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Morphological Characteristics of Apple Genotypes in Mudurnu (Bolu)

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Abstract

This research was carried out in the Mudurnu district of Bolu province to determine the morphological and chemical properties of 17 apple genotypes. Fruit and seed properties and soluble solids content, pH, titratable acidity, and fruit color (L*, a*, b*, chroma*, and hueº) were examined. Descriptive statistical analysis, principal component analysis, and hierarchical clustering analyses were used to determine the morphological and chemical properties of the genotypes. Fruit weights were determined as 29.06-126.30 g, fruit width as 30.55-74.00 mm, fruit flesh firmness as 2.40-7.00 kg/cm^2, soluble solids content as 12.00-18.21%, and pH as 2.93-5.30 in the examined genotypes. It was determined that G3 and G13 genotypes differed from the other genotypes regarding the examined properties. The genetic diversity identified in this study provides a valuable foundation for breeding programs aimed at developing new apple cultivars that are adapted to regional conditions and meet market demands. Particularly, the distinct genotypes such as G3 and G13 are significant due to their potential use as parents in future selection studies or hybridization programs.

***Key Words:** Apple**,** Genotypes, Selection, PCA, Pomological characteristics*

Introduction

Anatolia, thanks to the ecological opportunities offered by various climate zones and soil structures, allows the growth of many fruit species. Among these fruit species, the apple belongs to the *Malus* genus of the *Rosales* order, *Rosaceae* family, and *Pomoideae* subfamily (Kaşka, 1977). Its origin is the South Caucasus region, including Anatolia (Özbek, 1978). Apple, open to foreign pollination, produces many genotypes with the germination of heterozygous seeds. Today, many local and cultural apple varieties have emerged with selection studies conducted with genotypes (Karadeniz et al., 2013). There are 6,500 local apple varieties worldwide, and approximately 500 in Türkiye, suitable for different ecologies (Özmen and Çekiç, 2021).

The emergence of superior genotypes through targeted selection with selection breeding is an important step. Genotypes grown from natural seeds are valuable sources for increasing the quantity and quality of essential traits such as adaptation to ecological conditions, fruit characteristics, resistance to abiotic and biotic stresses, and nutritional quality due to environmental factors. The emergence of genotypes showing these superior traits is possible with selection breeding studies. Many researchers have used morphological and biochemical markers to reveal genetic diversity (Kaya and Balta, 2009; Bostan and Yılmaz, 2015; Vurgun and Aslantaş, 2016; Kara, 2022; Dumanoglu et al., 2018; Korkmaz and Okatan, 2021; Alan et. al., 2024), molecular (Vurgun, 2012; Güneş, 2017; Daler et al., 2017; Doğru Çokran et al., 2019; Koçyiğit, 2022; Bakır et al., 2022). Although these parameters are affected by genetic structure and environmental conditions, they provide valuable information about the differences and similarities between genotypes (Ebrahimi and Alipour, 2020). It is essential to maintain apple genetic diversity. The basic step in variety development and improvement is to collect and evaluate local germplasm. Multivariate analysis effectively interprets the relationships between genotypes for germplasm characterization (Al-Halabi, Muzher, 2015). This research aimed to determine the fruit traits of apple genotypes in Mudurnu/Bolu province and to reveal their diversity using multivariate analysis methods.

Material and Methods

This research was conducted on 17 apple genotypes grown from seeds found in nature in the Mudurnu district of Bolu province, where no cultural practices were applied. Ten fruit samples were selected to represent each genotype for evaluation. Fruit weight (g) and seed weight (g) were measured with a precision scale, and fruit length (mm), fruit width (mm), seed width (mm), and seed length (mm) were measured with a digital scale. Seed number was obtained by counting the seeds in the carpel of each genotype. Fruit flesh firmness (kg/cm^2) was determined with a hand penetrometer. Soluble solids content (SSC) (%) were determined with a hand refractometer. pH was determined using a pH meter and the titratable acidity (TA) titration method as a percentage. Fruit taste was determined by five panelists giving a score between 1-5. Fruit color (L*, a*, b*, Chroma*, and Hue°) was determined with a colorimeter.

Statistical Analysis

Descriptive statistical analysis was performed for fruit traits of genotypes. Principal Component Analysis (PCA) and Hierarchical Cluster Analysis were conducted to determine the relationships between the examined fruit traits and genotypes. JMP software was used in statistical analyses.

Results and Discussion

Descriptive statistical data of the characteristics examined in apple genotypes are given in Table 1. The analyzed genotypes showed wide variation. The coefficients of variation of the traits studied in genotypes varied between 8.92% (Seed length) and 69.68% (TA). It was determined that fruit and seed weight, seed number, TA, a*, b*, and Hueº values had high variation (% CV ≥ 35.00). This variability shows that some traits showed more variance than others. A high CV value can clearly distinguish the genotypes regarding these traits and indicate diversity and variability. It was determined that a lower % CV ≤35.00) was found in other pomological characteristics examined. This situation shows that apple genotypes are more consistent regarding these traits.

Fruit weight ranged between 29.06 and 126.30 g, and the coefficient of variation was 36.78% (Table 1). Fruit weight was determined as 26.59-273.75 g by Özmen and Çekiç, (2021), 65.40-205.30 g, Balta et al. (2015), 71.41-245.99 g, Kırkaya et al. (2014) 76.24-247.23g, Uzun et al. (2016) 75.52-191.95 g, Macit and Aydın (2021) 59.3-220.8 g, Özrenk et al. (2011), 20.90-139.30 g, Macit et al. (2021) reported it as 27.56-269.32 g. In our research, fruit length and width varied between 32.38-60.35 mm and 30.55-74.00 mm, respectively. The coefficients of variation are 12.44% and 15.10%, respectively. Fruit length and width were reported as 53.17-81.77 mm and 62.97-91.87 mm by Yarılgaç et al. (2009), 50.3-73.06 mm and 51.65 mm - 75.34 mm by Çöçen et al. (2019), 50.96-78.95 mm and 61.01-95.59 mm by Karadeniz et al. (2013) reported it as 53.14-62.07 mm and 63.46-73.79 mm, Bostan and Acar (2009) as 43.85-74.61 mm and 53.40-86.60 mm, Kırkaya et al. (2014) as 69.03-89.03 mm and 60.96-73.98 mm, Uzun et al. (2016) as 46.81-65.57 mm and 60.61-78.60 mm, Macit and Aydın (2021) as 48.3-67.3 mm and 50.4-85.0 m, Özrenk et al. (2011) as 32.8-54.3 mm and 35.4-60.3 mm. Findings from other researchers show a wide range of these properties. These findings show similar results to previous studies, but some differences may be due to genotypic and ecological conditions, especially genetic structure. Indeed, fruits are characterized by different shapes and sizes. Still, each fruit originates from the development of a single growing meristematic point, and the final size depends on the number of cell divisions and cell expansion during the development of the ovary and fruit. Individual fruit shape and size are determined by the fruit's genetics, phytohormones, and environment (De Mori and Cipriani, 2023) and can vary significantly among different genetic materials (Kumar et al., 2012).

In the genotypes, SSC varied between 12-18.21%, pH between 2.93-5.30, and TA between 0.17-1.88%. TA gave the highest coefficient of variation among the examined traits, at 69.68% (Table 1). Similarly, other researchers reported the SSC, pH and TEA values as 9.2-19.7%, 4.0-5.2%, 0.21-1.40% (Özmen and Çekiç, 2021), 8.40-14.25%, 3.03-4.10, and 0.16-1.08% % (Karakaya et al., 2016), 10.62-13.85%, 3.60-4.82% and 0.699-0.929% (Yarılgaç et al., 2009), 10.07-14.10%, 2.20-3.65% and 0.66-1.12% (Çöçen et al., 2019), 9.40-13.60%, 2.83-4.11% and 0.22-2.01% (Balta et al., 2015). In addition, Osmanoğlu and Balta (2021) reported the SSC values as 9.00-15.00%, Şenyurt et al. (2015) as 11.50-15.25%, and TA as 0.20-1.24%. Findings give slightly higher results than the findings of other researchers. However, SSC is one of the essential quality criteria in fruits, and SSC increases as fruit maturity progresses and reaches the maximum level on the harvest date. It is essential to evaluate SSC and other parameters such as TA and fruit flesh firmness, especially in determining maturity (Yer and Erdoğan, 2022).

In the genotypes examined, seed weight was determined as 0.12-0.55 g, seed length as 6.07-9.38 mm, seed width as 2.71-5.41 mm, and seed number as 1-10 (Table 1). They reported seed weight, seed length, seed width and seed number as 0.20-0.55 g, 7.46-10.59 mm, 3.84-5.58 mm and 3.5-10 pieces (Yarılgaç et al., 2009), 0.02-0.08 g, 7.23-9.11 mm, 3.45-5.28 mm and 3.50-7.25 pieces (Bostan and Acar, 2009), 0.20-0.55 g, 7.46-10.59 mm, 3.84-5.58 mm and 3.5-10 pieces (Karadeniz et al., 2013), respectively. Findings are parallel to those of other researchers.

Fruit flesh firmness values varied between 2.40-7.00 kg/cm^2, while fruit taste took values between 2-5 (Table 1). Fruit flesh firmness has been reported as 9.46-10.33 kg/cm^2 (Karadeniz et al., 2013), 6.45-10.90 kg/cm^2 (Uzun et al., 2016), 6.27-9.39 kg/cm^2 (Şenyurt et al., 2015), 5.04-9.40 kg/cm^2 (Çöçen et al., 2019), 4.33-7.11 kg/cm^2 (Karataş, 2021). Fruit ripening is a complex process that includes flavor, color, cell wall changes and softening, starch degradation, and aroma development, and contributes significantly to distinctive fruit qualities (De Mori and Cipriani, 2023). Fruit firmness is one of the most important quality characteristics in consumer preferences, and fruit firmness may vary depending on variety, location, and environmental factors (Kumar et al., 2018). This research findings are similar to the results of other researchers regarding fruit flesh firmness.

Fruit color values of the genotypes were measured as L*, a*, b*, Chroma*, and hue° values between 29.08-74.70, 7.09-38.50, 7.51-44.19, 13.60-45.83, respectively. The coefficients of variation of the fruit color values generally gave high values for the examined traits and these values were determined as L* 22.99%, a* 35.47%, b* 46.41, Chroma* 25.69% and hue° 49.39% (Table 1). . Özmen and Çekiç (2021) reported L* 42.31-79.96, a* 21.91-27.47, and b* values between 20.79-45.22. In addition to genetic and transcriptional regulation, environmental factors such as light, temperature, water, sugars, plant hormones, and anthocyanin biosynthesis may also be effective in the formation of color in apples (Chen et al., 2021).

The results of the heatmap hierarchical clustering analysis showing how apple genotypes are grouped according to their similarities are given in Figure 2. The heatmap shows the similarities and differences between the samples and the examined traits with a color scale. Red tones represent high values, and blue tones represent low values. The figure shows that 17 apple genotypes are clearly divided into different clusters. G3 and G13 genotypes (marked in green) form a separate cluster from the other genotypes, showing high values especially in fruit weight, fruit length, and color parameters (L*, b*, Hueº, Chroma). Regarding SSC, the G3 genotype differs from all genotypes, especially from the G9 genotype. Indeed, (Mir et al., 2017) reported a similar situation. Within the main cluster, G1, G12, G16, G7, G14, G8 and G2 genotypes form a subcluster; The genotypes G4, G6, G9, G10, G11, G5, G17 and G15 form another sub-cluster. It is observed that the genotypes show significant differences, especially in the seed number, TA, and a* parameters. The clustering between the traits in the lower part of the dendrogram shows that the fruit traits (weight, length, width) and color parameters (L*, b*, Hueº, Chroma) are closely related.

PCA analysis provides essential information about which traits can be evaluated together in breeding programs while determining the selection criteria of genotypes within populations. Principal Component Analysis (PCA) results effectively reveal the variation in pomological and biochemical traits of the examined apple genotypes. The first five principal components (PC) explain 80.09% of the total variation (Table 2). PC1 is the most effective component with 26.61% variation and has positive loadings, especially on color parameters (L*, b*, Chroma*, and Hue°) and fruit sizes (weight, length, and width). PC2 represents 19.92% variation and shows positive loadings on fruit weight, fruit width, and taste parameters, as well as negative loadings on the flesh firmness parameter. When the relationships between genotypes and traits distributed on PC1 and PC2 axes are examined in the biplot graph, G3 and G13 genotypes stand out with positive values on the PC1 axis. In contrast, G6, G10, and G4 genotypes differ on the PC2 axis (Figure 2). The close positioning of fruit width, weight, and length vectors shows that these traits are strongly correlated. While color parameters (L*, b*, Hue°) are positively grouped on the PC1 axis, fruit flesh firmness is negatively prominent on the PC2 axis. Similarly, Mir et al. (2017) reported that the first component is related to fruit color, while SSC values are related to the fourth component.

Table 1. Descriptive statistics of apple genotypes in terms of examined traits.

Traits	Min.	Max.	Mean	±Std Dev	CV%
Fruit weight (g)	29.06	126.30	58.21	21.41	36.78
Fruit length (mm)	32.38	60.35	47.00	5.85	12.44
Fruit width (mm)	30.55	74.00	49.73	7.51	15.10
Seed number (pieces)	1.00	10.00	5.69	2.69	47.31
Seed weight (g)	0.12	0.55	0.30	0.12	39.48
Seed length (mm)	6.07	9.38	7.74	0.69	8.92
Seed width (mm)	2.71	5.41	4.14	0.50	12.04
SSC (%)	12.00	18.21	15.32	1.79	11.66
pH	2.93	5.30	4.05	0.59	14.45
TA (%)	0.17	1.88	0.63	0.44	69.68
Taste	2.00	5.00	3.59	0.87	24.25
Fruit flesh firmness (kg/cm^2)	2.40	7.00	5.15	0.96	18.61
Fruit colour L*	29.08	74.70	49.45	11.37	22.99
Fruit colour a*	7.09	38.50	20.88	7.41	35.47
Fruit colour b*	7.51	44.19	20.49	9.51	46.41
Fruit colour Chroma*	13.60	45.83	30.46	7.82	25.69
Fruit colour Hue°	14.11	108.45	44.21	21.83	49.39

Table 2. Eigenvalues, total variance ratios, and eigenvectors of principal components for the studied apple genotypes.

Traits	PC1	PC2	PC3	PC4	PC5
Fruit weight (g)	0.24	0.42	0.14	0.00	0.12
Fruit length (mm)	0.24	0.26	0.35	-0.07	0.04
Fruit width (mm)	0.25	0.43	0.08	-0.01	0.13
Seed number (pieces)	-0.24	-0.07	0.27	-0.09	-0.15
Seed weight (g)	-0.06	0.21	-0.47	0.17	-0.06
Seed length (mm)	-0.01	0.31	-0.26	-0.05	-0.23
Seed width (mm)	0.12	0.09	0.13	-0.22	0.53
SSC (%)	0.14	-0.16	-0.24	0.01	0.55
pH	0.01	-0.11	0.15	-0.58	-0.10
TA (%)	0.05	0.05	0.18	0.64	-0.08
Taste	-0.23	0.32	-0.08	0.06	0.32
Fruit flesh firmness (kg/cm^2)	-0.04	-0.36	-0.27	0.07	0.32
Fruit colour L*	0.38	-0.19	-0.09	-0.20	-0.13
Fruit colour a*	-0.20	-0.18	0.43	0.23	0.15
Fruit colour b*	0.43	-0.17	-0.03	0.10	-0.06
Fruit colour Chroma*	0.36	-0.22	0.22	0.21	0.05
Fruit colour Hue°	0.42	-0.02	-0.18	0.07	-0.19
Eigenvalue	4.52	3.39	2.26	1.80	1.65
% of Variance	26.61	19.92	13.31	10.57	9.68
Cumulative %	26.61	46.53	59.84	70.41	80.09

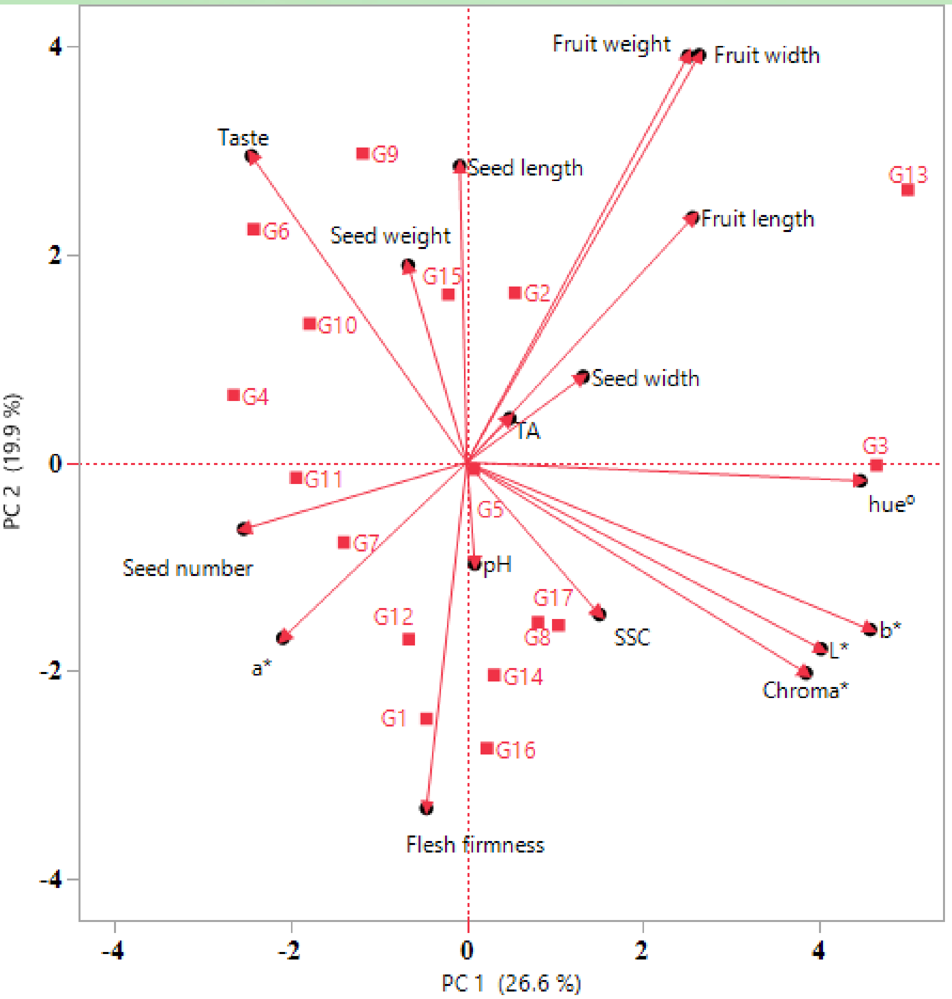

Figure 1. PCA analysis of the examined traits and genotypes

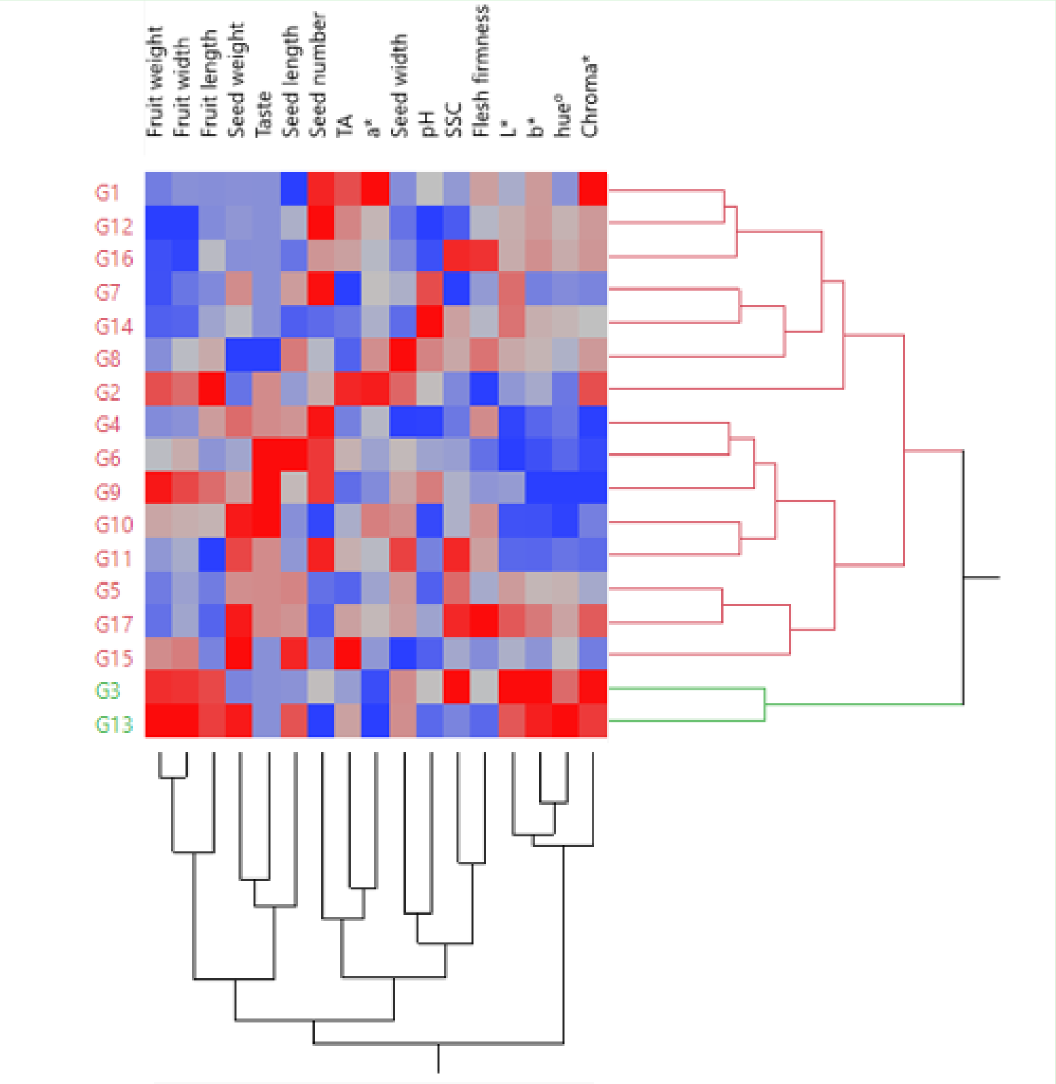

Figure 2. Hierarchical clustering analysis of apple genotypes and traits

Conclusion

This research investigated the pomological and biochemical properties of 17 apple genotypes collected from the Mudurnu/Bolu region. The research results revealed significant variation among the examined apple genotypes. A wide variation was observed in fruit weight (29.06-126.30 g), fruit length (32.38-60.35 mm), fruit width (30.55-74.00 mm), SSC (12.00-18.21%), pH (2.93-5.30), TA (0.17-1.88%) and fruit flesh firmness (2.40-7.00 kg/cm²) values. TA (69.68%) and color parameters (Hue° 49.39%, b* 46.41%) especially attracted attention due to their high coefficients of variation. According to PCA results, the first five components explained 80.09% of the total variation, PC1 (26.61%) was found to be effective especially on color parameters and fruit sizes, and PC2 (19.92%) was found to be effective on fruit weight, width, and taste. Hierarchical cluster analysis revealed that G3 and G13 genotypes were separated from other genotypes and showed superior characteristics, especially in fruit weight, length, and color parameters. Strong relationships were determined between fruit characteristics and color parameters. This research has made significant contributions to the characterization of apple genetic resources in the Mudurnu region, and the superior genotypes (especially G3 and G13) can be considered as parents in future breeding studies. In addition, the trait groups determined as a result of PCA and cluster analysis provide essential information on which traits can be evaluated together while establishing selection criteria in apple breeding programs. As a result, this study has provided valuable data for protecting, evaluating, and using regional apple genetic resources in breeding programs.

Conflict of interest statement

The authors declare that there is no conflict of interestregarding the publication of this paper.

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