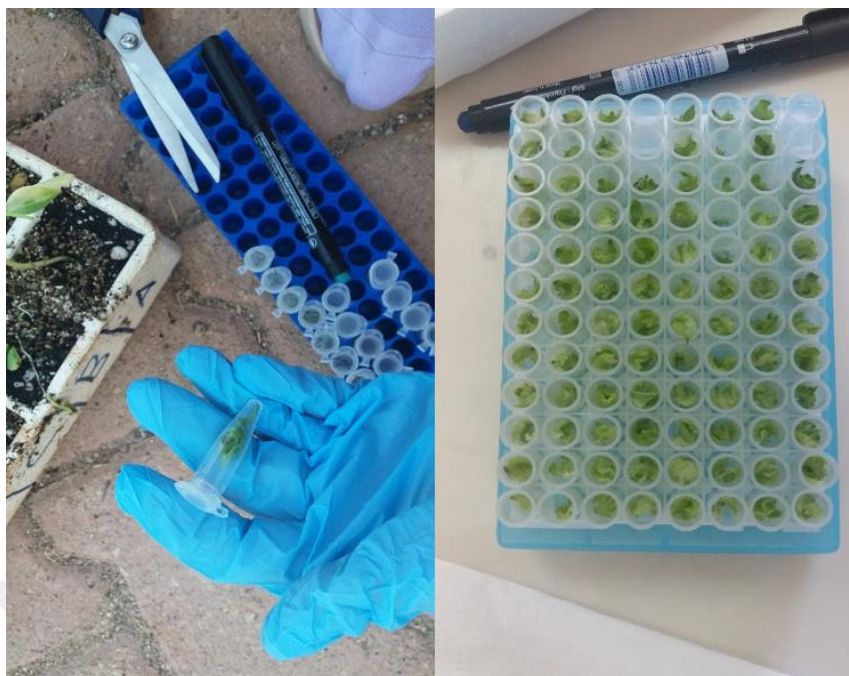


Figure 3.14. Taking plant samples in a tube and 96 well plates

To extract the necessary compounds, stainless steel beads (3 gr) were placed within the plates containing the leaves to grind them effectively.

A solution of 150 μ l of CTAB was added to the mixture and subjected to homogenize on the TissueLyser at 30 Hz for 1 min or grinded mechanically with hands using micro pestle.

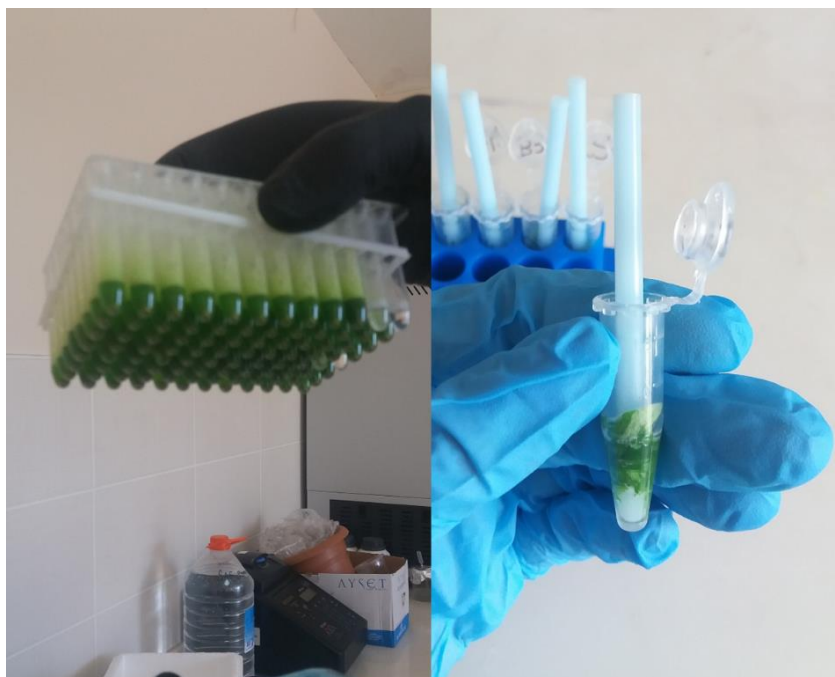


Figure 3.15. Grinded leaves with TissueLyser and mechanically with micro pestle

After a brief centrifugation of 40 sec at 4000 rpm, an additional 300 μ l of CTAB was added. The CTAB and plant extract mixed then incubated in a water bath at 65°C for 45 min.

450 μ l Chloroform : Isoamyl Alcohol (24:1) was added to the each sample, vortexed until the mixture becomes homogeneous and another round of centrifugation at 4000 rpm for 40 sec was carried out.

Following the centrifugation process, supernatant (the upper phase) 150 μ l was delicately transferred to new tubes 1.5 mL tubes.

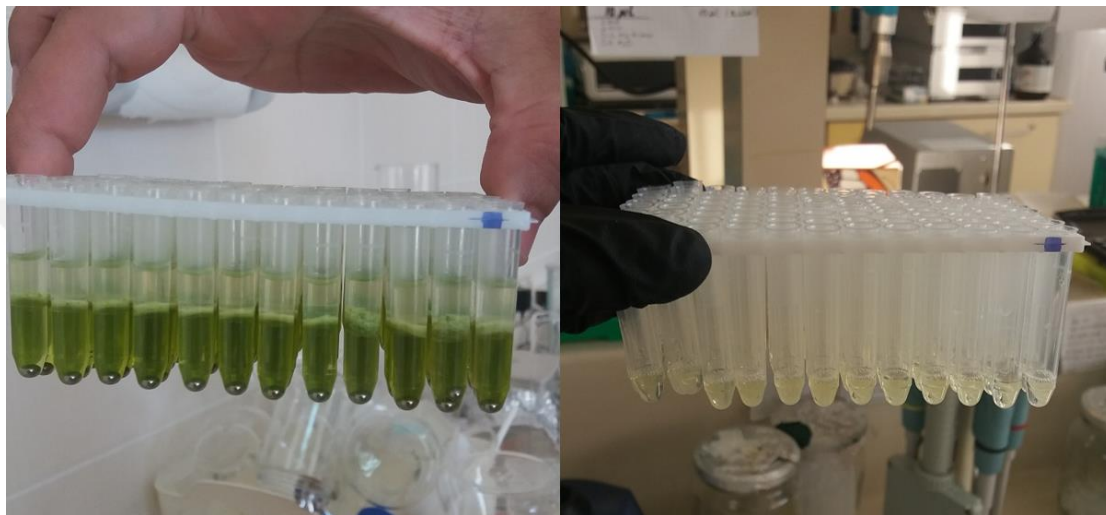


Figure 3.16. Steps after adding a Chloroform:Isoamyl Alcohol where two phases are evident and the supernatant is transferred to new tubes

Added 150 μ l of ice-cold Isopropanol to each sample, left in -20°C overnight.



Figure 3.17. After adding ice-cold Isopropanol

The next day, samples were centrifuged at 4°C for 20 min.

To refine the extract, isopropanol was poured, and an aliquot of 150 ml of 70% ethanol was added, followed by another centrifugation at 4°C for 15 min.

Post this step, the ethanol was removed and pellets dried at room-temperature than added 100 µl of distilled water, left to settle overnight on the bench, and eventually stored at -20°C for subsequent usage.



Figure 3.18. View of obtained DNA

DNA quality determination

To determinate a DNA yield and purity was used BioDrop (Anonymous 9). The ratio of the absorbance at 260 nm divided by the value at 280 nm is the most often used purity calculation. The ratio of A260 to A280 in high-quality DNA is between 1.7 and 2.0. Although a ratio of 1.6 does not mean that the DNA cannot be used for any purpose, lower ratios suggest that there are more contaminants present (Anonymous 10).

3.2.3.2. SRAP, PCR set-up

SRAP Primer Information

Table 3.3. shows the SRAP primers, important for genetic analysis, including forward (Me1 to Me13) and reverse (Em1 to Em16) primers, integral to the Polymerase Chain Reaction (PCR) process used in this research (Li 2001).

Table 3.3. Used SRAP primers

Primer	Forward (5' - 3')	Primer	Reverse (3' - 5')
Me1	TGAGTCCAAACCGGATA	Em1	GACTGCGTACGAATTAAT
Me2	TGAGTCCAAACCGGAGC	Em2	GACTGCGTACGAATTTGC
Me3	TGAGTCCAAACCGGAAT	Em3	GACTGCGTACGAATTGAC
Me4	TGAGTCCAAACCGGACC	Em4	GACTGCGTACGAATTTGA
Me5	TGAGTCCAAACCGGAAG	Em5	GACTGCGTACGAATTAAC
Me6	TGAGTCCAAACCGGACA	Em6	GACTGCGTACGAATTGCA
Me7	TGAGTCCAAACCGGACG	Em7	GACTGCGTACGAATTCAA
Me8	TGAGTCCAAACCGGACT	Em8	GACTGCGTACGAATTCAC
Me9	TGAGTCCAAACCGGAGG	Em9	GACTGCGTACGAATTCAG
Me10	TGAGTCCAAACCGGAAA	Em10	GACTGCGTACGAATTCAT
Me11	TGAGTCCAAACCG GAAC	Em11	GACTGCGTACGAATTCTA
Me12	TGAGTCCAAACCGGAGA	Em12	GACTGCGTACGAATTCTC
Me13	TGAGTCCAAACCGGAAG	Em13	GACTGCGTACGAATTCTG
		Em14	GACTGCGTACGAATTCTT
		Em15	GACTGCGTACGAATTGAT
		Em16	GACTGCGTACGAATTGTC

Table 3.4. PCR set up information

Reagent	Concentration of stocks	1x Reaction (μl)
Milli-Q-water		7.8
Green GoTaq Reaction Buffer	5x	1.5
MgCl ₂	25 mM	1.5
dNTPs	10 mM	1
Primer F	10 μM	1
Primer R	10 μM	1
GoTaq G2 DNA Polymerase	5 U/μl	0.2
Total Volume		14.0
Add template		1.0
Reaction Volume		15.0

Table 3.4, 3.5. outlines the PCR program, specifying the temperature and time conditions for each step. For each polymerase chain reaction (PCR), a 15 μL reaction mixture was prepared, comprising 1X PCR buffer, 1.5 mM Mg²⁺, 1 mM dNTPs, 2 μM forward and reverse primers, 1U Taq DNA polymerase, and 30 ng of DNA. The PCR reactions were conducted using the Biorad T100 Thermal Cycler. The PCR profile commenced with an initial denaturation at 94 °C for 2 minutes. Subsequently, 5 cycles, each consisting of denaturation at 94 °C for 1 minute, annealing at 35 °C for 1 minute, and elongation at 72 °C for 1 minutes, were carried out. This was succeeded by 35 cycles, wherein the annealing temperature was increased to 50°C, with a final elongation step of 1 minutes at 72 °C.

Table 3.5. PCR program information for SRAP primers

Step	Temperature	Time
1	94 °C	2:00 min
2	94 °C	1:00 min
3	35 °C	1:00 min
4	72 °C	1:00 min
5	Go to 2, 5x	
6	94 °C	1:00 min
7	50 °C	1:00 min
8	72 °C	1:00 min
9	Go to 6	35X
10	4 °C	forever

Table 3.6. details the equipment and materials used in the PCR process, including the PCR machines, agarose gel composition, ladders, and electrophoresis conditions.

The resulting PCR products were ran in electrophoresis on a 2% agarose gel in 0.5X TBE buffer, stained with ethidium bromide. Gel analysis was conducted under UV light using the gel imaging system, allowing for the observation and recording of distinct bands. This SRAP-PCR procedure facilitated the examination of genetic markers and polymorphisms in the DNA samples (for details Table 3.6.).

Table 3.6. Equipments and materials for PCR

Equipment	Details
PCR machine	Biograd T100 Thermal Cycler
Agarose gel	2 % agarose with 0.5x TBE Buffer + 4 ul Ethidium Bromide
Ladders	3 µl of GeneRuler 100bp (Hibrogen)
PCR product	15.0 µl
Electrophoresis	100V 2-4 hours

3.2.3.3. Genotyping for Fusarium resistance

DNA extraction was performed using the CTAB method as described previously. Following extraction, the DNA concentrations were adjusted to a final concentration of 10 ng/mL using MTE Buffer (10 mM Tris-HCl, pH 8.0; 1 mM EDTA) for PCR amplification.

For genotyping, a cleaved amplified polymorphic sequence (CAPS) marker linked to the Fom-1 gene, as reported by Oumouloud et al. (2015), and a sequence characterized amplified region (SCAR) marker linked to the Fom-2 gene, as reported by Oumouloud et al. (2012), were employed. These markers, whose utility and robustness have been previously validated (Chikh-Rouhou et al 2018; Meighan et al 2020), were selected based on their ability to distinguish between resistant and susceptible alleles. The utilization of these functional markers facilitated accurate identification of the genotypes tested, enabling differentiation between resistant and susceptible alleles, thereby enhancing the efficiency and reliability of the genotyping process.

Table 3.7. Primer sequences used for the genomic DNA amplification

Marker name	Primer sequences
Fom-1568F	5'-ATGAGTTTTGATAGTTTCATAAG-3'
Fom-1568R	5'-GAACACTCCCTTAGATACTT-3'
Fom2 - R408	5'-GAGAAATTTGCAATGGGTGG-3' 5'-TTACACTATTATTGCTCAACTTGC-3'

In the Table 3.8 given the PCR program information for amplifying the Fom-1 and Fom-2 markers. For Fom-1, the program involved an initial denaturation step at 94°C for 3 minutes, followed by 34 cycles of denaturation at 94°C for 45 seconds, annealing at 55°C for 45 seconds, and extension at 72°C for 45 seconds, with a final extension at 72°C for 5 minutes. Similarly, for Fom-2, the program included an initial denaturation at 94°C for 2 minutes, followed by 29 cycles of denaturation at 94°C for 45 seconds, annealing at 59°C for 1 minute, and extension at 72°C for 2 minutes, with a final extension at 72°C for 5 minutes.

Table 3.8. PCR program information for Fom-1 primers

Step	Temperature	Time
1	94 °C	3:00 min
2	94 °C	0:45 min
3	55 °C	0:45 min
4	72 °C	0:45 min
5	Go to 2	34X
6	72 °C	5:00 min
7	4 °C	forever

Table 3.9. PCR program information for Fom-2 primers

Step	Temperature	Time
1	94 °C	2:00 min
2	94 °C	0:45 min
3	59 °C	1:00 min
4	72 °C	2:00 min
5	Go to 2	29X
6	72 °C	5:00 min
7	4 °C	forever

3.2.6. Anthracnose and powdery mildew observations

A field evaluation of anthracnose and powdery mildew susceptibility was conducted on 30 Kyrgyz melon accessions, 15 Uzbek accessions, and a single wild type accession. Disease severity was scored on a 0-to-5 scale, with 0 indicating no visible disease symptoms and 5 representing the most severe infection. This assessment in an open-field setting aimed to provide insights into the natural resistance levels of these melon germplasm resources against these prevalent fungal diseases.

3.2.7. Statistical analysis

3.2.7.1. Qualitative and quantitative data analysis

To distinguish the correlation between morphological characteristics used a Pearson's correlation coefficient, PCA and UPGMA cluster analysis based on morphological characteristics were all completed using Minitab and Past 4.3. software.

3.2.7.2. Molecular data analysis

Data Scoring: Amplified products of SRAP markers were scored as 1/0 (1 = presence of band, 0 = absence of band).

Polymorphism Information Content (PIC) was calculated based on the scored data. Primer Index and Resolving Power (Rp) Calculation. Multiplex Ratio (MR), Effective Multiplex Ratio (EMR), and Marker Index (MI) Calculation. Principle Coordinate Analysis (PCoA) and Analysis of Molecular Variance (AMOVA) performed using GenAlEx V6.5.

Genetic similarity between genotypes was calculated using on Jaccard's similarity (J) coefficient by DendroUPGMA program (Garcia et al 1999) and unweighted pair group method average (UPGMA) dendrogram was constructed using SAHN clustering algorithm of NTSYSpc, performed by Phylogeny/evolution category from EXPASY Tools (Duvaud et al 2021) and ITOL online tool for the display and annotation of phylogenetic tree (Letunic and Bork 2021).

Principal Coordinate Analysis (PcoA) was performed using Past 4.3. software.

The STRUCTURE software 2.3.4 by Pritchard, Stephens and Donnelly (2000) and Falush, Stephens and Pritchard (2003), Code by Pritchard, Falush and Hubisz, Version 2.3.4 (Jul 2012) was run at desired K values (5000 burn-in periods, 50,000 MCMC replicates; ancestry model: admixture model, Allele frequency correlated, K = 1 to 10, Iterations = 10). Calculating ΔK (Delta K) involves using the rate of change in the log likelihood of the data between successive K values in a STRUCTURE analysis to infer the optimal number of populations (K). For calculating and evaluation of K was used Structure selector (Li and Liu 2018).

4. RESULTS AND DISCUSSION

4.1. Seeds

In the Table 4.1. described different characteristics related to melon seeds, including size, width, shape, and color. Seed size is classified into five categories based on length, ranging from very small (<5 mm), small (5-8 mm), medium (9-12 mm), large (13-16 mm) to very large (>16 mm).

The width of the seeds is categorized as small (<2.1), medium (2.1-2.5), and large (>2.5). Seed color is divided into two categories: whitish and cream yellow. In Table 2 shown detailed information about seed's length, width, shape and color.

Seed shape (Fig.1) showed in two variations: not pine-nut shape (1) and pine-nut shape(2).

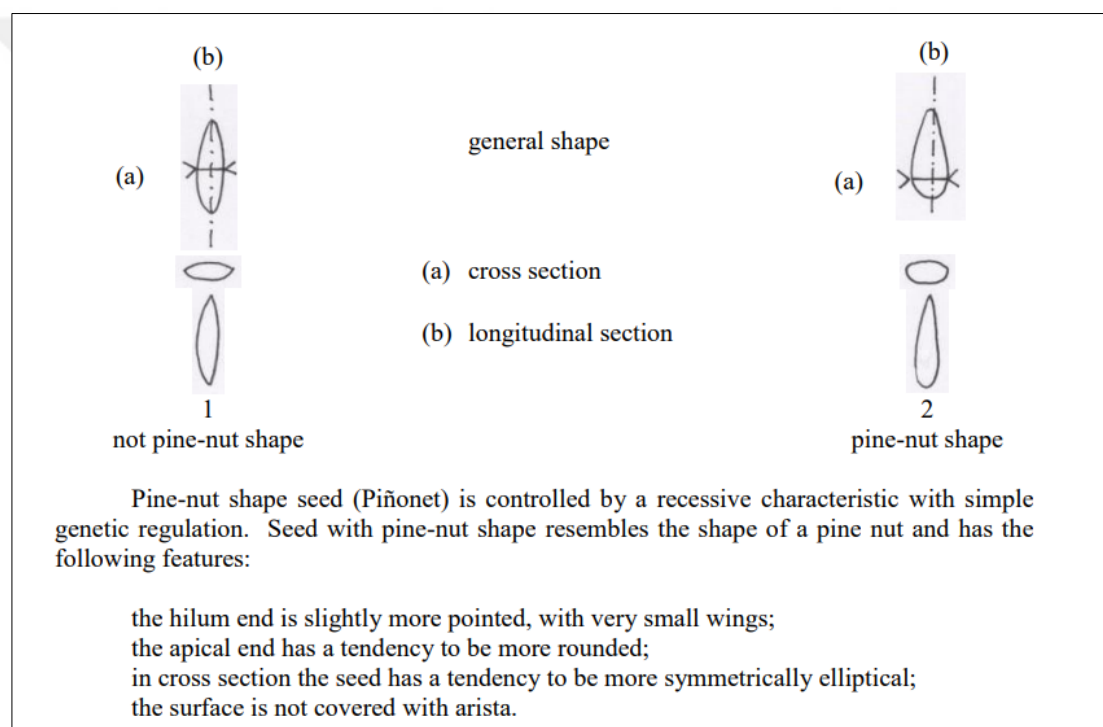


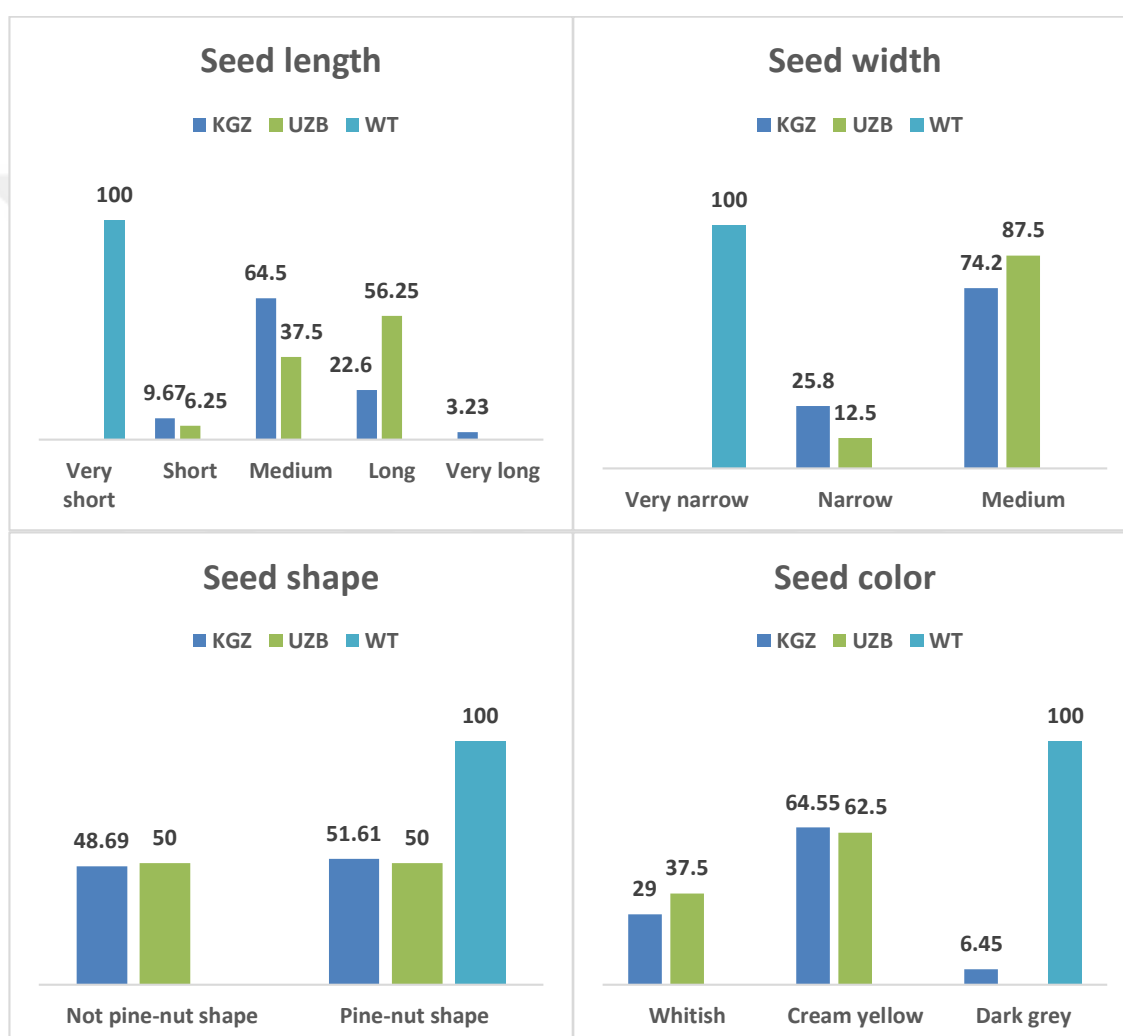
Figure 4.1. Seed shape types (Anonymous 3)

Table 4.1. Length, width, shape and color of seeds of Kyrgyz, Uzbek and wild type genotypes

№	Genotype	Seed: length	Seed: width	Seed: shape	Seed: color
Kyrgyz genotypes					
1	KGZ-1	5	3	1	2
2	KGZ-2	4	3	2	2
3	KGZ-3	3	3	2	2
4	KGZ-4	3	3	2	2
5	KGZ-5	3	3	2	1
6	KGZ-6	3	3	2	1
7	KGZ-7	3	3	2	2
8	KGZ-8	3	3	2	1
9	KGZ-9	3	3	1	2
10	KGZ-10	2	2	1	2
11	KGZ-11	3	3	1	2
12	KGZ-12	4	3	1	2
13	KGZ-13	2	2	1	2
14	KGZ-14	3	3	2	3
15	KGZ-15	3	3	2	3
16	KGZ-16	4	3	1	2
17	KGZ-17	4	3	1	2
18	KGZ-18	4	3	1	2
19	KGZ-19	3	2	1	1
20	KGZ-20	3	3	1	2
21	KGZ-21	4	2	1	2
22	KGZ-22	3	3	2	1
23	KGZ-23	3	2	1	2
24	KGZ-24	3	2	2	1
25	KGZ-25	3	2	2	2
26	KGZ-26	3	3	2	1
27	KGZ-27	2	2	2	1
28	KGZ-28	3	3	1	2
29	KGZ-29	4	3	2	1
30	KGZ-30	3	3	2	2
31	KGZ-31	3	3	1	2
Uzbek genotypes					
32	UZB-1	4	3	1	2
33	UZB-2	3	3	2	2
34	UZB-3	3	2	1	2
35	UZB-4	4	3	2	1
36	UZB-5	2	2	2	1
37	UZB-6	4	3	1	2
38	UZB-7	4	3	1	2
39	UZB-8	4	3	1	2
40	UZB-9	4	3	1	1
41	UZB-10	3	3	2	1

Table 4.1. Continued

41	UZB-10	3	3	2	1
42	UZB-11	3	3	1	2
43	UZB-12	3	3	2	1
44	UZB-13	4	3	2	1
45	UZB-14	4	3	1	2
46	UZB-15	3	3	2	2
47	UZB-16	4	3	2	2
48	WT-1	1	1	2	3

**Figure 4.2.** Seed length, width, shape, color evaluation results

The provided data on seed length, width, shape and color (Figure 4.2.) reveals interesting patterns in seed size distribution among the genotypes: KGZ (Kyrgyz), UZB (Uzbek), and WT (Wild Type). The seed size analysis reveals variations among genotypes. KGZ primarily has medium (64.5%) and long (22.6%) seeds, with shorter and very long seeds being less frequent. UZB exhibits a wider distribution with a majority of long seeds (56.25%) followed by medium (37.5%) and a smaller portion of short seeds

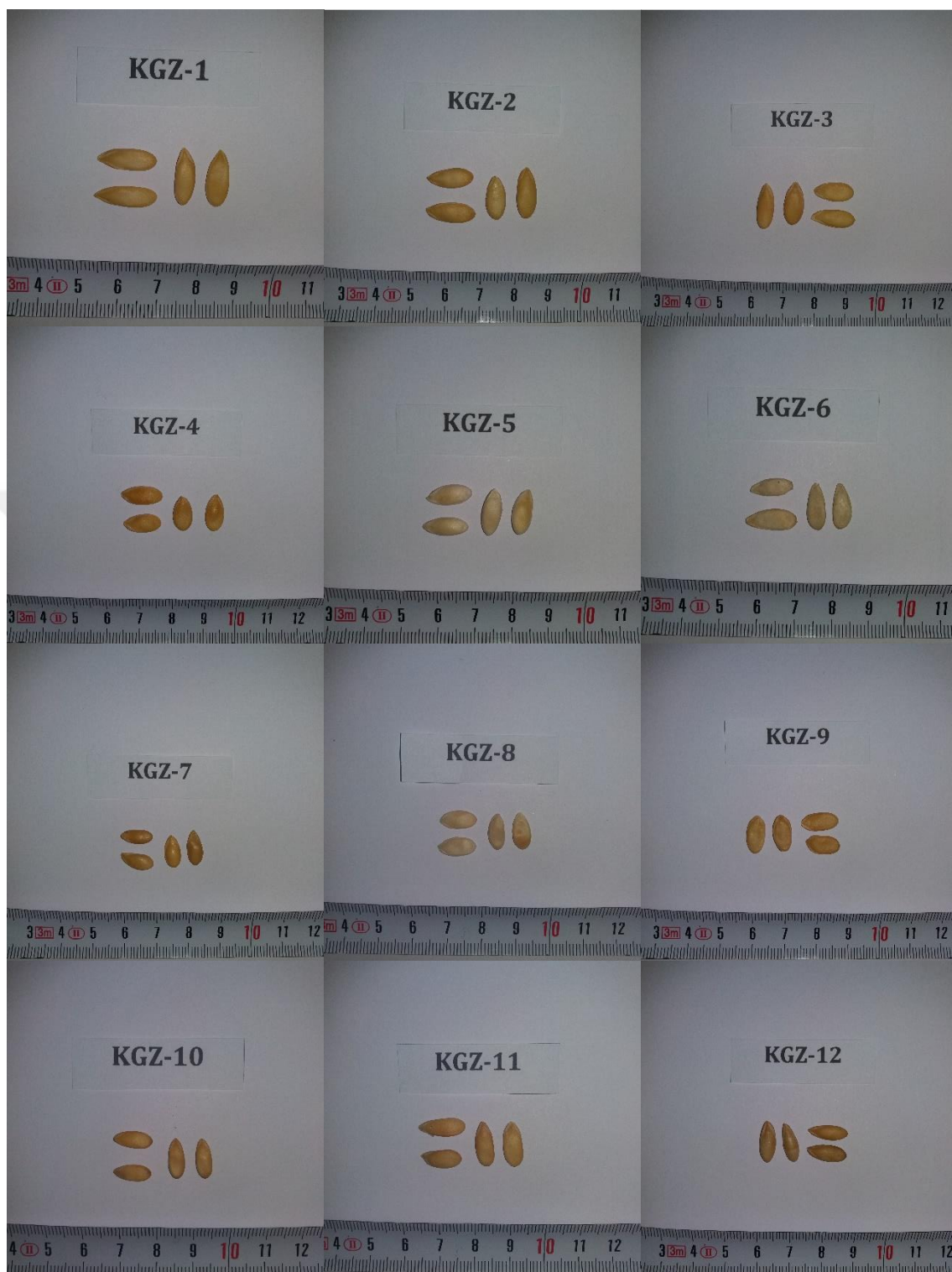
(6.25%). The wild type displays a unique pattern with all seeds categorized as very short, suggesting a distinct genetic influence on seed size regulation within this group.

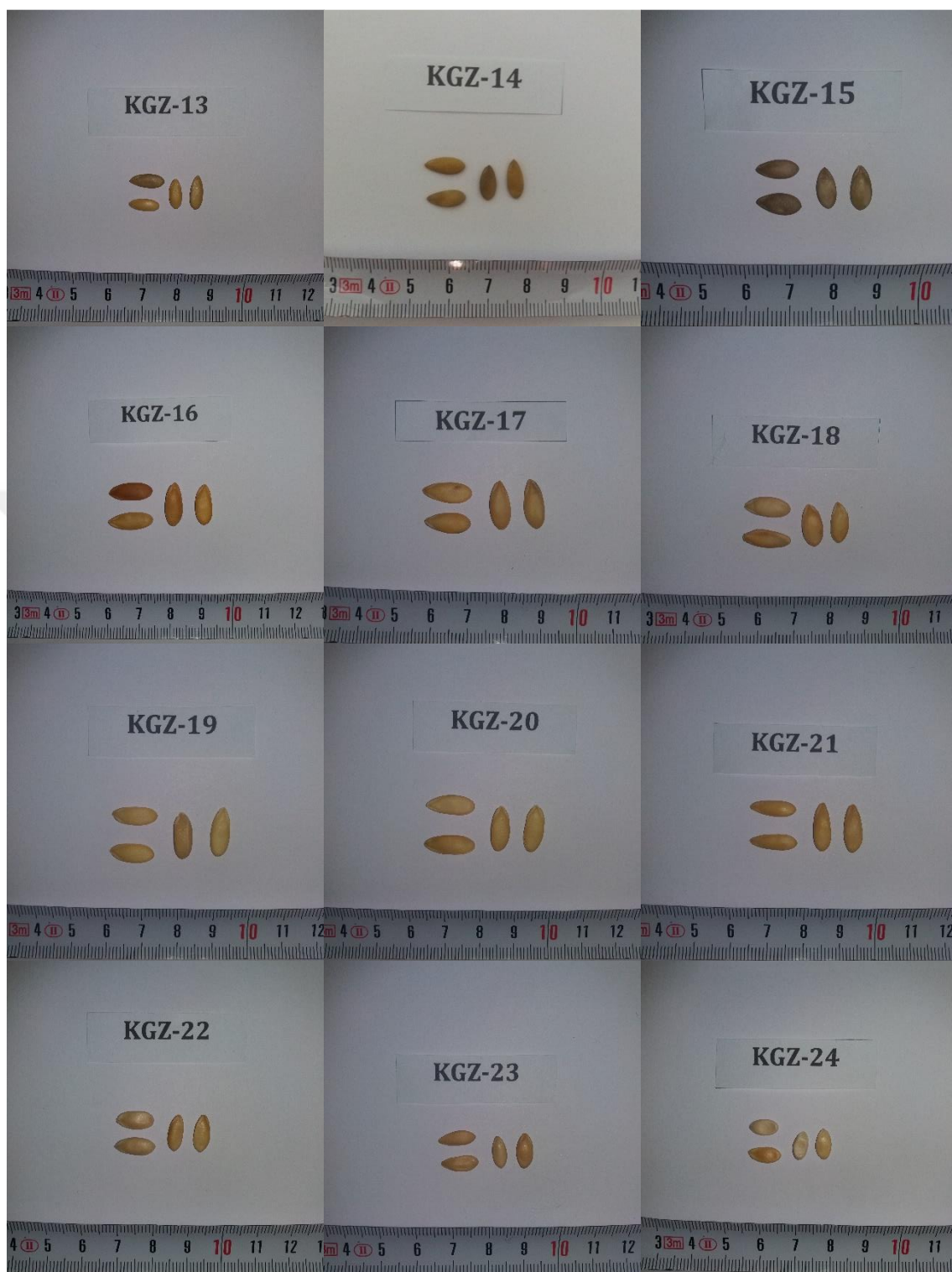
The investigation of seed width across genotypes revealed that the WT has very narrow seed width, while 74.2% of KGZ seeds fell within the "Medium" width category, with the remaining 25.8% classified as "Narrow." UZB melons displayed a wider range of seed widths, with 87.5% categorized as "Medium" and 12.5% classified as "Narrow."

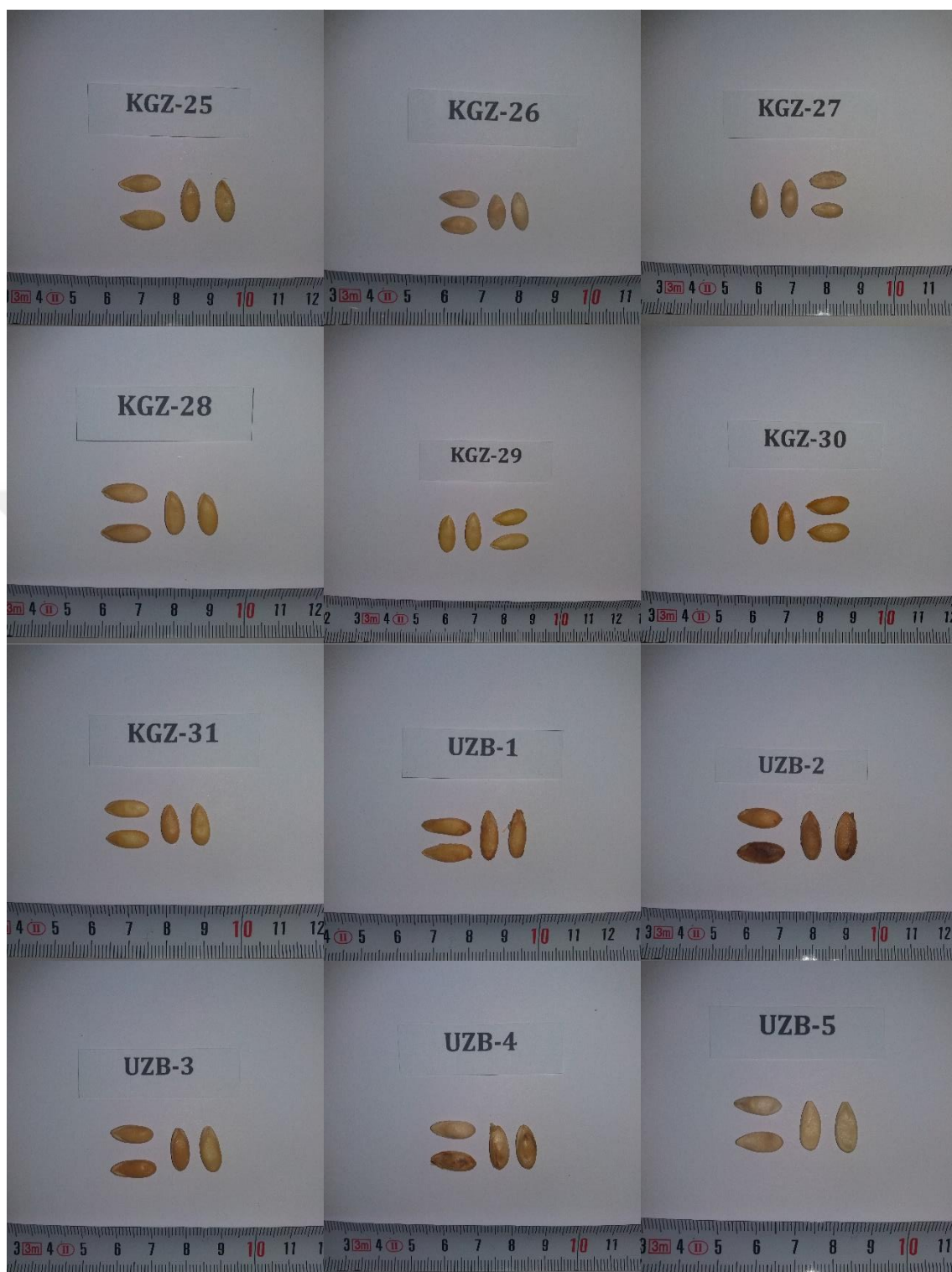
The analysis of seed shape distribution among genotypes reveals the following insights. Both KGZ and UZB genotypes exhibit a near-equal distribution between seeds categorized as "Not pine-nut shape" and "Pine-nut shape." In KGZ, approximately 48.69% of seeds are classified as "Not pine-nut shape," while 51.61% fall into the "Pine-nut shape" category. Similarly, in the UZB genotype, 50% of seeds are categorized as "Not pine-nut shape" and the remaining 50% exhibit a "Pine-nut shape". The WT showed "Pine-nut shape".

Can and Tütken (2022) also evaluated seed weight and length. Kyrgyz accessions continued to display dominance, with Kg-H and J-01 producing the heaviest seeds. Consistent with observations in other traits, YYÜ-30 consistently had the lowest seed weight. Seed length mirrored this trend, with Kg-H and Ç-07 accessions boasting the longest seeds, while the Manas-4 accession exhibited the shortest.

Aierken et al. (2011) explored the genetic diversity of Hami melon, a Chinese variety with four subtypes (cassaba, chandalak, ameri, and zard). The study compared the DNA of 120 melon samples, including 24 Hami melons. Interestingly, all Hami melons had large seeds, similar to melons grown in Spain and the US, while eastern China's Conomon melons were all small-seeded. Notably, melons from Central Asia displayed both seed sizes.







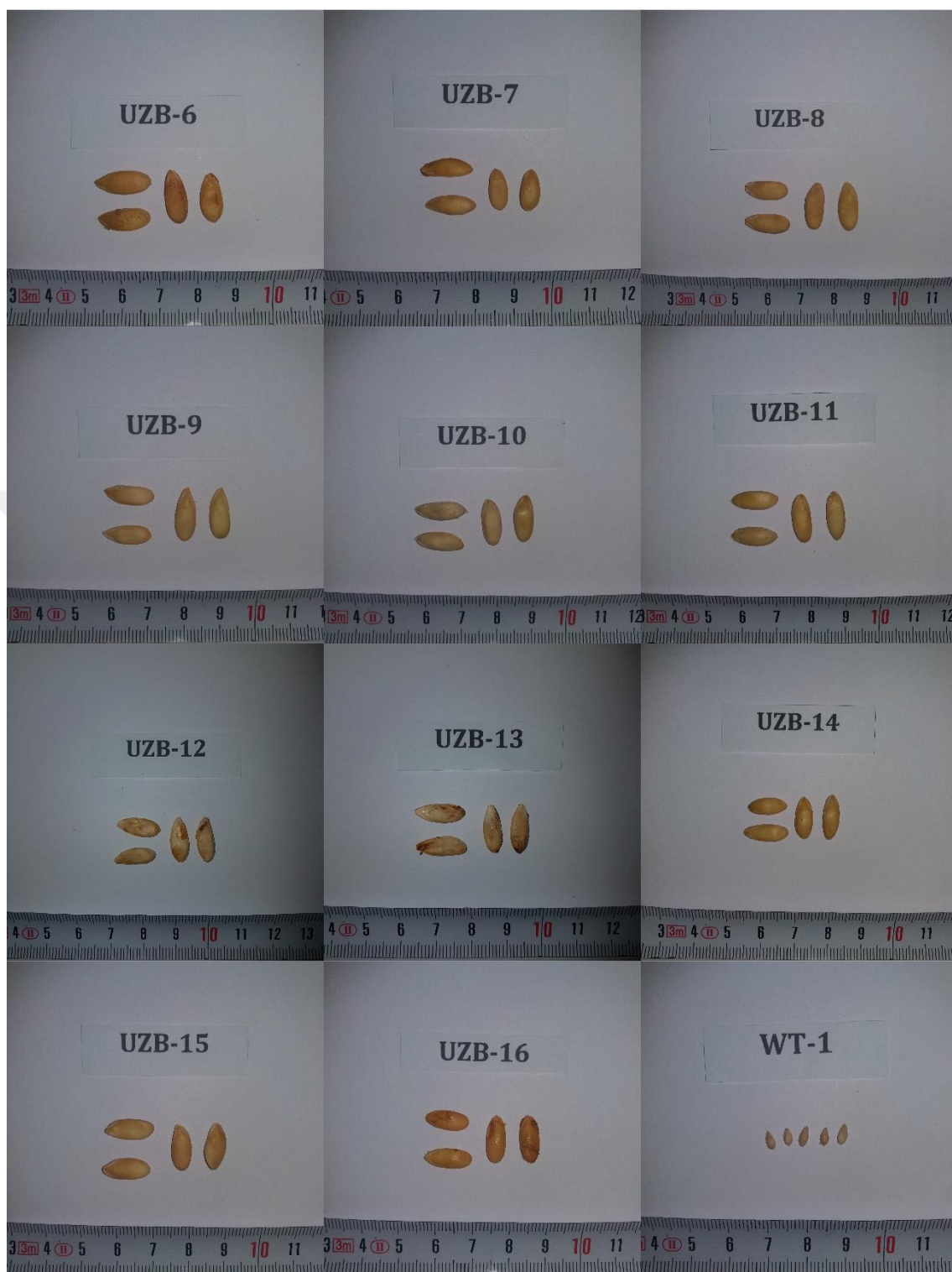


Figure 4.3. Diversity of seeds analyzed in research; KGZ 1 – 31 is Kyrgyz genotypes, UZB 1 – 16 Uzbek genotypes, and wild type showed as WT – 1

4.2. Morphological analysis

4.2.1. Leaf

The study investigated the leaf characteristics of 48 genotypes, encompassing diverse geographic origins. The majority originated from Kyrgyzstan (31 genotypes), followed by Uzbekistan (16 genotypes). Additionally, a single wild variety from Turkey was included for comparative purposes, allowing researchers to assess potential variations across a broader geographical range. This diverse collection of genotypes provided valuable insights into the morphological diversity of these plants across their natural habitats.

4.2.1.1. Leaf characteristic results in greenhouse conditions

The examination of morphological traits among KGZ, UZB, and WT genotypes (Table 4.2) revealed distinct patterns across various characteristics.

Leaf length, KGZ genotypes exhibit a range of leaf lengths from 21.5 to 36 cm, with KGZ-11 displaying the longest leaf and KGZ-12 and KGZ-13 the shortest. UZB genotypes also show variability in leaf lengths, ranging from 24 to 31 cm, with UZB-4 having the longest leaf and UZB-5 the shortest. The wild type (WT-1) has the shortest leaf length among all groups, measuring only 19 cm.

KGZ genotypes exhibit varying lengths from the end of the petiole till the apex, ranging from 11.5 to 16 cm, with KGZ-6 displaying the longest and KGZ-17 the shortest. UZB genotypes show similar variations in this trait, with lengths ranging from 10 to 13 cm. WT-1 displays the shortest length in this trait among all groups, measuring only 6 cm.

Leaf widths among KGZ genotypes range from 21 to 38 cm, with KGZ-6 having the widest leaf and KGZ-21 the narrowest. UZB genotypes demonstrate leaf widths ranging from 26.5 to 31 cm, with UZB-7 exhibiting the widest leaf and UZB-3 the narrowest. The wild type (WT-1) displays the narrowest leaf width among all groups, measuring only 14 cm.

Petiole lengths range from 17 to 32.5 cm among KGZ genotypes, with KGZ-9 having the longest petiole and KGZ-4 the shortest. UZB genotypes exhibit petiole lengths ranging from 22 to 38.5 cm, with UZB-8 displaying the longest petiole and UZB-3 the shortest. The wild type (WT-1) shows the shortest petiole length among all groups, measuring only 13 cm.

KGZ genotypes demonstrate variations in the distance between two nodes, ranging from 9.5 to 16 cm. UZB genotypes show similar variations in this trait, with distances ranging from 10 to 16 cm. WT-1 exhibits the shortest distance between nodes among all groups, measuring only 6 cm.

Stem thickness varies from 7.1 to 12.48 mm among KGZ genotypes, with KGZ-12 and KGZ-13 having the thinnest stems and KGZ-1 the thickest. UZB genotypes demonstrate stem thickness ranging from 8.28 to 13.43 mm, with UZB-10 having the

thinnest stem and UZB-7 the thickest. The wild type (WT-1) displays the thinnest stem among all groups, measuring only 5 mm.

Between groups KGZ and UZB genotypes generally exhibit overlapping ranges in most traits, indicating similarities in morphological characteristics.

The wild type (WT-1) consistently demonstrates distinctively different morphological features compared to both KGZ and UZB genotypes, particularly in leaf length, leaf width, and petiole length.

Table 4.2. Leaf characteristics of Kyrgyz and Uzbek genotypes in greenhouse conditions

№	Genotype	Leaf length (cm)	Leaf length from the end of petiole till apix (cm)	Leaf width (cm)	Petiole length (cm)	Distance between 2 nodes (cm)	Stem thickness (mm)
1	KGZ-1	29	23	34	26.5	13	11.38
2	KGZ-2	35	22	33	32	11	11.32
3	KGZ-3	28	20	33.5	25	11.3	11.68
4	KGZ-4	26	19.5	27	19	10	12.48
5	KGZ-5	22.5	22	33.5	26	11	10.3
6	KGZ-6	28.5	36	38	28	11.5	10.42
7	KGZ-7	23	18.5	23	21.5	9.5	7.31
8	KGZ-8	32	25.5	32	30	14.5	11.01
9	KGZ-9	35	27.5	35.5	31.5	12.5	10.34
10	KGZ-10	33	24	28.5	26	11	10.15
11	KGZ-11	36	24	35	22	16	11.48
12	KGZ-12	21.5	16	21	17	9.5	7.61
13	KGZ-13	21.5	16	21	17	9.5	7.61
14	KGZ-14	27	22.5	26	31.5	11.5	8.91
15	KGZ-15	29	23	27	26	12	9.75
16	KGZ-16	29	23	28	31	13	9.93
17	KGZ-17	31	16.5	32.5	31	11.5	11.14
18	KGZ-18	31	22	25.5	29	10	9.6
19	KGZ-19	30	23	31	28	14.5	10.55
20	KGZ-20	29	21.5	29.5	32.5	14	11.85
21	KGZ-21	26	21	25	31	13	8.52
22	KGZ-22	26	21	25	31	13	8.52
23	KGZ-23	25.5	18.5	27	22.5	11	9.18
24	KGZ-24	25.5	18.5	27	22.5	11	9.18
25	KGZ-25	27	19.5	27	28.5	13.5	10.8
26	KGZ-26	14.5	11.5	13.5	10	9.5	7.1
27	KGZ-27	14.5	11.5	13.5	10	9.5	7.1
28	KGZ-28	30	21.5	31	24.5	10.5	11.3
29	KGZ-29	27	22	29.5	29.5	11	10.3
30	KGZ-30	28	18.5	27	29.5	13	10.64
31	KGZ-31	29	19	27	23	12.5	8.35

Table 4.2. Continued

31	UZH-1	29	22	28	33	12	11.33
33	UZH-2	29	22	28	33	12	11.33
34	UZH-3	27.5	20.5	26.5	24.5	10	10.56
35	UZH-4	30.5	22.5	31	28.5	16	11.3
36	UZH-5	24	19	28	28	13	9.97
37	UZH-6	29	20.5	27	22	11	10.16
38	UZH-7	30	20	31	34	12	13.43
39	UZH-8	29	21	30.5	38.5	12	10.51
40	UZH-9	28	20.5	28	34	12	10.89
41	UZH-10	26	25	28	30	10	8.28
42	UZH-11	32	24.5	31	27	13	9.75
43	UZH-12	27	23	29	28.5	11.5	9.13
44	UZH-13	28	22	27	27	13	8.62
45	UZH-14	30	23	27	28	13	10.62
46	UZH-15	30	19	30.5	29	10.5	9.35
47	UZH-16	31	22	31	24	11	11.09
48	WT-1	19	15	14	13	6	5

4.2.1.2. Leaf characteristic results in open field conditions

In examining leaf length among the different genotypes of leaf samples from the open field group (Table 4.3), KGZ-20 stood out group with the longest leaves at 22 cm. On the other hand, KGZ-32 displayed the shortest leaf length at 11. Within the UZH group, UZH-14 exhibited the highest leaf length (19.5 cm), whereas UZH-12 had the lowest (13.5 cm). The WT group, represented by WT-1, consistently featured shorter leaf lengths compared to both KGZ and UZH genotypes, with WT-1 recording the smallest leaf length at 14 cm.

KGZ-6 emerged as the leader in leaf width among KGZ genotypes in the open field, boasting the widest leaves at 38 cm. In the UZH group, UZH-10 showcased the broadest leaves (19 cm), while UZH-9 had the narrowest (16 cm). The WT group, as represented by WT-1, consistently demonstrated smaller leaf widths across all genotypes, with a leaf width of 16 cm.

For petiole length, KGZ-24 held the top position within KGZ genotypes in the open field, featuring the longest petioles at 17.5 cm. In the UZH group, UZH-8 displayed the lengthiest petioles (16.5 cm), while UZH-9 exhibited the shortest at 13 cm. The WT group, represented by WT-1, consistently presented shorter petiole lengths across all genotypes, with a minimum of 10 cm.

Analyzing the distance between nodes revealed variations among genotypes. KGZ-11 exhibited the widest gap (16 cm) among KGZ genotypes in the open field, while KGZ-18 had the narrowest (6.5 cm). UZH-16 showcased the largest gap (10.8 cm) within the UZH group, and UZH-7 featured the smallest gap (7 cm). The WT group, represented by WT-1, consistently demonstrated smaller gaps between nodes compared to KGZ and UZH genotypes.

Regarding stem thickness, KGZ-10 and KGZ-27 led the KGZ genotypes in the open field, featuring the thickest stems at 12.48 mm. UZB-4 displayed the thickest stems (10.3 mm) within the UZB group, while UZB-9 had the thinnest at 4.95 mm. The WT group, represented by WT-1, consistently showcased thinner stems compared to both KGZ and UZB genotypes, with a minimum thickness of 3.9 mm.

Table 4.3. Morphological characteristics of Kyrgyz, Uzbek and wild type genotypes in open field conditions

№	Genotype	Leaf length (cm)	Leaf length from the end of petiole till apix (cm)	Leaf width (cm)	Petiole length (cm)	Distance between 2 nodes (cm)	Stem thickness (mm)
1	KGZ-1	20	15	20.5	26	12	9
2	KGZ-2	20.5	14.5	21.2	18.5	10	8
3	KGZ-3	14	14	21	31	8	8
4	KGZ-4	17	13	16.5	21	9	10
5	KGZ-5	21.5	17.5	23	27	9	8.56
6	KGZ-6	14	10	14	27	13	8.31
7	KGZ-7	18	15	19	23	7	5.68
8	KGZ-8	17.5	15	18.5	31	8.5	9.62
9	KGZ-9	21	16	22	30	10	8.71
10	KGZ-10	18	13	16.5	27	8	8.31
11	KGZ-11	18.5	14	18	22	6.5	8.69
12	KGZ-12	17	14	17.5	22.5	10.5	5.24
13	KGZ-13	17.4	13.2	18	22	13.5	8.91
14	KGZ-14	17	16	17.5	28	7	7.62
15	KGZ-16	22	18	23	30	7.5	9.01
16	KGZ-16	15	12	15	22	10	7.98
17	KGZ-17	15.5	13	18.5	17	6.5	9.79
18	KGZ-18	19	14.3	18	31	7.5	8.12
19	KGZ-19	20	15	21	22	6.5	9.38
20	KGZ-20	22	18	21	26	8.5	10.01
21	KGZ-21	17	13	16.5	22	8.5	8.31
22	KGZ-22	16.5	12	18.5	19	10	9.21
23	KGZ-23	18.5	15	18.5	20	6	9.11
24	KGZ-24	19	17.5	20	14	8.5	8.59
25	KGZ-25	16	13	19	26	14	9.85
26	KGZ-26	13.5	10.5	15	24	7.5	6.01
27	KGZ-27	15	12.5	17.5	24	8	8.98
28	KGZ-28	22	18	22	16.5	8	10.1
29	KGZ-29	17.5	13.5	17	19	11	10.13
30	KGZ-30	19	16	23	30	10	10.32
31	KGZ-31	19	15	24	26	9	8.24
32	UZB-1	11	8	11	14	9	4.5
33	UZB-2	18	13	21	18	11	8.2
34	UZB-3	19	15	22	19	14	9.1

Table 4.3. Continued

35	UZH-4	17	14.5	19	15	10	10.3
36	UZH-5	18	14	18	17	14	10
37	UZH-6	19	14	18.5	15.5	9	7.01
38	UZH-7	16	14	18	17	7	5.25
39	UZH-8	17	13	16.5	16	9	5.75
40	UZH-9	15	13	16	17	8	4.95
41	UZH-10	17.5	15.5	19	29	10	8.01
42	UZH-11	18.5	14	18	26	14	7.5
43	UZH-12	13.5	11.5	18	17	13	5.75
44	UZH-13	13.5	11.5	18	17	10.6	9.4
45	UZH-14	19.5	16.5	19.5	25	8	9.32
46	UZH-15	18	14.5	18	22	10.5	9.09
47	UZH-16	18	16	24	18	10.8	10.3
48	WT-1	14	11.5	16	10	5	3.9

4.2.1.3. Leaf characteristics result comparison between greenhouse and open field

When comparing the leaf lengths of genotypes between greenhouse and open field conditions, notable variations are observed. For instance, in the greenhouse, KGZ-1 exhibits a leaf length of 29 cm, whereas in the open field, this measurement reduces to 20 cm. A similar trend is seen in KGZ-2, KGZ-3, and other KGZ genotypes, suggesting a consistent impact of cultivation environments on leaf length. This pattern is also apparent in UZH and WT genotypes, emphasizing the influence of growing conditions on this particular trait.

Differences in leaf width become apparent when comparing greenhouse and open field results. KGZ-6, which boasts the widest leaves in the greenhouse at 38 cm, experiences a considerable reduction to 14 cm in the open field. UZH-10 follows a similar trend, displaying broader leaves in the greenhouse compared to the open field. This indicates a nuanced response of certain genotypes to varying cultivation environments, resulting in distinct leaf width outcomes.

Petiole length exhibits notable variations between greenhouse and open field conditions. For instance, KGZ-24 displays the longest petioles in the greenhouse at 22.5 cm, while in the open field, this measurement decreases to 14 cm. UZH-8 also experiences a significant reduction in petiole length when transitioning from the greenhouse to the open field. These findings underscore the substantial impact of environmental factors on the morphology of plant structures such as petioles.

Analyzing stem thickness discrepancies, KGZ-5 stands out with a substantial increase in stem thickness in the open field compared to the greenhouse. This trend is consistent across various genotypes, highlighting a potential correlation between cultivation conditions and stem thickness. Further investigation is warranted to unravel the underlying factors influencing these variations in plant characteristics between greenhouse and open field settings.

Comparing the leaf characteristics between genotypes within different growing conditions provides valuable insights into their morphological adaptations. In the greenhouse environment, KGZ genotypes demonstrate a mean leaf length of 27.42 cm, whereas UZB genotypes have slightly longer leaves with a mean of 28.74 cm. The wild type (WT) genotype exhibits shorter leaves in the greenhouse, measuring 19 cm on average.

When focusing on the length from the end of the petiole to the apex, KGZ and UZB genotypes show comparable values in both greenhouse and open field conditions, indicating consistent leaf elongation patterns. However, the wild type genotype tends to have shorter lengths in both environments, with means of 15 cm and 11.5 cm in the greenhouse and open field, respectively.

Moving on to leaf width, UZB genotypes consistently display wider leaves compared to KGZ genotypes in both greenhouse and open field conditions. In the greenhouse, UZB genotypes have a mean leaf width of 29.1 cm, while KGZ genotypes measure 27.97 cm. Similarly, in the open field, UZB genotypes have a mean width of 18.9 cm, whereas KGZ genotypes measure 19.1 cm. The wild type genotype consistently exhibits the narrowest leaves among all groups, with means of 14 cm and 16 cm in the greenhouse and open field, respectively.

Regarding petiole length, UZB genotypes have longer petioles compared to KGZ genotypes in both environments, with means of 29.4 cm and 25.6 cm in the greenhouse and 19.23 cm and 24.02 cm in the open field, respectively. The wild type genotype consistently shows the shortest petiole lengths among all groups, with means of 13 cm and 10 cm in the greenhouse and open field, respectively.

Stem thickness follows a similar trend, with UZB genotypes exhibiting thicker stems compared to KGZ genotypes in both environments. In the greenhouse, UZB genotypes have a mean stem thickness of 10.33 mm, while KGZ genotypes measure 9.86 mm. In the open field, UZB genotypes have a mean thickness of 8 mm, whereas KGZ genotypes measure 8.64 mm. The wild type genotype consistently displays the thinnest stems among all groups, with means of 5 mm and 3.9 mm in the greenhouse and open field, respectively.

Lastly, considering the distance between two nodes, UZB genotypes generally have a greater distance compared to KGZ genotypes in both environments. In the greenhouse, UZB genotypes have a mean distance of 12.03 cm, while KGZ genotypes measure 11.6 cm. In the open field, UZB genotypes have a mean distance of 10.59 cm, whereas KGZ genotypes measure 9 cm. The wild type genotype displays the shortest distances between nodes among all groups, with means of 6 cm and 5 cm in the greenhouse and open field, respectively. These detailed comparisons highlight distinct morphological differences between genotypes and the influence of growing conditions on their leaf characteristics.

Similarly, UZB genotypes display variations in leaf dimensions between greenhouse and open field conditions, indicating genotype-specific responses to varying environmental cues. Contrasting the genotypes across conditions reveals broader trends,

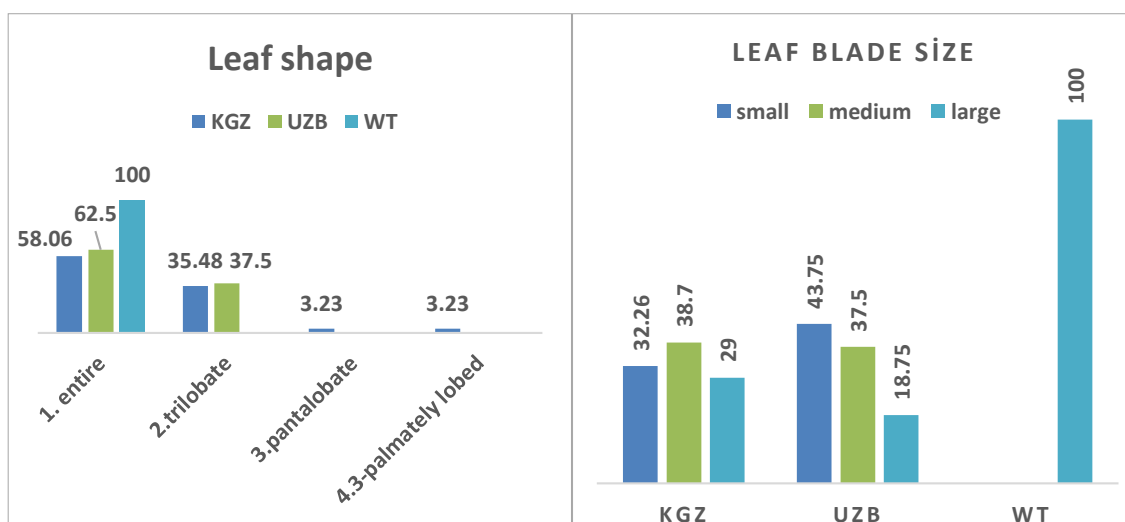
with UZB genotypes generally showing longer and wider leaves compared to KGZ genotypes, regardless of the cultivation environment.

Moreover, the wild type genotype exhibits unique leaf characteristics, such as shorter and narrower leaves and thinner stems, highlighting inherent genetic differences. Overall, the differences observed in leaf characteristics between genotypes and environments highlight the significant influence of both genetic factors and growing conditions. KGZ genotypes tend to display longer and wider leaves in greenhouse settings compared to UZB genotypes, while the wild type genotype exhibits distinctively different leaf traits, including shorter and narrower leaves and thinner stems. Environmental conditions, particularly in the greenhouse, play a crucial role in shaping leaf morphology, suggesting the importance of optimizing growing conditions for desired plant characteristics and overall productivity.

In reserach of Can (2020) showed significant variation among the genotypes for Leaf length, the longest leaf was observed in Ç-07 (16.27 cm), followed by YYÜ-13 (14.76 cm); the shortest leaves were found in Kav-3 (7.38 cm) and Kg-C (7.75 cm) and leaf width, the widest leaves belonged to YYÜ-13 (22.92 cm) and Ç-07 (20.1 cm). Kg-E (9.34 cm) and Kg-C (10.25 cm) had the narrowest leaves.



Figure 4.4. Different types of leaf samples



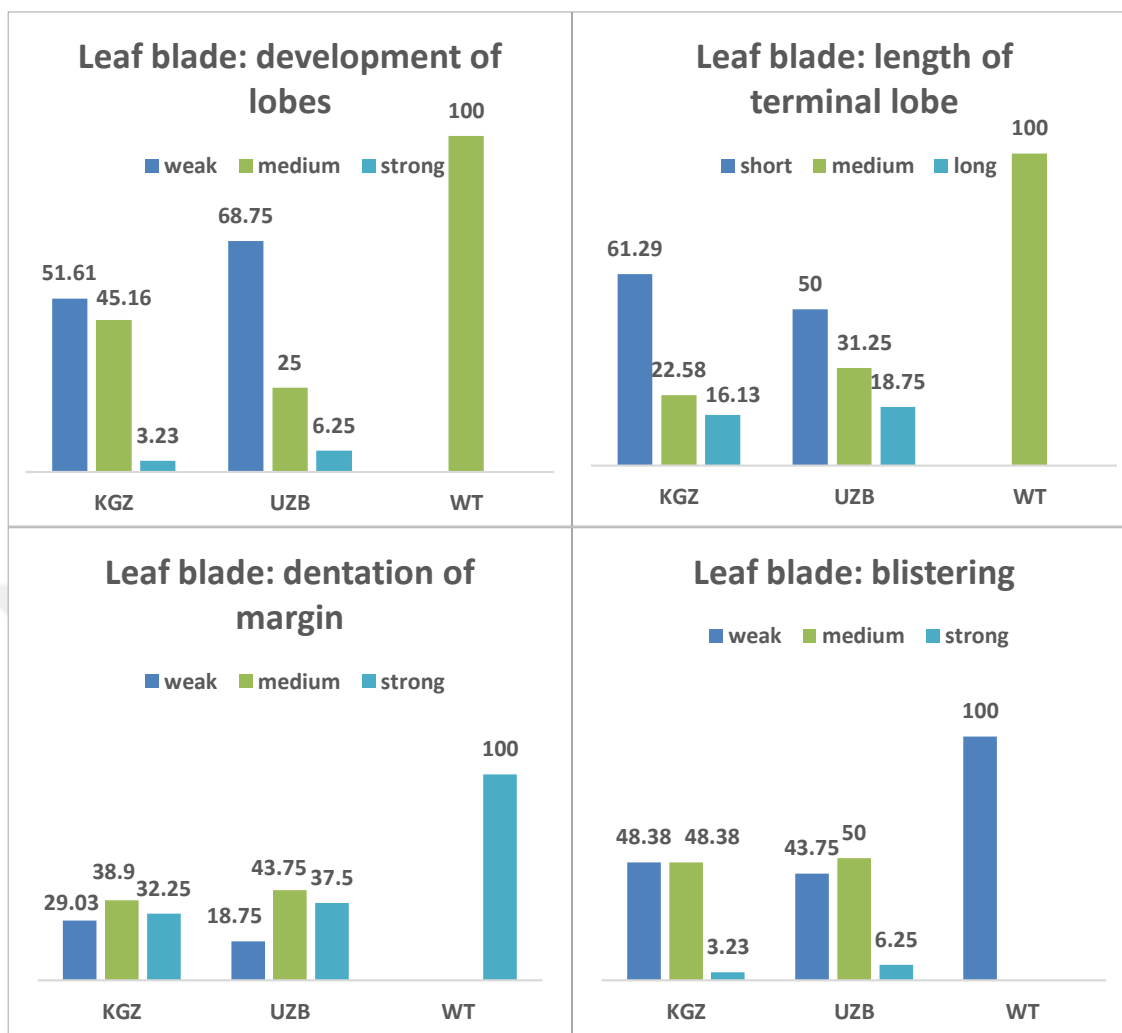


Figure 4.5. Leaf morphologic trait results of genotypes

KGZ and UZB melons mostly have entire leaf shape (around 60%). KGZ melons show slightly more variation, with some trilobate and even rarer, more lobed leaves. In contrast, wild type melons only have entire leaves.

KGZ melons show the most variation in leaf blade size, with nearly equal portions of small (32%), medium (39%), and large leaves (29%). UZB melons have mostly small (44%) and medium (37%) leaf blade sizes, with fewer large ones (19%). WT melon leaves blade sizes are large (100%).

Lobe development in melon leaves varies among different genotypes. In KGZ and UZB melons, weak lobe development is predominant, with the majority of leaves exhibiting this trait (52% for KGZ and 69% for UZB). However, there are differences in the distribution of lobe development levels between the two genotypes. While KGZ shows a moderate portion of leaves with medium development (45%), UZB has a significant portion with medium development (25%). Strong lobe development is rare in both KGZ (3%) and UZB (6.25%). WT melons predominantly display leaves with

medium lobe development (100%), indicating a distinct pattern compared to KGZ and UZB.

In analyzing the leaf blade length of the terminal lobe, was observed that KGZ melons are most diverse, with many short (61%), medium (23%) and long (16%) terminal lobes. UZB melons lean towards short (50%) and medium (31%) with fewer long (19%) lobes. Wild type melons has medium lobes.

Leaf margin dentation varies across the melon genotypes. KGZ melons show a relatively spread with weak (29%), medium (39%), and strong (32%) dentation. UZB melons have a higher proportion of medium dentation (44%) with some weak (19%) and strong (37%) leaves. WT leaves have strong dentation.

Leaf blade blistering among the melon genotypes shows that KGZ melons exhibit a near-equal distribution of weak (48%) and medium (48%) blistering, with a minimal presence of strong blistering (3%). Conversely, UZB melons show a slight preference for medium blistering (50%), with a significant portion experiencing weak blistering (44%) and a very small percentage exhibiting strong blistering (6%). WT melons display weak blistering.

The comparison of leaf morphology among cultivated (KGZ and UZB) and wild type melons reveals important insights into the impact of domestication and genotype on leaf traits. Cultivated melons exhibit greater diversity in leaf characteristics compared to wild type melons, suggesting that human selection during domestication may have favored specific leaf traits. KGZ melons display the highest variation in leaf shape and dentation, whereas UZB melons tend to have entire leaves with medium dentation, indicating potential genotype-specific preferences. In contrast, WT melons exhibit uniformity in certain traits such as entire leaves, strong dentation, and weak blistering, possibly reflecting adaptations to the wild environment. Additionally, variations in lobe development, blade length, and blistering rates across genotypes suggest potential responses to environmental stresses, with KGZ melons appearing more susceptible compared to UZB and WT melons.

Koca and Paksoy (2023) observed significant variations in leaf dimensions among melon genotypes from the Kırıkkale region. Their study revealed a difference of nearly 8 cm in leaf width, with genotypes like Sulakyurt 2 having the narrowest (10.06 cm) and Balışeyh 2 exhibiting the widest leaves (17.92 cm). Similarly, petiole length varied by almost 5 cm, with Keskin 10 showing the shortest (7.84 cm) and Balışeyh 2 having the longest petioles (12.76 cm). Leaf length also displayed notable variation of approximately 4.3 cm. The shortest leaves were observed in Keskin 10 (5.02 cm), while Bahşılı 4 genotypes possessed the longest leaves (9.36 cm).

In the research of Can (2020) examined the leaf characteristics of 48 genotypes collected from various regions of Kyrgyzstan (35) and Turkey (13). The results showed that 25% of the genotypes had 5-lobed leaves (pentalobat) and the remaining 75% had entire leaves (integrated), as shown in Figure 4.2. Among the Kyrgyz genotypes (35), 85.7% had entire leaves (30) and 14.2% had pentalobat leaves (5). Of the Turkish genotypes (13), 6 had entire leaves and 7 had pentalobat leaves. The leaf characteristics evaluations showed that 25% of the genotypes had 5-lobed leaves (pentalobat) and the

remaining 75% had entire leaves (integrated), as shown in Figure 4.2. Among the Kyrgyz genotypes (35), 85.7% had entire leaves (30) and 14.2% had pentalobate leaves (5). Of the Turkish genotypes (13), 6 had entire leaves and 7 had pentalobate leaves. Examining leaf blade shape, most genotypes (77%) had flat leaves, while 23% were pointed (acuminate). Notably, Kyrgyz melons were predominantly flat (90%), while Turkish melons showed more variation, with a nearly equal split between flat and pointed leaves.

Szamosi et al. (2010) studied Turkish and Hungarian genotypes and found that 62% were heart-shaped, while 38% were acuminate. Liu et al. (2004) characterized 72 melon genotypes using 35 morphological traits, including leaf blade shape, which contributed to principal component analysis. Sensoy et al. (2007) also utilized this UPOV criterion. Additionally, Trimech et al. (2013) found that terminal lobe length, which determines leaf blade shape, was highly correlated with morphological characterization, contributing to principal component analysis. Sensoy and Sahin (2012) classified 30 genotypes based on terminal lobe and found that 3.3% were acuminate, 6.6% were moderately long, and 90.1% were entire.

Plant leaves are essential for photosynthesis, gas exchange, nutrient distribution, and water transport (Tsukaya, 2006). Leaf shape and deeply lobed leaves can improve heat transfer and reduce leaf temperature. Additionally, leaf structure and lobes affect the amount of shade produced by the leaf, which directly influences the amount of light the plant actively uses for photosynthesis (Niklas, 1989; Vogel, 2009). Soltani et al. (2010) characterized Iranian melon genotypes using molecular and morphological markers. In their study, leaf characteristics, along with other traits, contributed 9.9% to the explanation of morphological characterization in a factor analysis. Zhang et al. (2012) recorded five types of leaf shapes in Asian melon and cucumber genotypes: entire, cordate, triangular, reniform, and pentalobate. Erdoğan (2016) reported that 67% of 94 local genotypes collected from the Lakes Region of Turkey had entire leaves, 5.3% had three-lobed leaves, 8.5% had five-lobed leaves, 16% had three-lobed and five-lobed leaves, and 3.2% belonged to other groups.

4.2.2. Fruit

4.2.2.1. Fruit characteristic results of genotypes in greenhouse conditions

In the assessment of fruit weight across different genotypes, each group: Kyrgyz (KGZ), Uzbek (UZB), and Wild type (WT) (Table 4.4), reveals distinct characteristics. Within the Kyrgyz genotypes, KRZ-9 stands out with the highest fruit weight at 2.87 kg, while KGZ-10 exhibits the lowest weight at 1.35 kg. Turning to Uzbek genotypes, UZB-16 leads the group with the highest fruit weight of 2.78 kg, and UZB-10 demonstrates the lowest within the Uzbek category at 1.09 kg. In the case of the Wild genotype, WT-1 shows a relatively lower fruit weight at 0.13 kg compared to the other groups. Comparing across all genotypic groups, UZB-16 emerges with the highest fruit weight, showcasing its superiority in this trait. Conversely, WT-1 records the lowest fruit weight among all genotypes.

Analyzing fruit length across different genotypes shows that, in the Kyrgyz group, KGZ-9 displays the highest fruit length at 30.7 cm, while KGZ-16 has the shortest length at 15 cm. In the Uzbek genotypes, UZB-16 leads with the highest length at 35 cm, and

UZB-13 exhibits the lowest within the Uzbek category at 21.9 cm. Turning to the wild genotype, WT-1 shows a relatively lower fruit length at 7.8 cm compared to the other groups. When comparing across all genotypic groups, UZB-16 stands out with the highest fruit length, indicating its superiority in this trait. Conversely, WT-1 records the lowest fruit length among all genotypes.

Analyzing width within groups, in the Kyrgyz group, KGZ-5 stands out with the widest fruit at 23 cm, while KGZ-4 exhibits the narrowest width at 27 cm. Among Uzbek genotypes, UZB-1 records the highest width at 17.5 cm, and UZB-3 displays the lowest within the Uzbek category at 11 cm. In the wild genotype, WT-1 shows a relatively modest fruit width at 15.5 cm compared to the other groups. Considering the broader comparison across all genotypic groups, KGZ-5 has the widest fruit width, indicating its prominence in this trait. Conversely, UZB-3 records the narrowest fruit width among all genotypes.

In the diameter of seed pot trait, within the Kyrgyz group, KGZ-4 has the largest seed pot diameter at 8.2 cm, while KGZ-10 exhibits the smallest at 5.6 cm. Turning to the Uzbek genotypes, UZB-2 records the highest value at 8.5 cm, and UZB-3 has the lowest within the Uzbek category at 6 cm. In the wild type, WT-1 shows a moderate diameter at 3.5 cm compared to other groups. In the broader comparison, KGZ-4 has the largest seed pot diameter, while WT-1 has the smallest. Within each group, KGZ-4, UZB-2, and WT-1 are notable for their respective seed pot diameters.

Skin thickness among the Kyrgyz group, KGZ-17 has the thickest skin at 1.57 mm, while KGZ-18 displays the thinnest at 0.43 mm. Within the Uzbek genotypes, UZB-9 records the highest skin thickness at 0.9 mm, and UZB-5 has the lowest within the Uzbek category at 0.41 mm. In the wild type genotype, WT-1 exhibits a moderate skin thickness at 0.45 mm compared to other groups. In the broader comparison, KGZ-17 has the thickest skin, and UZB-5 has the thinnest. KGZ-17, UZB-9, and WT-1 emerge as distinctive genotypes within their respective groups.

Within the Kyrgyz group in second skin thickness trait, KGZ-17 again stands out with the thickest second skin at 11.13 mm, while KGZ-16 displays the thinnest at 3.25 mm. Among Uzbek genotypes, UZB-9 records the highest second skin thickness at 10.64 mm, and UZB-3 has the lowest within the Uzbek category at 4.04 mm. In the wild type, WT-1 shows a relatively moderate second skin thickness at 1.34 mm compared to other groups. Considering the broader comparison, KGZ-17 has the thickest second skin, and WT-1 has the thinnest. KGZ-17, UZB-9, and WT-1 are distinctive genotypes within their respective groups.

Fruit flesh thickness, in the Kyrgyz group, KGZ-5 stands out with the thickest fruit flesh at 8.56 cm, while KGZ-7 displays the thinnest at 5.68 cm. Among Uzbek genotypes, UZB-10 records the highest fruit flesh thickness at 29.28 cm, and UZB-3 has the lowest within the Uzbek category at 4.04 cm. In the wild genotype, WT-1 shows a relatively moderate fruit flesh thickness at 11.49 cm compared to other groups. KGZ-5, UZB-10, and WT-1 are distinctive genotypes within their respective groups.

Can and Tütken (2022) further emphasized the importance of flesh thickness, another crucial trait for commercially desirable melons. Here too, Kyrgyz accessions

from the germplasm impressed. Manas-6 and Oş-02 accessions displayed the most substantial flesh, measuring over 43 mm thick. In contrast, the YYÜ-30 accession consistently underperformed in this category, exhibiting the least amount of flesh. This highlights the potential of Kyrgyz melons as breeding resources for cultivars with superior flesh thickness.

Table 4.4. Fruit characteristics of Kyrgyz, Uzbek and wild type genotypes in greenhouse conditions

№	Genotype	Weight (kg)	Length (cm)	Width (cm)	Diameter of seed pot (cm)	Skin thickness (mm)	Second skin thickness (mm)	Fruit flesh thickness (cm)
1	KRZ-1	2.6	21	16.5	7	0.96	7.38	37.32
2	KRZ-2	2.36	22.5	15.2	7.9	0.68	4.47	35.17
3	KRZ-3	2.545	22	16.2	7.8	0.4	10.09	38.15
4	KRZ-4	1.905	22.2	15.1	8.2	1	3.55	41.92
5	KRZ-5	1.59	17.5	14.6	5.5	0.92	3.68	49.1
6	KRZ-6	1.95	20.5	14.7	6.2	1.1	10.16	46.49
7	KRZ-7	1.85	23.8	13.2	6.5	0.54	5.65	31.65
8	KRZ-8	1.8	20	14.7	3.8	0.66	7.75	36.46
9	KRZ-9	2.87	30.7	14.4	5.2	0.92	9.37	44.43
10	KRZ-10	1.35	16	14.4	5.6	0.76	9.12	37.76
11	KRZ-11	2.88	30.5	13	6	0.84	6.61	41.25
12	KRZ-12	1.715	19.5	15.7	7.8	0.69	9.9	34.51
13	KRZ-13	1.22	18.8	13.2	5	1.08	10.42	35.9
14	KRZ-14	1.22	18.8	13.2	5	1.08	10.42	35.9
15	KRZ-15	1.885	21	14.9	6	1.35	10.64	36.27
16	KRZ-16	1.855	27.2	11.8	5.2	0.86	3.25	32.09
17	KRZ-17	1.61	20	14.7	3.8	1.57	11.13	33.16
18	KRZ-18	2.1	25.8	13.3	6	0.43	9.46	35.15
19	KRZ-19	2.25	31	12.5	6	0.83	8.09	30.37
20	KRZ-20	2.345	30.5	12.9	5	0.57	5.36	44.59
21	KRZ-21	2.365	20	17	6	0.52	5.46	39.82
22	KRZ-22	2.16	27	14	7	0.48	4.61	38.82
23	KRZ-23	2.16	27	14	7	0.48	4.61	38.82
24	KRZ-24	1.415	18.5	13.2	6.8	0.48	5.59	35.1
25	KRZ-25	1.415	18.5	13.2	6.8	0.48	5.59	35.1
26	KRZ-26	1.56	26.5	12.5	5.5	0.72	4.29	29.23
27	KRZ-27	1.83	16.5	12.2	6.5	0.69	4.14	30.2
28	KRZ-28	1.83	16.5	12.2	6.5	0.69	4.14	30.2
29	KRZ-29	1.525	24.8	11.7	5.3	1.05	5.88	29.62
30	KRZ-30	1.705	23.8	12.3	5	0.9	8.63	34.77
31	KRZ-31	2.25	31	12.5	6	1.06	5.63	36.9
32	UZB-1	2.15	15.9	17.5	7	1	6.25	40.18
33	UZB-2	2.03	22.6	14.8	8.5	0.54	8.26	29.6
34	UZB-3	1.3	21.9	11	6	0.43	4.04	35.63

Table 4.4. Continued

35	UZB-4	1.74	24.5	13	7	0.58	4.45	29.78
36	UZB-5	1.415	15.3	14.3	7.5	0.41	5.47	29.68
37	UZB-6	1.44	24	13	6	0.58	3.55	39.74
38	UZB-7	2.115	28	13	6.7	0.39	5.49	31.63
39	UZB-8	1.845	25.5	12.7	6.2	0.65	6.45	32.28
40	UZB-9	2.13	17.8	16.4	7.2	0.9	7.18	42.02
41	UZB-10	1.09	23.3	11.5	5.8	0.85	29.28	3.12
42	UZB-11	2.04	22	15.2	6.5	0.51	6.59	36.47
43	UZB-12	1.83	24.5	12.8	5.2	0.91	8.99	39.5
44	UZB-13	2.235	28	13.5	5.7	0.81	3.7	41.15
45	UZB-14	2.285	20	16.5	7	0.48	3.61	36.16
46	UZB-15	2.375	32	12.2	6.5	0.67	4.49	32.34
47	UZB-16	2.785	35	15	6	1.35	10.64	36.27
48	WT	0.13	7.8	5.5	3.5	0.45	1.34	11.49

4.2.2.2. Fruit characteristic results of genotypes in open field conditions

Table 4.5 provides an analysis of fruit characteristics among genotypes under open field conditions.

Analysing weight within the Kyrgyz (KGZ) group, KGZ-25 demonstrates the highest fruit weight at 7.75 kg, signifying exceptional performance. In contrast, KGZ-4 exhibits the lowest weight (2.8 kg), showcasing variability within the Kyrgyz genotypes. In the Uzbek (UZB) group, UZB-13 excels with the maximum weight of 8.79 kg, highlighting its superiority. Conversely, UZB-10 displays the lowest weight, illustrating diversity within Uzbek genotypes. Representing the wild type, WT-1 shows the lowest weight, emphasizing its distinct trait in this characteristic. Comparing the three genotype groups, UZB-16 stands out with the highest fruit weight (5.94 kg), while KGZ-5 has the lowest, underscoring diversity within the groups.

Length analysis in the Kyrgyz group, KGZ-29 exhibits the maximum length at 34.5 cm, emphasizing its notable performance. KGZ-32 has the shortest length (8 cm), showcasing intra-group variation. Within the Uzbek group, UZB-16 has the highest length (35 cm), highlighting its distinctiveness. On the other hand, UZB-5 displays the lowest length, demonstrating diversity within Uzbek genotypes. For the Wild Type, WT-1 shows the smallest length, marking a unique trait. Comparing the groups, UZB-16 stands out with the longest fruit, while KGZ-32 has the shortest, indicating diversity across genotypes.

Width analysis in the Kyrgyz group, KGZ-18 demonstrates the maximum width at 40 cm, showcasing its significant performance. KGZ-17 exhibits the smallest width, indicating variability within Kyrgyz genotypes. Within the Uzbek group, UZB-16 has the widest fruit (15 cm), emphasizing its uniqueness. UZB-10 has the narrowest width, revealing diversity among Uzbek genotypes. For the wild type, WT-1 displays the smallest width, marking a distinct characteristic. Comparing the groups, UZB-16 stands out with the widest fruit, while KGZ-17 has the narrowest, highlighting diversity.

Diameter of seed pot analysis of the diameter of the seed pot, KGZ-9 within the Kyrgyz group and UZB-9 within the Uzbek group exhibit the largest seed pot diameters at 10.4 cm and 10.5 cm, respectively. In contrast, WT-1 showcases the smallest seed pot diameter, emphasizing its specific trait in this dimension.

Skin thickness analysis in KGZ-19 displays the most substantial skin thickness within the Kyrgyz group at 0.62 mm, while UZB-16 exhibits the highest skin thickness in the Uzbek group at 1.35 mm. WT-1, representing the Wild type, manifests a relatively moderate skin thickness at 0.45 mm.

Second skin thickness analysis in UZB-16 stands out with the most substantial second skin thickness at 13.22 mm, underscoring its unique trait within the Uzbek genotypes. KGZ-25 also displays a notable second skin thickness at 22.28 mm, emphasizing its distinctive characteristic. In contrast, WT-1 exhibits a relatively moderate second skin thickness at 0.74 mm.

Fruit flesh thickness analysis in UZB-16 leads in fruit flesh thickness with the highest mean value at 7.5 cm, showcasing its distinctive characteristic within the Uzbek group. KGZ-16 also exhibits a substantial fruit flesh thickness at 5.1 cm, highlighting its unique trait. In comparison, WT-1 displays the lowest fruit flesh thickness.

In a comparative context, UZB-16 stands out with the highest fruit flesh thickness, showcasing its unique trait among all genotypes. Conversely, WT-1 exhibits the lowest fruit flesh thickness. Analyzing the diameter of the seed pot across groups reveals nuanced variations, with KGZ-9, UZB-9, and WT-1 showcasing distinctive traits. In terms of weight, UZB-13 emerges as the heaviest among all genotypes, while WT-1 demonstrates the lowest weight, emphasizing its singular characteristic within the study.

Koca and Paksoy (2023) conducted a morphological characterization study on melon genotypes in the Kırıkkale region of Turkey. Their research aimed to establish a foundation for future breeding programs through genetic examinations. They analyzed 58 genotypes collected from various districts in 2021, evaluating traits like leaf dimensions, lobing, color, and flower characteristics using UPOV guidelines. Interestingly, all examined genotypes displayed shallow leaf lobing and a heart-shaped leaf base. Flower sex was also uniform, with all plants exhibiting an andromonoecious condition (having both male and female flowers). While some morphological similarities were observed in traits like hypocotyl and leaf dimensions, statistically significant differences were found between genotypes from various districts ($p < 0.05$; 0.001).

Fruit size emerged as a critical factor in Can and Tütken's (2022) investigation of melon accessions for breeding potential. Kyrgyz melons exhibited a distinct advantage in both fruit length and diameter. Notably, Ç-04 and Ç-05 accessions displayed impressive lengths exceeding 28 cm, while Manas-4 and YYÜ-30 accessions exhibited the smallest dimensions, measuring around 10 cm. This dominance extended to fruit diameter, with Kyrgyz accessions Manas-6 and Kg-D boasting the thickest rinds, contrasting significantly with the notably thin rind observed in YYÜ-30.

Table 4.5. Fruit characteristics of Kyrgyz, Uzbek and wild type genotypes in open field conditions

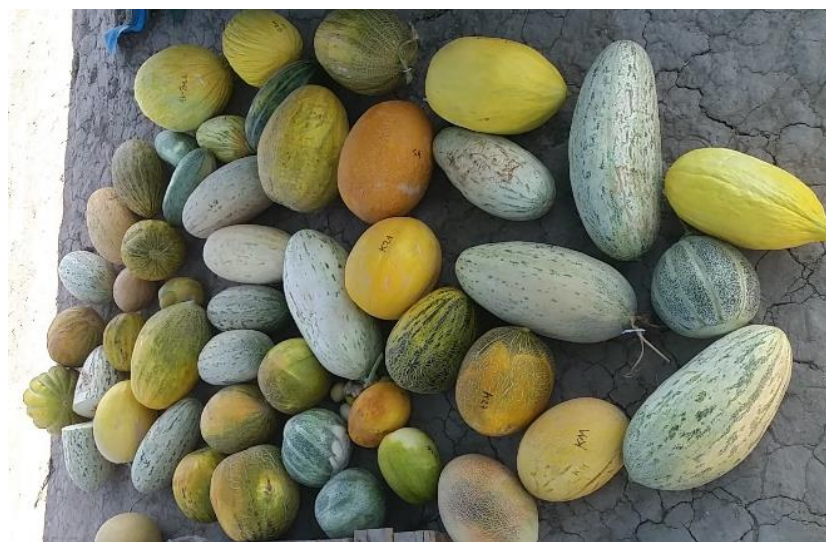
№	Genotype	Weight (kg)	Length (cm)	Width (cm)	Diameter of seed pot(cm)	Skin thickness (mm)	Seconder skin thickness (mm)	Fruit flesh thickness (mm)
1	KGZ-1	5.04	22	23.5	13	0.79	3.18	53.47
2	KGZ-2	4.16	34	14	6.2	0.44	6.87	37.53
3	KGZ-3	3.693	25	19	9	0.48	6.78	49.93
4	KGZ-4	2.808	17.5	8.5	7	0.43	5.04	51.1
5	KGZ-5	5.577	29	15.7	8	0.37	6.8	41.02
6	KGZ-6	2.037	16.5	15.8	8.2	0.61	2.68	32.43
7	KGZ-7	5.522	24	21.5	5	0.42	11.84	47.99
8	KGZ-8	1.84	14.5	13	9	0.67	11.25	46.36
9	KGZ-9	6.54	36	21.2	10.4	0.43	2.09	60.7
10	KGZ-10	3.126	23	16.5	6.2	0.9	3.78	55.06
11	KGZ-11	2.864	24.5	15.5	6.5	0.36	5.68	44.07
12	KGZ-12	4.601	17.34	18	8	0.78	8.24	60.11
13	KGZ-13	1.299	16	13.2	5.5	0.16	2.05	32.94
14	KGZ-14	3.426	26	17.5	7.2	0.74	8.42	48.24
15	KGZ-15	3.66	25	18.8	7.5	0.47	5.07	48.78
16	KGZ-16	3.952	25	19.5	9.2	0.62	4.85	51.36
17	KGZ-17	2.079	18.5	15.2	6.8	0.41	6.55	42.28
18	KGZ-18	5.605	40	17	7	0.86	6.42	48.63
19	KGZ-19	6.995	44	19	8	0.62	12.08	58.77
20	KGZ-20	3.113	34	13	5.5	0.94	7.49	47.4
21	KGZ-21	4.579	24	21	11	0.67	9.08	55
22	KGZ-22	3.252	23	18	9.5	0.61	3.76	44.61
23	KGZ-23	3.65	23	21	6.75	0.59	3.56	49
24	KGZ-24	1.254	16.5	12.8	5.3	0.69	3.54	39.62
25	KGZ-25	7.759	34	24	12	0.51	22.28	69.52
26	KGZ-26	1.229	16	13	6.5	0.67	4.39	40.12
27	KGZ-27	3.352	22.5	17.5	7	0.85	4.85	52.25
28	KGZ-28	6.161	43	20	12	0.81	7.22	30.39
29	KGZ-29	3.164	34.5	14.5	7	0.91	10.55	29.38
30	KGZ-30	4.49	39.5	16.2	7	0.88	2.65	51.74
31	KGZ-31	5.203	39.5	17	7	0.73	9.86	34.91
32	UZB-1	3.25	34	14.5	5.5	0.69	6.56	48.81
33	UZB-2	3.54	29.5	17.5	10	0.44	2.89	28.64
34	UZB-3	4.746	34	18.5	8	0.53	5.14	49.35
35	UZB-4	5.221	13.3	18.2	7.5	0.74	3.13	55.95
36	UZB-5	2.442	16	16.5	9.2	0.62	3.38	38.91
37	UZB-6	5.17	44	16.5	7	0.57	7.52	47.99
38	UZB-7	4.05	35.5	15.6	6.5	0.69	7.38	48.32
39	UZB-8	7.312	36.5	20.9	10.5	0.57	16.21	43.22
40	UZB-9	3.885	22	19.8	8	0.52	10.06	52.66
41	UZB-10	2.979	30	16	6.5	0.75	5.72	42.52

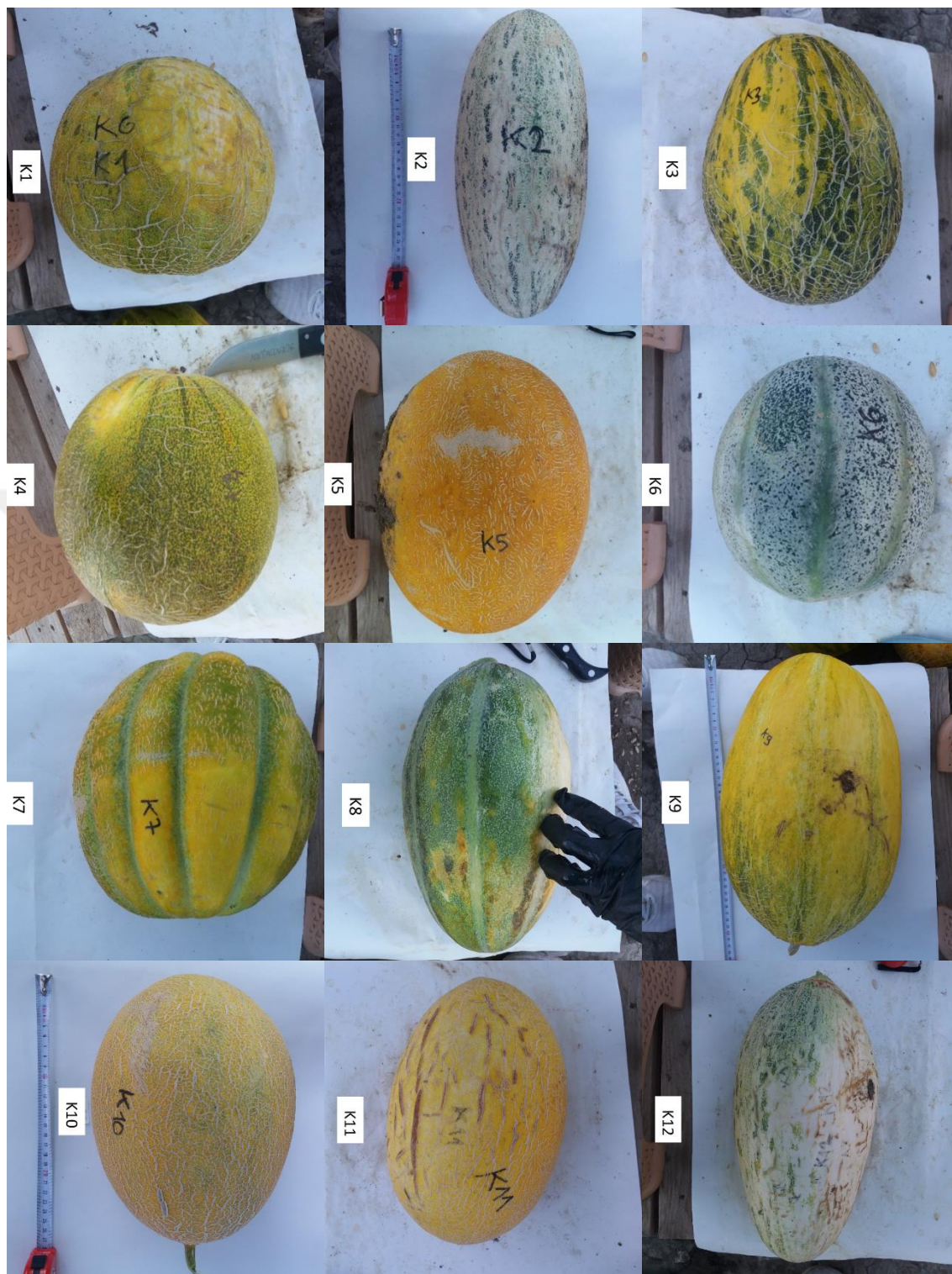
Table 4.5. Continued

42	UZH-11	6.039	33	20.5	9.5	0.82	14	63.47
43	UZH-12	2.403	29.5	14.5	6.5	0.25	7.71	39.35
44	UZH-13	8.796	33	26	14	0.28	6.59	49.94
45	UZH-14	2.696	32	13.6	6.5	0.56	3.53	39
46	UZH-15	1.872	27	11.3	6	0.71	6.43	28
47	UZH-16	5.947	31	12	10	0.65	13.22	75.96
48	WT-1	0.58	5.681	4.052	3.257	0.32	0.74	6.8

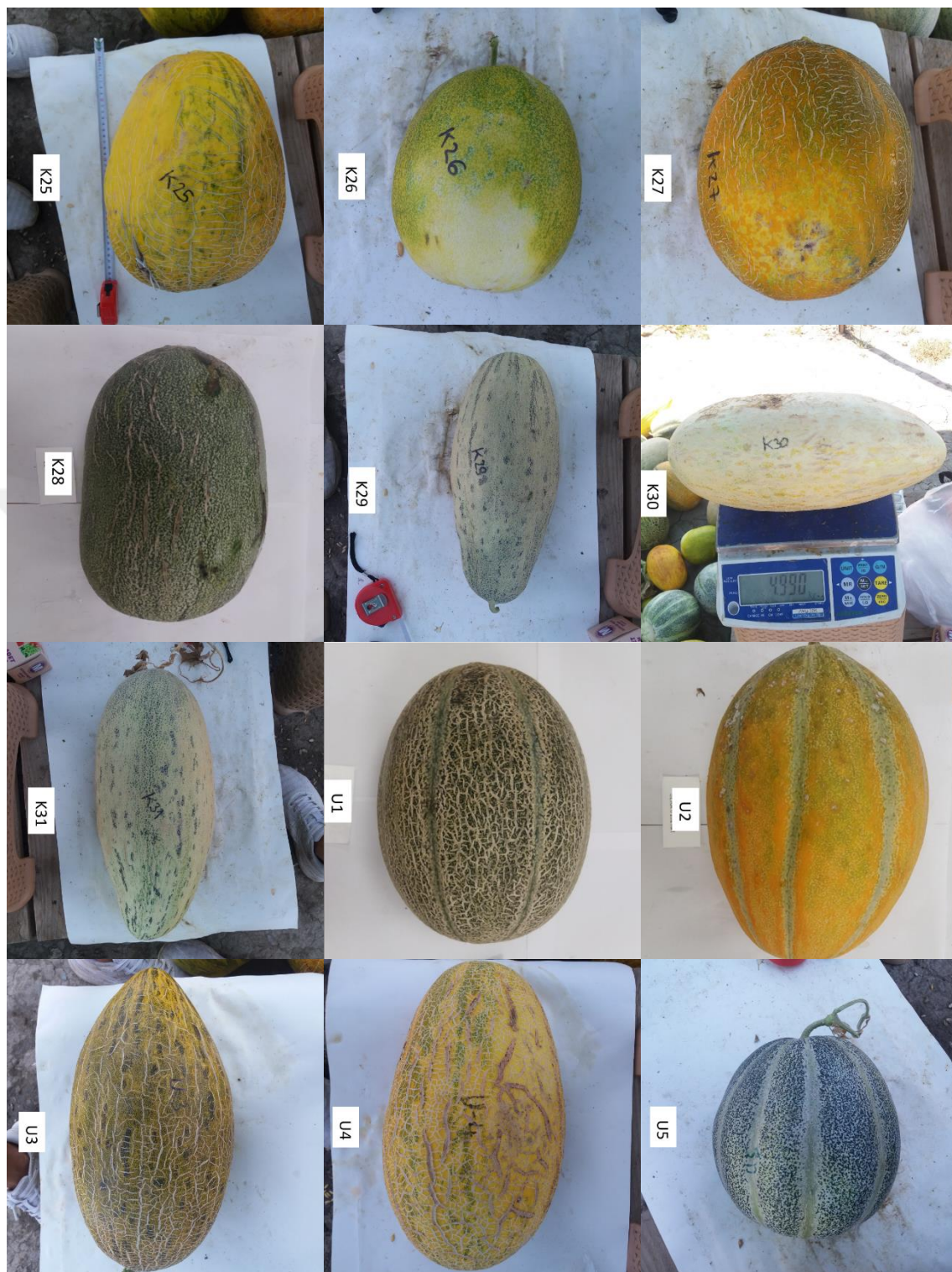
Melon genotypes exhibit a diverse range of fruit sizes and morphologies, with a significant portion of this variability originating from genotypes and wild melon forms in Central Asia (Dhillon et al., 2012; Roy et al., 2012). The primary factors contributing to this diversity are the width and length of the fruits, influenced by the activity of genes determining fruit gender. While melon is recognized as one of the most diverse species within the Cucumis genus, the genetic mechanisms controlling its phenotypic variations remain largely unknown and unexplored (Monforte et al., 2004).

Studies conducted by Lázaro et al. (2017) on Spanish genotypes reported a fruit width of 15.46 cm and a fruit length of 22.83 cm. Similarly, Guliyev et al. (2018) found that Azerbaijani genotypes exhibited a fruit length ranging from 15.28 to 29.87 cm and a fruit width between 14.88 and 24.2 cm. In comparison to these findings, the genotypes under investigation in this study demonstrate fruit lengths longer than those observed in Spanish genotypes and comparable to Azerbaijani genotypes. Interestingly, the fruit width of the studied genotypes is shorter than that of Azerbaijani genotypes but aligns closely with the Spanish genotypes.

**Figure 4.6.** Fruits harvested from the open field







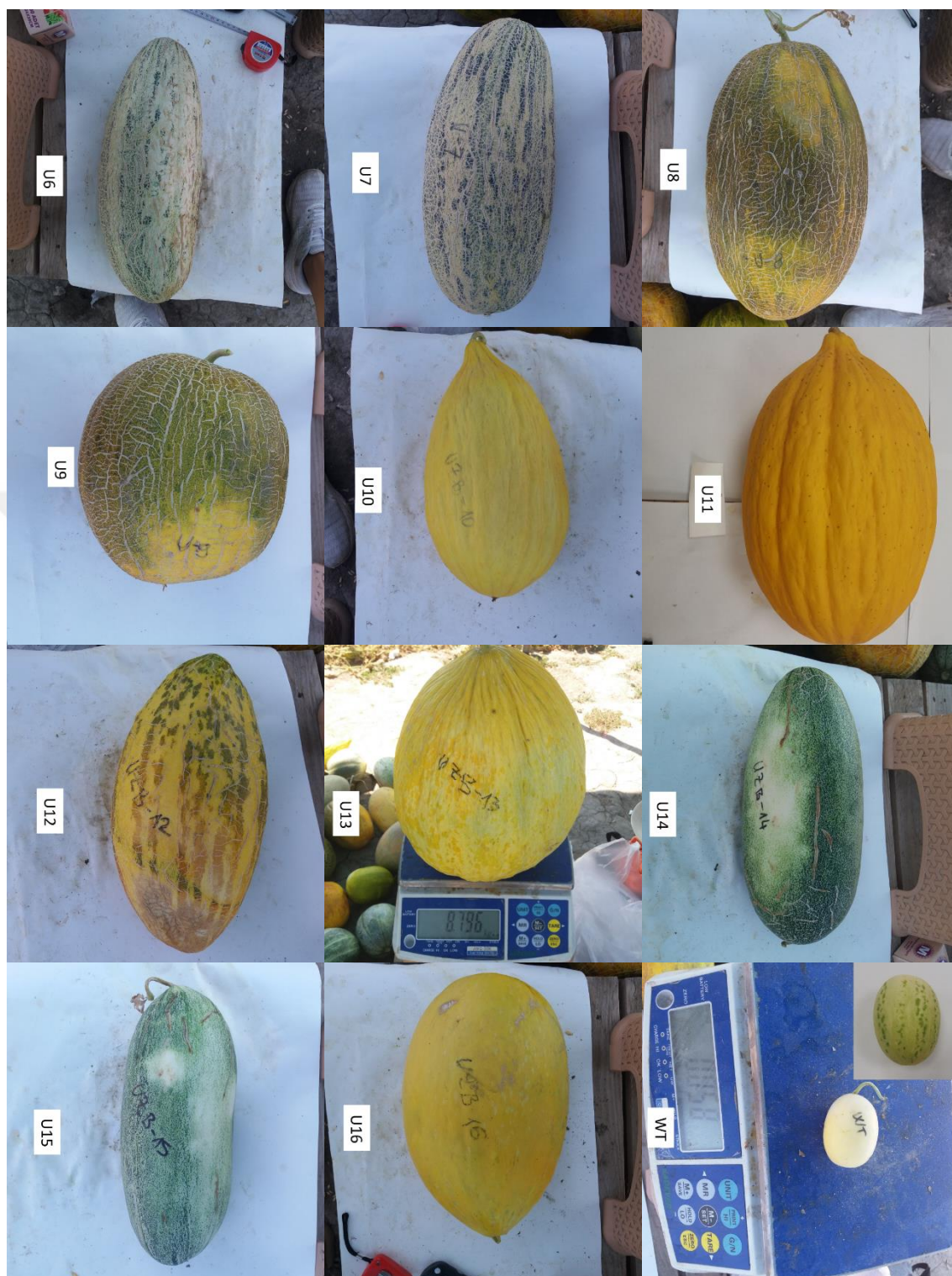
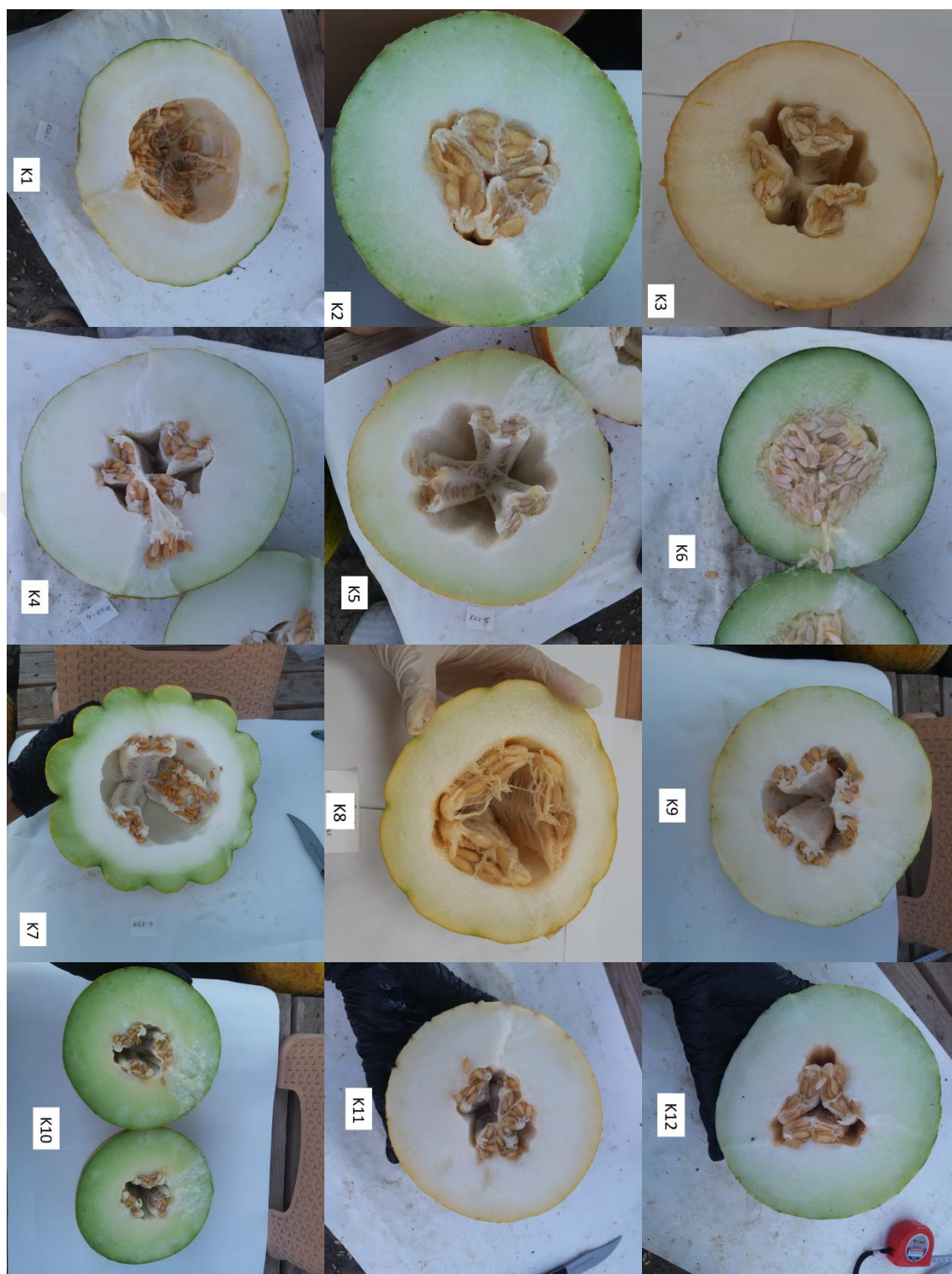
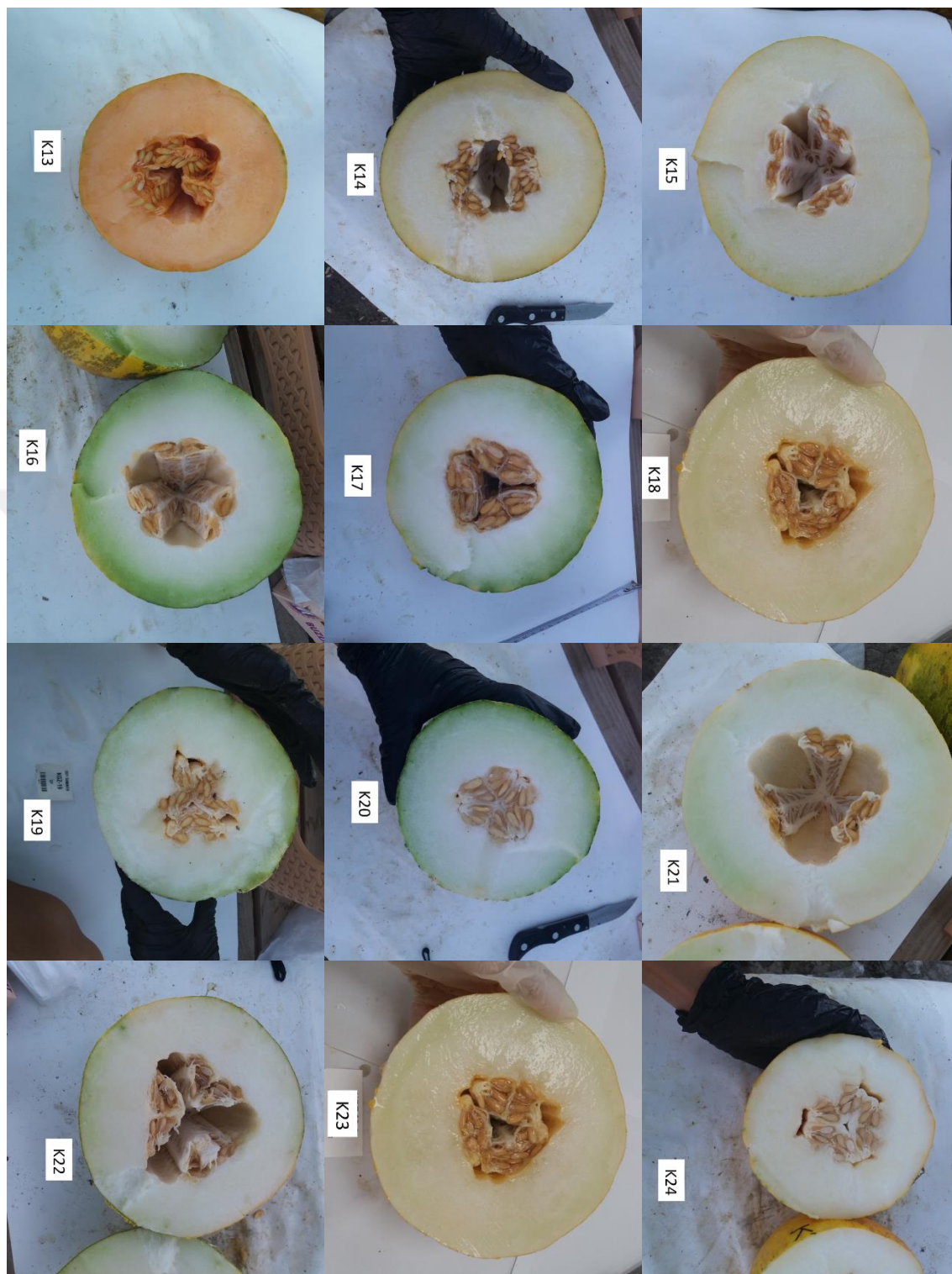


Figure 4.7. Fruit images of Kyrgyz and Uzbek melon genotypes







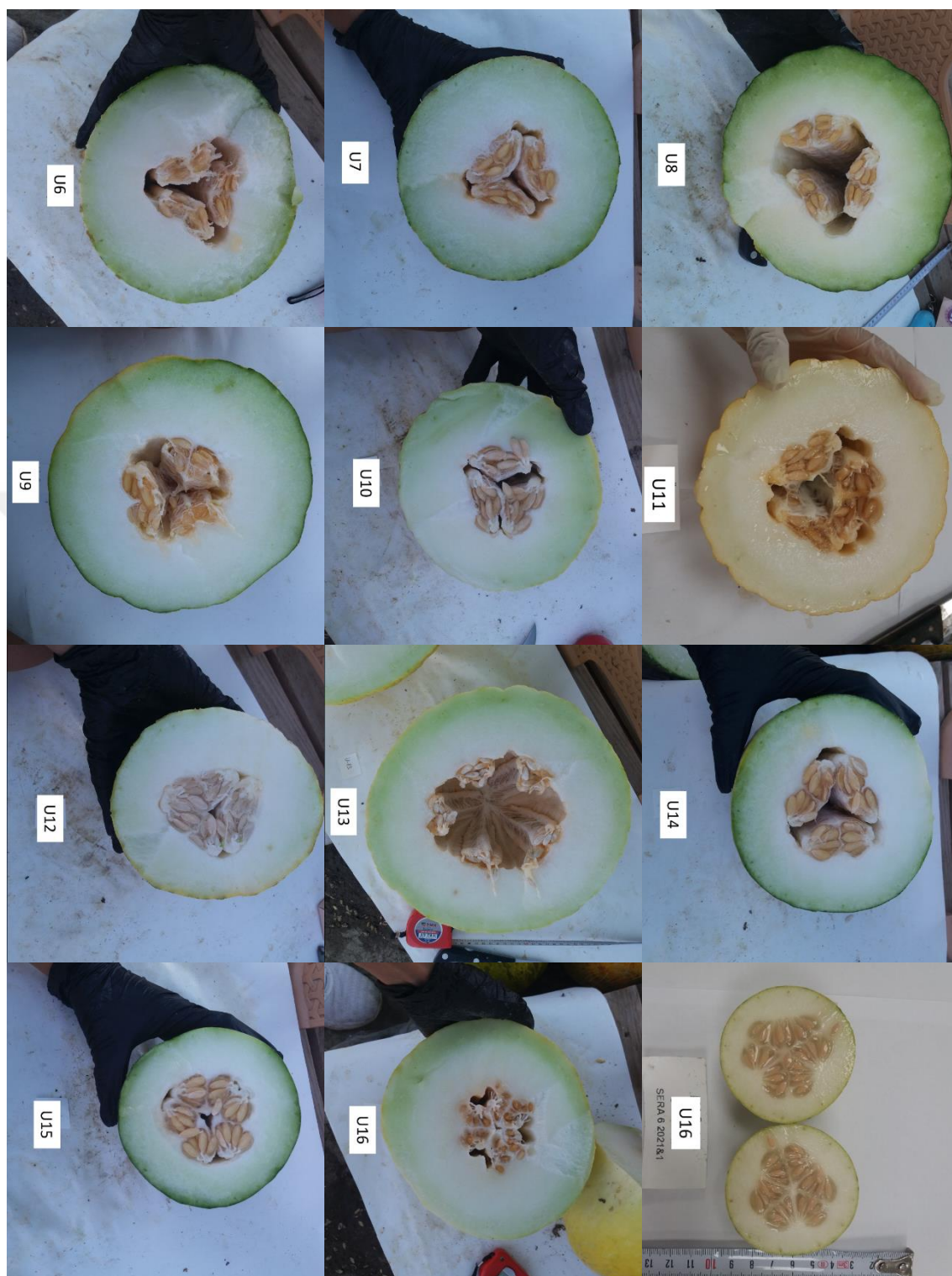


Figure 4.8. Cross-section images of Kyrgyz and Uzbek melon genotypes

4.2.2.3. Comparison of some fruit characteristics of genotypes from two different conditions

Table 4.6. Mean compare results of 3 groups in two conditions

Genotypes	Weight (kg)	Length (cm)	Width (cm)	Diameter of seed pot (cm)	Skin thickness (mm)	Seconder skin thickness (mm)	Fruit flesh thickness (mm)
KGZ/Greenhouse	1.87	22.88	13.84	6.06	0.8	6.94	36.65
UZB	1.97	23.77	13.9	6.55	0.69	7.48	33.47
WT	0.13	7.8	5.5	3.5	0.45	1.34	11.49
KGZ/Open field	4.33	28.3	17.11	7.88	0.63	6.74	46.93
UZB	4.83	30.55	17	8.2	0.59	7.47	47
WT	0,58	5,681	4,052	3,257	0,32	0,74	6,8

Table 4.6 and Figure 4.7. presents the mean values of seven morphological traits (weight, length, width, diameter of seed pot, skin thickness, second skin thickness, and fruit flesh thickness) for three melon genotypes (KGZ, UZB, WT) grown under two conditions (Greenhouse, Open field).

KGZ melons demonstrate substantial improvements in all studied characteristics, with the exception of skin thickness, when comparing the greenhouse and open field environments. Fruit flesh thickness experiences the most significant rise at 33%, followed by length at 24% and weight at 30%. Like KGZ, UZB melons exhibit improvements in all assessed characteristics, with the exception of skin thickness, when cultivated in an open field as opposed to a greenhouse.

The fruit flesh thickness has the most significant growth, with a 40% rise, followed by the length, which increases by 29%, and the weight, which increases by 145%. In comparison to the other genotypes, wild-type (WT) melons exhibit a notable reduction in size and possess a thinner skin, irrespective of the prevailing growing conditions. Although the open field setting results in marginal enhancements in the majority of attributes for WT, the overall disparity is considerably less pronounced in comparison to KGZ and UZB.

Weight of all genotypes show a substantial increase in weight when grown in the open field compared to the greenhouse. This suggests that the open field environment provides better conditions for fruit development and weight gain. Length and width, similar to weight, both length and width increase for all genotypes in the open field. This indicates that open field cultivation allows for better fruit expansion compared to the greenhouse environment.

Diameter of seed pot of the diameter of the seed pot shows a slight increase in the open field for KGZ and UZB, but remains nearly the same for WT. This suggests that seed pot size might be less influenced by the growing environment compared to other traits.

Skin thickness of both primary and secondary skin thickness decrease slightly for all genotypes grown in the open field compared to the greenhouse. This could be due to factors like increased sun exposure and temperature fluctuations in the open field, leading to thinner skin development. Fruit flesh thickness of all genotypes show the most

significant increase in fruit flesh thickness when grown in the open field. This suggests that the open field environment is more favorable for flesh development and potentially higher fruit yield. Open field cultivation generally leads to larger fruits with thicker flesh for KGZ and UZB genotypes compared to the greenhouse environment. WT melons show the least difference between the two growing conditions, suggesting potential adaptation to different environments or inherent limitations in growth potential. Skin thickness seems less influenced by the growing environment compared to other measured traits.

Figure 4.8 shows in a detail variations in skin texture, shape, color, and other characteristics of young and ripe fruits across different melon genotypes.

Flower Sex Expression: Inflorescence characterization revealed contrasting patterns in flower sex expression. Kyrgyz genotypes displayed a mixed distribution, with 84% exhibiting hermaphroditic (monoecious) flowers and 16% showing functionally male (andromonoecious) flowers. Conversely, all Uzbek genotypes and the Wild Type group exclusively produced hermaphroditic flowers.

Dot Density: Analysis of dot density in young melon fruits showed genotypic differences. Kyrgyz fruits displayed the most variation, ranging from nearly absent (6.5%) to very dense (23%), with sparse (29%) and medium (25%) densities also observed. Uzbek genotypes exhibited a broader range, with similar frequencies for absent (19%) and sparse (19%) categories, followed by medium (25%) and dense (25%) categories. Wild type fruits had a medium density of dots.

Dot Size: Analysis of dot size on young melon fruits showed that Kyrgyz melons displayed the most diverse distribution, with small (19%), medium (51%), and large (29%) dots represented. Conversely, Uzbek melons showed a higher concentration of small dots (44%), followed by medium (31%) and large (25%). Wild Type fruits exhibited medium-sized dots.

Dot Contrast: The contrast between dots and the background color on young melon fruits varied across groups. Kyrgyz melons exhibited the most variation, with weak (26%), medium (16%), and strong (58%) contrast observed. Uzbek melons had a more even distribution, with similar proportions for weak (31%) and medium (31%) contrast, and a dominant presence of strong contrast (44%). Wild Type fruits displayed a medium level of contrast.

Groove Coloring: Young melon fruits displayed distinct patterns in groove coloring. Kyrgyz melons exhibited the most diverse range, with a significant presence of absent or very weak coloring (84%), followed by weak (10%), medium (3%), and strong coloring (3%). In contrast, Uzbek melons showed a more uniform distribution, with no fruits exhibiting weak coloring, and similar proportions for medium (6%) and strong (6%) coloring, while the majority (66%) displayed absent or very weak coloring. All Wild Type fruits exhibited absent or very weak groove coloring.

Groove Color Intensity: Young melon fruits revealed distinct patterns in groove color intensity. Both Kyrgyz and Uzbek melons displayed a remarkable similarity, with a dominant presence of light-colored grooves (94%) and a small proportion exhibiting

medium intensity (6%). No strong coloring was observed in either group. Interestingly, Wild Type melons had an even lighter groove color.

Fruit Shape: Longitudinal sections of fruits showed distinct patterns between melon groups. Kyrgyz melons exhibited the most diverse range of shapes, including a significant presence of circular fruits (32.25%) and varying proportions of ovate, medium elliptic, and other less common shapes. Uzbek melons also showed a mix of shapes, with ovate being the most prevalent (25%), followed by medium elliptic (18.75%) and a smaller presence of other categories. Wild type fruits had a broad elliptic shape.

Maximum Diameter Position: The analysis of maximum diameter position in melon fruits revealed distinct patterns. Kyrgyz melons displayed the most diverse distribution, with 10% having the widest part towards the stem end, 74% in the middle, and 16% towards the blossom end. Uzbek melons showed a preference for a central diameter (56.25%), with a significant portion (37.5%) having a wider blossom end compared to only 6.25% with a wider stem end. Wild Type fruits exhibited a maximum diameter at the middle.

Peduncle Length: The analysis of peduncle length in young melon fruits displayed variations between genotypes. Kyrgyz melons displayed the most diverse distribution: 13% with short peduncles, 42% with medium length, and 45% with long peduncles. Uzbek melons exhibited a different pattern, with a higher prevalence of medium-length peduncles (69%), followed by short (19%) and long (12%). Wild Type fruits possessed medium-length peduncles.

Peduncle Thickness: Young melon fruits revealed distinct patterns in peduncle thickness. Kyrgyz melons displayed the most variation, with 26% having thin peduncles, 64% having medium thickness, and 10% having thick peduncles. Uzbek melons showed a more balanced distribution, with 12.5% having thin peduncles, 50% having medium thickness, and 37.5% having thick peduncles. Wild Type fruits appeared to have a medium-sized peduncle.

Darkening Area Around Peduncle in Young Fruits: Kyrgyz melons exhibited the greatest variation in the extent of darkening around the peduncle. Nearly a third (29%) lacked darkening entirely, with the remaining fruits showing a range of small (19.35%), medium (32.25%), and large (19.35%) darkened zones. Conversely, Uzbek melons predominantly showed minimal or no darkening (over 56%), with a smaller proportion exhibiting small (6.25%), medium (25%), and large (12.5%) darkened areas. Wild Type fruits displayed an intermediate level of darkening.

Fruit Skin Color: Kyrgyz melons displayed the most diverse range of ripe fruit skin colors, with yellow (32%), green (42%), and grey (26%) all well-represented. Uzbek melons exhibited a similar trend, but with green skin being the most dominant (56%), followed by yellow (31%) and grey (13%). Interestingly, Wild Type fruits exhibited white skin, contrasting with the colored skin observed in the cultivated varieties.

Fruit Skin Color Intensity: Variations in ripe fruit skin color intensity were observed. Kyrgyz melons displayed the greatest variation, with fruits categorized as light-colored (42%), medium intensity (45%), and dark (13%). In contrast, Uzbek melons

showed a preference for medium intensity skin (63%), with a significant portion having lighter skin (31%) and a smaller percentage with darker skin (6.25%). Wild Type fruits, with their white skin, displayed the darkest coloration in this category.

Surface Dot Density and Size: Both dot density and size varied among the melon genotypes. Kyrgyz melons exhibited the most diverse distribution in both categories. Dot density ranged from absent or very sparse (over half at 55%) to sparse (23%), medium (16%), and dense or very dense (3% each). Dot size ranged from small (56%) to medium (38%) and large (6%). Uzbek melons displayed a somewhat similar pattern for dot density, with a higher prevalence of sparse dotting (31%) and a significant portion having medium density (31%). Notably, Wild Type fruits lacked dots entirely, or had very sparse dotting. In terms of size, Uzbek melons showed a stronger preference for smaller dots (61%) compared to Kyrgyz melons.

Dot Color in Ripen Fruits: Variations in dot color were observed, suggesting genetic influences on dot development. Kyrgyz melons displayed the most diverse spread, with green (51.6%) being the most prevalent dot color, followed by yellow (38.7%) and white dots (9.7%). In contrast, Uzbek melons showed a complete absence of white dots and a balanced distribution between yellow (50%) and green (50%) colored dots. Wild Type fruits displayed small, white dots.

Dot Color Intensity: A clear distinction is observed in dot color intensity. Kyrgyz melons exhibit the most diverse distribution, with a significant presence of light-colored dots (51%), followed by medium (39%) and dark (10%). Uzbek melons show a more balanced distribution with a slight preference for light-colored dots (44%), followed by medium (31%) and dark (25%), Wild Type fruits exclusively possess light-colored dots.

Patch Density: Variations are evident in patch density. Kyrgyz melons display a wider range, with over half (52%) showing absent or very sparse patches, followed by sparse (29%), medium (16%), and dense (3%). Uzbek melons exhibit a more restricted distribution, with the majority (62%) having absent or very sparse patches, followed by a significant portion with medium density (25%) and a smaller presence of sparse patches (13%). Wild Type fruits completely lack patches, or have only very sparse patches.

Patch Size: Patch size also demonstrates variations among genotypes. Kyrgyz melons showed the most diverse spread, with a dominant presence of small patches (61%), followed by medium (29%) and large (10%). Uzbek melons display a stronger preference for small patches (75%), with a considerably smaller proportion having medium (19%) and large (6%) sized patches. Wild Type fruits exclusively possess small patches.

Fruit Warts: The presence or absence of fruit warts is another distinguishing characteristic. Kyrgyz and Uzbek melons exhibit a high prevalence of warts, with 87% and 81% respectively, Wild Type fruits entirely lack warts.

Peduncle Attachment: The maturity-stage attachment of the peduncle reveals further differences. Kyrgyz melons predominantly show medium attachment (84%), with a small presence of weak attachment (13%). Uzbek melons exhibit a more even distribution, with a dominant presence of medium attachment (68.75%), followed by

weak (12.5%) and strong attachment (18.75%). Wild Type fruits had medium peduncle attachment at maturity.

Fruit Base Shape: The final characteristic examined is the shape of the fruit base. Kyrgyz melons display a diverse range, with a significant portion having a rounded base (71%), followed by pointed (13%) and truncate (16%) shapes. Uzbek melons show a preference for a rounded base (56.25%), followed by pointed (31.25%) and truncate (12.25%) shapes. Interestingly, Wild Type fruits exclusively possess a rounded base shape.

Fruit Apex Shape: The genotypes showed distinct variations in fruit apex shape. Kyrgyz melons display a dominance of rounded shapes (55%), followed by truncate (39%) and pointed (6%) apices. Uzbek melons show a similar trend with a preference for rounded apices (63%), followed by truncate (25%) and pointed (13%) shapes. Wild Type fruits showed a truncate apex shape.

Fruit Grooves: The presence and strength of expression of grooves on the fruit surface vary. Both Kyrgyz and Uzbek melons display a high prevalence of absent or very weakly expressed grooves (80% and 81% respectively). This characteristic is also observed in Wild Type fruits.

Fruit Groove Width and Depth: The presence of grooves on the fruit surface appears minimal across all genotypes. Both Kyrgyz and Uzbek melons, along with Wild Type fruits, predominantly exhibit absent or very weakly expressed grooves, with frequencies exceeding 80% in each case.

Fruit Groove Color: The analysis of fruit groove color revealed that smooth fruit, lacking grooves, is the most prevalent characteristic across all genotypes: Kyrgyz (77%), Uzbek (69%), and Wild Type (100%). However, for the minority of melons that do exhibit grooves, both Kyrgyz and Uzbek melons display a variety of colors, including white (Kyrgyz: 3%, Uzbek: 12%), yellow (Kyrgyz: 6%, Uzbek: 12%), and green (Kyrgyz: 13%, Uzbek: 6%).

Fruit Surface Creasing: Surface creasing displayed minimal variation. Both Kyrgyz and Uzbek melons predominantly exhibited absent or very weak creasing (97% and 81% respectively), with a very small proportion showing weak creasing. Wild Type fruits also lacked significant surface creasing.

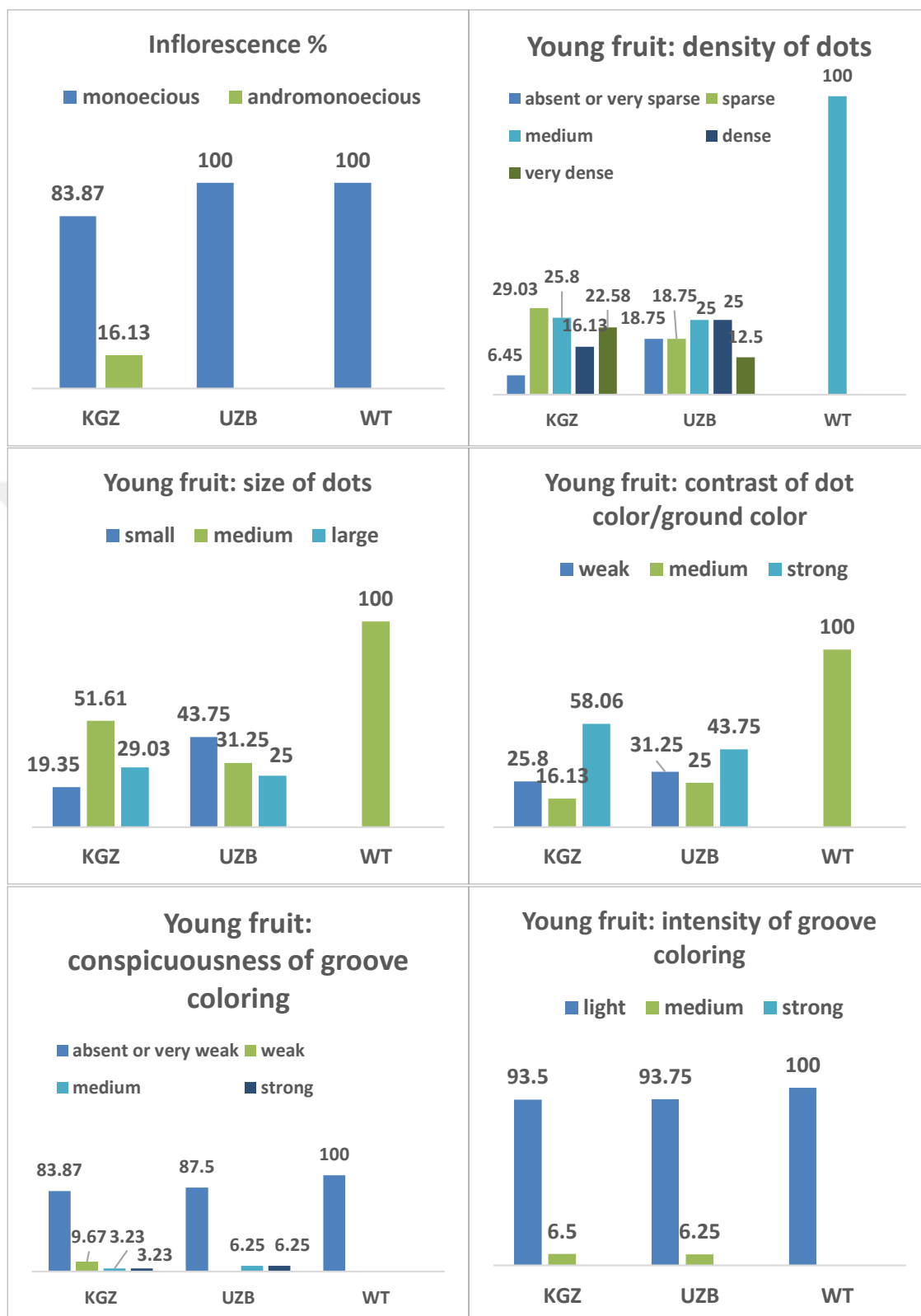
Presence of Fruit Cork: A clear distinction exists between the genotypes regarding fruit cork formation. While Wild Type fruits consistently possess cork, Kyrgyz and Uzbek melons exhibit a mix of fruits with (45% and 37% respectively) and without (55% and 63% respectively) cork formation.

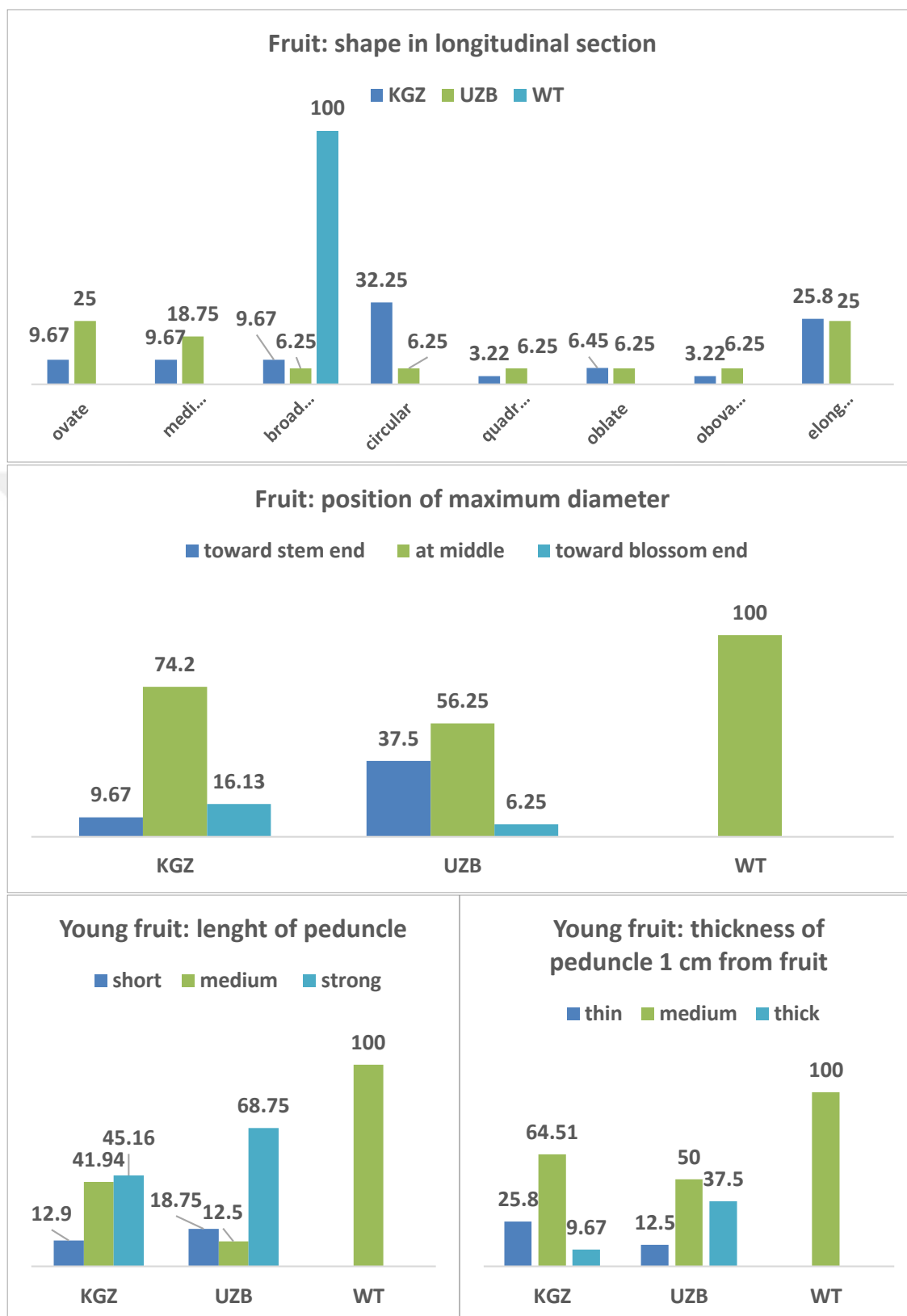
Cork Layer Thickness: Variations are evident in the thickness of the cork layer when present. Kyrgyz melons display a wider range, with a dominant presence of very thin cork (68%), followed by thin (19%), medium (10%), and thick (3%). Uzbek melons exhibit a more even distribution, with a majority having thin cork (56%), followed by very thin (37%) and a smaller portion with medium thickness (6%). Wild Type fruits possess a very thin cork layer.

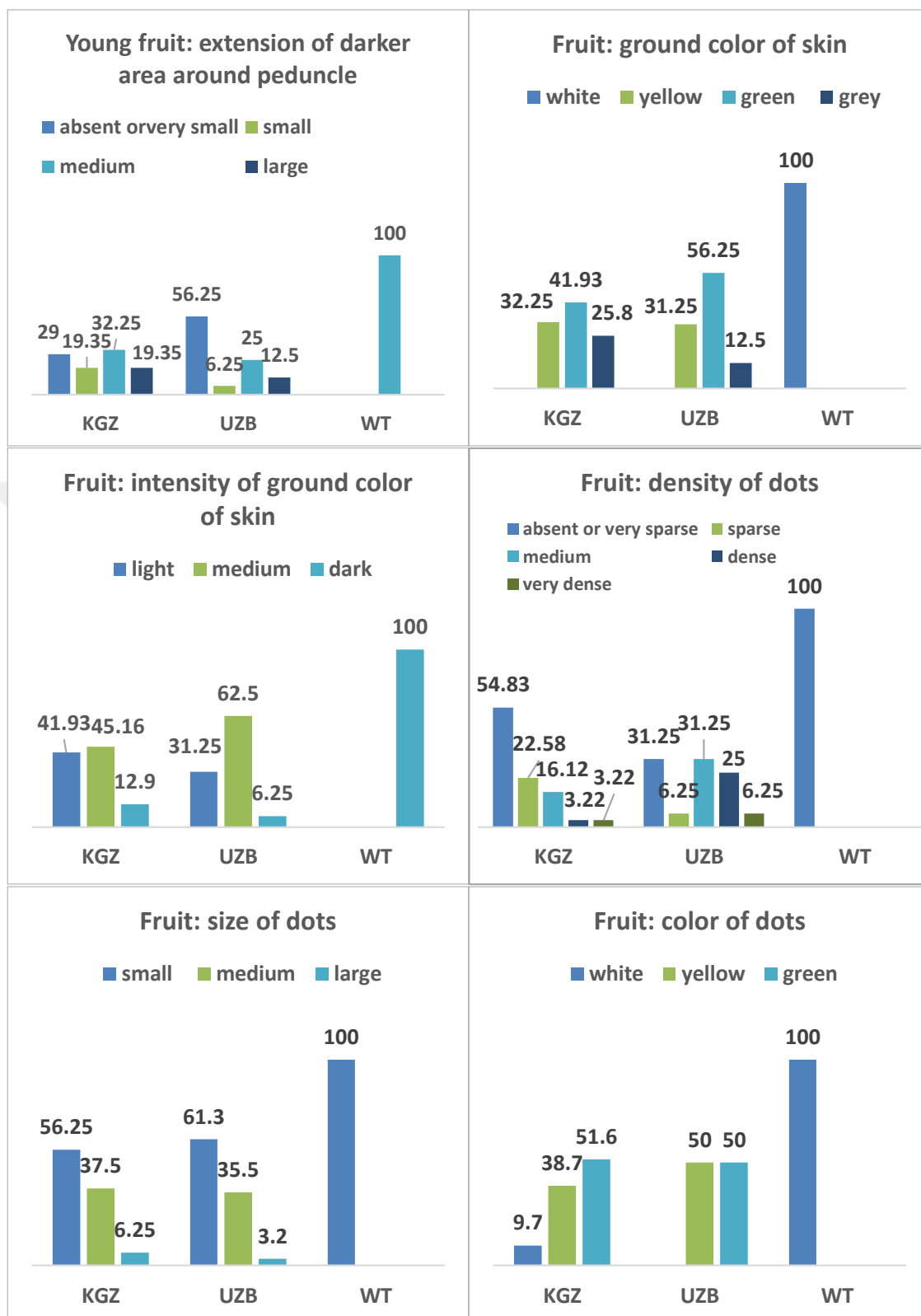
Fruit Cork Formation Pattern: The pattern of cork formation also varies among genotypes. Kyrgyz melons show a diverse distribution, with a significant presence of fruits exhibiting dots only (29%), followed by a combination of dots and linear patterns (45%), linear patterns alone (16%), and less frequent occurrences of linear and netted patterns (3% and 7% respectively). Uzbek melons display a more prominent presence of dots only (50%), followed by a combination of linear and netted patterns (25%), and a smaller proportion exhibiting linear patterns alone (6%) or a combination of dots and linear patterns (13%). Wild Type fruits exhibit a dots-only pattern of cork formation.

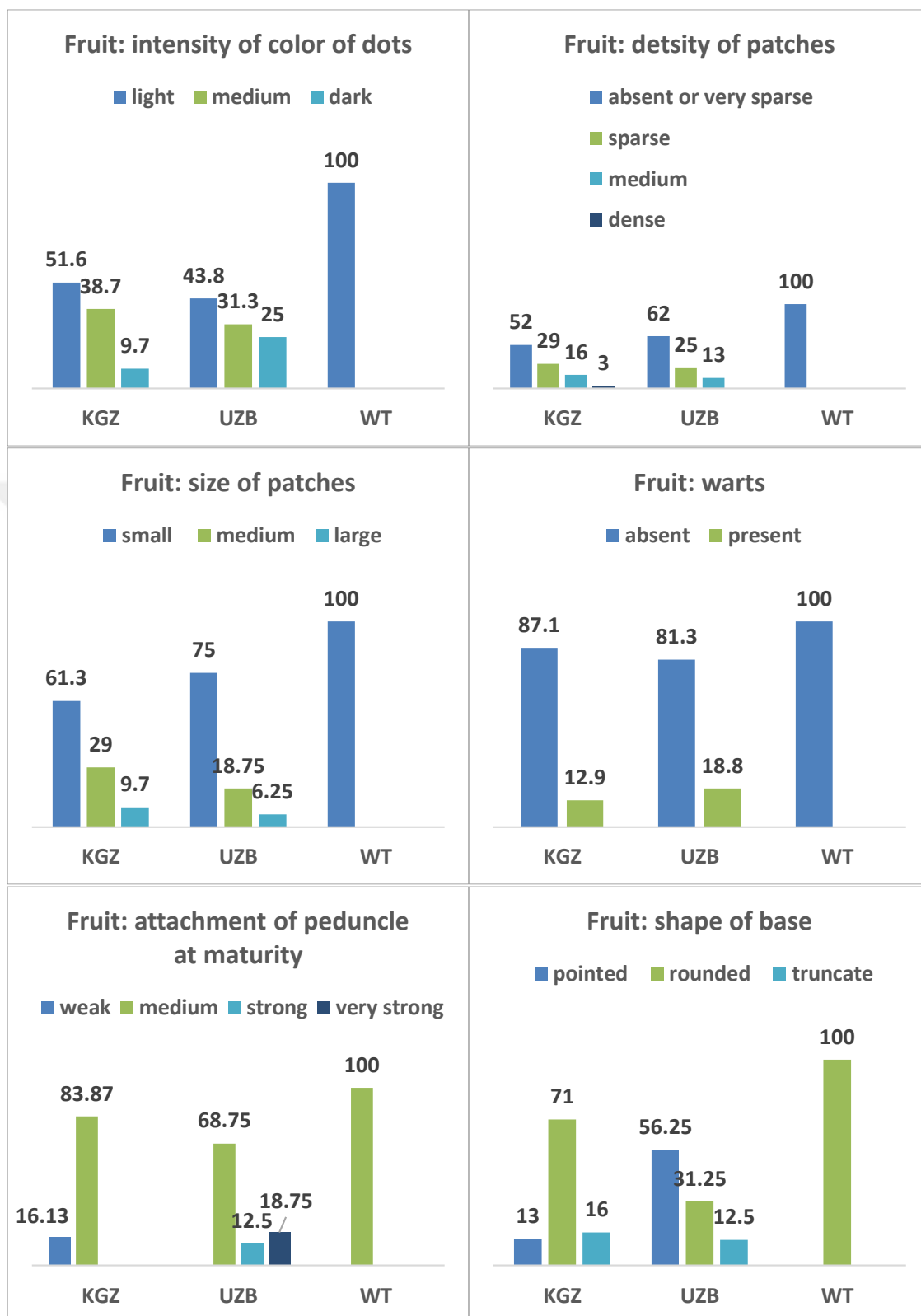
Fruit Flesh Firmness: Kyrgyz and Uzbek melons exhibit a similar distribution, with a dominant presence of medium firmness (48% and 44% respectively), followed by soft (39% and 19% respectively) and firm (19% and 37% respectively) flesh. Wild Type fruits had the firmest flesh among the genotypes.

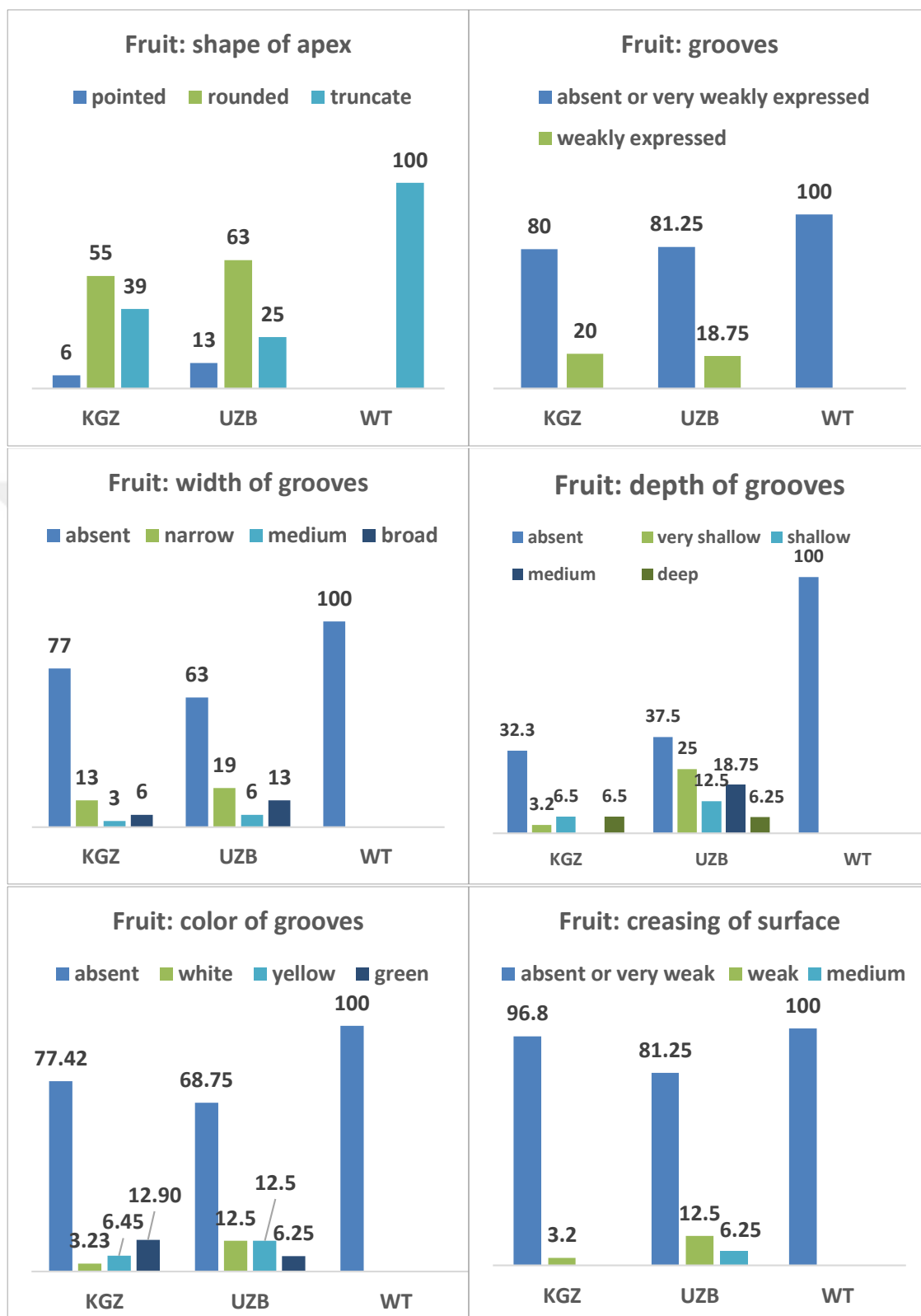












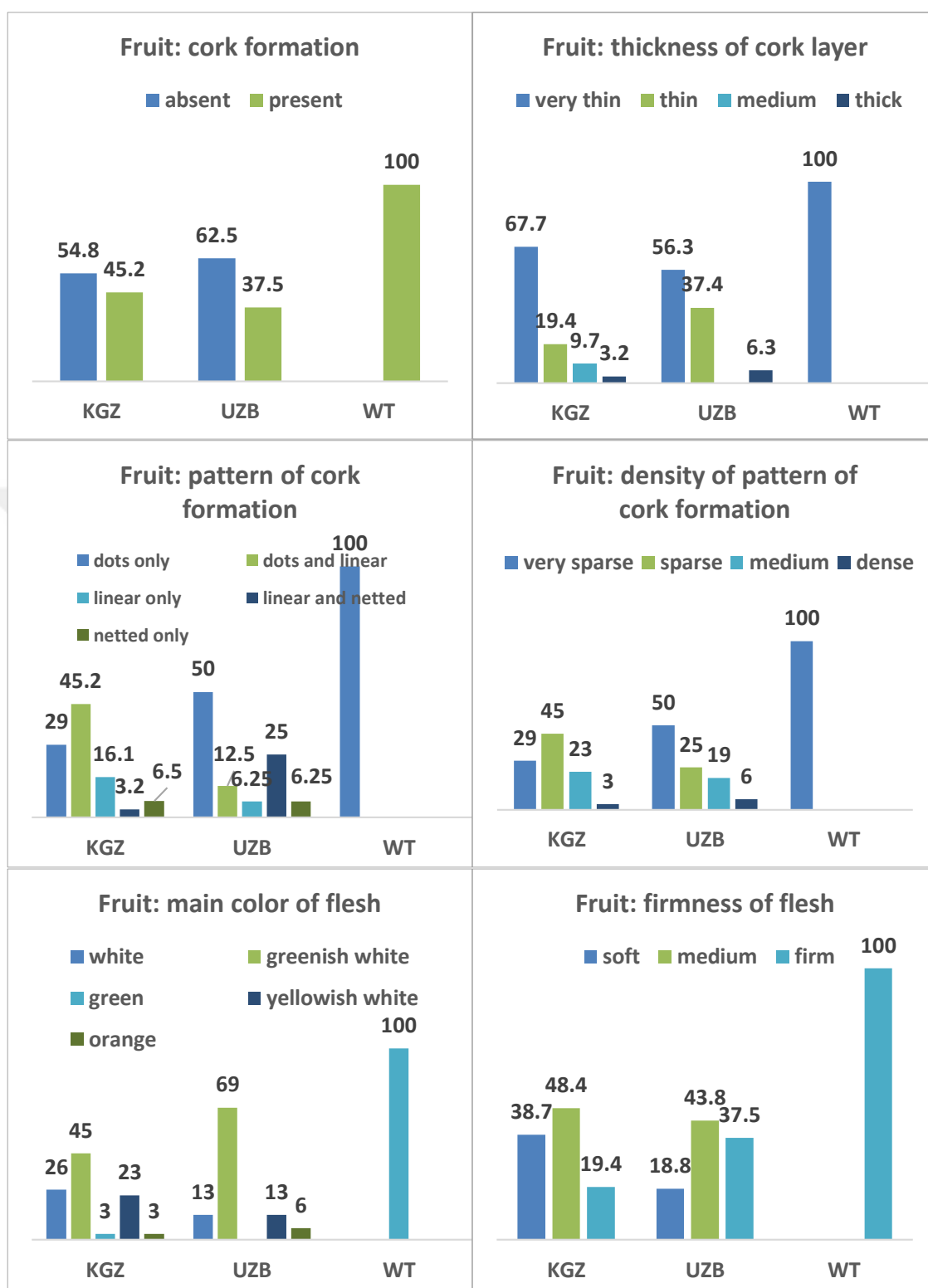


Figure 4.9. Morphological trait results of genotypes

4.3. Biochemical analysis

4.3.1. TSSC, pH, TA

Table 4.7. Biochemical analysis results (TSSC, pH, TA) of Kyrgyz, Uzbek and wild type genotypes from greenhouse and open field conditions

№	Greenhouse	TSSC	pH	TA	Open field	TSSC	pH	TA
1	KGZ-1	8	6.35	0.33	KGZ-1	6.5	4.82	0.81
2	KGZ-2	6.3	5.95	0.3	KGZ-2	4.4	5.3	0.87
3	KGZ-3	4.7	5.54	0.23	KGZ-3	6	4.98	1.15
4	KGZ-4	6	6.61	0.13	KGZ-4	5.1	4.87	1
5	KGZ-5	8.4	6.46	0.31	KGZ-5	8.4	5.11	1.85
6	KGZ-6	5.9	6.65	0.8	KGZ-6	3	5.37	0.72
7	KGZ-7	4	6.21	0.15	KGZ-7	6	5.96	0.81
8	KGZ-8	6.5	6.51	0.22	KGZ-8	6.8	6.1	0.83
9	KGZ-9	8.3	6.12	0.26	KGZ-9	5.5	5.18	0.73
10	KGZ-10	5.8	6.24	0.27	KGZ-10	4.9	6.47	0.83
11	KGZ-11	7.5	6.1	0.18	KGZ-11	4.7	5.98	1.16
12	KGZ-12	7.2	6.3	0.22	KGZ-12	3.3	4.81	1.26
13	KGZ-13	5.7	6.43	0.18	KGZ-13	4.2	6.37	1.08
14	KGZ-14	5.7	6.43	0.18	KGZ-14	3.7	6.45	0.95
15	KGZ-15	6.1	6.82	0.14	KGZ-15	6	6.6	0.98
16	KGZ-16	5.8	6.01	0.19	KGZ-16	2.6	4.34	1.1
17	KGZ-17	4.6	5.76	0.25	KGZ-17	3.9	5.79	0.6
18	KGZ-18	7.2	6.21	0.24	KGZ-18	3.1	5.77	0.44
19	KGZ-19	4.2	5.99	0.2	KGZ-19	2.7	4.92	0.53
20	KGZ-20	5.8	6.06	0.22	KGZ-20	2.8	5.53	0.7
21	KGZ-21	10	6.2	0.33	KGZ-21	8.4	5.96	1.39
22	KGZ-22	4.6	5.76	0.25	KGZ-22	6.2	6.16	1.01
23	KGZ-23	4.6	5.76	0.25	KGZ-23	5.9	5.75	0.62
24	KGZ-24	4.5	5.88	0.19	KGZ-24	4.1	5.1	0.75
25	KGZ-25	4.5	5.88	0.19	KGZ-25	4.3	5.73	0.52
26	KGZ-26	5.5	5.98	0.21	KGZ-26	2.5	5.12	0.89
27	KGZ-27	5.2	5.98	0.26	KGZ-27	3.1	4.62	0.93
28	KGZ-28	5.2	5.84	0.26	KGZ-28	7.4	5.34	1.4
29	KGZ-29	7	6.19	0.28	KGZ-29	4.2	5.63	0.91
30	KGZ-30	4.5	6.09	0.14	KGZ-30	4.8	5.27	1.45
31	KGZ-31	7.2	5.95	0.33	KGZ-31	3.2	4.73	1.1
32	UZB-1	5.5	5.95	0.33	UZB-1	4.3	5.21	0.93
33	UZB-2	5.5	6.01	0.21	UZB-2	4.02	5.25	0.59
34	UZB-3	4.3	5.96	0.32	UZB-3	2.7	5.63	0.61
35	UZB-4	6.4	6.26	0.17	UZB-4	4.4	5.1	1.64
36	UZB-5	5	5.97	0.77	UZB-5	3.1	5.6	0.49
37	UZB-6	3.9	5.61	0.3	UZB-6	3.4	5.41	0.59
38	UZB-7	4.4	5.56	0.22	UZB-7	3.2	4.51	1.17
39	UZB-8	5.3	5.86	0.23	UZB-8	2.5	5.35	0.56
40	UZB-9	5.5	5.73	0.36	UZB-9	2.6	4.96	0.8

Table 4.7. Contunied

41	UZB-10	3.7	5.81	0.31	UZB-10	3.9	5	0.86
42	UZB-11	8.4	5.64	0.44	UZB-11	4.2	5.29	1.02
43	UZB-12	7	6.17	0.25	UZB-12	4.2	5.17	0.44
44	UZB-13	6.4	6.26	0.29	UZB-13	6.2	5.49	0.98
45	UZB-14	8.1	5.81	0.44	UZB-14	6.3	5.23	0.52
46	UZB-15	7.2	6.07	0.29	UZB-15	5.2	5.16	1.09
47	UZB-16	6.4	6.22	0.3	UZB-16	5.1	4.85	0.59
48	WT-1	3.1	4.7	1.27	WT-1	2.9	4.34	1.09

In the Table 4.7. presents the biochemical analysis results for Total Soluble Solids Content (TSSC), pH, and Total Acidity (TA) of different genotypes under greenhouse and open field conditions, categorized into three groups: KGZ, UZB, and WT and table 4.8. shows descriptive statistics.

Greenhouse conditions; in the greenhouse, KGZ genotypes exhibit variable TSSC levels ranging from 4.0 to 10, with an average pH of approximately 6.23 and TA values between 0.13 and 0.33. Notably, KGZ-21 demonstrates the highest TSSC of 10 and KGZ-6 has the highest TA of 0.8 among KGZ genotypes. In contrast, UZB genotypes show TSSC values ranging from 3.7 to 8.4, with an average pH of around 5.99 and TA values between 0.17 and 0.44. UZB-11 exhibits the highest TSSC of 8.4, while UZB-4 has the lowest TA of 0.17. The wild type (WT) genotype demonstrates relatively lower TSSC levels ranging from 3.1 to 3.3, with an average pH of approximately 4.7 and TA values between 1.09 and 1.27.

Open Field Conditions; in the open field, KGZ genotypes display TSSC levels ranging from 2.5 to 8.4, with an average pH of around 5.43 and TA values between 0.44 and 1.85. KGZ-5 demonstrates the highest TSSC of 8.4, while KGZ-12 exhibits the highest TA of 1.26 among KGZ genotypes. Conversely, UZB genotypes show TSSC values ranging from 2.5 to 6.2, with an average pH of approximately 5.16 and TA values between 0.44 and 1.02. UZB-14 has the highest TSSC of 6.3, while UZB-3 demonstrates the highest TA of 1.02. In the open field, the WT genotype maintains consistent characteristics with relatively lower TSSC levels ranging from 2.9 to 4.8, an average pH of approximately 4.59, and TA values between 0.52 and 1.45.

Significant changes in Total Soluble Solids Content (TSSC), pH, and Total Acidity (TA) were seen within and across genotypes and settings, as indicated by the analysis. The KGZ genotype group demonstrated significant variations in total suspended solids concentration (TSSC) and pH levels between greenhouse and open field environments, with a tendency towards higher values in the greenhouse setting. In contrast, the UZB genotype group exhibited comparable patterns, but with varying degrees, suggesting that genotype-specific reactions to environmental condition were observed. In addition, the WT genotype group exhibited comparable biochemical measures in both greenhouse and open field settings, indicating that the genotype traits remain stable regardless of environmental fluctuations.

Can and Tütken (2022) explored the sweetness of the melons, measured by soluble solid content (SSC). The Ç-08 accession emerged as the clear leader, boasting the highest SSC value, indicating superior sweetness. Conversely, YYÜ-13 and YYÜ-19 accessions consistently underperformed in terms of sweetness, suggesting potential limitations for breeding programs focused on this characteristic.

The flavor profile of most fruits results from the interplay of sugar and organic acid levels, along with specific volatile compounds. While excessive acidity in melons is associated with diminished fruit quality, a moderate concentration of acids can enhance the overall palatability of the fruit (Tang et al., 2010). Typically, sour melons are characterized by ripe fruit pH values <5, while sweet melons exhibit pH values above 6 during maturity (Cohen et al., 2012).

Research on taste attributes has indicated that non-sour melon lines possess higher citric and malic acid levels in ripe fruits compared to isogenic lines derived from sour genotypes (Burger et al., 2003b). The genetic factor governing taste and acidity in melon fruit flesh is attributed to a single dominant locus known as So (Sour) or PH (Burger et al., 2003b; Harel-Beja et al., 2010).

Previous studies have reported melon pH values ranging from 4.5 to 6.7 (Cohen et al., 2012). Erdogan (2016) found an average pH value of 6.13 in melon genotypes from the lakes region, while Dal et al. (2017) observed pH values in their breeding lines ranging from 4.27 to 6.61. Melon genotypes originating from Iran and Afghanistan were reported to have pH values ranging between 4.19 and 5.7 (Bagheriyan et al., 2015). In the breeding populations created by Harel-Beja et al. (2010), the pH values of the parent lines varied between 4 and 6.5. The consistent similarity between these studies suggests that there is generally no significant deviation in pH values among different melon genotypes.

4.3.2. Leaf color

L*, a*, b* values determined from leaf samples taken from greenhouse and open field are given in Table 4.8 and graphical version shown in Figure 4.9.

Table 4.8. L*, a*, b* values of leaf samples taken from greenhouse and open field

Greenhouse	L	a	b	Open field	L	a	b
KGZ-1	39,55	-9,08	14,41	KGZ-1	38,17	-10,39	17,03
KGZ-2	41,54	-12,54	20,45	KGZ-2	39,24	-9,84	17,01
KGZ-3	50,07	-15,73	28,49	KGZ-3	37,12	-11,3	15,94
KGZ-4	45	-9,94	16,81	KGZ-4	40,89	-5,53	13,5
KGZ-5	42,51	-10,46	18,51	KGZ-5	36,82	-6,58	15,55
KGZ-6	42,53	-10,31	15,16	KGZ-6	36,21	-6,61	15,06
KGZ-7	37,08	-5,56	15,71	KGZ-7	39,56	-6,6	15,93
KGZ-8	35,34	-11,15	15,46	KGZ-8	38,68	-9,65	16,88
KGZ-9	37,8	-9,88	15,4	KGZ-9	36,8	-10,07	18,6
KGZ-10	46,66	-13,71	23,47	KGZ-10	39,78	-7,65	16,39
KGZ-11	39,47	-6,67	14,34	KGZ-11	34,52	-3,26	12,5
KGZ-12	42,58	-11,74	19,51	KGZ-12	32,21	-5,32	16,83

Table 4.8. Continued

KGZ-13	31,8	-4,41	11,15	KGZ-13	34,17	-9,31	16,79
KGZ-14	40,96	-12,13	18,33	KGZ-14	34,71	-5,82	11,73
KGZ-15	39,06	-10,03	14,51	KGZ-15	40,35	-6,07	11,62
KGZ-16	42,93	-11,46	21,38	KGZ-16	36,51	-7,92	14,32
KGZ-17	38,62	-10,97	15,95	KGZ-17	37,1	-13,21	18,75
KGZ-18	39,48	-10,96	17,69	KGZ-18	37,27	-8,19	17,58
KGZ-19	41,06	-13,63	20,35	KGZ-19	38,06	-8,67	14,86
KGZ-20	37,99	-10,51	15,29	KGZ-20	38,37	-11,29	20,08
KGZ-21	41,11	-11,7	17,52	KGZ-21	36,03	-5,21	11,29
KGZ-22	36,99	-7,7	11,33	KGZ-22	41,83	-8,19	17,37
KGZ-23	40,35	-6,07	11,62	KGZ-23	35,2	-6,26	12,13
KGZ-24	41,29	-4,72	17,65	KGZ-24	38,78	-6,95	11,7
KGZ-25	38,01	-11,01	14,4	KGZ-25	39,69	-8,57	17,94
KGZ-26	37,97	-5,05	13,11	KGZ-26	30,14	-3,6	11,69
KGZ-27	39,29	-12,76	19,31	KGZ-27	39,17	-6,49	13,94
KGZ-28	38,73	-14,76	16,39	KGZ-28	40,62	-12,58	18,35
KGZ-29	45,32	-13,64	21,53	KGZ-29	36,64	-10,73	14,05
KGZ-30	36,7	-12,04	13,47	KGZ-30	38,24	-12,37	17,3
KGZ-31	39,87	-9,69	15,87	KGZ-31	37,77	-8,37	14,2
UZB-1	38,24	-8,02	14,36	UZB-1	34,86	-9,51	13,27
UZB-2	48,92	-13,69	24,54	UZB-2	36,7	-9,29	16,64
UZB-3	39,5	-9,36	17,86	UZB-3	37,23	-10,32	16,75
UZB-4	38,08	-7,29	10,14	UZB-4	38,76	-9,86	15,89
UZB-5	35,86	-7,2	10,58	UZB-5	37,73	-7,63	16,56
UZB-6	35,12	-9,31	11,45	UZB-6	38,29	-12,16	16,33
UZB-7	37,38	-5,49	13,5	UZB-7	39,16	-12,03	18,21
UZB-8	43,6	-14,14	21,25	UZB-8	39,89	-7,06	17,13
UZB-9	41,18	-13,01	19,82	UZB-9	39,52	-13,82	20,01
UZB-10	64,77	-3,38	4,75	UZB-10	38,04	-5,97	14,32
UZB-11	40,48	-11,33	17,51	UZB-11	37,03	-5,46	15,39
UZB-12	47,57	-14,19	24,6	UZB-12	39,8	-11,32	18,71
UZB-13	39,77	-6,67	16,19	UZB-13	38,57	-11,69	17,75
UZB-14	35,42	-9,08	13,22	UZB-14	35,85	-8,09	15,45
UZB-15	43,15	-11,34	17,53	UZB-15	40,84	-8,86	17,69
UZB-16	44,94	-11,77	18,79	UZB-16	39,71	-8,75	16,45
WT	42,76	-8,49	14,14	WT	37,08	-6,29	9,14

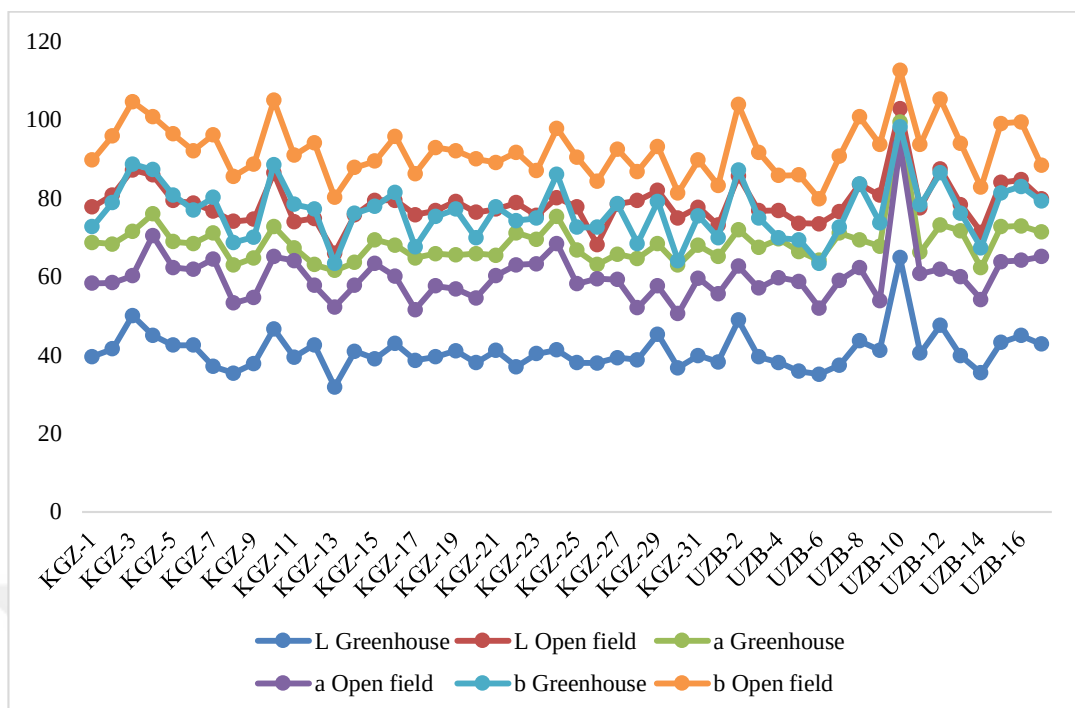


Figure 4.10. Display of the leaf color data of L^* , a^* , b^* values

Table 4.8 presents the L^* , a^* , b^* values of leaf samples obtained from both greenhouse and open field environments, encompassing different genotypes including KGZ, UZB, and WT. These values correspond to the brightness (L^*), redness (a^*), and yellowness (b^*) color attributes of the leaves, providing insights into their visual appearance and potential physiological characteristics.

Within the KGZ genotype group, the L^* values range from 31.8 to 50.07, a^* values range from -15.73 to -3.26, and b^* values range from 11.15 to 28.49. Noticeable variations are observed between greenhouse and open field conditions. In the greenhouse, leaf samples generally exhibit higher L^* values, indicating greater brightness, while in the open field, L^* values tend to be lower, suggesting reduced brightness. Additionally, differences in a^* and b^* values indicate variations in the redness and yellowness attributes of the leaves, reflecting potential differences in chlorophyll content and overall leaf pigmentation. These variations within the KGZ genotype group highlight the influence of environmental factors on leaf coloration and potentially, on physiological processes such as photosynthesis and stress response (Judkins and Wander 1950).

Similarly, within the UZB genotype group, the L^* values range from 35.12 to 64.77, a^* values range from -14.19 to -3.38, and b^* values range from 4.75 to 24.6. Distinct patterns in L^* , a^* , and b^* values are observed between greenhouse and open field environments. While L^* values may vary indicating differences in brightness, variations in a^* and b^* values suggest alterations in leaf pigmentation and potentially, in physiological responses to environmental conditions such as light intensity and temperature.

For the WT genotype, the luminance (L) values exhibit notable differences between greenhouse and open field conditions, with a recorded value of 42.76 in the

greenhouse, indicating relatively brighter leaves, compared to 37.08 in the open field, suggesting a decrease in brightness outdoors. Regarding chromaticity, the a-coordinate reflects a shift towards green hues, with values of -8.49 in the greenhouse and -6.29 in the open field, indicating a slight reduction in the shift towards green in outdoor settings. Similarly, the b-coordinate, representing the shift towards yellow hues, demonstrates differences between the environments, with values of 14.14 in the greenhouse and 9.14 in the open field, suggesting a decrease in the shift towards yellow in outdoor conditions.



4.4. Molecular analysis

4.4.1. SRAP results

Prechecking of primers involved testing 208 combinations of ME 1-13 forward and EM 1-16 reverse SRAP primers. The results showed a range of 0-8 bands (Figure 4.11, 4.12). For further investigation, combinations giving 6 or more bands were selected.

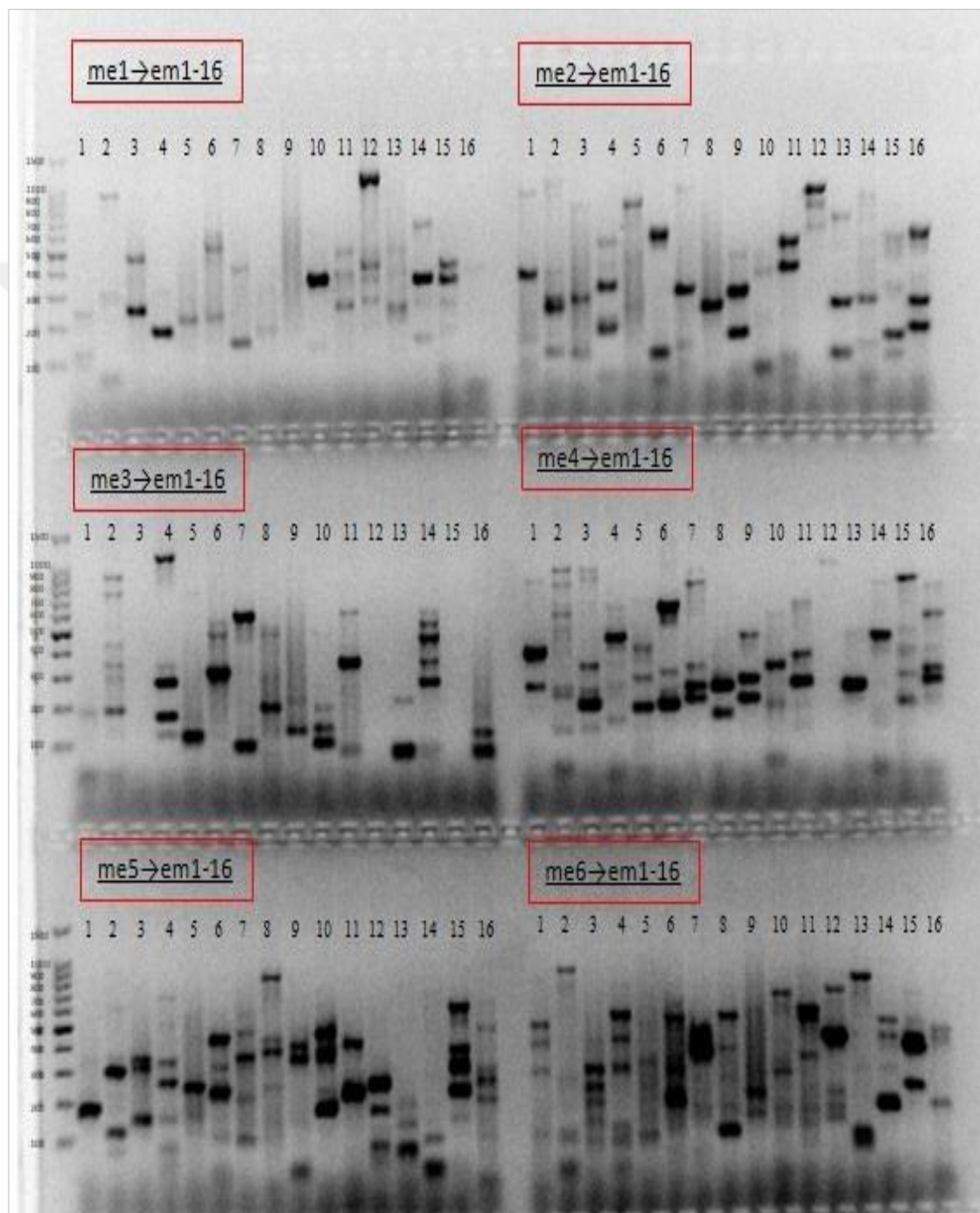


Figure 4.11. Cross-checking results of Me 1-6 forward and Em 1-16 reverse primers

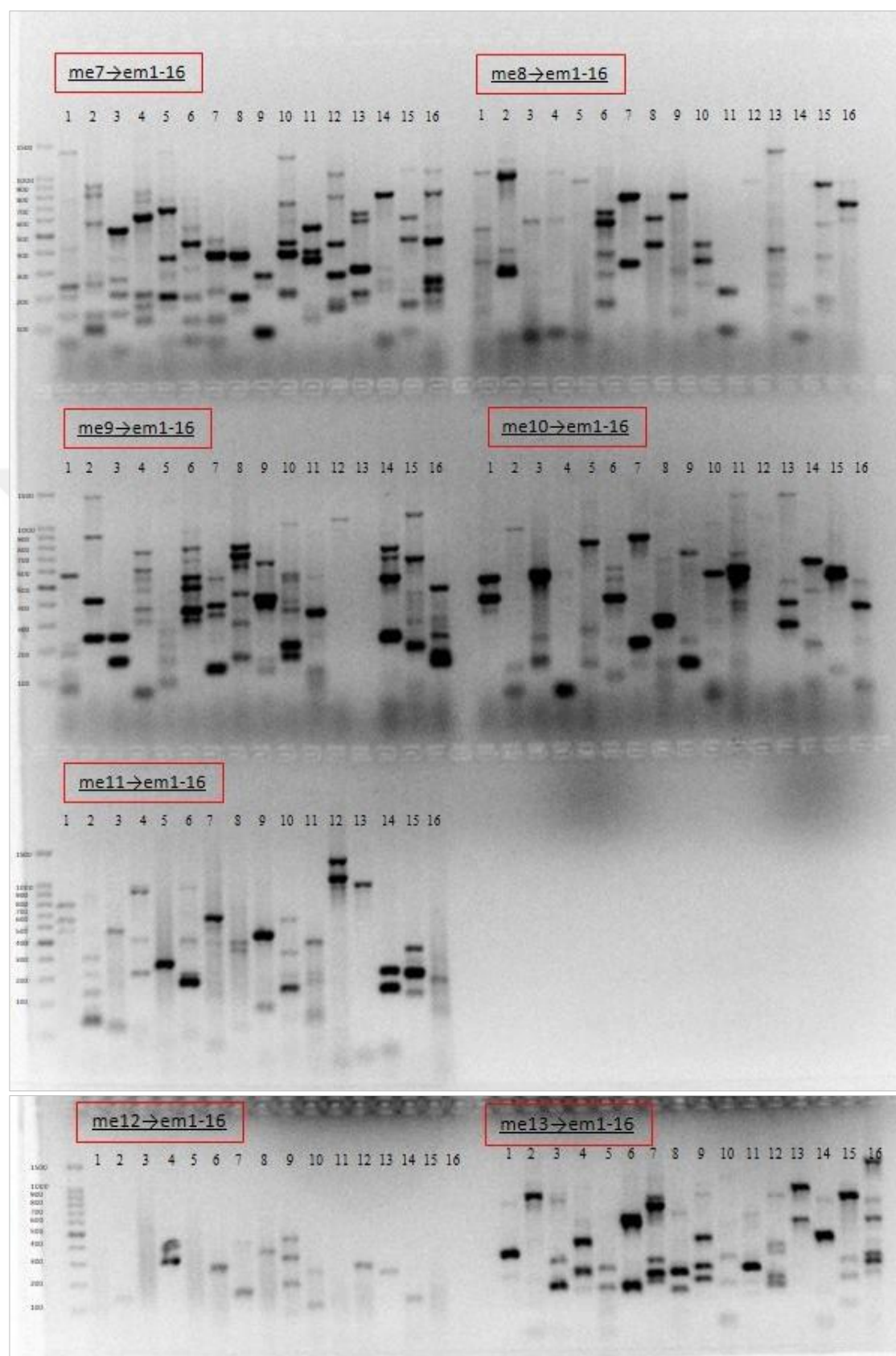


Figure 4.12. Cross-checking results of Me 7-13 forward and Em 1-16 reverse primers

The selected combinations for detailed PCR running are based on pre-screening results, specifically targeting combinations that produced 6 or more bands (Table 4.9). These combinations include various forward (Me1-Me13) and reverse (Em1-Em16) primers. Each combination represents a potential target region for further analysis in the study.

Table 4.9. Chosen combinations for detailed pcr running that gave 6 or more bands on pre-screening

Me3 – Em2	Me5 – Em15	Me7 – Em16
Me3 – Em4	Me6 – Em4	Me8 – Em6
Me3 – Em14	Me6 – Em6	Me9 – Em6
Me4 – Em2	Me7 – Em1	Me9 – Em10
Me4 – Em6	Me7 – Em2	Me9 – Em14
Me4 – Em15	Me7 – Em4	Me9 – Em15
Me4 – Em16	Me7 – Em6	Me13 – Em7
Me5 – Em4	Me7 – Em10	Me13 – Em12

The Table 4.10. provides an overview of the features of chosen SRAP amplified products, with each combination of SRAP markers exhibiting a specific range of band sizes, total bands (TB), polymorphic bands (PB), fraction of polymorphism (FP), polymorphic information content (PIC), and primer index (PI), as well as the overall range, mean, and sum for these features.

The chosen SRAP amplified products, as outlined in Table 4.10, display variations in several key traits across different primer pairs. For instance, considering the band size range, primer pairs exhibit diverse span lengths, from as low as 100 base pairs to as high as 3000 base pairs. This variation in band size may reflect differences in the genomic regions targeted by the primers and the resulting amplification efficiency.

Total bands (TB) also vary among the primer pairs, with some combinations yielding fewer bands (e.g., Me4+Em15 with 5 bands) and others producing more bands (e.g., Me4+Em6 with 10 bands). This discrepancy in total bands could be attributed to differences in the specificity and amplification efficiency of the primer pairs across the genomic regions of interest.

Similarly, the number of polymorphic bands (PB) differs across primer pairs, ranging from 3 bands (e.g., Me3+Em4) to 9 bands (e.g., Me9+Em10 and Me13+Em7). This variability suggests that certain primer pairs may be more effective at capturing genetic variation within the studied genotypes compared to others.

Table 4.10. Features of chosen SRAP amplified products used for analysis of genetic diversity of genotypes

SRAP marker	Band size (base pairs)	Total bands (TB)	Polymorphic bands (PB)	Fraction of polymorphism (FP)	Polymorphic information content (PIC)	Primer index (PI)
Me3+Em2	150-1000	7	7	1	0.48	1.64
Me3+Em4	150-1200	6	3	0.5	0.42	0.82
Me3+Em14	200-1200	9	7	0.78	0.44	1.28
Me4+Em2	130-800	7	6	0.86	0.35	1.41
Me4+Em6	100-700	10	8	0.8	0.48	1.31
Me4+Em15	250-600	5	4	0.8	0.48	1.31
Me4+Em16	200-1500	5	5	1	0.39	1.64
Me5+Em4	150-700	7	5	0.71	0.4	1.16
Me5+Em15	200-1350	8	8	1	0.44	1.64
Me6+Em4	100-900	10	9	0.71	0.47	1.16
Me6+Em6	150-1500	7	7	1	0.4	1.64
Me7+Em1	100-1500	8	8	1	0.21	1.64
Me7+Em2	100-900	9	5	0.56	0.35	0.92
Me7+Em4	100-1500	9	7	0.78	0.33	1.28
Me7+Em6	100-1000	9	7	0.78	0.5	1.28
Me7+Em10	100-3000	9	7	0.78	0.47	1.28
Me7+Em16	150-1000	7	5	0.71	0.28	1.16
Me8+Em6	150-1000	7	6	0.86	0.39	1.41
Me9+Em6	100-800	9	7	0.78	0.49	1.28
Me9+Em10	180-3000	9	9	1	0.47	1.64
Me9+Em14	200-2000	6	4	0.67	0.48	1.10
Me9+Em15	100-2000	8	8	1	0.5	1.64
Me13+Em7	200-1500	9	9	1	0.33	1.64
Me13+Em12	150-900	8	6	0.75	0.42	1.23
Range/	100-3000	188	157	0.83	0.42	1.35

MR (multiplex ratio) = TB/TP = 188/48 = 3.9

EMR (effective multiplex ratio) = MR × FP

MI (marker index) = EMR × Mean PIC

A total of 188 scoreable bands were obtained from 24 SRAP primers and then was used to reveal the genetic variation in a population of 48 melon genotypes, and 157 of the obtained bands showed polymorphism (Table 4.10).

Accordingly, the lowest polymorphic band production per primer was obtained from primer pairs Me4+Em15 and Me4+Em16 with 4 and 5 polymorphic bands, while the highest band production was obtained from primer Me4+Em6, Me5+Em15 with 10 bands. Primers pairs Me3+Em2, Me4+Em16, Me5+Em15, Me6+Em6, Me7+Em1, Me9+Em10, Me9+Em15 and Me13+Em7 showed 100% polymorphism. While the average polymorphism % of the primers studied was 83, the lowest polymorphism rate was found to be 50% in the Me3+Em4 primer pair.

The mean polymorphism information content (PIC) value was calculated as 0.42 for 48 melon genotypes. The minimum PIC value was obtained from 0.21 from

Me7+Em1 primer, while the highest PIC value (0.5) was obtained from Me7+Em6 and Me9+Em15 primer pair.

The primer index (PI) for the primers ranged from 0.82 (Me3+Em4) to 1.64 (Me3+Em2, Me4+Em16, Me5+Em15, Me6+Em6, Me7+Em1, Me9+Em10, Me9+Em15, Me13+Em7). The average PI value was calculated as 1.35.

Three different molecular marker types were used in Aziz's study (2023) to evaluate the genetic diversity of 57 melon genotypes: universal rice primer (URP), sequence-related amplified polymorphism (SRAP), conserved DNA derived polymorphism (CDDP), and inter-retrotransposon amplified polymorphism (IRAP). Significant genetic variation between groups was found in the SRAP analysis.

Researchers (Tanaka et al., 2022) explored the genetic diversity of melons along the Silk Road, focusing on Kazakhstan. They measured seed size and analyzed the DNA of 87 melon varieties using various markers. Interestingly, most Kazakh melons had large seeds, except for a couple of wild varieties. The analysis also revealed three main types of genetic material within the cytoplasm (the non-chromosomal part of the cell) of these melons. Two of these types were dominant in Kazakhstan and surrounding regions, suggesting a shared ancestry. Further analysis using DNA markers revealed two distinct genetic groups and one mixed group among the Kazakh melons. Notably, the mixed group was more frequent in the eastern part of the Silk Road, including Kazakhstan.

Yilmaz et al. (2021) analyzed the morphological and genetic characteristics of local *Cucumis melo* L. (melon) accessions that had been collected from several locations in northern Cyprus and Turkey using SRAP markers. The 32 melon accessions were divided into two groups based on morphology data, and our molecular data revealed that 56 bands in total were produced using 11 SRAP primer combinations, 11 of which were polymorphic at the molecular characterisation stage. The percentage rate of polymorphism changed between 0.69 - 0.96%.

Zhang (2012) studied eighteen *Cucumis* accessions (nine *C. sativus* and nine *C. melo*) that were collected from the three South Asian nations with the highest *Cucumis* diversity. Twenty-three qualitative and nine quantitative traits were measured. Of the nine quantitative traits, fruit weight values showed the greatest divergence, and among the eighteen accessions, there was significant diversity in twenty-three qualitative traits. There were not many genetic differences between any of the *C. sativus* and *C. melo* accessions. Despite their notable physical differences, the eighteen accessions studied in this study were found to have a close genetic link. This study's knowledge on unique *Cucumis* germplasms will help with breeding programs.

Zhang (2012) also used SRAP technology to identify the hybrid seed purity of one melon cultivar and to investigate the genetic relationships of 12 additional melon cultivars. A total of 78 polymorphic bands were amplified and 13 out of 40 SRAP markers were tested. Based on SRAP, clustering analysis revealed that the genetic variation index values of 12 melon cultivars ranged from 0.263 to 0.921. UPGMA phylogenetic analysis was able to classify these cultivars into 2 groups and 5 subgroups.

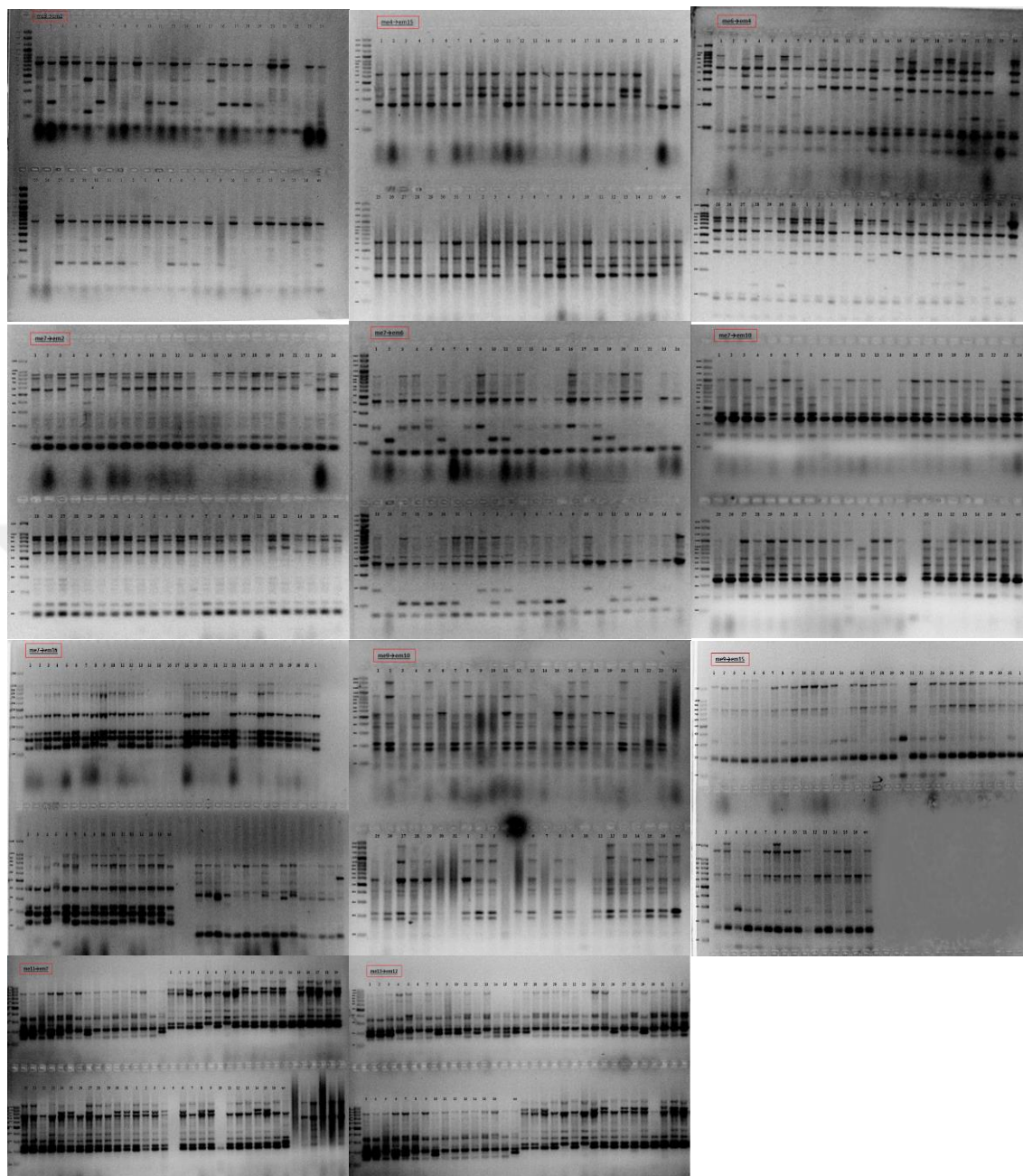


Figure 4.13. Representative PCR profiles obtained with SRAP primers.

Yildiz (2011) carried out another study to examine the genetic relationships between 63 Turkish melon (*Cucumis melo* L.) genotypes that were collected from different regions. The investigation involved comparing the molecular ISSR, SRAP, and RAPD markers of the Turkish melon genotypes with those of 19 foreign genotypes to investigate the taxonomic relationships and genetic variation of Turkish melon germplasm. Genetic similarity within groups varied from 0.46 to 0.96. Similar clusters were created by dividing genotypes that were related or that were collected from similar regions. The genotypes of the Southeastern Anatolian group were clearly distinguished from those of the Group cantalupensis (sweet) and Group inodorus. These findings supported Turkey's standing as the secondary center of melon genetic variation.

4.4.2. Fusarium PCR results

The analysis examined the resistance of melon genotypes of Kyrgyz, Uzbek and wild type to Fusarium wilt disease caused by Fom1 and Fom2 using PCR technique (Table 4.11). The PCR results, visualized on a gel, reveal the presence or absence of specific alleles associated with resistance to Fom1 and Fom2.

A significant part (21 out of 30) of displayed Kyrgyz genotypes indicative of Fom-1 resistance based on the PCR results. This includes accessions like KGZ-1, KGZ-2, KGZ-3, KGZ-4, KGZ-7, KGZ-10, KGZ-11, KGZ-14, KGZ-15, KGZ-16, KGZ-17, KGZ-18, KGZ-23, KGZ-24, KGZ-26, KGZ-28, KGZ-30, KGZ-31 showing the RR genotype, suggesting complete resistance to Fom1. Interestingly, KGZ-4, KGZ-9, KGZ-13 and KGZ-25 exhibited a mixed pattern, which due to the presence of both RR and rr individuals within the accession. Specifically, KGZ-4, KGZ-5, KGZ-8, KGZ-21, KGZ-22, and KGZ-27 all possess genotypes indicative of susceptibility (rr).

Uzbek accessions UZB-3, UZB-4, UZB-6, UZB-9, UZB-15, and UZB-16 displayed the homozygous Fom-1 resistant genotype (RR), indicating a high resistance to Fom-1. Conversely, accessions like UZB-10 and UZB-14, UZB-12 (33% of all examined plants), possessed the homozygous susceptible genotype (rr), suggesting susceptibility to Fom-1 infection. Interestingly, UZB-5, UZB-7 (partially resistant in 50% of individuals), and UZB-12 (partially resistant in 66% of individuals) exhibited the Rr genotype, indicative of partial resistance.

The wild type melon accession exhibited a resistance to Fom1.

The Kyrgyz germplasm displayed a range of resistance levels. Some accessions, like KGZ-3 (partially resistant in 50%), KGZ-9, KGZ-10, KGZ-14 (partially resistant in 66%), KGZ-15, KGZ-22 (partially resistant in 40%), KGZ-24, KGZ-25, KGZ-26, KGZ-27 (partially resistant in 20%), exhibited genotypes suggestive of complete resistance (RR) to Fom2. Unfortunately, a significant portion of the Kyrgyz accessions, including KGZ-1, KGZ-2, KGZ-3 (50%), KGZ-4, KGZ-5, KGZ-6, KGZ-7, KGZ-8, KGZ-11, KGZ-12, KGZ-13 (75%), KGZ-14 (33%), KGZ-16, KGZ-17, KGZ-18, KGZ-19, KGZ-20, KGZ-21, KGZ-27 (60%), KGZ-28, KGZ-30, and KGZ-31, showing genotypes indicative of susceptibility (likely rr) to Fom2.

The Uzbek germplasm offered fewer accessions with complete resistance. Only UZB-8, UZB-10, UZB-11 (66%), UZB-14 (66%) displayed genotypes suggesting resistance to Fom2. Similar to the Kyrgyz lines, UZB-11 and 14 exhibited mixed populations with some individuals being susceptible. The majority of Uzbek accessions, including UZB-2, UZB-3, UZB-4, UZB-5, UZB-6, UZB-7, UZB-9, remaining portion (33%) of UZB-11, UZB-12, UZB-14 (33%), UZB-15, and UZB-16, displaying genotypes indicative of susceptibility to Fom2.

The wild type accession displayed a mixed response, with half the individuals resistant and the other half susceptible.

Several accessions from both regions, including KGZ-3, KGZ-10, KGZ-14, KGZ-15, KGZ-24, KGZ-25, and KGZ-26, and UZB-8, displayed resistance to both Fom1 and

Fom2 races. These accessions, along with the wild type (partially resistant in 50% of individuals), represent promising candidates for breeding programs focused on developing melon cultivars with durable resistance against Fusarium wilt. It's important to remember that further confirmation through pathogen inoculation is crucial to definitively determine the actual resistance levels of these accessions.

Table 4.11. Results of PCR for Fom1 and Fom2

Genotype	Plant no	Fom1 (Fusarium 0,2)	Fom2 (Fusarium 0,1)	Genotype	Plant no	Fom1 (Fusarium 0,2)	Fom2 (Fusarium 0,1)	Genotype	Plant no	Fom1 (Fusarium 0,2)	Fom2 (Fusarium 0,1)
KGZ-1	1	RR	rr	KGZ-10	1	RR	R	KGZ-19	3	RR	rr
	2	RR	rr		2	RR	R		4	RR	rr
	3	-	rr		3	RR	R	KGZ-20	1	RR	rr
KGZ-2	1	RR	rr	KGZ-11	1	RR	rr		2	RR	rr
	2	RR	rr		2	RR	rr		3	RR	rr
	3	RR	rr	KGZ-12	1	rr	rr	KGZ-21	1	rr	rr
KGZ-3	1	RR	R		2	rr	rr		2	rr	rr
	2	RR	rr		3	rr	rr		3	rr	-
KGZ-4	1	rr	rr		4	rr	rr		4	rr	rr
	2	-	-	KGZ-13	1	Rr	rr		5	rr	rr
	3	RR	rr		2	-	R		6	rr	rr
	4	rr	rr		3	-	rr	KGZ-22	1	rr	rr
	5	rr	rr		4	-	rr		2	rr	rr
	6	rr	rr	KGZ-14	1	RR	-		3	rr	R
KGZ-5	1	rr	rr		2	RR	rr		4	rr	R
	2	rr	rr		3	RR	R	KGZ-23	1	RR	rr
	3	rr	rr		4	RR	R		2	RR	rr
	4	rr	rr	KGZ-15	1	RR	R		3	RR	rr
KGZ-6	1	-	-		2	RR	R		4	-	rr
	2	rr	rr		3	RR	R	KGZ-24	1	RR	R
	3	rr	rr	KGZ-16	1	-	rr		2	RR	R
	4	rr	rr		2	RR	rr	KGZ-25	1	RR	R
	5	rr	rr		3	RR	rr		2	RR	R
	6	rr	rr		4	RR	rr		3	RR	R
KGZ-7	1	RR	rr	KGZ-17	1	RR	rr		4	RR	R
	2	RR	rr		2	RR	rr		5	RR	R
	3	RR	rr	KGZ-18	1	RR	rr		6	Rr	R
	4	RR	rr		2	RR	rr	KGZ-26	1	RR	R
	5	RR	-		3	RR	rr		2	RR	R
KGZ-8	1	rr	rr		4	RR	rr		3	RR	R
	2	rr	rr		5	RR	rr		4	RR	R
	3	rr	rr		6	RR	rr		5	RR	rr
	4	rr	rr	KGZ-19	1	RR	rr	KGZ-27	1	-	-
KGZ-9	1	Rr	R		2	RR	rr		2	-	rr

Table 4.11. Continued

KGZ-27	3	rr	R	UZB-2	3	rr	rr	UZB-9	2	-	-
	4	rr	R	UZB-3	1	RR	rr		3	RR	rr
	5	rr	rr		2	-	rr		4	RR	rr
	6	rr	rr	UZB-4	1	RR	rr	UZB-10	1	-	R
KGZ-28	1	RR	rr		2	RR	rr		2	rr	R
	2	RR	-	UZB-4	3	RR	rr	UZB-11	1	-	R
KGZ-30	1	RR	rr		4	RR	rr		2	rr	rr
	2	RR	rr		5	RR	rr		3	-	R
	3	RR	rr	UZB-5	1	Rr	rr	UZB-12	1	rr	rr
KGZ-31	1	RR	rr		2	Rr	rr		2	Rr	rr
	2	RR	rr		3	Rr	rr		3	Rr	rr
	3	RR	rr	UZB-6	1	RR	rr	UZB-14	1	-	R
	4	RR	rr		2	RR	rr		2	rr	rr
	5	RR	rr		3	RR	rr		3	-	R
WT-1	1	RR	R	UZB-7	1	RR	rr	UZB-15	1	RR	rr
	2	RR	rr		2	Rr	rr	UZB-16	1	RR	rr
	3	RR	rr	UZB-8	1	RR	R		2	RR	rr
	4	RR	R		2	RR	R		3	RR	rr
UZB-2	1	rr	rr		3	RR	R		4	RR	rr
	2	rr	rr	UZB-9	1	RR	rr				

RR: Homozygous dominant

Rr: Heterozygous

rr: Homozygous recessive

-: Missing data

Sabahi et al. (2020) investigated the genetic makeup of *Fusarium oxysporum* f. sp. melonis (Fom), a fungus causing wilt disease in melons. They focused on strains from Iran, a region with a long history of melon cultivation. By analyzing the DNA of 33 Fom strains, the researchers discovered 40 new genes potentially linked to causing disease in melons. Was identified nine distinct groups (lineages) of Fom based on their genetic similarities. Interestingly, some geographically distant lineages shared similar disease-causing genes, suggesting these fungi can swap genetic material (horizontal gene transfer). This process may contribute to the emergence of new and more harmful Fom strains. The study also identified a specific lineage (Race 1.2) that can bypass the defenses (resistance genes) typically used in melons. This race was found in three lineages, with two being particularly common in Iran. Furthermore, the researchers discovered a new variant of a gene that normally helps the fungus evade detection by melon resistance proteins. This new variant allows the fungus to infect even melons bred to resist Fom.

Researchers in Tunisia (Chikh-Rouhou et al. 2021) conducted a study to find new sources of resistance against *Fusarium* wilt disease in melons at 27 local melon varieties obtained from farmers. The molecular analysis showed that 13 of the varieties carried a specific resistance gene (Fom-1) - seven had two copies (homozygous) and six had one copy (heterozygous). This gene provides resistance against races 0 and 2 of the *Fusarium* wilt fungus. Additionally, two other varieties had a different resistance gene (Fom-2) in

a single copy, offering protection against races 0 and 1. Two varieties displayed a high level of resistance even against the particularly aggressive race 1.2.

Sebastiani et al. (2017) investigated the genetic basis of resistance to *Fusarium oxysporum* f. sp. *melonis* race 1.2 (FOM1.2) in melon and the molecular mechanisms underlying the melon-FOM1.2 interaction. Through RNA-Seq analysis, they identified differentially expressed genes (DEGs) in resistant (NAD) and susceptible (Charentais-T) melon genotypes at 24 and 48 hours post-inoculation (hpi) with FOM1.2. NAD showed a prompt activation of defense responses, with a higher number of DEGs compared to Charentais-T. Gene Ontology (GO) enrichment analysis highlighted GO terms related to fungal infection response and pathways involving calcium-mediated signaling and hormone crosstalk, indicating their crucial roles in NAD's resistance to FOM1.2.

Miller et al. (2017) studied NBL genes potentially linked to melon resistance against Fom races and PRSV. The presence of extra NB domains and splice variants suggest complex regulatory mechanisms. Fungal Avr homologs challenge the "gene-for-gene" model, highlighting the need for further investigation into their role. Proteomic analysis revealed up-regulated melon proteins and fungal proteins in xylem sap, offering insights into plant defense responses and potential virulence factors. These findings pave the way for future research on NBL gene function, Avr homolog interactions, and development of molecular markers for breeding resistant melon cultivars.

Oumouloud et al. (2015) identified the Fom-1 gene linked to melon resistance against *Fusarium* wilt races 0 and 2. They cloned and sequenced the gene, revealing variations in resistant melons that potentially affect protein function. Fom-1 expression increased upon fungal infection, suggesting its role in defense. The predicted Fom-1 protein structure aligns with disease resistance genes. Most importantly, they developed CAPS markers based on single nucleotide polymorphisms in Fom-1, allowing for efficient screening of melon germplasm for resistance in breeding programs.

In the investigation of Oumouloud et al. (2013) was researched the resistance of various melon accessions against *Fusarium* wilt, with a specific focus on race 1.2. While the conventional understanding portrays resistance to race 1.2 as predominantly recessive and polygenic, their findings hinted at the presence of race-specific effects in certain instances. The study encompassed the inoculation of melon seedlings with six Fom isolates employing two distinct procedures, followed by a meticulous assessment of symptom severity spanning four weeks. Interestingly, the 'tray immersion' inoculation method emerged as more adept at discerning subtle resistance factors linked to polygenic partial resistance. Notably, several melon accessions showed resistance against all Fom isolates, underscoring a broad-spectrum resistance profile.

4.4.3. Anthracnose and powdery mildew observations

An observation of anthracnose and powdery mildew susceptibility was conducted on various melon genotypes, including Kyrgyz (KGZ), Uzbek (UZB), and wild type (WT) accessions (Table 4.12). The observations were scored on a scale of 0 (no symptoms) to 5 (very intense symptoms).

Several accessions exhibited high susceptibility (scores of 4 or 5) to anthracnose, including KGZ-1, KGZ-3, KGZ-4, KGZ-5, KGZ-7, KGZ-9, KGZ-12, KGZ-17, KGZ-19, KGZ-21, KGZ-22, KGZ-25, KGZ-30, and most Uzbek accessions (UZB-2, UZB-3, UZB-4, UZB-5, UZB-6, UZB-8, UZB-15). A few accessions showed moderate susceptibility (scores of 2 or 3), including KGZ-2, KGZ-6, KGZ-10, KGZ-11, KGZ-13, KGZ-16, KGZ-23, KGZ-24, KGZ-27, KGZ-28, and some Uzbek accessions (UZB-4, UZB-7, UZB-9, UZB-10, UZB-11, UZB-14). Encouragingly, KGZ-13, KGZ-14, KGZ-15 displayed low susceptibility (score 1) to anthracnose and only UZB-12 showed completely resistance to anthracnose. The wild type accession (WT-1) showed low susceptibility to anthracnose.

Similar to anthracnose, several accessions were highly susceptible (scores of 4 or 5) to powdery mildew, including KGZ-22, KGZ-23, KGZ-24, KGZ-25, KGZ-26, KGZ-30 and most Uzbek accessions (UZB-2, 3, 4, 5, 8, 15). A larger portion of accessions showed moderate susceptibility (scores of 2 or 3) to powdery mildew compared to anthracnose. This includes KGZ-1, KGZ-2, KGZ-3, KGZ-6, KGZ-7, KGZ-8, KGZ-11, KGZ-12, KGZ-16, KGZ-17, KGZ-19, KGZ-21, KGZ-23, KGZ-24, KGZ-28, from Uzbek genotypes UZB-2, UZB-3, UZB-4, UZB-5, UZB-6, UZB-8, UZB-11, UZB-15.

Table 4.12. Results of observation for anthracnose and powdery mildew

Genotype	Anthracnose Observation (0- 5)**	Powdery mildew observation (0- 5)**	Genotype	Anthracnose Observation (0- 5)**	Powdery mildew observation (0- 5)**
KGZ-1	4	2	KGZ-24	3	4
KGZ-2	2	1	KGZ-25	5	5
KGZ-3	5	3	KGZ-26	5	5
KGZ-4	4	1	KGZ-27	2	1
KGZ-5	4	1	KGZ-28	3	1
KGZ-6	3	3	KGZ-30	5	5
KGZ-7	5	2	KGZ-31	4	2
KGZ-8	4	3	WT-1	1	1
KGZ-9	5	3	UZB-2	4	2
KGZ-10	2	2	UZB-3	4	2
KGZ-11	3	3	UZB-4	3	2
KGZ-12	4	3	UZB-5	4	2
KGZ-13	2	2	UZB-6	5	2
KGZ-14	1	1	UZB-7	2	1
KGZ-15	1	0	UZB-8	4	2
KGZ-16	3	2	UZB-9	3	1
KGZ-17	4	3	UZB-10	2	1
KGZ-18	5	2	UZB-11	3	2
KGZ-19	4	2	UZB-12	0	1
KGZ-20	5	2	UZB-14	3	1
KGZ-21	4	2	UZB-15	4	2
KGZ-22	4	4	UZB-16	1	1
KGZ-23	3	4			

'0' no symptoms

'5' symptoms are very intense

Low susceptibility (scores of 0 or 1) to powdery mildew exhibited in genotypes KGZ-2, KGZ-4, KGZ-5, KGZ-14, KGZ-27, KGZ-28, UZB-7, UZB-9, UZB-10, UZB-12, UZB-14, UZB-16, making them potentially valuable for breeding programs.

The wild type accession (WT-1) showed low susceptibility to powdery mildew.

Overall, the analysis revealed a range of susceptibility levels to both anthracnose and powdery mildew within the melon germplasm. Notably, some accessions, like KGZ-13, KGZ-14, KGZ-15, and UZB-12, displayed low susceptibility to both diseases. These resistant genotypes offer promising resources for developing disease-resistant melon cultivars.

4.5. Statistical analysis

4.5.1. Morphological analysis

4.5.1.1. Descriptive statistics of morphological traits

Table 4.13. Descriptive statistics of morphological characteristics examined in the studied Kyrgyz, Uzbek and wild type accessions

Variable	Character	Mean	SD	CV%	Min	Max
Q1	Leaf blade: size	4.83	1.58	32.88	3	7
Q2	Leaf blade: development of lobes	3.95	1.16	29.46	3	7
Q3	Leaf blade: length of terminal lobe	4.16	1.53	36.83	3	7
Q4	Leaf blade: dentation of margin	5.2	1.55	29.89	7	7
Q5	Leaf blade: blistering	4.12	1.16	28.12	3	7
Q6	Leaf shape	1.45	0.65	44.64	1	1
Q7	Inflorescence: sex expression	1.1	0.3	27.96	1	2
Q8	Young fruit: density of dots	5.2	2.55	48.98	1	9
Q9	Young fruit: size of dots	5	1.59	31.39	3	9
Q10	Young fruit: contrast of dot color/ground color	5.5	1.72	31.38	3	7
Q11	Young fruit: conspicuousness of groove coloring	1.54	1.47	95.52	1	7
Q12	Young fruit: intensity of groove coloring	3.12	0.48	15.66	3	5
Q13	Young fruit: length of peduncle	5.75	1.46	25.49	3	7
Q14	Young fruit: thickness of peduncle 1 cm from fruit	4.95	1.27	25.63	3	7
Q15	Young fruit: extension of darker area	3.54	2.28	64.59	1	7
Q16	Fruit: position of maximum diameter	1.93	0.56	28.98	1	3
Q17	Fruit: shape in longitudinal section	4.5	2.54	56.52	1	8
Q18	Fruit: shape	3.12	2.23	71.59	1	9
Q19	Fruit: ground color of skin	2.85	0.77	27.03	1	4
Q20	Fruit: intensity of ground color of skin	4.41	1.3	29.48	3	7
Q21	Fruit: density of dots	3.12	2.45	78.56	1	9
Q22	Fruit: size of dots	3.91	1.16	29.72	3	7
Q23	Fruit: color of dots	2.41	0.64	26.77	1	3
Q24	Fruit: intensity of color of dots	4.29	1.45	33.97	3	7

Table 4.13. Continued

Q25	Fruit: detsity of patches	2.25	1.63	72.48	1	7
Q26	Fruit: size of patches	3.83	1.29	33.75	3	7
Q27	Fruit: warts	2.16	2.85	131.69	1	9
Q28	Fruit: attachment of peduncle at maturity	5.12	1.26	24.69	3	9
Q29	Fruit: shape of base	1.87	0.64	34.13	1	3
Q30	Fruit: shape of apex	2.27	0.6	26.86	1	3
Q31	Fruit: grooves	1.18	0.39	33.22	1	2
Q32	Fruit: width of grooves	1.25	2.23	178.89	3	7
Q33	Fruit: depth of grooves	1.1	2.08	188.90	3	7
Q34	Fruit: color of grooves	0.6	1.08	179.83	3	3
Q35	Fruit: creasing of surface	1.33	1.19	89.32	1	7
Q36	Fruit: cork formation	4.33	3.98	91.98	1	9
Q37	Fruit: thickness of cork layer	2	1.59	79.89	1	7
Q38	Fruit: pattern of cork formation	2.14	1.22	56.86	1	5
Q39	Fruit: density of pattern of cork formation	2.83	1.74	61.49	1	7
Q40	Fruit: maximum width of flesh in	5.12	1.51	29.48	3	7
Q41	Fruit: main color and hue of flesh	2.29	1.14	50.08	1	5
Q42	Fruit: firmness of flesh	4.83	1.47	30.58	3	7
Q43	Greenhouse: leaf length	27.68	4.4	15.90	14.5	36
Q44	Greenhouse: leaf length from the end of petiole till apix	20.9	3.87	18.56	11.5	36
Q45	Greenhouse: leaf width	27.92	5.08	18.22	13.5	38
Q46	Greenhouse: petiole length	26.13	5.9	22.59	10	38.5
Q47	Greenhouse: distance between 2 nodes	11.73	1.81	15.46	6	16
Q48	Greenhouse: stem thickness	9.81	1.6	16.33	5	13.43
Q49	Greenhouse: length of stem torn	2.2	0.43	19.91	1.39	3.31
Q50	Open field: leaf length	17.61	2.41	13.70	11	22
Q51	Open field: leaf length from the end of petiole till apix	14.13	2.06	14.59	8	18
Q52	Open field: leaf width	18.77	2.65	14.15	11	24
Q53	Open field: petiole length	22.02	5.35	24.33	10	31
Q54	Open field: distance between 2 nodes	9.41	2.29	24.39	5	14
Q55	Open field: stem thickness	7.59	2.63	34.75	0.8	1.03
Q56	Greenhouse: fruit weight	1.92	0.5	26.14	0.13	2.88
Q57	Greenhouse: fruit length	23.43	5.24	22.38	7.8	35
Q58	Greenhouse: fruit width	13.92	1.56	11.21	11	17
Q59	Greenhouse: diameter of seed pot	6.17	1.09	17.74	3.5	8.5
Q60	Greenhouse: shelf thickness	0.75	0.27	36.44	0.39	1.57
Q61	Greenhouse: seconder shelf thickness	6.95	4.12	59.39	1.34	2.93
Q62	Greenhouse: fruit flesh thickness	35.05	7.56	21.58	3.12	49.10
Q63	Greenhouse: TSSC	6.07	1.57	25.96	3.1	10
Q64	Greenhouse: pH	6.04	0.34	5.72	4.7	6.82
Q65	Greenhouse: TA	0.29	0.19	64.24	0.13	1.27
Q66	Open field: fruit weight	4.02	1.82	45.39	0.58	8.8
Q67	Open field: fruit length	27.36	8.97	32.80	5.68	44

Table 4.13. Continued

Q68	Open field: fruit width	16.79	3.96	23.59	4.052	26
Q69	Open field: diameter of seed pot	7.89	2.18	27.64	3.257	14
Q70	Open field: shelf thickness	0.6	0.18	30.80	0.16	0.94
Q71	Open field: seconder shelf thickness	6.85	4.08	59.60	0.740	2.23
Q72	Open field: fruit flesh thickness	46.12	11.7	25.36	6.8	7.6
Q73	Open field: TSSC	4.04	1.79	44.49	1.2	8.4
Q74	Open field: pH	5.36	0.54	10.19	4.34	6.6
Q75	Open field: TA	0.90	0.31	34.83	0.44	1.85
Q76	Seed: length	3.25	0.72	22.44	1	5
Q77	Seed: width	2.75	0.48	17.59	1	3
Q78	Seed: shape	1.52	0.5	33.20	1	2
Q79	Seed: color	1.75	0.56	32.28	1	3

Descriptive statistics (Table 4.13) examined the descriptive statistics (mean, standard deviation, coefficient of variation) for 79 morphological and biochemical characteristics of 48 genotypes, categorized into three groups.

Leaf blade size (Q1) exhibited a mean of 4.83 (SD = 1.589), indicating a moderate degree of variability (CV% = 32.88%). Similarly, leaf blade development of lobes (Q2) had a mean of 3.95 (SD = 1.166) and a CV% of 29.46%, with values ranging from 3 to 7. The length of the terminal lobe (Q3) showed a mean of 4.16 (SD = 1.534) and a CV% of 36.83%.

In contrast, leaf blade dentation of margin (Q4) displayed a higher mean of 5.208 (SD = 1.55) and a CV% of 29.89%, with values clustered around 7, suggesting less variability within this characteristic. Leaf blade blistering (Q5) also exhibited moderate variability, with a mean of 4.12 (SD = 1.160) and a CV% of 28.12%. Leaf shape (Q6) showed the highest coefficient of variation at 44.64%, with a mean of 1.4583 (SD = 0.65), indicating considerable diversity within this trait.

Inflorescence sex expression (Q7) had a mean of 1.1 (SD = 0.3) and a CV% of 27.96%, suggesting some variability in this characteristic across the examined accessions. The mean density of dots on young fruit is 5.2, with a standard deviation of 2.5, indicating considerable variability among the accessions. The CV is 48.98%, suggesting a moderate level of dispersion relative to the mean. On average, the size of dots measures 5.08, with a standard deviation of 1.59, showing moderate variability across the examined accessions (CV% = 31.39%).

The mean contrast of dot color to ground color is 5.5, with a standard deviation of 1.72, suggesting moderate variability (CV% = 31.38%). However, the conspicuousness of groove coloring exhibits substantial variability, with a mean of 1.54 and a high standard deviation of 1.47, resulting in a notably high coefficient of variation (CV% = 95.52%).

In contrast, the intensity of groove coloring displays less variability, with a mean of 3.12 and a standard deviation of 0.48 (CV% = 15.66%). The mean length of the peduncle measures 5.75, with a standard deviation of 1.46, indicating moderate variability

(CV% = 25.49%). These findings highlight the diverse nature of young fruit characteristics and underscore the importance of considering multiple factors in phenotypic analysis across different accessions.

The mean position of the maximum diameter of the fruit (Q16) is 1.93, with a SD of 0.56. The CV of 28.98% indicates moderate variability in this characteristic among the accessions. The shape of the fruit in longitudinal section (Q17) has an average value of 4.5, accompanied by a relatively high standard deviation of 2.54. The CV of 56.52% reflects considerable variability in fruit shape among the examined accessions. Moreover, the mean shape of the fruit (Q18) is 3.12, with a notably high standard deviation of 2.23. The CV of 71.59% suggests substantial variability in fruit shape across the accessions. Additionally, the mean ground color of the skin (Q19) is 2.85, with a standard deviation of 0.77. The CV of 27.03% indicates moderate variability in this characteristic among the accessions.

The intensity of the ground color of the skin (Q20) averages at 4.41, with a standard deviation of 1.3. The CV of 29.48% indicates moderate variability in intensity among the examined accessions. The density of dots on the fruit (Q21) has a mean value of 3.12, with a high standard deviation of 2.45. The CV of 78.56% reflects substantial variability in dot density across the accessions. Similarly, the mean size of dots on the fruit (Q22) is 3.91, with a standard deviation of 1.16. The CV of 29.72% indicates moderate variability in dot size among the examined accessions.

The color of dots on the fruit (Q23) averages at 2.41, with a standard deviation of 0.64. The CV of 26.77% indicates moderate variability in dot color among the accessions. One of the characteristics examined is the intensity of color of dots (Q24), which has a mean value of 4.29 and a standard deviation of 1.45. The CV is 33.97%, indicating moderate variability in the intensity of dot color among the accessions. This variability in dot color intensity can significantly influence the visual appeal and market value of the fruit.

Another characteristic, the density of patches (Q25), exhibits a mean value of 2.25, with a high standard deviation of 1.63 and a CV of 72.48%. This substantial variability in patch density among the accessions suggests diverse patterns of patch distribution across the fruit surface.

Additionally, the size of patches (Q26) has a mean value of 3.83, with a standard deviation of 1.29 and a CV of 33.75%. This indicates moderate variability in patch size among the examined accessions, which can influence the overall appearance and texture of the fruit skin.

Other characteristics such as the presence of warts (Q27), attachment of peduncle at maturity (Q28), and shape of the base (Q29) and apex (Q30) also exhibit variability across the accessions, as indicated by their respective coefficients of variation.

4.5.1.2. PCA and heatmap

A PCA was performed with 79 studied morphological and biochemical traits.

The findings of a principal component analysis (PCA) are presented in Table 4.14. This table provides information on the eigenvalues, proportion of variance explained, and cumulative percentage of variance explained by each principal component. The analysis of eigenvalues, which indicate the extent to which each component captures variation, indicates that the first principal component (PC1) has the greatest value of 9.32, accounting for 11.8% of the overall variance. The eigenvalues of subsequent components demonstrate a decrease, suggesting a reduction in their contributions to the overall variance. The extent to which each component accounts for variance varies, ranging from 11.8% for PC1 to 1.3% for PC22, exhibiting a progressive decrease.

The cumulative percentage of variation indicates that the initial 23 components account for a substantial amount of the dataset's variability, explaining 88.2% of the overall variance. This implies that although the dataset exhibits complexity, a significant portion of its variability can be adequately captured by a very limited selection of major components. This enables a more efficient analysis process while preserving crucial information.

Table 4.14. Eigenanalysis of the correlation matrix

No	Eigenvalue	Proportion%	Cumulative %	No	Eigenvalue	Proportion%	Cumulative %
1	9.32	11.8	11.8	13	2.11	2.7	70.3
2	8.08	10.2	22	14	1.88	2.4	72.7
3	6.4	8.1	30.1	15	1.73	2.2	74.9
4	4.95	6.3	36.4	16	1.68	2.1	77.1
5	4.06	5.1	41.6	17	1.57	2	79.1
6	3.7	4.7	46.1	18	1.36	1.7	80.8
7	3.41	4.3	50.6	19	1.29	1.6	82.4
8	3.03	3.8	54.4	20	1.27	1.6	84.1
9	2.78	3.5	57.9	21	1.16	1.5	85.5
10	2.69	3.4	61.3	22	1.11	1.4	86.9
11	2.63	3.3	64.7	23	1.01	1.3	88.2
12	2.36	3	67.7				

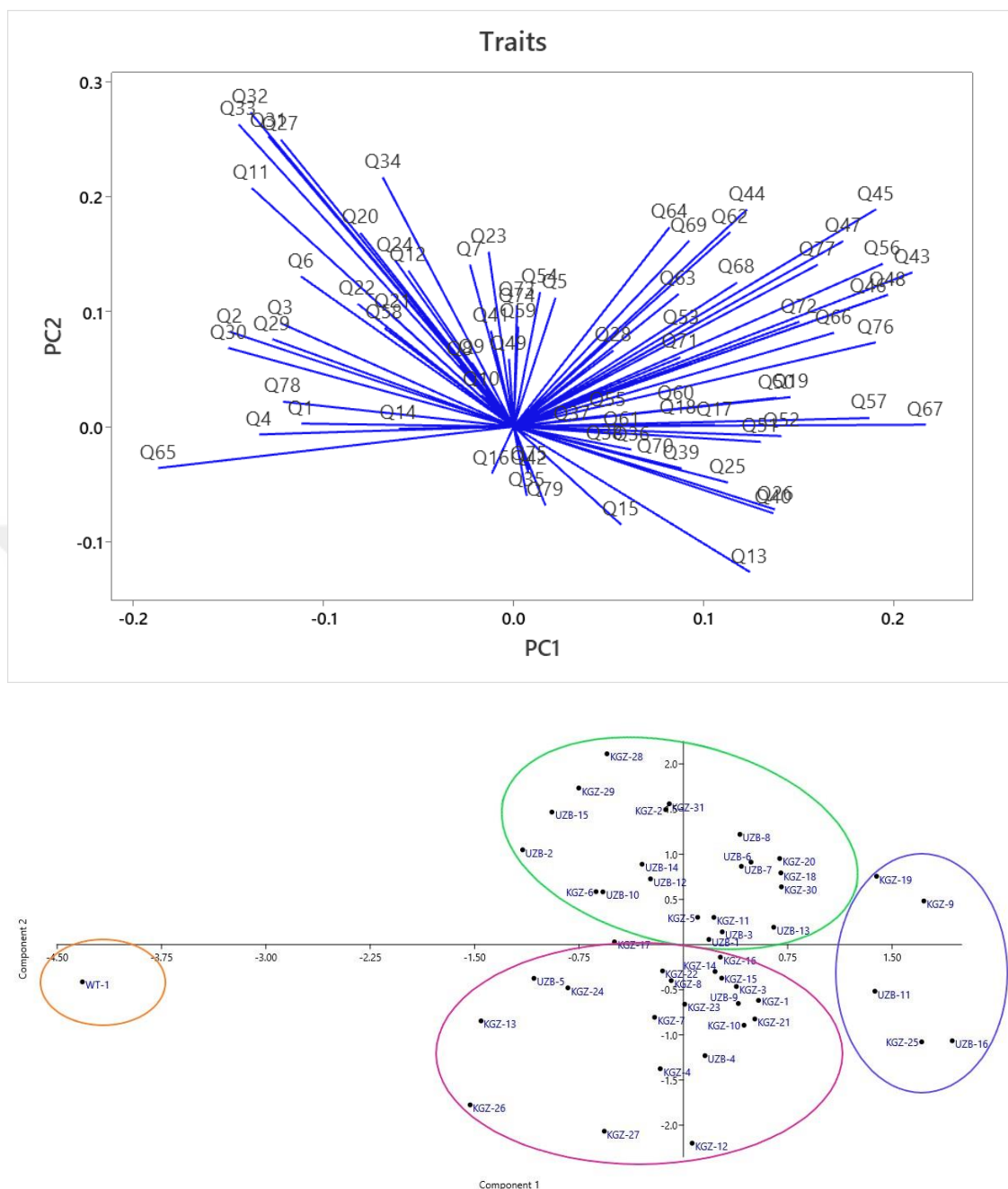


Figure 4.14. PCA of morphological characteristics of genotypes

For visualization, correlation and clarification of the 79 morphological traits considered to the 48 genotypes, was performed PCA (Fig.4.14) and heatmap clustering (Fig. 4.15). The present findings revealed that heatmap clustering revealed four major clusters. The first cluster was comprised of leaf blade size, development of lobes and length of terminal lobes in leaf blade, leaf blade dentation of margin, thickness of peduncle 1 cm from fruit in young fruit, position of maximum diameter in fruit, shape of base and apex, seed shape and TA in greenhouse, whilst the second major cluster was associated with the leaf shape, conspicuousness and intensity of groove coloring in young fruit, intensity of ground color of skin, size and intensity of color of dots in young fruit,

fruit warts, width, depth and color of grooves, density of cork formation and fruit width. The third cluster included blistering of leaf shape, sex expression, color of dots, main color of hue of flesh, length of stem, distance between 2 nodes, TSSC and pH. The remaining traits are all located in cluster 4.

UPGMA-based dendrogram (Fig. 4.14) constructed using the 79 phenotypic and morphological traits revealed four distinct clusters among the melon genotypes. The majority of genotypes resided within two main groups, each further divided into subgroups. A distinct third group encompassed genotypes KGZ-9, KGZ-19, KGZ-25, UZB-11, and UZB-16, while the fourth group comprised solely of the wild type accession.

Figure 4.15 shows a heatmap and a correlation matrix to effectively visualize the relationships between 79 morphological traits measured in 48 melon genotypes. This combined approach offers a powerful tool for dissecting the patterns of co-variation and divergence among these traits across the genotypes.

The heatmap leverages color intensity to represent the correlation coefficients between trait pairs. More intense colors, here is dark blue, light blue, purple indicate positive correlations. Conversely, weaker correlations or a lack thereof are depicted by green, yellow and and red squares, suggest negative correlations. Knowing the specific morphological traits measured would allow for a more meaningful interpretation of the correlations, enabling researchers to link the observed patterns to specific phenotypic characteristics.

By effectively utilizing the heatmap and correlation matrix (Figure 4.15) alongside the considerations mentioned above, researchers can glean valuable insights into the intricate morphological trait relationships within the 48 melon genotypes.

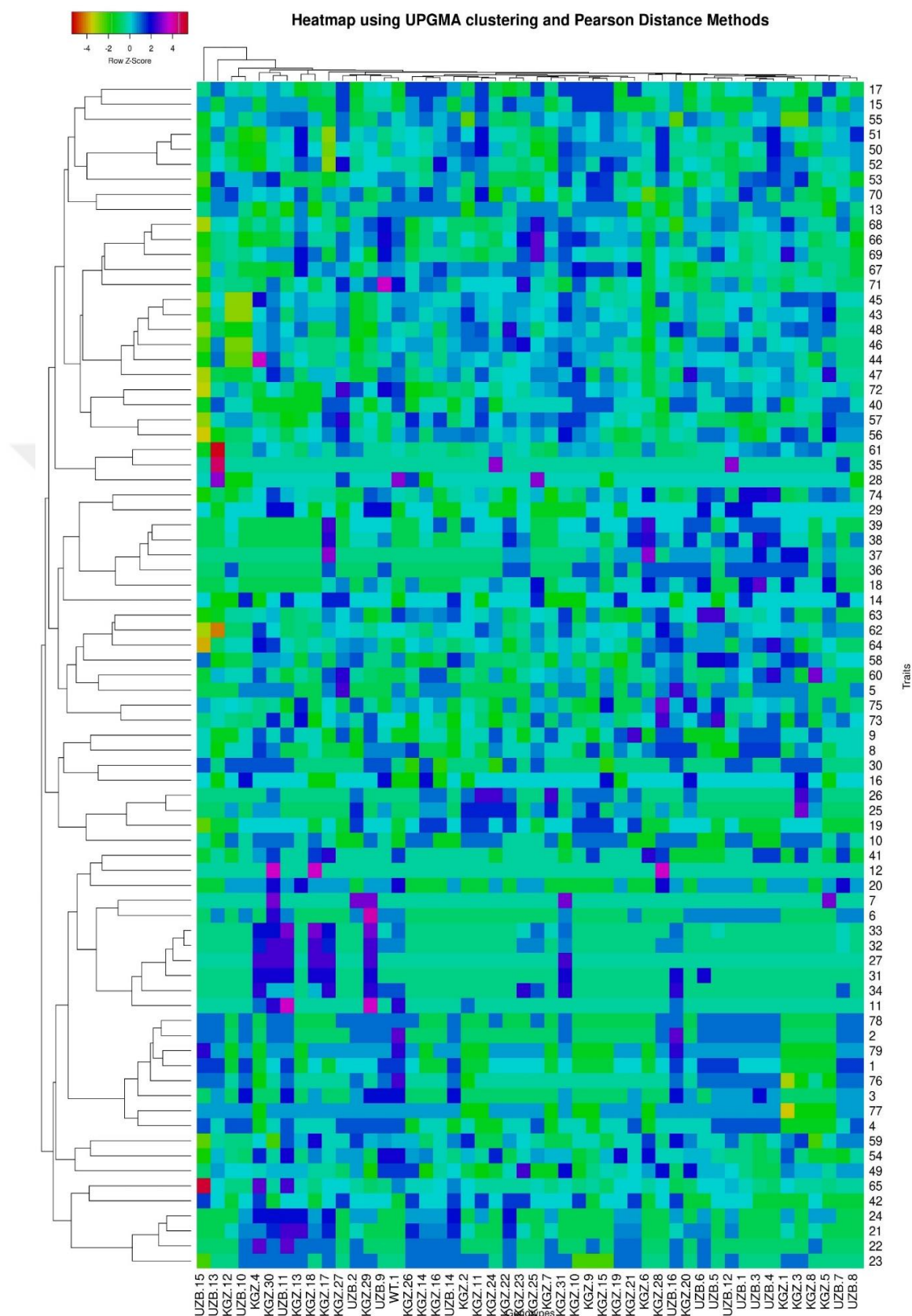


Figure 4.15. Heatmap and correlation matrix for morphological traits

4.5.2. Molecular analysis

4.5.2.1. Analysis of Molecular Variance

Table 4.15. Analysis of molecular variance (AMOVA) in melon populations using SRAP

Source	Est. Var.	%	Stat	Value	P(rand >= data)
Among Pops	2.734	12%	PhiPT	0.116	0.016
Within Pops	20.860	88%	PhiPT max	0.779	
Total	23.594	100%	Phi'PT	0.149	

Probability, P(rand >= data), for PhiPT is based on standard permutation across the full data set.

$\text{PhiPT} = \text{AP} / (\text{WP} + \text{AP}) = \text{AP} / \text{TOT}$

AP = Est. Var. Among Pops, WP = Est. Var. Within Pops

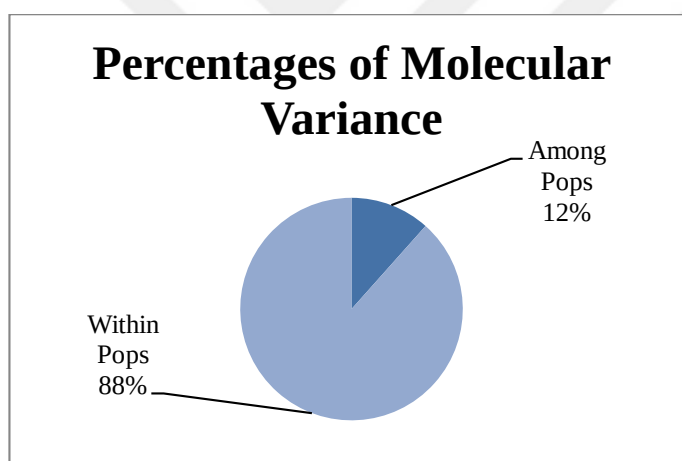


Figure 4.16. Results of Analysis of Molecular Variance as a graph

The Analysis of Molecular Variance (AMOVA) results (Table 4.15, Figure 4.16) shows the genetic structure within three distinct populations: Kyrgyz melon genotypes (Pop1), Uzbek melon genotypes (Pop2), and wild type (Pop3). Among these populations, the estimated variance between different groups is recorded, representing approximately 12% of the total genetic variation. This parameter determines the genetic dissimilarities between populations, with the highest variance observed in Pop1, denoting Kyrgyz genotypes. Within each population, varying levels of estimated variance are evident, with Pop3, the wild type, demonstrating the lowest variance, encompassing a substantial 88% of the total genetic variation. This underscores the considerable genetic diversity intrinsic to individual populations, particularly notable in Uzbek melon genotypes (Pop2). The PhiPT value, a population differentiation, is computed at 0.116, indicating that 11.6% of the genetic variation can be explained by differences within populations.

Table 4.16. Band Frequencies, Estimated Allele Frequencies and Estimated Heterozygosity by Pop

Mean and SE over Loci for each Pop						
Pop		Na	Ne	I	He	uHe
Pop1	Mean	1.787	1.477	0.414	0.277	0.282
Pop2	Mean	1.612	1.489	0.394	0.270	0.279
Pop3	Mean	0.606	1.000	0.000	0.000	0.000
Grand Mean and SE over Loci and Pops						
		Na	Ne	I	He	uHe
Total	Mean	1.335	1.322	0.269	0.183	0.187
Percentage of Polymorphic Loci						
Population	%P					
Pop1	81.38%					
Pop2	69.68%					
Pop3	0.00%					
Mean	50.35%					

Na = No. of Different Alleles

Ne = No. of Effective Alleles = $1 / (p^2 + q^2)$

I = Shannon's Information Index = $-1 * (p * \ln(p) + q * \ln(q))$

He = Expected Heterozygosity = $2 * p * q$

uHe = Unbiased Expected Heterozygosity = $(2N / (2N-1)) * He$

Where for Diploid Binary data and assuming Hardy-Weinberg Equilibrium, $q = (1 - \text{Band Freq.})^{0.5}$ and $p = 1 - q$

The genetic diversity analysis reveals notable distinctions among the studied populations, with implications for their conservation. The Kyrgyz genotypes (Pop1) exhibit the highest levels of genetic diversity, characterized by a relatively large number of distinct alleles (Na) and effective alleles (Ne) per locus. This indicates a rich genetic reservoir within the Kyrgyz melon population, offering potential advantages for breeding programs and adaptive responses to environmental challenges. The observed heterozygosity (He) and unbiased expected heterozygosity (uHe) values further support the notion of considerable genetic variability within this population.

In contrast, the Uzbek genotypes (Pop2) demonstrate slightly lower levels of genetic diversity compared to the Kyrgyz genotypes, as evidenced by the slightly reduced Na and Ne values. However, Pop2 still maintains a moderate level of genetic diversity, suggesting adaptive potential and resilience to environmental pressures. The presence of polymorphic loci in both Pop1 and Pop2 underscores the genetic heterogeneity within these cultivated melon populations.

The wild type melon population (Pop3) exhibits markedly lower genetic diversity metrics, with a substantially lower Na value and lack of polymorphic loci. This is expected, as the wild type serves as a reference genotype against which the cultivated populations are compared. While the wild type may lack the genetic variability seen in cultivated populations, its inclusion in the analysis provides valuable context for understanding the genetic diversity landscape of cultivated melons.

These findings highlight the importance of conserving and managing the genetic diversity present within cultivated melon populations, particularly in the Kyrgyz and Uzbek genotypes, to ensure their long-term sustainability and resilience in the face of changing environmental conditions. Further research into the genetic basis of traits

associated with adaptation and stress tolerance in melons may inform breeding strategies aimed at enhancing crop resilience and productivity.

4.5.2.2. Principal Coordinates Analysis (PCoA) and cluster analysis

Figure 4.17 displays a visualization of the genetic relationships among 48 melon genotypes, generated through Principal Coordinates Analysis (PcoA) using SRAP markers based on Euclidean distance. Each circle on the plot represents a distinct melon genotype, positioned based on its genetic similarity to others as revealed by the SRAP marker profiles. Tight clusters of circles depict genotypes with a high degree of shared genetic variation. Conversely, genotypes positioned further apart possess more divergent genetic makeup, potentially harboring unique agronomic or quality attributes.

Eigenvalues and eigenvectors were employed in PcoA analysis to ascertain the significance of distinct genetic determinants and the distinct genetic profiles exhibited by each group. Eigenvalues play a crucial role in comprehending the extent to which individual genetic factors contribute to the overall variety. Greater eigenvalues indicate that specific genetic features exert a more significant influence on the observed diversity. Conversely, eigenvectors serve as genetic profiles for each group, providing insights into the distinct genetic composition of the Kyrgyz, Uzbek, and wild type genotypes.

Based on the scattering analysis PCoA was also performed to determine the genetic diversity and four main groups were formed. The analysis separates the genotypes into four main groups, accounting for 16% (PCoA1) and 11% (PCoA2) of the total variation, respectively. The main two groups in green and red circles represent genotypes with higher genetic similarity. A third group, containing genotypes KGZ-26, UZB-4, UZB-5, and UZB-10, appears distinct from the two main clusters. This suggests these genotypes share a unique genetic structure compared to the majority. Interestingly, KGZ-14 stands out as a separate entity in the PCoA plot. This isolated position indicates significant genetic divergence from all other genotypes, potentially signifying unique traits or agronomic characteristics.

The PCoA analysis complements the cluster analysis by providing a visual representation of genetic diversity. The observed groupings and KGZ-14's distinctiveness are valuable insights for breeders. Genotypes within the main clusters can be targets for breeding within similar genetic backgrounds, while KGZ-14 might be a promising source of novel traits due to its genetic divergence. While PCoA offers valuable insights, additional information like the specific traits measured and breeding goals would be helpful for a more comprehensive interpretation and this analysis effectively highlights the genetic diversity within the melon genotypes using SRAP markers.

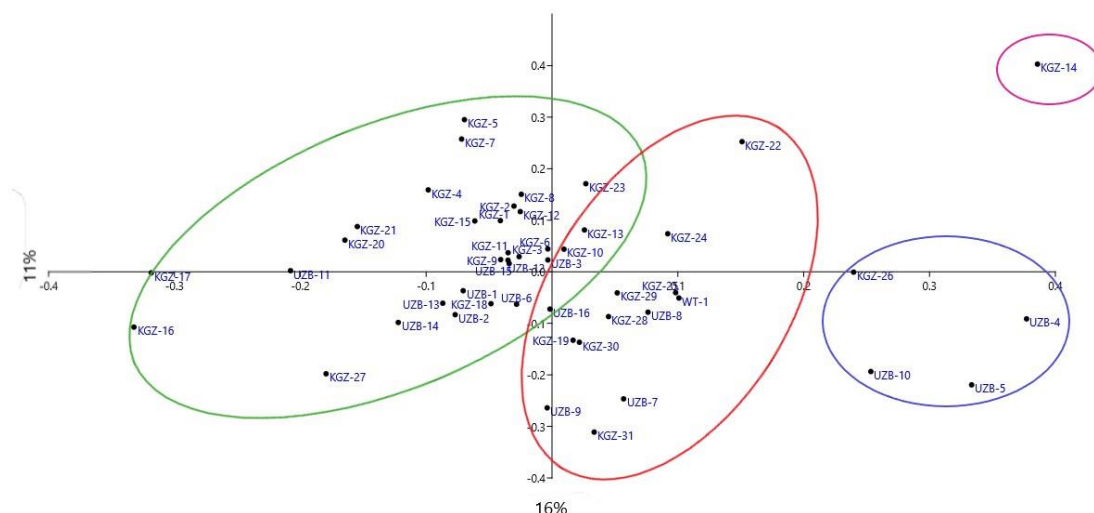


Figure 4.17. Genetic clustering of 48 cultivars based on PcoA using SRAP markers

The classification of 48 genotypes based on SRAP marker band patterns using the Jaccard similarity coefficient and the UPGMA algorithm shown in Figure 4.18. According to the resulting dendrogram, genotypes can be classified into four groups. Group 1 divided into two subgroups, which included, (1) KGZ-28, UZB-7, KGZ-30, KGZ-31, KGZ-18, KGZ-19, KGZ-27, UZB-1, KGZ-6, KGZ-29, UZB-12, UZB-13, UZB-14, UZB-16, UZB-15, UZB-8, UZB-2, UZB-6, and (2) included KGZ-12, KGZ-13, KGZ-2, KGZ-10, KGZ-11 genotypes, and Group 2 included KGZ-7, KGZ-22, KGZ-23, KGZ-8, KGZ-5, KGZ-3 and KGZ-4 genotypes. Group 3 is divided into two subgroups: (1) the first subgroup included UZB-5, UZB-10, KGZ-14, UZB-4, KGZ-25, KGZ-26, KGZ-24 and UZB-9 genotypes; and (2) the second subgroup included KGZ-21, UZB-11, KGZ-20, KGZ-16, KGZ-17 AND KGZ-9 genotypes. Group 4 included KGZ-1 and KGZ-15 genotypes.

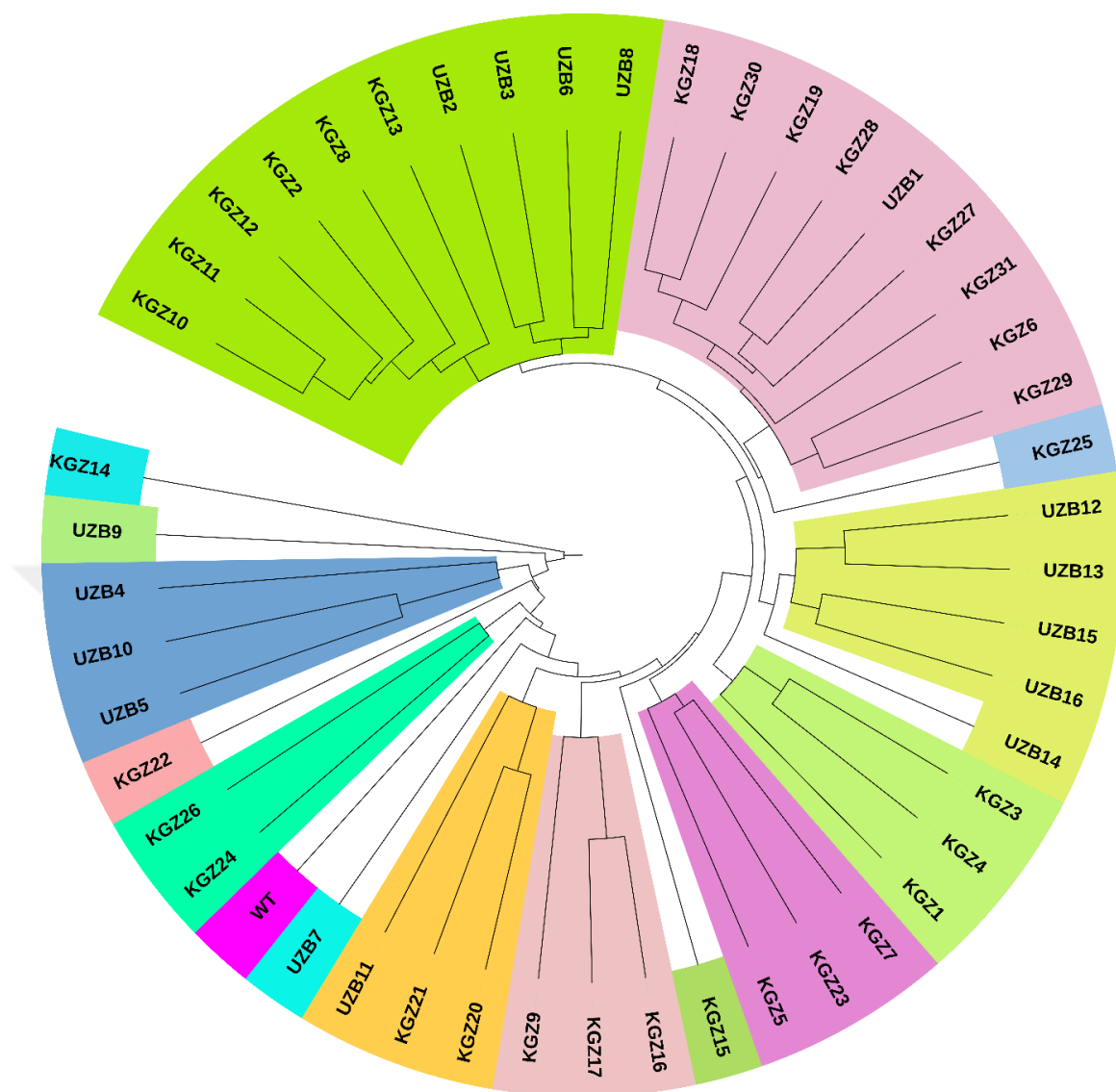


Figure 4.18. Cluster analysis of studied genotypes by Ward's grouping method using Euclidean distances

4.5.2.4. Population structure analysis

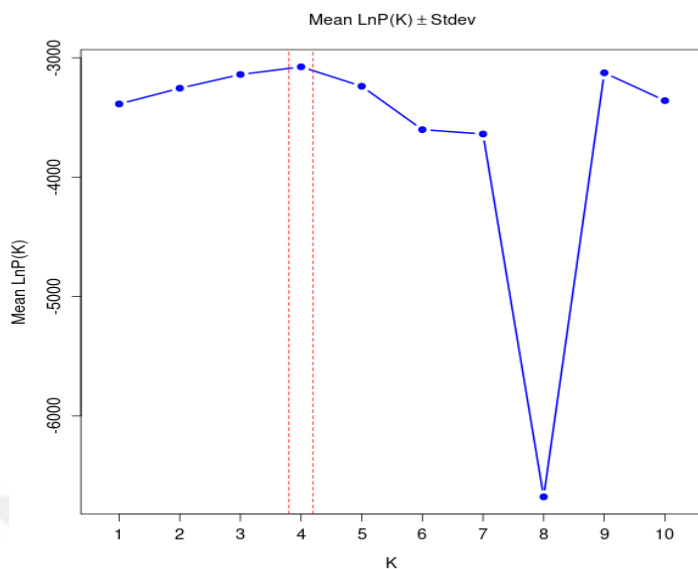


Figure 4.19. Delta K (ΔK) graph obtained by Structure Selector

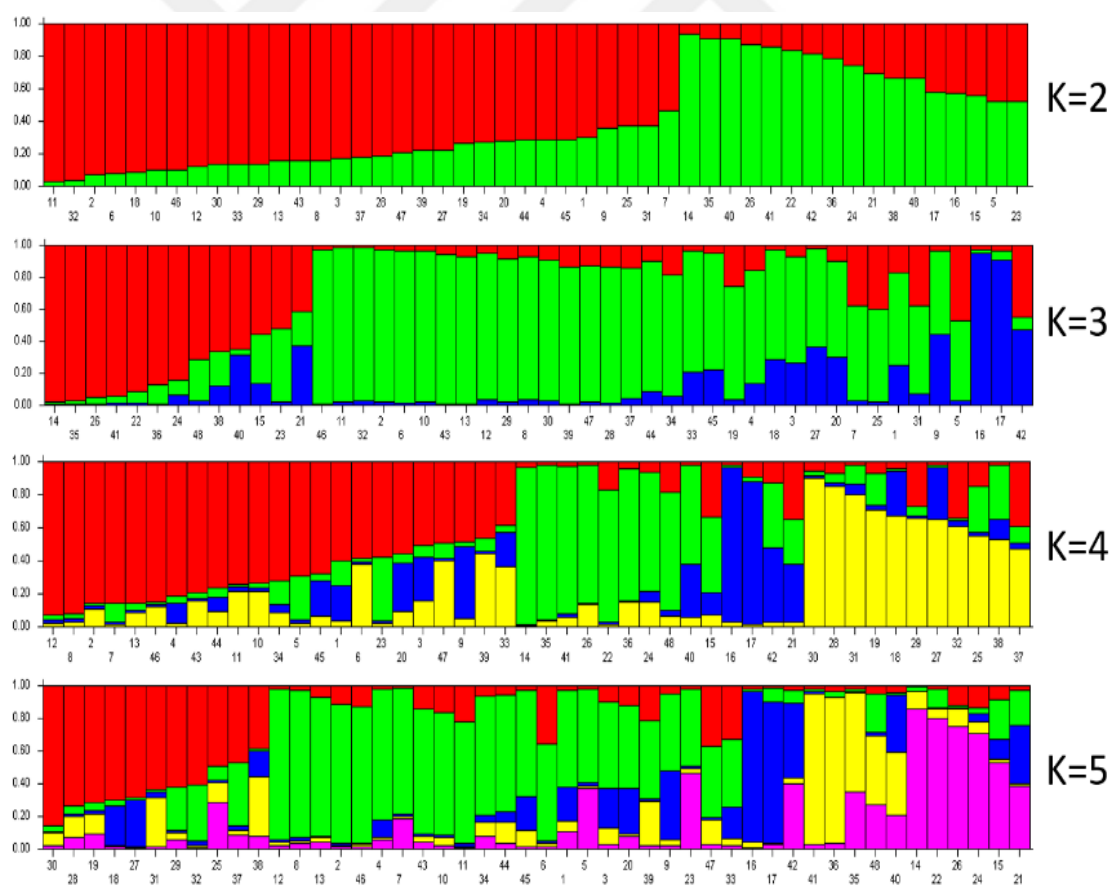


Figure 4.20. Clustering analysis of genotypes with Structure Software, highest ΔK bar plots showed in numerical order

The results from the STRUCTURE analysis reveal important insights into the population structure and genetic diversity within the studied samples. The analysis was conducted with desired ΔK values ranging from 1 to 10, and the optimal number of populations (ΔK) was determined to be 4 based on the highest value of ΔK .

The inferred clusters show the overall proportion of the samples in each of the 4 clusters. Cluster 1 has the highest proportion with 38.9%, followed by Cluster 4 with 24.1%, Cluster 2 with 23.8%, and Cluster 3 with 13.2%.

The average distances (expected heterozygosity) between individuals within the same cluster provide information about the genetic diversity within each cluster. Cluster 2 exhibits the highest expected heterozygosity (0.3), indicating greater genetic diversity within this cluster compared to others.

The structure analysis reveals the presence of four distinct genetic clusters within the studied samples, each characterized by varying levels of genetic diversity and differentiation.

5. CONCLUSION

The assessment of morphological and genetic resemblances across different melons, encompassing both cultivated and wild varieties, is of utmost importance in preserving genetic diversity and facilitating breeding initiatives. A total of 48 genotypes were utilized in this investigation, consisting of 31 Kyrgyz genotypes, 16 Uzbek genotypes, and 1 wild genotype.

The results obtained are summarized below.

1. The analysis of seed size, width, and shape revealed distinct patterns among the genotypes. KGZ displayed a preference for medium and long seeds, while UZB exhibited a wider distribution with a majority of long seeds, the wild type seeds displayed a unique pattern with all seeds categorized as very short and very narrow. Seed shape analysis in KGZ and UZB showed a near-equal distribution between "Not pine-nut shape" and "Pine-nut shape".
2. Leaf characteristics between genotypes showed that UZB genotypes generally exhibited wider leaves and longer petioles compared to KGZ genotypes, under both greenhouse and open field conditions. The wild type consistently displayed unique features, with shorter and narrower leaves and thinner stems. Environmental impact on leaf morphology showed that growing conditions significantly influenced leaf characteristics. Greenhouse cultivation generally resulted in longer leaf lengths, wider widths, and longer petioles compared to the open field for most genotypes. Genotype-specific responses displayed that while UZB genotypes displayed broader trends of having wider and longer leaves, some KGZ genotypes exhibited longer leaves in the greenhouse environment compared to UZB genotypes. The wild type consistently maintained distinct leaf morphology across environments, highlighting its inherent genetic differences.
3. Cultivated melon genotypes (KGZ and UZB) exhibit greater leaf morphological diversity compared to wild type melons, suggesting domestication pressures played a role in shaping leaf traits. This highlights the potential for human selection during domestication to favor specific leaf characteristics that may have enhanced growth, yield, or stress tolerance in cultivated varieties.

KGZ melons display the highest variation in leaf shape (entire, trilobate, rare lobed) and dentation (weak, medium, strong), potentially reflecting selection for specific leaf characteristics during domestication. This adaptability might be beneficial in diverse growing conditions. UZB melons tend towards entire leaves with moderate dentation, indicating possible genotype-specific preferences during domestication. Breeders may have favored these traits for reasons such as improved light interception, reduced water loss, or potential pest resistance. Wild type melons exhibit uniformity in leaf shape (entire), dentation (strong), and blistering (weak), potentially reflecting adaptations to the wild environment. These characteristics may enhance survival in untamed settings. Variations observed in lobe development, blade length, and blistering across genotypes suggest potential responses to environmental stresses. KGZ melons, with their wider range of leaf morphologies, might be more susceptible to certain stresses

compared to UZB and wild type melons, which exhibit more uniformity in these traits.

4. The evaluation of fruit characteristics in melon genotypes, accessions grown under open field conditions revealed notable variation compared to greenhouse cultivation. While both environments supported fruit development, open fields demonstrably yielded fruits with greater weight and size across all genotypes. This trend is evident in weight, length, and width measurements. Genotypes such as KGZ-25 (7.75 kg), UZB-13 (8.79 kg), KGZ-29 (34.5 cm), and UZB-16 (35 cm) exhibited exceptional performance under open field conditions, highlighting the potential for increased fruit production outdoors. Notably, these values often surpassed those observed under greenhouse cultivation, suggesting that open fields might be better suited for maximizing fruit size and weight in certain genotypes. UZB genotypes, particularly UZB-13 and UZB-16, displayed a propensity to outperform other groups when cultivated in open fields. UZB-16 excelled in weight, length, width, and fruit flesh thickness, suggesting potential advantages for open field production due to its ability to translate these factors into commercially desirable fruit. Conversely, genotypes like KGZ-25 achieved exceptional weight but displayed slightly less impressive dimensions compared to UZB-16. This highlights the possibility of genotype-specific responses to open field environments.
5. The analysis of morphologic traits on melon genotypes revealed distinct variations in multiple traits, especially when compared to the Wild Type (WT) melons. Kyrgyz melons exhibited greater diversity in flower sex expression, dot density, dot size, and fruit shape, with significant proportions of both hermaphroditic and male flowers. They showed the most variation in dot density, size, and contrast, and a wide range in groove coloring, fruit shapes, and peduncle lengths. Uzbek melons displayed a more uniform distribution in many traits, with all plants producing hermaphroditic flowers and more consistent patterns in dot and patch density, fruit skin color, and peduncle thickness. Both groups predominantly had light-colored grooves and minimal fruit surface creasing. Compared to WT melons, which exhibited uniform traits such as white skin, medium dot density, small dots, and light-colored grooves, both KGZ and UZB genotypes showed greater phenotypic diversity. WT melons lacked warts and had a rounded base and truncate apex, differing from the varied shapes observed in the cultivated varieties. Moreover, WT fruits consistently possessed cork formation, while KGZ and UZB melons displayed a mix of cork presence and absence. Overall, Kyrgyz melons showed the most phenotypic diversity, Uzbek melons displayed more uniformity, and Wild Type melons had distinct, consistent characteristics.
6. The biochemical analysis of Total Soluble Solids Content (TSSC), pH, and Total Acidity (TA) in melons under greenhouse and open field conditions revealed significant genotypic and environmental differences. KGZ genotypes exhibited higher TSSC and pH, and variable TA, with the highest values observed in greenhouse conditions. UZB genotypes had lower TSSC and pH but showed similar trends in TA. WT genotypes consistently displayed lower TSSC and pH, with stable TA across both environments. Leaf color analysis indicated that

greenhouse conditions generally resulted in higher brightness (L^*) and varied redness (a^*) and yellowness (b^*) compared to open field conditions. KGZ and UZB genotypes demonstrated notable environmental influences on leaf coloration, suggesting physiological adaptations, while WT genotypes maintained consistent leaf traits across conditions.

7. The analysis of SRAP amplified products across 24 primers in 48 melon genotypes reveals substantial genetic variation. Band sizes ranged from 100 to 3000 base pairs, with 188 scoreable bands identified, 157 of which were polymorphic. Polymorphic band production varied, with the highest (10 bands) in primers Me4+Em6 and Me5+Em15, and the lowest (4 and 5 bands) in Me4+Em15 and Me4+Em16. Average polymorphism was 83%, with some primers achieving 100%. The mean polymorphism information content (PIC) was 0.42, indicating moderate genetic diversity, with PIC values ranging from 0.21 to 0.5. The primer index (PI) varied from 0.82 to 1.64, averaging 1.35.
8. The analysis of melon genotypes demonstrated varied resistance to Fusarium wilt caused by Fom1 and Fom2. PCR results showed that 70% of Kyrgyz genotypes and several Uzbek accessions (UZB-3, UZB-4, UZB-6, UZB-9, UZB-15, UZB-16) were completely resistant to Fom1, while other genotypes exhibited partial or complete susceptibility. Regarding Fom2 resistance, fewer accessions showed complete resistance, with mixed patterns observed in both Kyrgyz and Uzbek germplasm. Some accessions demonstrated resistance to both Fom1 and Fom2, including KGZ-3, KGZ-10, KGZ-14, KGZ-15, KGZ-24, KGZ-25, KGZ-26, and UZB-8, as well as the wild type. These accessions are promising candidates for breeding programs aimed at developing Fusarium wilt-resistant melon cultivars, although further pathogen inoculation tests are needed to confirm resistance levels.
9. The observation of anthracnose and powdery mildew susceptibility between melon genotypes showed a range of responses within the accessions. Many genotypes exhibited high susceptibility to both diseases, with some showing moderate susceptibility and a few displaying low susceptibility or resistance. Notably, KGZ-13, KGZ-14, KGZ-15, and UZB-12 demonstrated low susceptibility to both anthracnose and powdery mildew, suggesting potential for breeding disease-resistant melon cultivars. These results emphasize the need of resistant genotype identification and utilization in breeding efforts targeted at improving melon disease resistance, as well as the significance of genetic diversity in melon germplasm.
10. The statistical analyses employing PCA, heatmap clustering, and UPGMA dendrogram construction effectively unraveled the complexities of morphological diversity within the melon genotypes. PCA successfully captured a substantial portion of the total variance (88.2%) with a limited number of principal components, facilitating further exploration of the underlying data structure. UPGMA cluster analysis further categorized the genotypes into four distinct clusters, with the wild type accession forming a separate group and the cultivated

genotypes exhibiting varying degrees of relatedness based on their morphological profiles.

11. The utilization of AMOVA and PCoA methodologies yielded comprehensive insights into the genetic composition and diversity within the melon genotypes. AMOVA analysis underscored significant genetic differentiation (11.6%) among the three populations, with Kyrgyz melons demonstrating the highest level of genetic variance. Conversely, Uzbek genotypes displayed slightly diminished diversity yet sustained moderate levels, indicative of adaptability to environmental stressors. Notably, the wild type population exhibited the least genetic diversity, serving as a reference for cultivated populations. Principal Coordinates Analysis (PCoA) further delineated the genetic relationships among the 48 melon genotypes, discerning distinct clusters and accentuating unique genotypes such as KGZ-14, potentially harboring novel traits. Moreover, genotype classification based on SRAP markers delineated four principal groups, furnishing valuable insights for breeding strategies and conservation endeavors.
12. The use of STRUCTURE analysis on the examined samples yielded significant findings on their population structure and genetic variability. By doing an analysis, it was determined that there were four separate genetic clusters present in the samples. Each cluster corresponded to a distinct genetic group. Cluster 1 exhibited the highest abundance of samples, followed by Clusters 4, 2, and 3, resulting in varied proportions of samples distributed across the clusters. Furthermore, the examination of mean distances within each cluster revealed variations in genetic variety, with Cluster 2 demonstrating the greatest anticipated heterozygosity.

In conclusion, this research provides a complete understanding of the genetic and morphological diversity present within Kyrgyz, Uzbek melon populations and wild type. Through complex analysis, significant knowledge have been provided between genotype, environment, and phenotype, shedding light on the adaptive mechanisms and selection pressures that have shaped melon evolution. The identification of distinct genetic clusters and the characterization of unique genotypes underscore the rich genetic pool of variability available for breeding purposes. Moreover, the assessment of disease resistance, agronomic traits, and environmental responses provides crucial information for the development of resilient and high-yielding melon cultivars. This research contributes to the larger goal of sustainable agriculture by explaining the genetic foundations of crop diversity and offering valuable tools for crop improvement and conservation efforts in melon cultivation.

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ACADEMIC BACKGROUND

Doctorate 2017-2023	Akdeniz University Graduate School of Natural and Applied sciences, Department of Biotechnology, Antalya
Masters 2014-2016	Akdeniz University Graduate School of Natural and Applied sciences, Department of Horticulture, Antalya
Bachelor 2009-2014	Kyrgyz – Turkish Manas University Agriculture Faculty, Department of Horticulture, Bishkek/Kyrgyzstan
Erasmus+ Internship 01.10.2021-31.12.2021	Heinrich – Heine University Centre for Plant Genome Engineering

PUBLICATIONS

Articles published in international peer-reviewed journals

Aidai Muratbek Kyzy, Gözde Hafize Yildirim & Nuri Yilmaz (2023) Effects of vermicompost applications on chlorophyll content and flag leaf area in rice (*Oryza sativa* L.), *Cogent Food & Agriculture*, 9:2, 2272460, DOI: 10.1080/23311932.2023.2272460

Muratbek Kyzy, A., Yıldırım, G.H., Şavşatlı, Y. (2023). Effects of Nitrogen Fertilizer Doses on Some Germination Parameters in Bread Wheat (*Triticum aestivum* L.) and Examination with Scanning Electron Microscopy, *International Journal of Eastern Anatolia Science Engineering and Design*, 5(2), 289-298

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Papers presented in international scientific meetings and published in proceedings books

- 1- Muratbek kyzy, A. and Gozlekci, S. 2017. Selection studies on Kara-Alma walnut forest in Zhalal Abad of Kyrgyzstan. International congress of the new approaches and technologies for sustainable development.
- 2- Muratbek kyzy A. and Gozlekci S. 2017. Pome fruit potential of Kyrgyzstan. 2. National Soft Fruit Symposium. (Poster presentation)
- 3- Muratbek kyzy A. and Gozlekci S. 2016. Potential of walnut (*Juglans regia* L.) in Kyrgyzstan. 2. National Symposium on Walnut. (Oral Presentation)
- 4- Muratbek kyzy A. 2012. Moniliose in Apple trees. 1. National Plant Protection Congress. (Oral Presentation)

Books and book chapters

- 1- Uzun, A., Turgunbayev, K., Abdullaev, A., Pinar, H., Ozongul, Ş., Muratbekkizi, A., et al. 2018. Evaluation of Central Asia Apple Genetic Resources: Some Fruit and Tree Characteristics of Naturally Growing Apple Species in Kyrgyzstan, In: Innovative Approaches in Agriculture, Forestry and Aquaculture Sciences, Atik A., (Eds.), Gece Kitaplığı, Ankara, pp.89-99.

Projects

- 1- Uzun, A., Turgunbaev, K., Abdullaev, A., Pinar, H., Muratbek kyzy A. 2014-2015. Collection of fruit genetic resources in Central Asia, Storage, Characterization: Collection of apples Genetic Resources in Kyrgyzstan, Molecular Characterization and Storage, Research Project Participant in project held under cooperation Kyrgyz - Turkish Manas University and Erciyes University.