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Original scientific article

MORPHOLOGICAL AND MOLECULAR IDENTIFICATION OF HYBRID APRICOT GENOTYPES OBTAINED BY INTRA-SPECIFIC HYBRIDIZATION

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Apricot is one of the important stone fruits produced in the world. In this study, genetic variation was investigated based on SRAP marker technique and morphological data in 120 genotypes and parent plants obtained by inbreeding in some apricot cultivars such as Ninfa, Proce de Tyrinthe, Palstein, Hacıhaliloğlu, Hasanbey, Aprikoz and Kabaaşı. In the study, 15 different combinations of SRAP markers were used and a total of 105 scoreable bands were obtained and 76 of them were determined as polymorphic. The average base lengths of these primers are between 200-1700 bp, the average number of polymorphic bands per primer is 7.0. The mean polymorphism value is 71.64%. The similarity coefficient in the dendrogram created according to the UPGMA method differed between 0.61 and 0.96. According to the dendrogram, 2 main groups were formed. The closest genotypes have a similarity index of 0.96. In the morphological characterization analysis, 120 hybrid individuals were examined with 19 UPOV criteria. No variation was found in terms of petiole nectarium number, dominant numbers and petiole shape characteristics. Variations between hybrids were determined in terms of 16 characteristics such as plant development, plant habitus, amount of branching in the tree, leaf and shoot characteristics. 119 hybrids showed ‘reddish brown’ coloration, 87 hybrids medium leaf tip, and 116 plants 'double dentate' in terms of incisions of margin. 84 hybrids showed

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medium petiole incision, 101 hybrids showed medium petiole thickness, and 117 plants showed weak petiole anthocyanin coloration. It is predicted that the morphological and molecular analyzes of the hybrid plants will enable the development of new cultivars and rootstock candidate genotypes. With the results of this study, the genetic variations and morphological classifications determined in the genotypes will guide the further studies on hybrid breeding programs in apricots.

Keywords: apricot, hybridization, morphological characterization, SRAP marker, UPOV

INTRODUCTION

Apricot (*Prunus armeniaca* L.), a member of the *Rosaceae* family, is a very important commercial fruit grown in many countries and different climatic conditions around the world, especially in Mediterranean and Central Asian countries (BAILEY and HOUGH, 2006; ÇUHACI *et al*., 2021). According to FAO 2021 data; Apricot production in the world is 3,578 412 tons. Turkey, which has been on the first rank in apricot production in the world for years, supplies more than 22% of the total production with 800 thousand tons of production. 23.3% of the production areas in the world are in Turkey. In 2021, 156218 tons of apricot exports were made worldwide. Having a significant share in exports, Turkey exported approximately 87722 tons of dried apricots. Turkey is followed by Algeria, Uzbekistan and Pakistan in apricot production (FAO, 2022).

In recent years, due to the increase in demand for apricot varieties with different characteristics that based on consumer demands (size, taste, color, aroma, earliness, etc.), studies on breeding new varieties that distinguish in terms of fruit quality have gained importance (ÇALIŞKAN *et al*., 2012). Although progress has been made in the production of new apricot varieties in Turkey and other apricot producing countries, apricot breeding programs are still not sufficient (ÇUHACI et al., 2020). Genetic diversity is very important in breeding studies and especially wild species are included in the studies along with the cultivated varieties. Central Asia, China and Iran-Caucasus regions contain a significant variety of wild species populations (AKPINAR *et al*., 2010; YILMAZ and GÜRCAN, 2012).

Morphological characterization studies and phenotypic measurements are carried out in selection criteria such as affinity relations, productivity, resistance to environmental conditions in selected species for use in breeding studies Molecular methods are also used to support these measurements and to apply in cases where they are insufficient. With the current developments in biotechnology, molecular markers have been developed to identify genetic variations within and between species, to determine the degree of affinity and to classify them. It has been widely and successfully used in genetic analysis studies in recent years, and studies have made progress at the molecular level (HALASZ *et al*., 2010; TURKOGLU *et al*., 2010; EHLIZ *et al*., 2021).

Different molecular marker methods have been used by researchers in many DNA-based studies (ÖZKAYA *et al*., 2006). Due to the reproducibility problems such as the RAPD (Random Amplified Polymorphic DNA) technique, the changes that occur after transcription, and the low reliability of isoenzymes, researchers have started to use different molecular marker techniques to get exact and more reliable results (EHLIZ *et al*., 2021). One of these techniques, SRAP (Sequence-Related Amplified Polymorphism) molecular marker technique, is a PCR-based and

dominant marker system targeting ORFs (Open Reading Frames). The SRAP marker technique is distinguished in terms of being a cheap and simple method, having a high polymorphism rate, being suitable for studies such as gene tagging and cDNA fingerprinting, and easy sequencing the selected bands (LI and QUIROS, 2001). In addition, SRAP is used in genetic diversity determination studies, genetic mapping of different plant species, and gene tagging studies (BUDAK *et al*., 2004; FILIZ *et al*., 2009). The SCAR marker system was used to determine genetic variation by molecular characterization of many horticultural crops such as peach and nectarine (AHMAD *et al*., 2004), dates (GUO and LUO, 2006), citrus fruits (UZUN *et al*., 2009) and apricot (UZUN *et al*., 2010; PINAR *et al*., 2013).

Turkey, as a country with a large number of *Prunus* species, has a strong potential in this area. Despite this potential, there has not been much study on crossbreeding, especially in Prunus species, and studies have been limited. In this study, it was aimed to develop new cultivars and rootstock candidate genotypes with morphological and molecular identification of hybrid plants obtained by intraspecific hybridization in some apricot cultivars.

MATERIAL AND METHODS

Material

Plant Material

The hybrid genotypes used in the study were obtained from the crossing of apricot varieties such as Ninfa, Proce de Tyrinthe, Palstein, Hacıhaliloğlu, Hasanbey, Aprikoz and Kabaaşı. These genotypes were obtained from Erciyes University Agricultural Research and Application Center. The soil properties of this place are generally poor in organic matter, poor water holding capacity, and in terms of climate characteristics, the winters are cold and snowy, and the summers are hot and dry. Annual maintenance operations (fertilization, irrigation and pruning) are carried out routinely in the hybrid plot. The numbers and combinations of hybrid genotypes are given in Table 1.

Methods

Morphological Analysis

In order to determine some morphological characteristics of Apricot × Apricot hybrid plants obtained from 2018 and 2019 hybridizations (Figure 1), UPOV (The International Union for the Protection of New Varieties of Plants) criteria (Table 2) with the code TG/56/4(proj.3) were used.

Molecular Analysis

Molecular Marker Analysis

DNA isolation was performed according to the CTAB method developed by DOYLE *et al*. (1990) and modified from this protocol by GÜLŞEN *et al*. (2009). SRAP (Sequence-Related Amplified Polymorphism) markers were used for the amplification of DNA obtained in the molecular characterization analysis (BUDAK *et al*., 2004). A total of 40 different primer combinations were pretested and primer combinations giving scoreable bands are shown in Table 3.

Table 1. Apricot × Apricot hybrid plants used in morphological and molecular analysis

No	Genotypes	Abbr.	No	Genotypes	Abbr.	No	Genotypes	Abbr.
1	Ninfa	Ninfa	41	Ninfa × Aprikoz-5	NxA-5	81	Palstein × Kabaaşı-10	PxK-10
2	Proce de Tyrinthe	P. Tyrinthe	42	Ninfa × Aprikoz-6	NxA-6	82	Palstein × Kabaaşı-11	PxK-11
3	Palstein	Palstein	43	Ninfa × Aprikoz-7	NxA-7	83	P. Tyrinthe × Hasanbey-1	PTxH-1
4	Hacıhaliloğlu	Hacıhaliloğlu	44	Palstein × Hasanbey-1	PxH-1	84	P. Tyrinthe × Hasanbey-2	PTxH-2
5	Hasanbey	Hasanbey	45	Palstein × Hasanbey-2	PxH-2	85	P. Tyrinthe × Hasanbey-3	PTxH-3
6	Aprikoz	Aprikoz	46	Palstein × Hasanbey-3	PxH-3	86	P. Tyrinthe × Hasanbey-4	PTxH-4
7	Kabaaşı	Kabaaşı	47	Palstein × Hasanbey-4	PxH-4	87	P. Tyrinthe × Hasanbey-5	PTxH-5
8	Ninfa × Hasanbey-1	NxH-1	48	Palstein × Hasanbey-5	PxH-5	88	P. Tyrinthe × Hasanbey-6	PTxH-6
9	Ninfa × Hasanbey-2	NxH-2	49	Palstein × Hasanbey-6	PxH-6	89	P. Tyrinthe × Hasanbey-7	PTxH-7
10	Ninfa × Hasanbey-3	NxH-3	50	Palstein × Hasanbey-7	PxH-7	90	P. Tyrinthe × Hasanbey-8	PTxH-8
11	Ninfa × Hasanbey-4	NxH-4	51	Palstein × Hasanbey-8	PxH-8	91	P. Tyrinthe × Hasanbey-9	PTxH-9
12	Ninfa × Hasanbey-5	NxH-5	52	Palstein × Hasanbey-9	PxH-9	92	P. Tyrinthe × Aprikoz-1	PTxA-1
13	Ninfa × Hasanbey-6	NxH-6	53	Palstein × Hasanbey-10	PxH-10	93	P. Tyrinthe × Aprikoz-2	PTxA-2
14	Ninfa × Hasanbey-7	NxH-7	54	Palstein × Hacıhaliloğlu-1	PxHc-1	94	P. Tyrinthe × Aprikoz-3	PTxA-3
15	Ninfa × Hasanbey-8	NxH-8	55	Palstein × Hacıhaliloğlu-2	PxHc-2	95	P. Tyrinthe × Aprikoz-4	PTxA-4
16	Ninfa × Hasanbey-9	NxH-9	56	Palstein × Hacıhaliloğlu-3	PxHc-3	96	P. Tyrinthe × Aprikoz-5	PTxA-5
17	Ninfa × Hasanbey-10	NxH-10	57	Palstein × Hacıhaliloğlu-4	PxHc-4	97	P. Tyrinthe × Aprikoz-6	PTxA-6
18	Ninfa × Hacıhaliloğlu-1	NxHc-1	58	Palstein × Hacıhaliloğlu-5	PxHc-5	98	P. Tyrinthe × Aprikoz-7	PTxA-7
19	Ninfa × Hacıhaliloğlu-2	NxHc-2	59	Palstein × Hacıhaliloğlu-6	PxHc-6	99	P. Tyrinthe × Aprikoz-8	PTxA-8
20	Ninfa × Hacıhaliloğlu-3	NxHc-3	60	Palstein × Hacıhaliloğlu-7	PxHc-7	100	P. Tyrinthe × Aprikoz-9	PTxA-9
21	Ninfa × Hacıhaliloğlu-4	NxHc-4	61	Palstein × Hacıhaliloğlu-8	PxHc-8	101	P. Tyrinthe × Aprikoz-10	PTxA-10
22	Ninfa × Hacıhaliloğlu-5	NxHc-5	62	Palstein × Aprikoz-1	PxA-1	102	P. Tyrinthe × Kabaaşı-1	PTxK-1
23	Ninfa × Hacıhaliloğlu-6	NxHc-6	63	Palstein × Aprikoz-2	PxA-2	103	P. Tyrinthe × Kabaaşı-2	PTxK-2
24	Ninfa × Hacıhaliloğlu-7	NxHc-7	64	Palstein × Aprikoz-3	PxA-3	104	P. Tyrinthe × Kabaaşı-3	PTxK-3
25	Ninfa × Hacıhaliloğlu-8	NxHc-8	65	Palstein × Aprikoz-4	PxA-4	105	P. Tyrinthe × Kabaaşı-4	PTxK-4
26	Ninfa × Hacıhaliloğlu-9	NxHc-9	66	Palstein × Aprikoz-5	PxA-5	106	P. Tyrinthe × Kabaaşı-5	PTxK-5
27	Ninfa × Kabaaşı-1	NxK-1	67	Palstein × Aprikoz-6	PxA-6	107	P. Tyrinthe × Kabaaşı-6	PTxK-6
28	Ninfa × Kabaaşı-2	NxK-2	68	Palstein × Aprikoz-7	PxA-7	108	P. Tyrinthe × Kabaaşı-7	PTxK-7
29	Ninfa × Kabaaşı-3	NxK-3	69	Palstein × Aprikoz-8	PxA-8	109	P. Tyrinthe × Kabaaşı-8	PTxK-8
30	Ninfa × Kabaaşı-4	NxK-4	70	Palstein × Aprikoz-9	PxA-9	110	P. Tyrinthe × Kabaaşı-9	PTxK-9
31	Ninfa × Kabaaşı-5	NxK-4	71	Palstein × Aprikoz-10	PxA-10	111	P. Tyrinthe × Kabaaşı-10	PTxK-10
32	Ninfa × Kabaaşı-6	NxK-5	72	Palstein × Kabaaşı-1	PxK-1	112	P. Tyrinthe × Kabaaşı-11	PTxK-11
33	Ninfa × Kabaaşı-7	NxK-6	73	Palstein × Kabaaşı-2	PxK-2	113	P. Tyrinthe × Kabaaşı-12	PTxK-12
34	Ninfa × Kabaaşı-8	NxK-7	74	Palstein × Kabaaşı-3	PxK-3	114	P. Tyrinthe × Hacıhaliloğlu-1	PTxHc-1
35	Ninfa × Kabaaşı-9	NxK-8	75	Palstein × Kabaaşı-4	PxK-4	115	P. Tyrinthe × Hacıhaliloğlu-2	PTxHc-2
36	Ninfa × Kabaaşı-10	NxK-9	76	Palstein × Kabaaşı-5	PxK-5	116	P. Tyrinthe × Hacıhaliloğlu-3	PTxHc-3
37	Ninfa × Aprikoz-1	NxA-1	77	Palstein × Kabaaşı-6	PxK-6	117	P. Tyrinthe × Hacıhaliloğlu-4	PTxHc-4
38	Ninfa × Aprikoz-2	NxA-2	78	Palstein × Kabaaşı-7	PxK-7	118	P. Tyrinthe × Hacıhaliloğlu-5	PTxHc-5
39	Ninfa × Aprikoz-3	NxA-3	79	Palstein × Kabaaşı-8	PxK-8	119	P. Tyrinthe × Hacıhaliloğlu-6	PTxHc-6
40	Ninfa × Aprikoz-4	NxA-4	80	Palstein × Kabaaşı-9	PxK-9	120	P. Tyrinthe × Hacıhaliloğlu-7	PTxHc-7

Table 2. Some UPOV criteria in apricots

	Investigated Characteristics	*Explanations of Characteristics*
1	Tree: vigour	Weak, Medium, Strong, Very Strong
2	Tree: habit	Upright, Upright to spreading, Spreading, Drooping
3	Tree: degree of branching	Low, Medium, High
4	Young shoots: anthocyanin coloration	Weak, Medium, Strong
5	Coloration on one-year old shoots (on sunny side)	Tawny brown, Reddish brown, Purplish brown,
6	One-year shoots: bud size	Small, Medium, Large
7	Leaf blade length	Short, Medium, Long
8	Leaf blade width	Narrow, Medium, Broad
9	Leaf blade length / blade width	Slightly elongated, Moderately elongated, Very elongated
10	Leaf blade: intensity of green color of upper side	Light, Medium, Dark
11	Leaf blade: shape of base	Acute, Obtuse, Truncate, Cordate
12	Leaf blade: length of tip	Short, Medium, Long
13	Leaf blade: incisions of margin	Crenate, Bicrenate, Serrate, Biserrate
14	Petiole: length	Short, Medium, Long
15	Leaf: ratio length of blade / length of petiole	Low, Medium, High
16	Petiole: thickness	Thin, Medium, Thick
17	Petiole: anthocyanin coloration of upper side	Weak, Medium, Strong
18	The number of nectarium on the petiole	0-1, 2-3, >3
19	Nectarines on petioles	Low, Medium, High

Figure 1. Plant growth of apricot × apricot hybrids in field conditions

Table 3. List of SRAP primers used in pre-test in the research

Primer	*Sequence (Reverse)*	*Primer*	*Sequence (Forward)*
Em 1	5'-GACTGCGTACGAATTCAA-3'	Me 1	5'-TGAGTCCAAACCGGATA-3'
Em 2	5'-GACTGCGTACGAATTCTG-3'	Me 2	5'-TGAGTCCAAACCGGAGC-3'
Em 3	5'-GACTGCGTACGAATTGAC-3'	Me 3	5'-TGAGTCCAAACCGGACC-3'
Em 4	5'-GACTGCGTACGAATTTGA-3'	Me 4	5'-TGAGTCCAAACCGGACA-3
Em 5	5'-GACTGCGTACGAATTAAC-3'	Me 5	5'-TGAGTCCAAACCGGTGC-3
Em 6	5'-GACTGCGTACGAATTGCA-3'	Me 6	5'-TGAGTCCAAACCGGAGA-3
Em 7	5'-GACTGCGTACGAATTGAG-3'	Me 7	5'-TGAGTCCAAACCGGACG-3
Em 8	5'-GACTGCGTACGAATTGCC-3'	Me 8	5'-TGAGTCCAAACCGGAAA-3
Em 9	5'-GACTGCGTACGAATTTCA-3'	Me 9	5'-TGAGTCCAAACCGGAAC-3
Em 10	5'-GACTGCGTACGAATTCAT-3'	Me 10	5'-TGAGTCCAAACCGGAAT-3
Em 11	5'-GACTGCGTACGAATTAAT-3'	Me 11	5'-TGAGTCCAAACCGGAAG-3
Em 12	5'-GACTGCGTACGAATTTGC-3'	Me 12	5'-TGAGTCCAAACCGGTAG-3
Em 13	5'-GACTGCGTACGAATTCGA-3'	Me 13	5'-TGAGTCCAAACCGGTTG-3
Em 14	5'-GACTGCGTACGAATTATG-3'		
Em 15	5'-GACTGCGTACGAATTAGC-3'		
Em 16	5'-GACTGCGTACGAATTACG-3'		

PCR components were prepared by using 30 ng Template DNA, 1U Taq DNA polymerase enzyme, 0.25 mM each dNTP, 1 µM primer, 1.5µl 10X PCR buffer, 1.5 mM $MgCl_2$ and H_2O as PCR component in SRAP analysis.

PCR amplification in thermocycler is consisted of initial denaturation (3 min at 95°C), 45 seconds at 94°C, 1 min. at 35°C, 1 minute at 72°C, 45 sec. at 94°C, 35 cycles of 1 min. at 50°C in annealing and 1 min. at 72°C. The mixture obtained by adding 3 µl of loading buffer (20 ml of glycerol (40%), 30 ml of sterile water, 0.05 g of bromophenolblue) to the PCR products obtained from the PCR studies was loaded on a 2.5% agarose gel and carried out under 110V electric current for 3 hours. 1X TAE buffer was used in the preparation of the agarose gel and 25 µl (0.5 mg/ml) ethidium bromide solution was added into it. 100 bp and 1 kb DNA Ladder was loaded as standard in each electrophoresis procedure. After the electrophoresis, the gels were taken to the gel imaging device and the gel images were recorded on the computer under UV.

Data Analysis

A data matrix was formed by scoring bands as present (1) or absent (0) in all gel images obtained in molecular studies. These obtained data were analyzed in the computer package program NTSYS (Numerical Taxonomy Multivariate Analysis System, NTSYS-pcversion 2.11, Exeter Software, Setauket, N.Y., USA, Rohlf, 2000). The similarity indices were calculated according to the Dice (1945) method and the dendrogram was created according to the UPGMA (Unweighted Pair-Group Method with Arithmetic Average) method. The UPGMA method has been shown to be more successful than other methods in revealing the relationships between genotypes (MOHAMMADI and PRASANNA, 2003).

RESULTS AND DISCUSSION

Morphological Analysis

Figure 2 shows the characters that distinguish in the majority of 120 hybrid plants according to the morphological characterization analyses. Plant vigour was determined as weak, medium and high in hybrid individuals obtained from Apricot × Apricot combination. All three growth patterns were observed rather than typical plant growth in general combinations. The plant habit was determined as "drooping", "spreading" and “upright to spreading”. The amount of branching was determined as "low" or "high". In the parameter of anthocyanin coloration in young shoots, “weak”, “medium” and “strong” classes were formed. In terms of plant vigour, 78 plants showed 'medium' growth. Similarly, in the study conducted by Rezae et al., (2020) on apricot genotypes of the genus Prunus armeniaca, 42 genotypes showed 'medium' development.

In terms of plant habit, 76 hybrids showed ' upright to spreading' characteristics. According to the results of REZAE *et al*. (2020), 38 of 98 genotypes showed ' upright to spreading' characteristics. In terms of the amount of branching in the tree, 100 hybrids showed 'high' branching characteristics. In a study conducted by YILMAZ *et al*. (2012) on 93 *Prunus armeniaca* genotypes, 89.4% high branching was observed. In terms of anthocyanin coloration on young shoots, 61 hybrids showed 'medium' degrees. Similarly, in a study conducted by NESHEVA (2020), medium anthocyanin coloration was observed in most of the apricot hybrids (50 out of 58 hybrid plants).

Almost all genotypes (119 hybrids) showed ‘reddish brown’ coloration in the sun-exposed parts of one-year old shoots. According to the results of Rezae et al., (2020), reddish brown coloration was observed in 32 of 98 genotypes. 95 hybrids showed 'medium' size in terms of bud size of one-year old shoots, 113 hybrids 'medium' length in terms of leaf blade length, 110 hybrids 'medium' width in terms of leaf blade width, 89 hybrids 'medium' colors in terms of leaf blade green color intensity. Similar results were obtained in 61 of 98 genotypes in the study of Rezae *et al*. (2020).

In general, there were no differences in the ratio of leaf blade length / blade width and shape of base character in hybrid plants to all combinations. The reason for this situation can be explained by the fact that the changes in the genetic structure caused by hybridization affect the morphological characters. All of them showed 'truncate' features in terms of shape of base, 87 hybrids 'medium' in terms of length of leaf tip, and 116 plants 'double dentate' in terms of incisions of margin. In terms of petiole length, 84 hybrids showed "medium", 101 hybrids showed "medium" features in terms of petiole thickness, and 117 plants showed "weak" features in terms of petiole anthocyanin coloration. According to the results of REZAE *et al*. (2020), 43 genotypes showed 'weak' characteristics. The number of nectarium in the leaf was observed to be around 2-3 in all hybrids and nectarines on petiole was determined to be low in all hybrids. According to the results of REZAE *et al*. (2020), the number of nectariums around 2-3 was determined in 27 genotypes.

When similar studies are examined in general, commercial cultivars and cultivar candidates constitute the apricot genotypes used, and morphological analyzes were made on these genotypes. The difference in morphological characters in this study can be explained by the fact that the number of intraspecific hybrids and also the number of plant materials used is higher

than the studies in the literature. Another reason for the morphological variation in hybrid plants can be explained by the increase in the heterozygosity level of the hybrids.

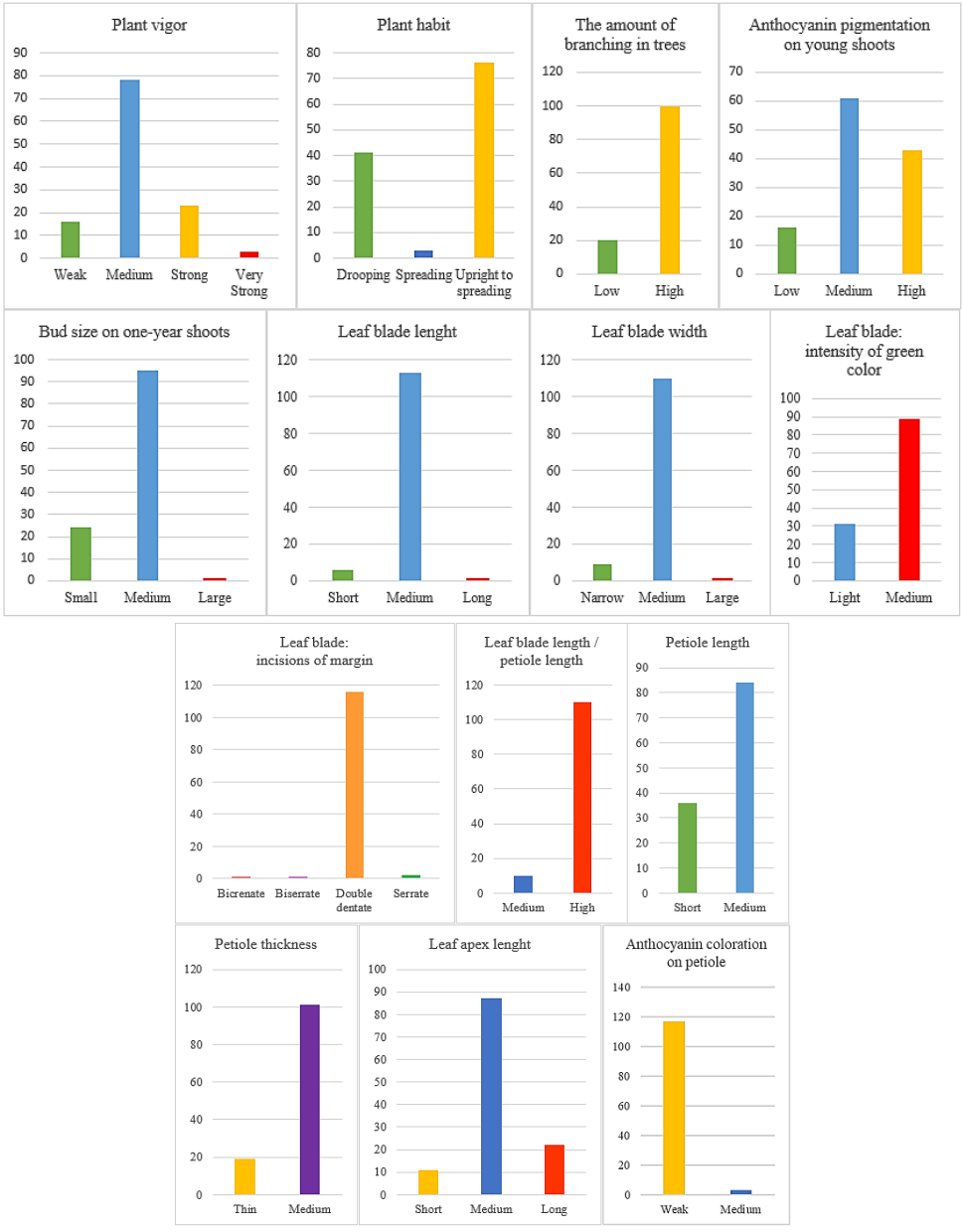

Figure 2. Distribution of some morphological features of apricot × apricot hybrid plants.

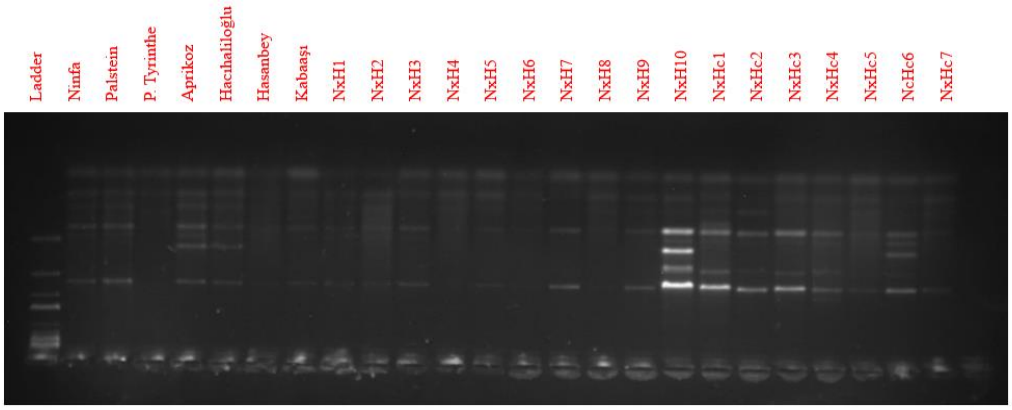

Figure 3. Gel image of Em2-Me3 SRAP primer combination in apricot × apricot hybrid plants.

Table 4. SRAP primers used in apricot × apricot hybrid plants

Primer	*Base Length*	*Total Number of Bands*	*Number of Polymorphic Bands*	*Polymorphism Rate (%)*
Em1-Me2	90-250	5	4	80.00
Em1-Me4	100-1010	6	5	83.33
Em2-Me3	100-600	9	5	62.50
Em4me4	120-500	6	5	83.33
Em4-Me9	100-800	8	7	87.50
Em6-Me4	100-600	6	4	66.67
Em6-Me6	90-500	8	4	50.00
Em7-Me12	200-250	5	4	80.00
Em5-Me7	600-750	2	1	50.00
Em7-Me9	150-700	9	6	66.67
Em10-Me9	250-1300	9	5	55.56
Em11-Me12	100-1700	13	11	84.62
Em14-Me4	90-700	6	4	66.67
Em8-Me8	150-1000	9	7	77.78
Em9-Me6	200-500	5	4	80.00
Mean	200-1700	7.0	5.06	71.64
Total	-	105	76	-

In the SRAP marker analyzes performed on plants obtained from Apricot × Apricot hybridization combinations (Figure 3). A total of 105 scoreable bands were obtained from 15 different primer combinations, and 76 of them were determined as polymorphic. The lowest number of bands was determined as 2 bands from the Em5-Me7 primer combination, and the highest number of scoreable bands was determined as 13 bands from the Em11-Me12 primer combination. The average base lengths of these primers are between 200-1700 bp, the average number of polymorphic bands per primer is 7.0 and the average number of polymorphic bands per primer is 5.06. The mean polymorphism value is 71.64%. Similar results were determined by UZUN *et al*. (2010) in the SRAP marker analysis performed on some domestic and foreign apricot cultivars, with an average of 5.4 bands per marker, 3.9 polymorphic bands per marker, and an average polymorphism percentage of 73%. Again, similar results were reported by LI *et al*. (2014) in the study in which the genetic relationships of different apricot cultivars with SRAP markers were determined, the average number of bands per marker was 13.1, the number of polymorphic bands per marker was 10.4, and the mean polymorphism rate was 79.6%.

The similarity coefficient in the dendrogram formed according to the UPGMA method differed between 0.61 and 0.96 (Figure 4). According to the dendrogram, 2 main groups were formed. In the first main group, individuals belonging to Ninfa × Hasanbey, Palstein × Aprikoz, Proce de Tyrinthe × Aprikoz hybrids were generally included. In this group, hybrid individuals belonging to Ninfa, Palstein, Proce de Tyrinthe mother parents and Aprikoz, Hasanbey, who were used as fathers to them, formed close groups. In particular, most hybrid individuals obtained from the Ninfa × Hasanbey combination were found to be similar to each other above the similarity index of approximately 0.86.

In the second main group of the dendrogram, the apricot varieties used as parents in the study showed distribution in the dendrogram with hybrid individuals. In this group, especially individuals obtained from Palstein × Hasanbey and Palstein × Aprikoz crosses formed close groups within themselves. In the UPGMA dendrogram, the closest individuals to each other are the hybrid individuals numbered Palstein × Hasanbey-7 and Palstein × Hasanbey-8 with a similarity index of 0.96 and are in the second main group of the dendrogram. There may be various reasons for the lack of a general grouping in the study. The most important factor that stands out among these is the difference in the genetic structure that emerges as a result of seed propagation.

In another similar study, 19 different primer combinations were used to determine genetic diversity with Srap markers in 57 apricot genotypes assumed to be grown from seed and collected from Sakıt valley, and similarity index was found between 0.75 and 0.94 among these apricot genotypes (PINAR *et al*., 2013). In the study carried out to determine the genetic relationship in local apricot cultivars grown in northern China using the SRAP marker technique, the genetic similarity index between apricot cultivars varied between 0.62 and 0.83 (LI *et al*., 2014). The similarity index in the SRAP, ISSR and DAMD marker analysis made in some domestic, foreign and hybrids of these varieties grown in Turkey differed between 0.65 and 0.87 (PINAR *et al*., 2017). The SRAP analysis performed on Apricot × Apricot hybrid plants has similar features with the studies in the literature, as well as different features. The difference can be explained by the fact that the apricot cultivars used are different and include hybrids between species, and the number of plant materials used is higher than the studies in the literature.

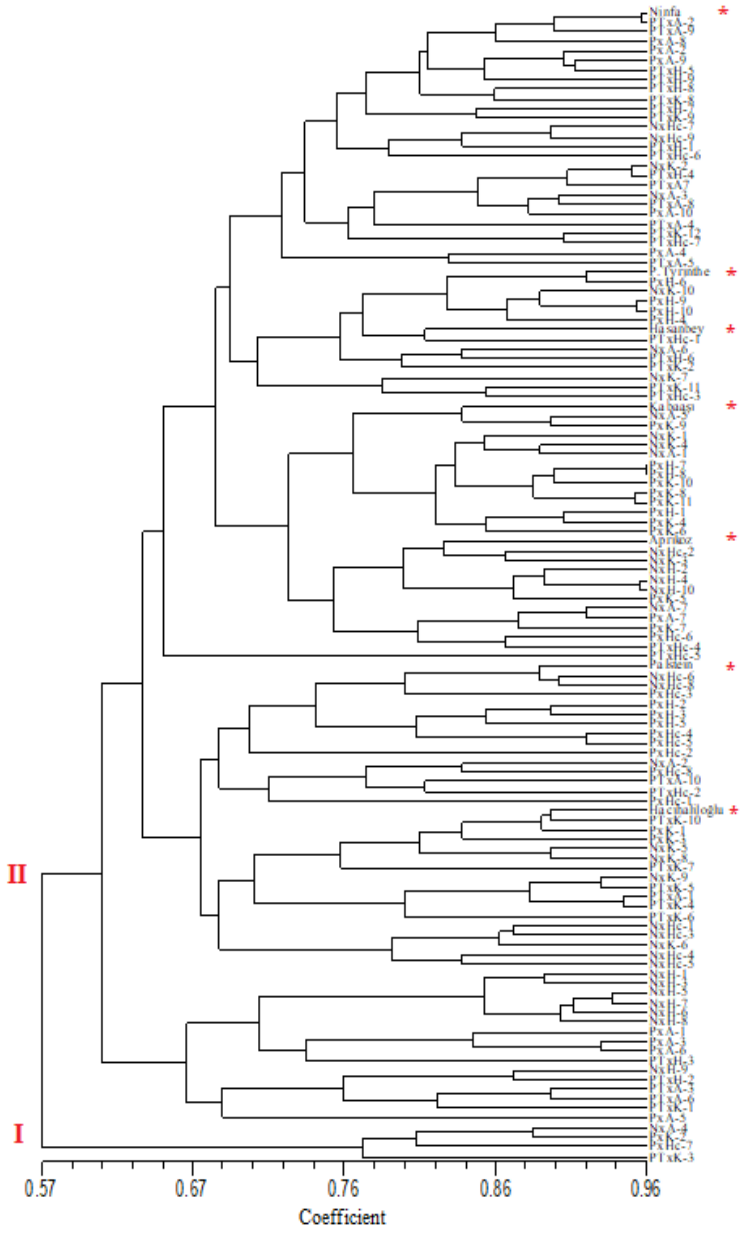

Figure 4. Dendrogram of UPGMA method in apricot × apricot hybrid plants
(Abbreviation explanations are given in Table 1)

CONCLUSION

In this study, it was aimed to determine the variation between genotypes by morphological classification according to UPOV criteria and molecular characterization of genotypes with the SRAP marker system in hybrid apricot genotypes obtained by intra-specific hybridization Significant variations between hybrids were detected in terms of 16 characteristics such as plant vigor, plant habit, amount of branching in plants, leaf and shoot characteristics. It is estimated that the morphological characterization of hybrid apricot genotypes will allow the selection of the genotypes having desired characters that can be used in further breeding programs. It is thought that the genetic characterization of hybrid apricot genotypes will contribute to the determination of combinations that can provide the highest variation. The results obtained can be an important reference for advanced apricot breeding programs and molecular researches.

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MORFOLOŠKA I MOLEKULARNA IDENTIFIKACIJA HIBRIDNIH GENOTIPA KASEIJA DOBIJENIH INTRASPECIFIČNOM HIBRIDIZACIJOM

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Izvod

Kajsija je jedna od važnih koštičavih voća koje se proizvode u svetu. U ovoj studiji, genetske varijacije su istraživane na osnovu SRAP markerske tehnike i morfoloških podataka u 120 genotipova i roditeljskih biljaka dobijenih inbridingom u nekim sortama kajsije kao što su Ninfa, Proce de Tirinthe, Palstein, Hacıhaliloglu, Hasanbei, Aprikoz i Kabaası. U studiji je korišćeno 15 različitih kombinacija SRAP markera i dobijeno je ukupno 105 traka od kojih je 76 određeno kao polimorfno. Prosečne dužine baza ovih prajmera su između 200-1700 bp, prosečan broj polimorfnih traka po prajmeru je 7,0. Srednja vrednost polimorfizma je 71,64%. Koeficijent sličnosti u dendrogramu kreiranom po UPGMA metodi bio je između 0,61 i 0,96. Prema dendrogramu formirane su 2 glavne grupe. Najbliži genotipovi imaju indeks sličnosti od 0,96. U analizi morfološke karakterizacije ispitano je 120 hibridnih jedinki po 19 kriterijuma UPOV. Nisu nađene varijacije u pogledu broja nektarijuma peteljki, dominantnog broja i karakteristika oblika peteljki. Varijacije između hibrida utvrđene su u pogledu 16 karakteristika kao što su razvoj biljke, habitus biljke, količina grananja u stablu, karakteristike listova i izdanaka. 119 hibrida je pokazalo „crvenkastosmeđu“ obojenost, 87 hibrida prosečan vrh lista, a 116 biljaka „dvostruku nazubljenu“ u smislu rezova na ivici lista. 84 hibrida su pokazala srednju inciziju peteljki, 101 hibrid je pokazao srednju debljinu peteljki, a 117 biljaka je pokazalo slabu antocijansku obojenost peteljki. Predviđa se da će morfološke i molekularne analize hibridnih biljaka omogućiti razvoj novih sorti i genotipova kandidata za podloge. Sa rezultatima ove studije, genetske varijacije i morfološke klasifikacije utvrđene u genotipovima će voditi ka daljim studijama o programima stvaranja hibrida kajsije.

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