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Research Article

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DETERMINATION OF LOCAL CHERRY TOMATO GENOTYPES' AGROMORPHOLOGICAL FEATURES IN TÜRKİYE AND KYRGYZSTAN

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Abstract: The purpose of this study was to ascertain some morphological traits and interrelationships of 36 genotypes of cherry tomatoes that were gathered from Türkiye and Kyrgyzstan. Measurements and observations include flower number of cluster, leaf length, leaf width, leaf attitude, fruit color, fruit neck shape, fruit cross-sectional shape, fruit weight, fruit firmness, time of maturity, number of locules, thickness of pericarp, and total soluble solid content, in accordance with the guidelines of the International Union for the Protection of New Varieties of Plants (UPOV). The genotypes T40 (62.7 g), T24 (50.8 g), T107 (50 g), T103 (41.4 g), and T105 (40.8 g) had the highest average fruit weights, whereas T3 (9.4 g) and K1 (10.6 g) had the lowest fruit weights. The pericarp had an average thickness of 3.82 mm and an average of 2.49 locules. A spherical fruit cross-section was observed in 97.2% of genotypes. Genotype K2 had the highest total soluble solids content (TTSC%) at 9.4%, whereas genotype K13 had the lowest TTSC% at 3.1%. To measure the data, Principal Component Analysis (PCA) was used. Five separate principle component axes were identified via PCA, and these axes together account for 75.57% of the dataset's variation. These principal components' eigenvalues, which varied from 1.07 to 3.24, showed how much variance was accounted for by each component. The PCA results showed that the genotypes T107, T40, T105, and T87 performed better in PC1 in terms of the number of locules, fruit weight, fruit cross-sectional shape, and pericarp thickness characteristics. Fruit color was influenced by genotypes T90 and T142, fruit firmness by genotype T40, and total soluble solids content by genotype T98. The indigenous cherry tomato varieties from Türkiye and Kyrgyzstan were shown to have a large amount of morphological variety, which may be useful for breeding initiatives in the future.

Keywords: Cherry tomato, Genetic resources, Morphological diversity

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1. Introduction

The tomato, a member of the genus *Solanum* in the Solanaceae family, is one of the most widely produced and cultivated vegetables globally (Rick, 1973; Taylor, 1986). Produced on 5 million hectares worldwide, it yields 186.8 million tons. China, India, Türkiye, and the United States are the top tomato-producing nations with Türkiye ranking third, having generated 13 million tons on 181,000 hectares (FAO, 2022).

Fresh, dried, and canned tomatoes are staples in any kitchen and are utilized in many parts of the world and the country (Günay, 2005). Due to their nutritional value and positive effects on human health, tomatoes have become an indispensable vegetable today (Hobson and Davies, 1971; Rao and Agarwal, 2000; Vural et al., 2000). The high economic and nutritional value has made tomatoes the subject of extensive research, from cultivation to breeding, both worldwide and in Türkiye. The widespread production of tomatoes has led to

varying demands in the global market. As with all plant species, the development of new breeding programs in tomatoes in response to changing demands has become a necessity. To achieve the highest yield and quality, the most appropriate cultivation methods, timing, and region-specific varieties must be utilized (Türkmen et al., 1992).

The success of breeding studies is limited by the genetic diversity in the gene pool used. Therefore, the development and preservation of the genetic pool are crucial. The conservation of genetic resources is essential for securing future plant production and, consequently, the future of humanity. Factors such as overuse, pollution, climate change, habitat loss, and genetic erosion threaten plant genetic resources. Thus, the preservation of plant genetic resources is of vital importance (Tan and İnal, 2003). Additionally, the increased use of hybrid and commercial varieties has led to the extinction of local populations, narrowing the

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genetic base (Altıntaş et al., 2016). Therefore, tomato genetic resources should be collected, recorded, and preserved appropriately. Effective use of plant genetic resources in breeding programs depends on systematically identifying of species and genus characteristics, tracking genetic changes, and recognizing key traits. To utilize genetic resources effeciently, the diversity within the population must be thoroughly investigated (Che et al., 2003).

For sustainable agriculture, local genetic resources must be collected, documented, recorded, and integrated into modern agriculture without undergoing genetic erosion. In the identifying of genetic resources, marker systems used in plant breeding are both morphological and genetic (Kayak, 2022). Morphological markers, traditionally used to determine relationships between plants, consist of distinguishable measurements and observations such as seed structure, plant, and fruit characteristics (Duman, 2019). Morphological variations are of great importance in plant breeding studies. Understanding the variations within cultivated species and the distribution of this variation is essential for implementing effective of breeding programs (Bliss, 1981).

In Türkiye, tomato varieties have been identified based on key characteristics such as fruit shape, fruit firmness, fruit flesh color, and fruit pH, with detailed morphological variations documented (Sönmez et al., 2015; Keskin et al., 2015; Kayak et al., 2022; Demir et al., 2024). Understanding the relationships between regional genetic resources, the traits that contribute to genotype variations, and the outcomes of growing them in different climates is crucial. Tomato breeding research can benefit from the identifying diverse genetic resources, as local varieties grown in different regions display significant heterogeneity. The morphological, phenological, and agronomic traits of these genotypes under field conditions must be understood for breeding research (Önemli and Önemli, 2023). This study aims to contribute to breeding studies and the expansion of the gene pool by examining how indigenous cherry tomato resources from Kyrgyzstan perform in Turkish environments. Characterizations of cherry tomatoes from Kyrgyzstan and Türkiye were conducted. Principal component analysis was used to identify the traits driving differences among genotypes, dendrograms were created, and cluster analyses were applied to interpret the results.

2. Materials and Methods

In the experiment, plant materials consisted of 36 genotypes in total, including 6 local genotypes from Kyrgyzstan and 30 local genetic materials from Türkiye. The plant materials used in the research were collected from the Mediterranean, Central Anatolia, and Black Sea regions, and all consisted of cherry tomatoes.

The study began with seedling cultivation in the greenhouse of the Department of Horticulture, Faculty of

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Agriculture at Selçuk University in 2022 and was conducted in the research and application field and laboratory.

Seed planting of the genotypes used in the research was carried out on March 28, 2022. On May 12, 2022, eight seedlings from each genotype were planted in the field at intervals of (100×50)×50 cm. All cultural practices such as plowing, soil cultivation, seed planting, seedling planting and harvesting were carried out properly.

For morphological observation, five plants from each genotype were selected for initial evaluation. Field observations (flowers number of cluster, leaf length, leaf width, leaf attitude) and fruit measurements (fruit color, fruit neck shape, fruit cross-section shape, fruit weight, fruit firmness, time of maturity, number of locules, thickness of pericarp, total soluble solid content) were recorded to determine agro-morphological characteristics. These measurements and observations were conducted based on UPOV parameters (UPOV, 2020).

In the study, the morphological characteristics of 6 local genotypes from Kyrgyzstan and 30 local cherry tomato genotypes from Türkiye were analyzed using Principal Component Analysis (PCA) using the JMP-14 computer software package for statistical analysis. The similarities and differences between the genotypes were determined by examining the tables and graphs generated from the PCA components.

3. Results and Discussion

The results of measurements and observations made on 36 local cherry tomato genotypes are presented below.

3.1. Leaf Characteristics

According to the evaluations, regarding leaf attitude, 8.3% of the genotypes were upright, 27.7% were semierect, 33.3% were horizontal, and 30.5% were semidrooping. In terms of leaf length, 66.6% of the genotypes had short leaves, 13.8% had medium-length leaves, and 19.4% had long leaves. For leaf width, 83.3% of the genotypes had narrow leaves, 11.1% had medium leaves, and 5.5% had wide leaves (Table 1).

Although these varying values are thought to be related to genetic diversity, ecological conditions and cultural practices are also considered partially affecting factors. Many studies have reported different values regarding leaf characteristics in tomatoes. Kayak et al. (2022) reported that 43.6% of the genotypes had semi-drooping leaves, 47.8% had horizontal leaves, and 8.5% had semierect leaves. Leaf length values were determined as 19.1% short, 20.2% medium, and 61.7% long; for leaf width, 32.9% of the genotypes had narrow leaves, 41.4% had medium leaves, and 26.5% had wide leaves. Salim et al. (2020) observed that 63.6% of the leaves were horizontal, 27.2% were semi-upright, and 13.6% were semi-drooping.

These findings suggest are both similarities and differences in leaf characteristics across various studies.

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No	Leaf Length	Leaf Width	Leaf Attitude	No	Leaf Length	Leaf Width	Leaf Attitude
K1	Short	Narrow	Semi-Erect	T85	Short	Narrow	Semi-Upright
K ₂	Short	Narrow	Semi-Erect	T86	Short	Narrow	Semi-Drooping
K ₅	Long	Medium	Semi-Drooping	T87	Short	Narrow	Horizontal
K6	Medium	Medium	Semi-Drooping	T88	Short	Narrow	Erect
K7	Medium	Medium	Semi-Drooping	T90	Long	Narrow	Horizontal
K13	Long	Wide	Semi-Drooping	T91	Short	Narrow	Semi-Drooping
T ₃	Short	Narrow	Erect	T92	Short	Narrow	Horizontal
T ₂₃	Short	Narrow	Horizontal	T94	Short	Narrow	Erect
T ₂₄	Short	Narrow	Horizontal	T97	Short	Narrow	Semi-Erect
T ₂₆	Short	Narrow	Horizontal	T98	Short	Narrow	Horizontal
T32	Medium	Narrow	Horizontal	T99	Short	Narrow	Horizontal
T40	Short	Narrow	Horizontal	T ₁₀₃	Short	Narrow	Semi-Drooping
T76	Short	Narrow	Semi-Erect	T ₁₀₄	Short	Narrow	Horizontal
$T77-1$	Long	Narrow	Semi-Erect	T ₁₀₅	Short	Narrow	Semi-Erect
T78	Medium	Narrow	Semi-Erect	T ₁₀₇	Long	Narrow	Horizontal
T79	Short	Narrow	Semi-Erect	T ₁₂₂ -1	Long	Wide	Semi-Drooping
T80	Short	Narrow	Semi-Drooping	T142	Long	Narrow	Semi-Drooping
T82	Medium	Medium	Semi-Erect	T190	Short	Narrow	Semi-Drooping

The variations may be attributed to genetic factors, as well as differences in growing conditions and environmental factors. The results of this study help us understand the extent of diversity in leaf characteristics among local genotypes and how this diversity may impact agricultural practices.

Table 1. Leaf characteristics of tomato genotypes

3.2. Fruit Characteristics

Cherry tomatoes exhibit a wide range of fruit characteristics. In our study, the number of flowers per cluster was found to be 44.4% with 3-5 flowers, 47.2% with 6-10 flowers, and 2% with more than 10 flowers. The time of fruit maturity was classified as 22.2% early and 77.7% medium. Fruit color was found to be 2.7% yellow, 91.6% red, and 5.5% brownish (Table 2). The genotypes with the highest fruit weight were T40 (62.7 g), T24 (50.8 g), T107 (50 g), T103 (41.4 g), and T105 (40.8 g), while the genotypes with the lowest fruit weight were T3 (9.4 g) and K1 (10.6 g). The average fruit weight was determined to be 24.32 g (Table 2).

Bhattarai et al. (2018) found that among tomato genotypes, 89.5% had red fruit, 5.8% had pink, and 4.7% had yellow; 4% were classified as very early, 5.5% as early, and 84.6% as medium, with 5.5% as late. Terzopoulos and Bebeli (2010) reported that among 36 tomato genotypes, 34.7% had orange fruit color, 29% had orange-red, 17.3% had red, and 15.5% had orangepink. Mutlu et al. (2007) found the fruit color distribution to be 1.12% yellow, 50.28% orange, 5.58% pink, and 43.02% red fruit colors. Kayak et al. (2022) identified 55.3% as medium, 10.6% as late, and 34% as early. They classified fruit colors as 1.06% light pink, 39.36% pink, 22.3% light red, 35.1% red, and 2.1% dark red. Kathayat et al. (2015) observed that the average fruit weight among 29 tomato genotypes ranged from 22.33 to 58.67 g. Figàs et al. (2014) reported fruit weight ranging from 2.7–511.6 g and yield per plant as 292–2,851 g. Keskin (2014) measured the average fruit weight in 17 tomato parent lines and 136 hybrids, finding it to be 147.8 g in hybrids and 156.4 g in parent lines. Another study reported average fruit weight to be between 127 and 155 g (Sönmez et al., 2015).

Fruit shape and firmness are important criteria for both consumers and transportation. In the study, the fruit neck section was classified as 2.7% slightly flattened, 86.1% round-oval, 8.3% ovate, and 2.7% egg-shaped. Fruit firmness was found to be 2.7% very soft, 16.6% soft, and 80.5% medium firmness. The fruit cross section shape was predominantly round (Table 2). In the transverse section of the fruit, 97.2% of the genotypes were classified as round, while 2.7% were classified as not round. Keskin et al. (2015) reported that 64.75% of the genotypes had medium firmness and 35.29% had firm fruit. Salim et al. (2020) found that 50% of the fruit shapes were round, 9.10% heart-shaped, 31.82% flat, and 4.54% elliptical and cylindrical in their tomato breeding lines. Bota et al. (2014) reported that among 171 local tomato genotypes, 50% had flat fruit, 31% had round fruit, and 19% had other shapes.

3.3. Principal Component Analysis (PCA)

The Principal Component Analysis (PCA) results include principal component (PC) axes, eigenvalues, variation, and total variance ratios, with factor loadings indicating the weight values of the principal components for various traits. Detailed results are provided in Table 3. It has been noted that PCA can be effectively used when the first two components explain more than 25% of the variance (Mohammadi and Prasanna, 2003; Seymen et al., 2019). The PCA analysis resulted in five independent principal component axes for 13 morphological characters, representing 75.57% of the total variation.

A= fruit color; B= fruit Shape; C= fruit cross section; D= fruit firmness; E= ripening time; F= number of flowers per cluster; G= fruit weight (g); H= number of seed cavities (per fruit); I= pericarp thickness (mm); G= soluble solid content (%).

Eigenvalues of 1 or greater for principal components indicate reliable weight values (Mohammadi and Prasanna, 2003). The eigenvalues of the first five principal components ranged from 1.07 and 3.24. For the factor loadings to be reliable in PCA, the principal component axes should explain 2/3 of the total variance (Özdamar, 2004). The analysis results show that the first five principal component axes explain more than 3/4 of the total variance (%75.57). Therefore, these axes were considered in the evaluation of analysis (Figure 1). The first principal component axis accounts for 24.93% of the total variation, while the second and third principal components cover 18% and 15.35% of the total variation, respectively.

Kal et al. (2020) reported that for 77 tomato genotypes, PC1 explained 16.8% of the total variance, PC2 explained 12.6%, and PC3 explained 10.2%. Evgenidis et al. (2011)

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found that PC1 explained 49.15% of the total variance, PC2 explained 29.63%, and PC3 explained 21.23%. Kayak et al. (2022) reported that PC1 explained 30.97% of the total variance, PC2 explained 42.28%, and PC3 explained 52.59%. Two major components resulted from the PCA conducted in accordance with the morphological findings, and it was reported that these two components explained 54.99% of the overall variation (Bahar et al. 2019).

Using PC1 and PC2 components, a Loading Plot was created to examine the mutual relationships among the traits. If the angle between vectors in the plot is <90 °, it indicates a positive relationship; if >90 °, it indicates a negative relationship; and if the angle is 90 °, there is no significant relationship (Danin-Poleg et al., 2001; Seymen et al., 2019).

Figure 1. Loading plot graph obtained from PC1 and PC2 in the PCA results.

Figure 2. Score plot derived from PC1 and PC2 in PCA.

Figure 1 shows that the highest correlation was found among number of locules, fruit weight, fruit cross-section shape, and thickness of pericarp. The highest negative correlation was found between leaf width and fruit firmness.

Using the PC1 and PC2 components, a score plot was created to evaluate the 36 cherry tomato lines (Figure 2). Upon examining Figure 2, it is observed that genotypes T107, T40, T105, and T87 exhibit the best performance concerning the parameters significant in PC1, such as the number of locules, fruit weight, fruit cross-section shape, and pericarp thickness. Regarding the total soluble solids content (TTSC) parameter, genotype T98 was found to be significant, while T90 and T142 were notable for the fruit color parameter, and T40 was significant for the fruit firmness parameter. This analysis demonstrates the significant variations and relationships among the different genotypes based on key morphological characteristics, highlighting the potential of specific genotypes for breeding programs focused on these traits. Although the methods used in tomato breeding studies are similar, differences arise in morphological characterizations. These differences are thought to stem from the rich genetic variation of tomatoes, rather than the success of the methods and applications.

4. Conclusion

In this study, the agro-morphological characteristics of 36 cherry tomato genotypes from Türkiye and Kyrgyzstan were evaluated using principal component analysis (PCA), and the relationships between these characteristics were interpreted. The research revealed differences in the morphological characteristics of the plants and fruits. As a result of the evaluations, the genotypes with the highest fruit weight were identified as T40 (62.7 g), T24 (50.8 g), T107 (50 g), T103 (41.4 g), and T105 (40.8 g), while the genotypes with the lowest fruit weight were T3 (9.4 g) and K1 (10.6 g). The average thickness of pericarp was 3.82 mm, the average number of locules was 2.49, and 97.2% of the genotypes were classified as having round fruit in cross-section shape, with 2.7% classified as not round. The highest TTSC ratio was observed in the K2 genotype at 9.4%. This genotype has an oval and round fruit shape and a medium maturation time. The lowest TTSC ratio was found in the K13 genotype at 3.1%. Based on these measurements and observations, the tomato genotypes were examined using PCA. Five independent principal component axes were obtained from the analysis. These axes represented 75.57% of the total variance, with eigenvalues ranging from 1.07 to 3.24. According to the PCA results, the genotypes T107, T40, T105, and T87 showed the best performance concerning the parameters important in PC1, such as the number of locules, fruit weight, fruit cross-section shape, and pericarp thickness. The T98 genotype was significant in terms of TTSC%, T90 and T142 in terms of fruit color, and T40 in terms of fruit firmness. High morphological variation was found among

the examined cherry tomato genotypes. These results indicate that different tomato genotypes show significant differences in various agro-morphological characteristics. Especially traits such as fruit weight, pericarp thickness, and TTSC ratio stand out as important criteria in the evaluation and breeding studies of genotypes. This data will guide genotype selection for future research.

Author Contributions

The percentage of the authors contributions is presented below. All authors reviewed and approved the final version of the manuscript.

C=Concept, D= design, S= supervision, DCP= data collection and/or processing, DAI= data analysis and/or interpretation, L= literature search, W= writing, CR= critical review, SR= submission and revision, PM= project management.

Conflict of Interest

The authors declared that there is no conflict of interest.

Ethical Consideration

Ethics committee approval was not required for this study because of there was no study on animals or humans.

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