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Bazı Kapya Biber (*Capsicum annuum* L.) Genotiplerinin Morfolojik Karekterizasyonu

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ÖZET

Solanaceae familyasının bir üyesi olan *Capsicum annuum* (Capia), meyve ve bitki özellikleri bakımından zengin bir genetik çeşitliliğe sahiptir. Bu çalışma, yeni hibrit kapya biber çeşitlerinin geliştirilmesi için arzu edilen morfolojik özelliklere sahip kapya biber genotiplerini seçmek amacıyla morfolojik karakterler kullanarak yerel popülasyonlar, standart ve hibrit çeşitlerden oluşturulan genetik havuzu karakterize etmeyi amaçlamıştır. Yüz on iki genotip 15 morfolojik (11 kalitatif ve 4 kantitatif) karakter kullanılarak karakterize edilmiş ve kalitatif karakterler gözlemlenirken kantitatif karakterler ölçülmüştür. Tek bitki seleksiyonu sonucunda belirlenen hatlar arasındaki ilişkiyi belirlemek için Küme ve Temel Bileşen Analizi (PCA) uygulanmıştır. Yapılan küme analizi sonucunda hatlar arasındaki morfolojik benzerliği değerlendirmek için dendrogram oluşturulmuş ve 15 değişkene dayalı olarak on dokuz grup belirlenmiştir. Temel bileşenler analizinde ise altı TB ekseni toplam varyasyonun %66,2' sini açıklamıştır. Çalışma sonucunda, biber hatları arasında yüksek morfolojik varyasyon tespit edilmiştir. Bitki özelliklerinde ki varyabilitenin değerlendirmesi, genetikçilere ve ıslahçılara biber ıslah programlarına dahil etmek üzere arzu edilen özelliklere sahip popülasyonların belirlemelerinde yardımcı olabilir.

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Morphological Characterization of Some Capia Pepper (*Capsicum annuum* L.) Genotypes

ABSTRACT

Capsicum annuum (Capia), a member of the *Solanaceae* family, has a rich genetic diversity in fruit and plant traits. To select Capia pepper genotypes with desirable morphological traits for the development of new hybrid capia pepper varieties, this study aimed to characterize genetic accessions generated from local populations, and standard and hybrid cultivars using morphological characters. One hundred and twelve genotypes were identified using 15 morphological traits (11 qualitative and 4 quantitative) and quantitative traits were measured while qualitative traits were observed. Cluster and Principal Component Analysis (PCA) was applied to determine the relationship between the lines identified as a result of single plant selection. As a result of the cluster analysis, a dendrogram was prepared to evaluate the morphological similarity between the lines, and nineteen groups were identified based on 15 variables. In Principal Component Analysis, six PC axes explained 66.2% of the total variation. As a result of the study, high morphological variability was observed among pepper lines. This evaluation of plant trait variability can assist geneticists and breeders in identifying populations with desirable characteristics for inclusion in pepper breeding programs.

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INTRODUCTION

Pepper (*Capsicum annuum* L.) is a crop with different colors ranging from green at the intermediate stage to yellow or red at maturity. Pepper is an important health protective factor that helps protect against common human diseases, especially due to the phenolic compounds, flavonoids, and carotenoids in its fruits, which can increase the vitamins perspective (Mady et al., 2005). According to Tüik (2023), capia pepper is one of the most widely cultivated crops in Turkey and has increased significantly in both open-field and greenhouse cultivation in recent years. In 2022, Faostat reported the world production of pepper at 36.972.494 metric tons and the estimated total production of pepper in Turkey at 3.018.775 metric tons. Considering this production data, Turkey has a rich genetic diversity of peppers with high cultivation value and important importance in terms of research and conservation. Correct identification and classification of botanical species is a crucial step in efficiently managing germplasm collections. Because this stage forms the basis of developing any plant species. In addition, many researchers have stressed the importance of morphological characterization as a fundamental step toward resolving taxonomic conflicts in many plant species (Moura et al., 2013; Ranjit et al., 2013; Gerrano et al., 2017; Olatunji & Afolayan, 2018).

It has been reported that due to the increased cultivation of improved varieties, a large portion of cultivated peppers are in constant danger of extinction along with the loss of genetic diversity (Sunday et al., 2021). In this context, morphological characterization studies are considered an important starting point for genotype selection from cultivars for breeding purposes (Oyelakin et al., 2019). These studies are also a useful genetic guide for selecting parental plants for hybridization (Singh, 2006). Due to the increasing cultivation of improved varieties, a large proportion of cultivated peppers have been reported to be in constant danger of extinction with a loss of genetic diversity (Sunday et al., 2021). Taia (2005) and Karaca (2013) reported that the use of morphological characters is the most valuable tool in selecting genotypes from varieties for crop improvement and breeding purposes. This process involves studying and evaluating the physical and structural characteristics of the plant, such as shape, size, color, and other visible traits. Evaluation of genetic diversity determined after morphological characterization is very important for determining unique traits, genetic variations, and potential sources of resistance to diseases, pests, and environmental stresses. In addition the genotypes identification and differentiation of different genotypes or cultivars based on their physical characteristics, such as plant height, leaf shape, fruit shape, color, and size. This information is crucial for maintaining genetic purity and integrity in breeding programs. Morphological characterization also provides valuable data for plant breeders to select and develop new pepper cultivars with desirable traits and enables them to make informed decisions on which genotypes to cross in line with breeding aims. Weerakoon and Somaratne (2010) also used morphological traits such as plant height, stem pubescence, fruit weight, flower color, and fruit shape to select pepper different genotypes for hybridization and breeding purposes. Sunday et al. (2021) used morphological traits such as fruit shape and color, fruit length (cm), fruit width (cm), and fruit wall thickness. All these morphological traits are very important in varietal selection and breeding programs. This is because fruit yield is determined by the vegetative characters. Numerous researchers in our country and around the world performed various characterizations on *C. annuum* L. species according to the fruit and plant characteristics, and the existing morphological variations were identified in detail (Başak, 2019; Belay et al., 2019; Lima et al., 2019; Santos et al., 2019; Hernández-Pérez et al., 2020; Khan et al., 2020; Ferdousi et al.,2021; Sunday et al.,2021; Tripodi et al., 2021; Bedjaoui et al.,2022; Gomes et al., 2022; Şahin et al., 2022; Çetin, 2023). To date, many characterization studies have been carried out on pepper, but morphological characterization studies on capia pepper are limited. It is known that breeders of capia pepper develop varieties through the selection of superior parents for various purposes. Therefore, understanding the level of genetic variation among pepper varieties through the use of morphological traits is important for the selection of suitable genotypes for crop improvement and breeding purposes. Accordingly, this study aimed to characterize the genetic pool established to select capia pepper genotypes with desirable morphological traits for future breeding studies.

MATERIAL and METOD

Plant material

The study material consisted of 112 Capia pepper genotypes, including 61 local populations from Kırşehir, 1 standard variety (Yalova Yağlık 28), and 50 hybrid varieties. Morphological observations and measurements were reported for 122 lines identified through morphological characterization studies on 775 plants at S1 stage.

Phenotypic Characters

Data for morphological characteristics were collected according to the UPOV (TG/76/8) protocol (UPOV, 2006). One hundred and twelve Capia pepper genotypes were cultivated in the fully automated R&D greenhouse at Kırşehir Ahi Evran University. On average, 8 plants of each genotype were planted based on seed emergence with spacing of 0.7m x 0.4m x 0.4m.

A total of fifteen phenotypic characters were evaluated. All characters were measured in the greenhouse at normal harvest time. One hundred and twenty genotypes were characterized using 15 morphological characters (11 qualitative and 4 quantitative), with qualitative characters observed and quantitative characters measured.

The qualitative characters included: Anthocyanin coloration in the internode (none/medium/high/very high), Plant grown habit (upright, semi-upright, prostrate), Leaf color (light green, green, dark green), Leaf shape (lanceolate, ovate, broad elliptic), Fruit attitude (erect, horizontal, drooping), Immature fruit color (light green, green, dark green), Mature fruit color (light red, red, dark red), Fruit cross-section shape (elliptic, angular, circular), Fruit tip shape (very acute, moderately acute, rounded, moderately depressed, very depressed),), Number of fruit loculus(predominantly two, equally two and three, predominantly three, equally three and four) and fruit stalk tip (absent, shallow, medium, deep, very deep). The quantitative characters were: Fruit length (cm), Fruit width (cm), Fruit flesh thickness (mm), and Seed cavity length (cm). Fruit character analyses were conducted on 3 fruits from each plant.

Statistical Analysis

The multivariate procedure in Minitab (MINITAB 19, 2019) was used for principal component analysis (PCA) and cluster analysis based on 15 morphological characters. In this analysis, the data obtained from the selected materials were scored according to the UPOV scale values, in order to identify patterns of variation within the Capia pepper accession groups.

RESULTS and DISCUSSION

Phenotypic Traits

Phenotypic characterization parameters showed a high variation in terms of some plant and fruit traits. When plant traits were evaluated, it was determined that 3 lines were prostrate (2.46%), 11 lines were semi-upright (9.02%) and 108 lines were upright (88.52%) in terms of plant attitude. In the study, the peppers that were determined to be prostrate and semi-upright in terms of plant attitude were non-types of village pepper, bell pepper, and ornamental pepper. In the gene collection, which showed high variation in terms of leaf color and shape, 58 lines were dark green (47.54%), 55 lines were green (46.08%) and 9 lines were light green (7.38%). In terms of leaf shape; 6 lines were broad elliptic (4.92%), 2 lines were lanceolate (1.64%) and 114 lines were ovate (93.44%). Finally, according to the intensity of anthocyanin in the internode; 19 lines were low (15.58%), 46 lines were medium (37.70%), 46 lines were high (37.70%) and 11 lines (9.02%) were absent anthocyanin in the internode. In a study conducted on interspecific hybrid populations of pepper, in terms of plant characteristics, 87 genotypes showed upright growth habits, while 11 genotypes showed semi-upright development. In terms of leaf shape, it was found that 7 genotypes had long leaves, 51 genotypes had medium leaves and 12 genotypes had short leaves, while in terms of leaf color, 53 genotypes had dark green leaves and the remaining genotypes had green leaves. As for anthocyanin in the internode level, while no anthocyanin formation was observed in 45 genotypes, it was reported that out of the remaining 43 genotypes, 24 showed moderate, 14 had low and 5 had very low (Pınar & Dilfiruz, 2022). According to the findings obtained, the gene collection exhibits a wide variation in terms of plant characteristics. This variation is very important in the design of breeding programs.

Upon a general assessment in terms of pomological characteristics, significant differences among the lines have been observed. The research findings indicate that, based on observations of fruit attitude, 2.46% of the fruits are upright, 8.20% are semi-upright, and 89.34% have drooping of the fruit, especially for plants with lower leaf density, which is a desired trait as it makes them more resistant to physiological disorders such as sunburn (Karaağaç, 2006). When examining the pre-maturity fruit color visually, it was observed that the colors range from green to dark green among the lines. 31.15% of the lines have green fruits, while 68.85% consist of dark green fruits. As fruits mature, a color transformation occurs. In capıa pepper, mature fruit color, which is very important both as a quality and a harvest parameter, was determined as 4.92% light red, 27.87% medium red, and 67.21% dark red. According to the study by Mutlu et al. (2009), the pre-maturity fruit color in most populations was green (92.97%), with 7.03% observed as yellow. The mature fruit color in the populations was reported to be red (54.59%), dark red (38.92%), and light red (5.41%), and in 2 populations (1.08%) a brown mature fruit color was observed.

In our study, when the cross-sectional shape of the fruits of the lines was evaluated, it was observed that the majority of 103 lines (84.43%) were triangular, while 19 lines (15.57%) were ovate. When the fruit tip shape was analyzed, it was determined that 2.46% were very depressed, 39.34% were depressed, 56.56% were peaked and 1.64% were very peaked. In terms of the number of fruit lobes, 35.25% of the lines had three lobes, 62.30% had two lobes and 2.45% had no lobes. Finally, when the stalk tip was analyzed, it was observed that 3 lines (2.46%) were deep, 7 lines (58.20%) were slightly deep and 48 lines (39.34%) had no stalk tip. Karaağaç (2006) reported that 60.7% of the genotypes were ovate-shaped when analyzed in terms of fruit cross-section. It was stated that the types with pointed fruit tips are more preferred in the market and three-lobed fruits are a desirable feature for the processing industry. However, it has been reported that two-lobed capia pepper fruits are preferred by consumers for roasting. The pomological traits characterized in our study show variation in parameters such as fruit color, fruit posture, fruit tip shape, number of fruit lobes and stem pit at different rates according to the lines. This variation is thought to be because the lines were collected from different locations and from a wide area and foreign pollination, which is common in pepper. This situation shows that the gene pool analyzed has a very heterogeneous structure.

In the study, the lowest seed cavity length was found to be 1.30 cm in line 122, while the highest was 9.20 cm in line 47 (Table 1). When fruit length and diameter values were evaluated, the shortest fruit length was 4 cm in line 8, while the longest fruit length was 20.40 cm in line 80. For fruit diameter, the smallest diameter was 2.10 cm in line 122, while the largest diameter was 6.50 cm in line 79. For flesh thickness, the lowest value was 2.54 mm in line 46, while the highest value was 6.95 mm in line 79 (Table 1). Consistent with our results, Mutlu et al. (2009) reported that in pepper, fruit length ranged from 1.4 to 18.5 cm, fruit diameter ranged from 0.7 to 7.3 cm, and fruit flesh thickness varied from 1 to 7 mm among populations. Similarly, Karaağaç (2006) found that in red pepper, fruit length ranged from 9.1 to 18.5 cm, fruit diameter varied from 4.5 to 6.8 cm, and fruit flesh thickness ranged from 3.3 to 5.8 mm. Panayotov et al. (2000) observed that in capia-type red peppers, fruit length ranged from 10.2 to 15.9 cm, fruit diameter ranged from 2.1 to 5.7 cm, and fruit flesh thickness ranged from 2.1 to 5.5 mm. Genetic relatedness among 122 red capıa pepper lines was determined using phenotypic markers at the end of the study. Some markers emphasized the differentiation among pepper genotypes phenotypically, as they showed more significant variations that caused significant distinctions. In conclusion, the importance of phenotypic variation in future pepper breeding programs was emphasized, and phenotypic traits were predicted to be useful in the differentiation of pepper genotypes.

Çizelge 1. S1 kademesindeki seçilen biber hatlarına ait kantitatif özellikler

Table 1. Quantitative characters of selected pepper lines at S1 level

Characters	Maximum	Genotype	Minimum	Genotype	Mean
Seed cavity length (cm)	9.20	47	1.30	122	3,38
Fruit width (cm)	6.50	79	2.10	122	4.37
Fruit length (cm)	20.40	80	4.0	8	12.70
Flesh thickness (mm)	6.95	79	2.54	46	4.10

Principal Component Analysis

In the study, PCA was also applied to group the pepper lines based on morphological and pomological observations and measured parameters, and to study the relationship between the parameters obtained.

It is reported that the evaluation of PC axes with eigenvalues greater than 1 in PCA analysis is a very reliable indicator (Özdamar, 2004; Kanal & Balkaya, 2021). Total variance ratios and cumulative variance values of the axes obtained as a result of the analysis were determined and interpretations were made accordingly. In the study, as a result of principal component analysis, 15 independent principal component axes were obtained in pepper lines and it was determined that there were 6 PC axes with eigenvalues greater than 1. It was determined that the cumulative variation of PC axes with eigenvalue greater than 1 represented 66.2% of the selected pepper lines (Table 2). When the values of the principal component axis were analyzed, it was found that the first principal component axis explained 20.2% of the total variation, the second principal component axis explained 12.2% of the variation, and the third principal component axis explained 10.4% of the total variation. In the study, it is accepted that the weight coefficient values in the components in terms of the criteria examined in the principal component analysis have significant weight if they are 0.3 and above (Brown, 1991; Taş, 2020). In this direction, the traits with high coefficients of 0.3 and above on the PC-1 axis were plant attitude (0.326), fruit tip shape (0.334), leaf shape (0.355), fruit attitude (-0.368), fruit length (-0. 442) and seed cavity length (-0.355), while stalk tip (0.392), sectional cross-sectional shape (0.473), fruit width (0.438) and fruit flesh thickness (0.486) were found to be significant on PC-2 axis (Table 2). The score plot and loading plot analyses are shown in Figure 1.

The studies conducted by Agyare et al. (2016) and Bozkalfa et al. (2017) emphasize the importance of characterizing genetic diversity in Capsicum species and local pepper genotypes through morphological and agronomic traits. The findings of Agyare et al. (2016) demonstrate that morphological traits effectively reflect genetic diversity in *Capsicum* species, with a genetic variance of 59.61%. The study by Bozkalfa et al. (2017) reveals that genetic distances among local pepper genotypes vary between 62% and 94%. These studies provide significant information for pepper breeding and the conservation of genetic diversity. The results of these research efforts show that the pepper gene pool possesses a high degree of heterogeneity, indicating the potential for its use in breeding programs aimed at improving resistance to diseases and pests, yield, and certain quality criteria. Supporting these breeding efforts with molecular characterization studies will ensure more effective use of the results obtained. Additionally, cluster analysis based on agronomic traits for distinguishing and identifying plant participation and group participation based on their similarities increases the possibility of determining heterotic effects from parents in the breeding populations and obtaining new superior genotypes.

Çizelge 2. S1 kademesindeki seçilen biber hatlarında temel bileşen analizine göre faktör grupları ve bunlara karşılık gelen TB eksenleri

Table 2. Factor groups and corresponding PC axes after principal component analysis for selected pepper lines at S1 level

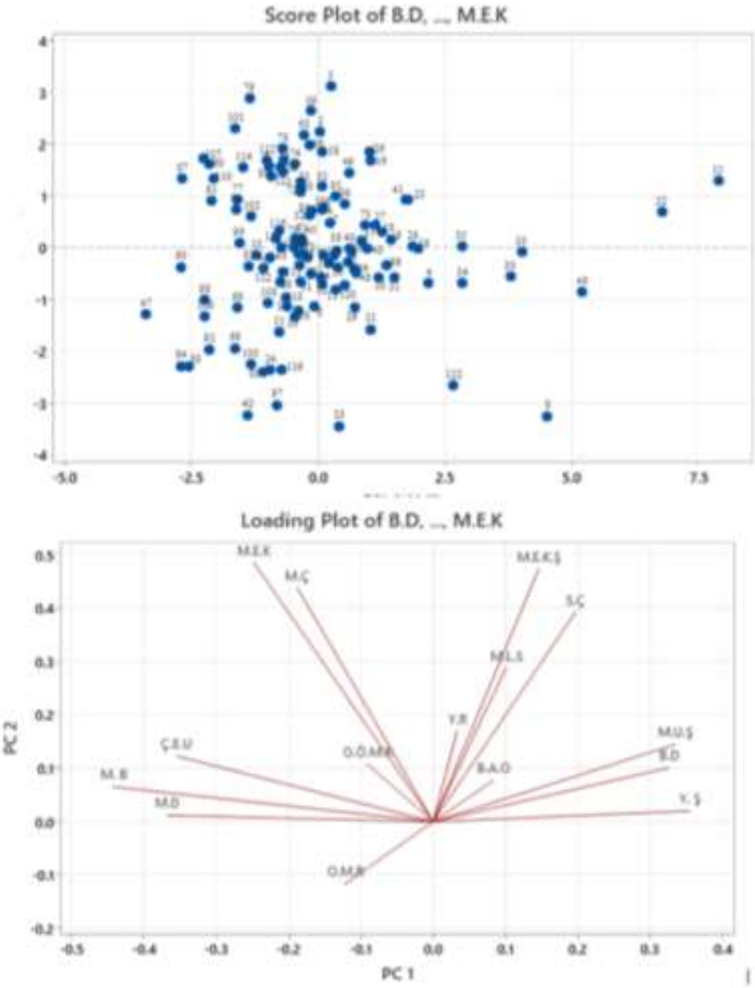
Eigenanalysis of the Correlation Matrix						
Eigenvalue	3.029	1.832	1.567	1.264	1.212	1.028
Proportion	0.202	0.122	0.104	0.084	0.081	0.068
Cumulative	0.202	0.324	0.429	0.513	0.594	0.662
Variable						
Eigenvalue	PC1	PC2	PC3	PC4	PC5	PC6
P.H	0.326	0.101	0.009	-0.012	-0.412	-0.141
L.C	0.033	0.169	-0.261	-0.678	0.083	0.134
L.S	0.355	0.020	0.002	-0.189	-0.283	0.197
A.C.I	0.084	0.078	-0.518	0.472	-0.094	0.062
F.A	-0.368	0.012	-0.166	0.247	0.197	-0.211
I.F.C	-0.091	0.108	-0.342	-0.359	0.216	-0.426
M.F.C	-0.122	-0.117	0.404	0.003	0.152	-0.395
F.C.S.S	0.146	0.473	0.139	0.018	0.210	-0.228
F T.S	0.334	0.144	-0.278	0.198	-0.090	-0.395
N.F.L	0.101	0.288	0.024	0.093	0.536	0.446
F.S.T	0.197	0.392	0.302	0.191	0.068	0.140
S.C.L	-0.355	0.123	-0.268	0.014	-0.238	0.301
F.L	-0.442	0.065	0.149	0.015	-0.264	0.075
F.W	-0.188	0.438	0.238	-0.075	-0.394	-0.098
F.F.H	-0.248	0.486	-0.129	0.022	-0.031	-0.066

Explanation: Plant grown habit (P.H),Leaf color (L.C), Leaf shape (L.S), Anthocyanin coloration in internode(A.C.I), Fruit attitude (F.A), Immature fruit color (I.F.C), Mature fruit color (M.F.C), Fruit cross-section shape (F.C.S.S), Fruit tip shape (F.T.S), Number of fruit loculus(N.F.L), fruit stalk tip (F.S.T), Seed cavity length (S.C.L), Fruit length (F.L), Fruit width (F.W), Fruit flesh thickness (F.F.T), Fruit flesh hardness (F.F.H).

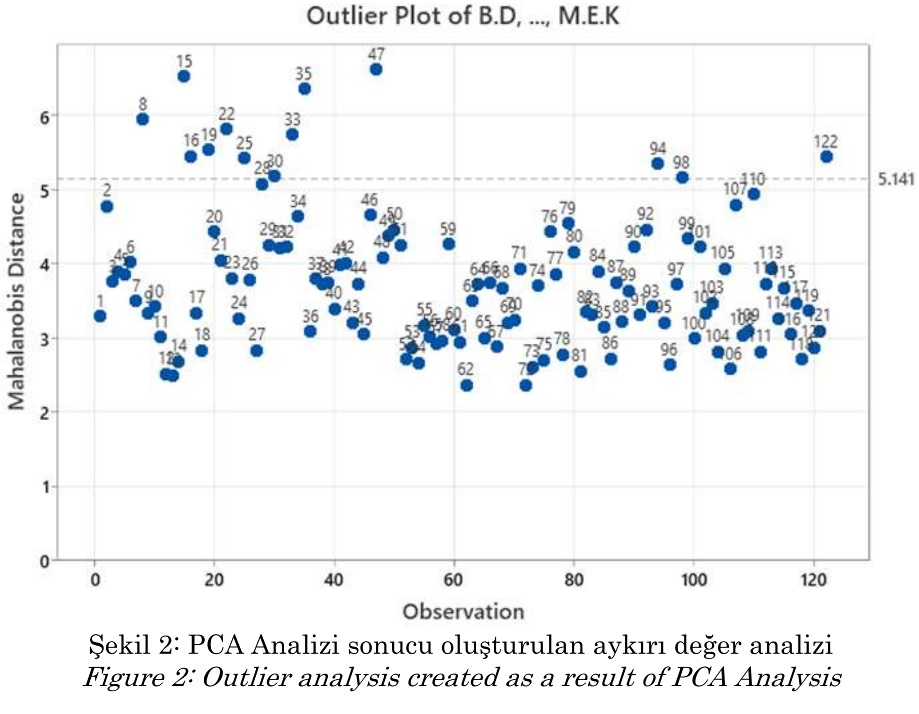
The outlier plot analysis conducted in our research data is also extremely important for detecting outliers containing extreme measurement values. Here, the calculated Mahalanobis distance is one of the statistical approaches used for outlier detection. Mahalanobis distance, which can be interpreted as a measure of distance, takes into account the covariance matrix calculated from the data to compute the distance between two points. Thus, it also considers the behavior of other points. The unit of the obtained distance is in terms of standard deviation along the line passing between two points, which is a value dependent on the data (Anonymous, 2023). Therefore, these lines possessing outliers in the gene pool can be characterized as atypical lines. Here, lines numbered 8, 15, 16, 19, 22, 25, 30, 33, 35, 47, and 122 exceeding a Mahalanobis distance of 5.141 have been identified as outliers (Figure 2).

Cluster Analysis

Cluster analysis was applied to the data obtained as a result of characterization. Using the data obtained after characterization studies, similarities-differences and groupings among pepper species, subspecies, or local varieties can be shown by using cluster analysis (Düzyaman & Vural, 2002; Rivera Martinez et al., 2004). It has been reported that cluster analysis is more reliable when 25% or more of the total variation can be explained by the first 2 or 3 axes (Mohammadi & Prassana, 2003). In the dendrogram formed as a result of cluster analysis according to the correlation matrix, the lines were defined as 19 groups. If the dendrogram is examined in general, it can be seen that it consists of 4 main groups. The first main group consists of 7 subgroups, the second main group consists of 3 subgroups, the third main group consists of 3 subgroups and the fourth main group consists of 5 subgroups (Figure 4). The genotypes in the groups formed as a result of the dendrogram are given in Table 3.



Şekil 1: PCA Analizi sonucu oluşturulan score plot ve loading plot analizleri
Figure 1: Score plot and loading plot analyses prepared based on PCA Analysis



Şekil 2: PCA Analizi sonucu oluşturulan aykırı değer analizi
Figure 2: Outlier analysis created as a result of PCA Analysis

Şekil 3: Çalışmada tip dışı olarak tespit edilen bazı hatların bir fotoğraf kesiti
Figure 3: A photo section of some of the lines identified as non-typical in the study

Çizelge 3: Dendrogram sonucunda oluşan gruplardaki genotipler
Table 3: Genotypes in the groups created as a result of the dendrogram

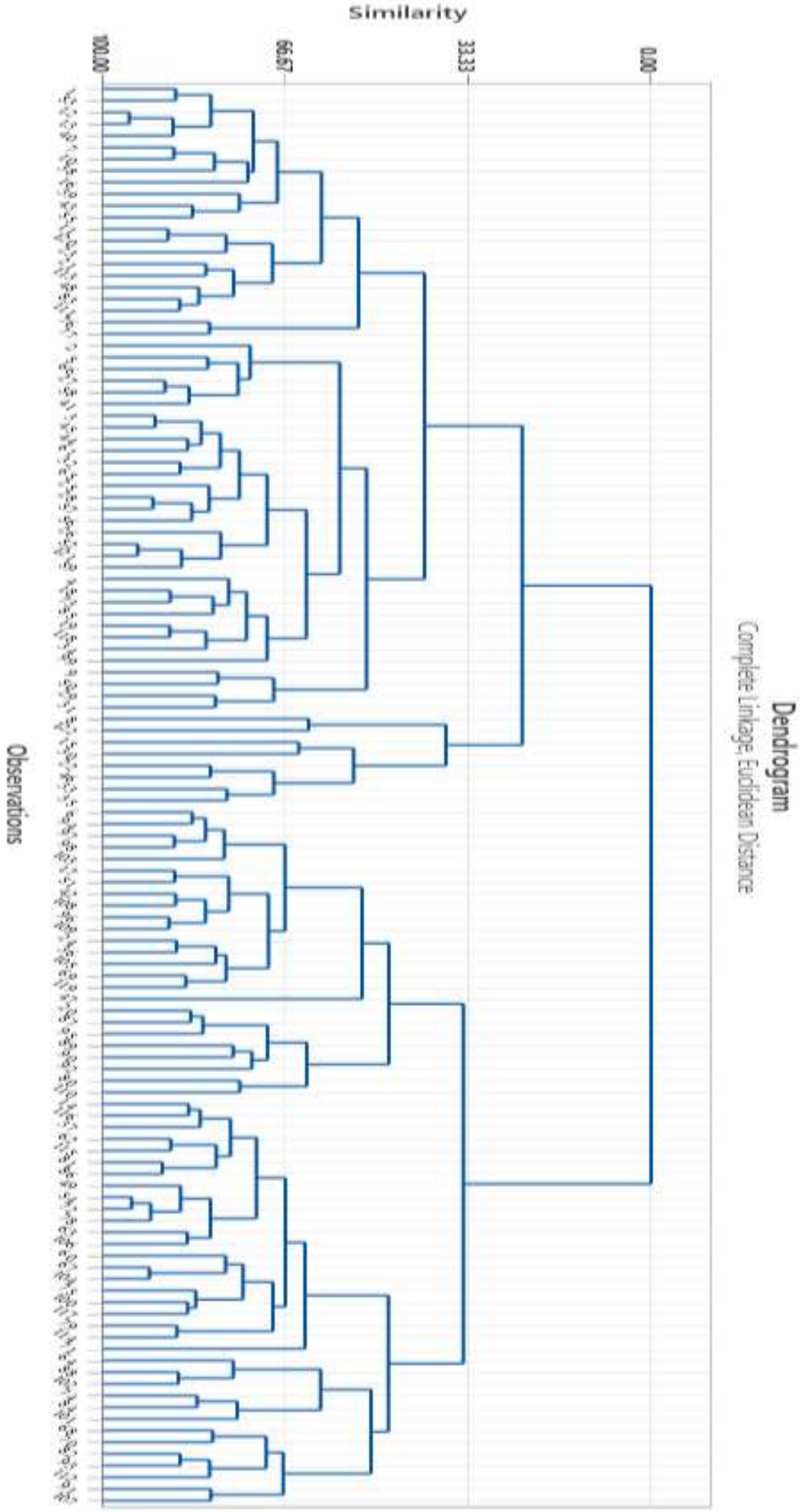
Group	Lines	Total Lines (pcs)
A	1. subgroup (1, 53, 12, 13, 40, 7, 10, 38, 16, 39, 43, 55), 2. subgroup (11, 120, 23, 21, 113, 48, 83, 111), 3. subgroup (76, 77), 4. subgroup (2, 5, 66, 27, 58, 41), 5. subgroup (3, 45, 44, 61, 32, 65, 25, 28, 57, 56, 26, 52, 121, 59), 6. subgroup (4, 18, 73, 85, 19, 118, 34, 99), 7. subgroup (9, 50, 29, 31).	54
B	1. subgroup (8, 122), 2. subgroup (15, 30), 3. subgroup (22, 46, 33, 35).	8
C	1. subgroup (6, 94, 97, 98, 103, 17, 51, 42, 108, 96, 109, 24, 36, 105, 65, 119), 2. yan grup (47), 3. subgroup (20, 87, 95, 89, 90, 92), 4. subgroup (80,110).	25
D	1. subgroup (14, 116, 37, 62, 115, 81, 86, 49, 54, 72, 78, 63, 106, 60, 67, 104, 75, 100, 117, 79, 114), 2. subgroup (71), 3. subgroup (64, 88, 102), 4. subgroup (74, 84, 101), 5. subgroup (68, 70, 82, 93, 112, 91, 107).	35

The general characteristics of the groups are given in detail below.

Group A: It was determined to be the group in which the most genetic material was clustered, with 54 lines among the groups formed as a result of cluster analysis (Table 3). The majority of lines in this group (44 lines) belonged to the local population. In this group, which consisted of seven subgroups, the plant attitude was erect/semi-erect, the leaf shape was oval, the fruit attitude was hanging/semi-erect, the fruit tip shape was pointed/depressed, and the presence of stalk tip was slightly deep/absent. According to the averages among the lines; the fruit length (11.96 cm) of the lines in this group was medium, fruit width (4.25 cm) was medium, seed cavity length (36.92 mm) was medium and fruit flesh thickness (4.51 mm) was medium.

Group B: It was identified as the group in which the least genetic material was clustered with 8 lines among the groups formed as a result of cluster analysis (Table 3). All lines in this group belonged to the local population and generally consisted of ornamental, dolma, and mini capia pepper types which are considered non-typical. In this group consisting of three side groups, the fruit attitude is upright/semi-upright, the fruit tip shape is depressed/very depressed and the fruit cross-sectional shape is square. According to the averages among the lines; the fruit length (6.91 cm) of the lines in this group was low, the fruit width (4.15 cm) was medium, the seed cavity length (19.13 mm) was low and the fruit flesh thickness (3.02 mm) was thin.

Group C: This group consists of a total of 25 lines (Table 3). Most of the lines in this group (17 lines) are hybrid variety extensions in the market. In this group, consisting of four lateral groups, plant attitude was upright, leaf shape was oval, fruit attitude was drooping, fruit tip shape was pointed/depressed, the number of fruit lobes was two, and the presence of stalk tip was not detected. According to the averages among the lines; the fruit length (15.64 cm) of the lines in this group was long, the fruit width (4.35 cm) was medium, the seed cavity length (40.06 mm) was high and the fruit flesh thickness (4.22 mm) was medium.



Şekil 4: Cluster analizi sonucunda elde edilen dendrogram
Figure 4: The dendrogram obtained as a result of the cluster analysis.

Group D: Among the groups formed in the dendrogram, the group with the highest number of lines (35 lines) is after group A (Table 3). The majority of lines in this group (30 lines) are commercial hybrids.

In this group, which consists of five subgroups, plant attitude is upright, leaf shape is oval, fruit attitude is drooping, fruit tip shape is pointed, fruit cross-sectional shape is square, and the presence of stem tip is slightly deep. According to the averages among the lines; the fruit length (16.29 cm) of the lines in this group is long, the fruit width (4.70 cm) is large, the seed cavity length (38.97 mm) is medium and the fruit flesh thickness (4.64 mm) is thin.

When the cluster analysis results were analyzed based on genotypes, it was found that in group A, lines 12-13 and 52-121 were very similar to each other, while lines 12-50 and 13-29 were the most distant lines. In group D, lines 54-72 were very similar to each other, while lines 54-64 were the most distant lines. These results will help to eliminate very similar genotypes and save work and time in breeding studies. In addition, the most distant genotypes are important in terms of a high positive heterosis rate as a result of future crosses between them.

CONCLUSION and RECOMMENDATIONS

Capsicum annuum L. is one of the most important vegetable crops grown and stands out both for its fresh consumption and for industrial use, in the world and Turkey. In conclusion, morphological characterization and selection of Capia pepper genotypes are vital steps in crop improvement, genetic diversity conservation, and ensuring the agricultural sustainability of this important crop. These processes enable the development of better-performing varieties, adaptation to changing environmental conditions, and the delivery of high-quality produce to meet market demands and are fundamental for the continued development and advancement of *Capsicum annuum* L. cultivation. This study aimed to characterize the gene pool created from standard, hybrid expansion, and local populations using morphological characters. At the end of the study, it was found that the six PC axes obtained from the PCA analysis represented 66.2% of the cumulative variation. This value indicates that this gene collection can help geneticists and breeders identify populations with desirable traits for inclusion in pepper breeding programs. In addition, four main groups were identified in the cluster analysis. To be used in different breeding studies, if the important criterion is Capia type pepper with long fruit and high fruit flesh thickness, the populations in groups C and D in the dendrogram showing the similarity coefficients between pepper samples can be selected. Again, if the criterion sought is plant and fruit attitude, these groups should be considered. In addition, if the populations that show a high similarity to the varieties we use as standard are included in breeding programs and evaluated, new varieties suitable for the market can be brought to the market. As a result of this study, sufficient morphological variability was found in the pepper lines. However, while it is difficult to reveal the difference between the types by morphological characterization, this difference can be revealed more easily and precisely by using molecular technical methods. Therefore, in the next stage of the study, characterization of the capia-type red pepper genotypes with these molecular breeding methods in the purpose-oriented breeding studies planned to be carried out in the future will allow more precise decisions to be made in the breeding studies.

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Author contribution statement

The contributions of all authors are defined as follows: study concept and design: A.N.Şavkan, O.Turkmen; data collection: A.N. Şavkan; analysis and interpretation of results: A.N.Şavkan, O.Turkmen, H. Başak; preparing a draft text: A.N.Şavkan, O.Turkmen. All authors reviewed the results and approved the final version of the article.

Compliance with ethical standards

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

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