Khazar Journal of Science and Technology Volume 5 №2 2021, 34-48

DOI: 10.5782/2520-6133.2021.5.2.34

Investigation of Variability of Apricot (*Prunus armeniaca* L.) Using Morphological, Pomological Traits and Microsatellite Markers

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Abstract

Based on 10 (morphological, pomological, phenological) traits and using 10 microsatellite molecular markers, 17 Azerbaijani apricot cultivars and accessions have been evaluated. All the genotypes manifested a high level of variability. Based on the size, fruits were divided into 2 groups: small fruits (< 40 g) and large fruits (> 40 g). Cultivars such as Ordubad eriyi, Ag erik, Mayovka (Terter) and Ag erik Gulnar with fruit weight above 70 g were estimated as very large**.** In general, fruits had yellow skin ground color and flesh color as well as high TSS. A high correlation was observed between bud break season and blossom season, bud break season and harvest season, bud break season and leaf fall season, blossom season and harvest season, blossom season and leaf fall season, harvest season and leaf fall season. However, a low or insignificant correlation was found between other pomological or phenological characteristics. According to the PCA results, 100% of the total variance among cultivars is attributed to the first seven components. NJ cluster analysis divided apricot cultivars into three main groups. The number of cultivars in the I, II and III clusters were, respectively, eight, seven and two. A total of 60 alleles, ranging from 3 to 9 alleles were revealed by molecular data obtained from microsatellite markers. The average of expected heterozygosity (He), observed heterozygosity (Ho) and polymorphism information content (PIC) were found to be 0.68, 0.77, and 0.63, respectively. The article presents the results of the first genetic diversity analysis of apricot cultivars from the regions. We believe the study will contribute to the effective management and sustainable utilization of apricot germplasm in future breeding programs in the regions.

Keywords: apricot, morphological and pomological traits, microsatellite markers

Introduction

Apricot (*Prunus armeniaca* L.) belonging to the Rosaceae family, is cultivated worldwide. As an important fruit in the Northern hemisphere, it represents the third most planted stone fruit species after peach and plum. Among all temperate fruits, apricot ranks as the seventh in terms of worldwide production. Apricots are native to China and Central Asia. They were the *subject* of successive *domestications twice*, one in Western Central Asia (Fergana valley, at the borders of Uzbekistan, Tajikistan, and Kyrgyzstan) and one in China (Vavilov, 1951; Faust et al., 1998). In these regions, apricots are cultivated mainly for fresh market, kernel production, and ornamental use. Apricot is mostly considered as a self-incompatible species, which fruit has no specific aroma (Zhebentyayeva et al., 2012).

Based on morphological and physiological traits, Kostina (1964) recognized four main eco-geographical groups: Central Asian, Irano-Caucasian, European, and Dzhungar-Zailij. Apricots from Central Asia and the Xinjing Province of China are genetically related to wild forms of P. armeniaca and differ from the East Asian apricots which are related to East Asian wild species. From the center of origin, apricot culture spreads to the Irano-Caucasian region, which included Azerbaijan and constituted the secondary center of apricot diversification following the Silk Road (Vavilov, 1951).

Apricots are grown almost in all regions of Azerbaijan, except very humid regions, for a long time. The cultivation of this plant is expanding every year. Different apricot genotypes are grown in regions of Azerbaijan such as Nakhchivan, Terter, Goranboy, Agdash, etc. In 2020, the total fresh apricot production of Azerbaijan was estimated to be 28977,4 metric tons. However, the available information about the morphological characteristics of apricot is limited. These evaluations are based on a wide range of characteristics such as phenological traits, fruit size, and tree vigor.

Genetic variability is known to be the prerequisite for any plant breeding program (Khush, 2002). New fruit cultivars are generally developed on the basis of genetic resources. Essential stages of any breeding program are germplasm collection and characterization, which are mainly performed by describing phenological, pomological, and morphological characteristics. Thus, plant breeding programs have widely used morphological criteria as important markers (Ogasanovic et al. 2007; Karimi et al. 2008). However, DNA-based molecular markers provide a very useful tool for genetic diversity investigation and identification of cultivars. Thus, the use of microsatellites (simple sequence repeats or SSRs) for molecular characterization and genetic diversity evaluation of different crop species has increased, due to their high polymorphism and wide distribution in the genome. Besides, they are highly

reproducible and co-dominant. Microsatellites have been used for genome mapping and cultivar characterization and variability evaluation in apricot (Raji et al., 2014).

We aimed to investigate the morphological and pomological traits and to perform molecular identification by using SSR primer pairs among 17 apricot genotypes from Terter, Goranboy, Agdash regions of Azerbaijan. Our research is an initial step for the national and international germplasm characterization and preservation of these valuable fruit trees for future breeding programs.

Materials and methods

Plant materials

Seventeen apricot cultivars and forms from Genetic Resources Institute of Azerbaijan (AGRI) were used as the study subjects. The plant material consisted of samples from the apricot germplasm collection located at Genetic Resources Institute of Azerbaijan (Table 1). This germplasm was originally collected from cultivars and forms of different cultivation regions of Terter, Goranboy, Agdash in Azerbaijan.

Morphological and Pomological Characterization

The primary selection criterion was based on the fruit and yield attributes of the genotypes (Table 1). Individual genotypes were marked in the field. The data were recorded at the time of fruit maturity during summer (June - July) seasons from 2016 to 2021 and data were pooled for analysis. Total numbers of fruits were counted per plant. Fruits from each genotype were randomly selected and data were collected on fruit length (mm), fruit weight (g), fruit width (mm) and TSS (^{0}Brix) in apricot genotypes. Fruit weight was measured using Sartorius balance with an accuracy of 0.001 g. The length and width of the fruit were measured with a digital Vernier caliper. The measurement of fruit length was made on the polar axis, i.e. between the apex and stylar end. The maximum width of the fruit was measured in the direction perpendicular to the polar axis.

Statistical methods such as principal component analysis and cluster analysis have been employed as powerful options for plant cultivar and accession screenings. As a tool for germplasm description, we have applied principal component analysis to study correlations among variables and establish relationships among cultivars (Asma and Ozturk., 2005). To identify the principal distinguishing characters of the variability the principal component analysis (PCA) was performed (Wani et. al., 2017). This method is commonly applied for the characterization of genetic

resources in such studies. In addition, Pearson correlation coefficients and correspondence analysis were applied to identify a putative redundancy and to discriminate the relevant informative traits (Krichen et al., 2014). The XLSTAT and SPSS software packages were used for the data analysis.

Molecular Characterization

In this study, we used 17 accessions. Before DNA extraction, young leaf tissue samples were stored at −80 ◦C. We applied the CTAB (cetyltrimethyl ammonium bromide) method of Doyle and Doyle (1990) to isolate genomic DNA. Electrophoresis was performed on 1% agarose gel to determine the DNA quality and it was quantified spectrophotometrically at 260 nm. A prepared DNA solution (10 ng/l) was stored at −20 ^{0}C. We chose 10 SSR primer pairs for the study. Fluorescently labeled M13 primer with 6-FAM, NED, PET and VIC were used for SSR fragment analysis and PCR was performed following the method described by Schuelke (2000). In brief, the PCR reaction mix consisted of 2 µl of 10x PCR buffer, 0,6 µl of 50 mM MgCl2, 2 µl of 10 mM dNTP, 0.15 µl of 10 µM of a sequence-specific forward primer with M13 tail at its 5′ end, 0.35 µl of 10 µM of a sequence-specific reverse primer, and 0.20 µl of 10 µM the universal fluorescent-labeled M13 primer, 0.2 µl 5U/µl Taq polymerase, and 3 µl of 25 ng/ µl sample DNA. The total reaction medium was brought up to 20 µl with distilled water. The PCR program consisted of 3 min an initial denaturation at 94 °C followed by 35 cycles of a 30 s denaturation step at 94 °C, a 40 s annealing step at 60 °C, and a 1 min extension step at 72 °C. Additional 7 min extension step was added to PCR program. Seven µL of PCR product were visualized on 3% agarose gel. 10 µL distilled water was added onto the remaining PCR product and stored at −20 °C until to use for fragment analysis. The stored PCR products for each multiplex were mixed. This concentration was further diluted 20 times and 0.75 µL of the diluted aliquot was mixed with 9 µL Hi-Di buffer and 0.25 µL LIZ 500 standard. The mixtures were kept at 95 °C 5 min, and then immediately were put on ice and finally loaded to capillary electrophoresis on a ABI 3500 (applied bio sysetms, Foster City, Calif., USA) located in Erciyes University, Kayseri, Turkey. DNA fragment sizes were determined using GeneMapper 4.1 software (Applied Biyosystems, Foster City, Calif., USA).

The neighbor-joining (NJ) method was used to construct and draw a dendrogram from the genetic similarity matrix using the DARwin 6 software (Perrier & Jacquemoud-Collet, 2006). A genetic similarity matrix based on the proportion of shared alleles was generated and the expected heterozygosity (He), observed heterozygosity (Ho) and polymorphism information content (PIC) were calculated using the PowerMarker V3.25 software (Table 2).

Table 1. List of apricot genotypes and their source city, used in this study.

No.	Cultivar	Source city
1	Zeynebi	Agdash
2	May Natiq	Agdash
3	Ag erik Gulnar	Agdash
4	Ag erik Elchin	Agdash
5	May Goranboy	Agdash
6	Mayovka	Agdash
7	Badami	Agdash
8	Shalakh	Agdash
9	Ordubad eriyi	Terter
10	Ag erik	Terter
11	Badam erik	Terter
12	Girmiziyanag	Terter
13	İrevan eriyi Shalakh	Terter
14	Mayovka	Terter
15	Ag erik Gejyetishen	Goranboy
16	Ag erik Tezyetishen	Goranboy
17	Badam erik	Goranboy

Table 2. Prunus SSR loci that were used in this study for the characterization of apricot genotypes.

Multiplex groups	Locus	Reference	Linkage Group	Position (From. To)
4-Fam	Gol061	Vera-Ruiz et al. (2011)	1	NA
1-Fam	PGS1.03	Soriano et al. (2012)	1	7320588–7320780
3-6-Fam	PGS1.20	Soriano et al. (2012)	1	8458901–8459094
4-Vic	PGS1.21	Soriano et al. (2012)	1	8527745–8527930
4-Ned	PGS1.23	Soriano et al. (2012)	1	8600638–8600792
2-Pet	PGS1.24	Soriano et al. (2012)	1	8668808–8668989
3-Vic	PGS1.252	Soriano et al. (2012)	1	8730677–8730761
2-6-Fam	96P10_SP6	Soriano et al. (2012)	1	8920241–8920383
3-6-Fam	ssrPaCITA5	Lopes et al. (2002)	1	11770142–11770214
4-Fam	ssrPaCITA17	Lopes et al. (2002)	1	NA

Results and discussion

Morphological and Pomological Characterization

Data in Table 3 represent 17 variables for the studied apricot germplasms. Bud break season for these germplasms in this region is generally from late February to mid-March, the full blossom is observed between early March and early April. A 15– 20-day variation in phenological phases was observed during the 6 years of study course. The germplasms Ag erik Gulnar, Ag erik Gecyetishen, Ag erik, and Ordubad eriyi demonstrated later blossom compared with others. The difference in blossoming periods of germplasms under the same geographical conditions might be a result of the total exposure temperature required. Later blossoming is an important factor for the protection from spring frosts in continental climates (Guleryuz 1988; Unal et al., 1999). In this region, late spring frosts end around mid-April and since all the cultivars and forms in germplasm blossomed before early April, they were all under the risk of spring frost damage.

There are large variations in harvest season between apricot cultivars and forms. Most cultivars were harvested between June and July. The earliest apricot cultivars were 'May Natiq', 'Ag erik Elchin', 'May Goranboy', 'Mayovka', 'Mayovka' (Terter). In this study, many cultivars were harvested in late May. The fruits of Zeynebi, Ag erik Gulnar, Badami, Shalakh, Ag erik Tezyetishen, Badam erik, Badam erik (Goranboy), Girmızıyanag, Irevan eriyi (Shalakh) were harvested on mid-June, while Ag erik Gecyetishen, Ordubad eriyi, Ag erik were harvested in late June. In the previous studies, the harvest data for apricot cultivars were in the range of 14 May-26 June in Spain (Ruiz & Egea, 2008), 11 June-10 September in Hungary (Hegedũs et al., 2010), 26 May-25 June in Italy (Lo Bianco et al., 2010). These differences could be due to climatic conditions in Terter, Goranboy, Agdash, where the climate is semi-arid, with hot summers and cold winters. These regions had high day-night temperature changes from February to May (>15°C) and maximum temperatures were >28°C in April and May. Therefore, the apricot cultivars could be early fulfilling degree-day thresholds from full-bloom to be harvested under these conditions. Ruml et al. (2010) indicated that the effect of growing degree-day thresholds on harvest time of apricots is very important for each apricot-producing region. The authors also reported that daily maximum temperatures were the most influential temperature variable for the ripening time of apricots. The fruit size is one of the most important fruit quality traits for fresh apricots. A high degree of variation is an important trait related to fruit size. Regarding the 'Apricot Descriptor' (IPGRI and CEC, 1984), the fruit weight for 'Ordubad eriyi'(100.2 g) , followed by 'Ag erik' (86.3 g), 'Mayovka' (Terter) (86.3 g), and 'Ag erik Gulnar' (71.1 g) were very large (>70 g), 'May Goranboy', 'Badam erik' and 'Ag erik Tezyetishen' were large (61-

70 g), ‘Badami’ and ‘Irevan eriyi’ (Shalakh) were medium-to-large (56-60 g) under ecological conditions of Terter, Goranboy, Agdash. The other cultivars ‘May Natiq’, ‘Mayovka’, ‘Girmiziyanag’, ‘Ag erik Gecyetishen’ and ‘Badam erik’ (Goranboy) (45-50 g) were medium, ‘Shalakh’ (43.1 g) small/medium and ‘Zeynebi’ and ‘Ag erik Elchin’ (10-20 g) small. The fruit weights of 2 accessions were less than 40 g indicating that they are small-fruited. This result is not compatible with the findings of Asma and Ozturk (2005) in Turkish apricots. Large fruits of ‘Ordubad eriyi’ make it a promising cultivar in apricot breeding programs to improve fruit size. In our study most genotypes had desirable fruit sizes. Attractive medium-sized fruits are desired for apricot cultivar breeding (Mratinić et al., 2011).

The fruit length and width was ranged from 11.4 mm to 70.8 mm and from 11.2 to 65.6 mm, respectively. The maximum value for FL was recorded in Ordubad eriyi, followed by Ag erik (63.8 mm), whereas minimum score was in Ag erik Elchin. The highest FWi was obtained in Ordubad eriyi, followed by Mayovka (Terter) (56.2 mm) and Ag erik (54.2 mm). As in previous parameter, the lowest fruit width was also recorded in Ag erik Elchin. The previous studies on apricot also reported a high variability among apricot cultivars regarding fruit-size traits (Badenes et al., 1998; Ruiz & Egea, 2008).

The TSS content is an important quality attribute, influencing notably the fruit taste. The levels of TSS in this study ranged from 10.2 ^{0}Brix (‘Mayovka’) to 20 ^{0}Brix (‘Shalakh’) with a mean of 14.5^{0}Brix, which is greater than the minimum (10 ^{0}Brix) established by the EU (European Union) to market apricots (R-CE No.112/2001). The high values for TSS were noted in genotypes Shalakh (20^{0}Brix) which is characterized by an excellent fruit taste (level of TSS >20^{0}Brix) and quality (Ayanoglu *et al*., 1995). Mayovka had the least amount of TSS. As seen in Table 3, the majority (53%) of the studied apricot cultivars were characterized by yellow skin ground color and flesh color. SGC for 4 cultivars, namely Ag erik Elchin, Badami, Ordubad eriyi, Mayovka (Terter) was orange. The skin ground color of Ag erik Gecyetishen was white and its flesh was cream color. Girmızıyanag had green-yellowish skin ground color.

Table 3. Description of apricot cultivars.

Varieties	**BBS**	**BS**	**HS**	**LFS**	**FW, g**	**FL, mm**	**FWi, mm**	**TSS (°Brix)**	**FC**	**SGC**
Zeynebi	2	2	2	2	11.1	16	14.8	15.1	1	1
May Natiq	1	1	1	1	48.6	46.8	44.8	14	1	1

Ag erik Gulnar	2	2	2	2	71.1	53.4	47.4	15.1	1	1
Ag erik Elchin	1	1	1	1	16.1	11.4	11.2	15.1	2	2
May Goranboy	1	1	1	1	62.8	54.6	52.4	14	1	1
Mayovka	1	1	1	1	49.6	36.6	39.8	10.2	1	1
Badami	2	2	2	2	60.1	52.4	50.8	15.1	2	2
Shalakh	2	2	2	2	43.1	41	35.8	20	1	1
Ordubad eriyi	3	3	3	3	100.2	70.8	65.6	15	2	2
Ag erik	3	3	3	3	86.3	63.8	54.2	13	1	3
Badam erik	2	2	2	2	65.9	53.2	46.1	16	1	1
Girmiziyanag	2	2	2	2	48.8	38.6	34.8	13	1	4
İrevan eriyi (Shalakh)	2	2	2	2	56.2	50.8	46.2	14	1	1
Mayovka (Terter)	1	1	1	1	86.3	58	56.2	13	2	2
Ag erik Gecyetishen	3	3	3	3	48.4	45.8	43.8	16	4	3
Ag erik Tezyetishen	2	2	2	2	68.4	51	44.6	14	1	3
Badam erik (Goranboy)	2	2	2	2	48.9	48.6	36.8	14.5	1	1

Correlation among variables

Several phenological and pomological characteristics were found to be highly correlated (Table 4). As expected, the highest values were recorded between bud break season and blossom season, bud break season and harvest season, bud break season and leaf fall season and blossom season and harvest season, blossom season and leaf fall season, harvest season and leaf fall season with maximum Pearson correlation index ($r=1.00$; $p < 0.01$). Strong positive correlations were also observed for fruit size parameters. Thus, fruits with larger sizes (both FL and FWi) had a higher weight. The Pearson correlation indices of fruit weight with fruit length and width were determined as $r = 0.948$ and $r = 0.941$, respectively. Fruit size traits (FL, FWi, FW) were negatively correlated with the amount of total soluble solids, however, they were not statistically significant. This is in agreement with the results of Badenes et al. (1998) who reported a high correlation ($r=0.87$) between bud break and blossom season and also a correlation (to a lesser extent) between bud break and harvest season ($r=0.79$).

Table 4. Correlation matrix among variables studied.

	BBS	BS	HS	LFS	FW	FL	FWi	TSS	FC
BS	1.000**								
HS	1.000**	1.000**							
LFS	1.000**	1.000**	1.000*						
FW	0.337	0.337	0.337	0.337					
FL	0.396	0.396	0.396	0.396	0.948**				
FWi	0.293	0.293	0.293	0.293	0.941**	0.973**			
TSS	0.307	0.307	0.307	0.307	-0.199	-0.080	-0.161		
FC	0.319	0.319	0.319	0.319	0.027	0.019	0.095	0.177	
SGC	0.419	0.419	0.419	0.419	0.203	0.100	0.089	-0.187	0.376

Correlations significant ($p < 0.05$). Abbreviations: TS, tree size; BBS, bud break season; BS, blossom season; HS, harvest season; LFS,

leaf fall season; FW, fruit weight; PW, pit weight; KW, kernel weight; SGC, skin ground color; FC, flesh color; KT, kernel taste; PFR,

flesh/pit ratio; BRIX, total solids soluble; TA, total acidity; Y, yield.

**Correlation is significant at 0.01. Abbreviations: BBS, bud break season; BS, blossom season; HS, harvest season; LFS, leaf fall season; FW, fruit weight; FL, fruit length; FWi, fruit width; TSS, total solids soluble; FC, flesh color; SGC, skin ground color.

Correlations significant ($p < 0.05$). Abbreviations: TS, tree size; BBS, bud break season; BS, blossom season; HS, harvest season; LFS,

leaf fall season; FW, fruit weight; PW, pit weight; KW, kernel weight; SGC, skin ground color; FC, flesh color; KT, kernel taste; PFR,

flesh/pit ratio; BRIX, total solids soluble; TA, total acidity; Y, yield.

Principal component analysis (PCA)

About 100% of the total variance among genotypes was explained by the first seven components (Table 5). PC1 which represents bud break season, blossom season, harvest season, and leaf fall season accounted for about 50.78% of total variance.

PC2 that includes fruit weight, fruit length, and fruit width comprised about 24.28% of overall variance. PC3 consisted of SGC constituted about 11.96% of total variance. Table 6 shows the amount of loading factors for each character in the first five principal components. As observed in PCA, the first three components represented 87.02% of total variance. This value is higher than those of reported by Raji et al. (2014), Asma and Ozturk (2005), and Yilmaz et al. (2012) (54, 70, and 73%, respectively).

Table 5. Eigen values, variance%, and cumulative% of first seven factors contributing to 100% of total variance

PC	Eigenvalue	Variability (%)	Cumulative %
1	5.08	50.78	50.78
2	2.43	24.28	75.06
3	1.20	11.96	87.02
4	0.84	8.44	95.46
5	0.39	3.91	99.37
6	0.05	0.50	99.87
7	0.01	0.13	100.00

Table 6. Zoading factor of variables in the first five principal components (PCs)

Variable	PC_1	PC_2	PC_3	PC_4	PC_5
BBS	0.941	-0.295	-0.064	-0.135	-0.075
BS	0.941	-0.295	-0.064	-0.135	-0.075
HS	0.941	-0.295	-0.064	-0.135	-0.075
LFS	0.941	-0.295	-0.064	-0.135	-0.075
FW, g	0.612	0.762	0.001	0.052	0.093
FL, mm	0.654	0.725	-0.151	0.085	0.050
FWi, mm	0.578	0.782	-0.065	0.184	-0.008
TSS (°Brix)	0.212	-0.505	-0.631	0.402	0.375
FC	0.367	-0.289	0.423	0.746	-0.213
SGC	0.470	-0.148	0.759	-0.095	0.414

Molecular Characterization

Polymorphism and diversity of SSR markers

Microsatellite primer pairs revealed a total of 60 alleles with a mean value of 6 alleles per locus, ranging from 3 alleles (PGS1.252 and ssrPaCITA5) to 9 alleles (PGS1.20 and ssrPaCITA17) (Table 7). Zhang, Q.P et al. (2013) reported a total of 318 alleles and the mean value of 15.14 alleles per locus in 94 apricot cultivars using SSR primers. Gürcan et al. (2015) reported 230 alleles in 239 apricot cultivars using 18 SSR loci. With ten SSR primer pairs, the total number of alleles and the mean value of alleles per locus in 39 apricot cultivar were 53 and 5.3, respectively (Raji et al., 2014). The average number of 7 alleles per locus is also higher than that found by Hormaza et al. (2002) and Sanchez-Perez et al. (2005) in apricot (4.1 and 3.9, respectively). The high value of average alleles per locus (6) confirms that SSRs are very useful markers for the identification of apricot cultivars. Our results showed successful cross-species transferability of SSR primers identified in different Prunus species to study genetic diversity in apricot. The average number of genotypes was 6.7, ranging from 9 in PGS1.20 and ssrPaCITA17 locus to 3 in PGS1.252 locus. The higher number of genotypes represents more power of loci for discriminating genotypes, as were detected in PGS1.20 and ssrPaCITA17. Excepted heterozygosity among loci ranged from 0.44 in ssrPaCITA5 to 0.82 in PGS1.03 with an average of 0.68. The average expected heterozygosity reported for apricot cultivars was 0.79, 0.75, 0.63, and 0.63 (Zhang et al., 2013; Gürcan et al., 2015; Bourguiba et al., 2012; Raji et al., 2014). Observed heterozygosity also ranged from 0.35 in ssrPaCITA5 to 0.94 in ssrPaCITA17, with an average of 0.77. The observed heterozygosity reported by Gürcan et al. (2015) ranged from 0.30 to 0.94 with an average of 0.63 in 239 apricot accessions from different eco-geographical groups. The average value of PIC was 0.63, with a minimum of 0.38 in ssrPaCITA5 locus and a maximum of 0.79 in PGS1.03 loci. The PIC value was similar in apricot (0.586) as reported by Bourguiba et al. (2012).

A NJ dendrogram based on the shared allele distance was used for grouping the apricots. (Fig. 1). The dendrogram generated from the cluster analysis divided 17 genotypes into three main groups (Fig 1). The first group consisted of 8 genotypes (Badami, Ag erik Gulnar, Shalakh, Ag erik Tezyetishen, Badam erik, May Goranboy, Girmiziyanag, Badam erik) that are 47.06% of the total genotypes with the highest fruit length, fruit diameter, fruit weight, medium TSS. Seven genotypes (May Natiq, Zeynebi, Ag erik Gecyetishen, Mayovka, Ag erik Elchin, Shalakh and Mayovka (Terter)) comprised the second group, which contains 41.18% of the total genotypes in this population. It had the low to high fruit weight, low to medium fruit length, fruit width, low to high TSS. The third cluster consisted of two genotypes (Ag erik, Irevan eriyi (Shalakh) characterized by medium to high fruit weight, medium fruit length, fruit width, and TSS.

Table 7. Variability parameters of 10 SSR markers on 17 apricots investigated genotypes.

Primer name	Ng	Na	He	Ho	PIC
Gol061	7	4	0.66	0.65	0.60
PGS1.03	8	7	0.82	0.82	0.79
PGS1.20	9	9	0.75	0.82	0.71
PGS1.21	7	7	0.64	0.94	0.58
PGS1.23	5	5	0.67	0.88	0.62
PGS1.24	7	6	0.70	0.59	0.66
PGS1.252	3	3	0.52	0.88	0.41
96P10_SP6	8	7	0.80	0.82	0.77
ssrPaCITA5	4	3	0.44	0.35	0.38
ssrPaCITA17	9	9	0.78	0.94	0.75
Mean	6,7	6	0.68	0.77	0.63

Ng, the number of genotypes; Na, the number of alleles; He, expected heterozygosity; Ho, observed heterozygosity; PIC, polymorphism information content.

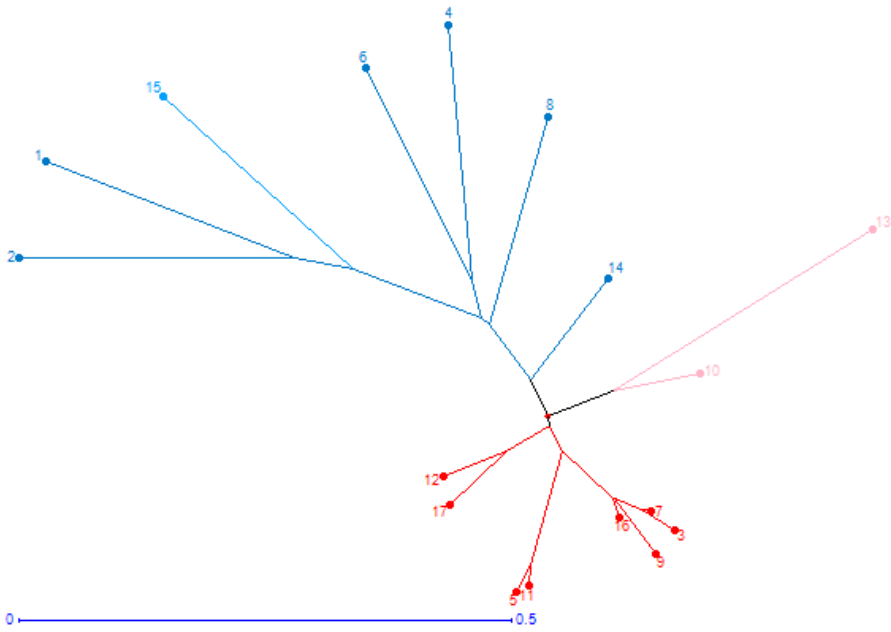

Figure 1. Neighbor-joining dendrogram based on simple matching dissimilarity matrix showing relationships among the 17 apricot accessions. Figure 1 with cluster 1 in red, cluster 2 in blue, and cluster 3 in pink.

Conclusion

For the first time in Azerbaijan, the extant apricot germplasm of Terter, Goranboy, Agdash regions has been evaluated for the purpose of plant sustainable utilization. The research results showed great biodiversity among Azerbaijan apricots. This variation could be used in apricot-breeding programs to improve fruit quality, extend ripening season, and late flowering season. For breeding large fruit-sized cultivars for better marketability and returns to the growers, Azerbaijani apricot cultivars are particularly important due to the large variation in fruit size. Based on this evaluation, 15 genotypes with fruit sizes greater than 40 g were identified. Cultivar "Ordubad eriyi" with the largest fruit (100.2 g) represents a highly precious variety that may be employed to breed large-sized apricots in future breeding programs. SSR molecular markers are of great importance for these breeding programs. In this study, polymorphism of 10 SSR loci from different *Prunus* species was reported. According to the results of the research, *Prunus* SSR loci are highly conserved and can be applied in apricot breeding programs to maximize genetic variability for generating new cultivars for cultivation under Azerbaijan conditions.

References

Agriculture, Erzurum
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Asma, B. M. & Ozturk, K. (2005). Analysis of morphological, pomological and yield characteristics of some apricot germplasm in Turkey. Genet. Resour. Crop Ev. 52, 305–313.

Ayanoglu, H., Kaska, N. & Yildiz, A. (1995). Investigations on adaptations of early apricot cultivars in Mediterranean region. Proceedings of the Second National Horticultural Congress, p.159-163, Adana, Turkey.

Badenes, M.L., Martinez-Calvo, J. & Llácer G. (1998). Analysis of apricot germplasm from the European Eco geographical group. Euphytica 102(1):93-99.

Bourguiba, H., Audergon, J., Krichen, L., Trifi-Fara, N., Mamouni, A., Trabelsi, S., D'Onofrio, C., Asma, B., Santoni, S. & Khadari, B. (2012). Loss of genetic diversity as a signature of apricot domestication and diffusion into the Mediterranean Basin. BMC Plant Biol. 2012, 12–49.

Decroocq, S. A., Chague, P., Lambert, G., Roch, J. M., Audergon, F., Geuna, R., Chiozzotto, D., Bassi, L., Dondini, S., Tartarini, J., Salava, B., Krska, F., Palmisano, ˇ I. & Karayiannis, V. (2014). Selecting with markers linked to the PPVres major QTL is not sufficient to predict resistance to Plum pox virus (PPV) in apricot. Tree Genet. Genomes 10, 1161–1170.

Doyle, J. J. & Doyle, J.L. (1990). Isolation of plant DNA from fresh tissue. Focus 12, 13–15.

Faust, M., Surányi, D. & Nyujtó, F. (1998). Origin and dissemination of apricot. Hort. Rev. 22, 225–266.

Guleryuz, M. (1988). A study on breeding by selection of wild apricots quality and resistance to spring frosts in erzincan plain. Professor thesis, Ataturk University Faculty of Agriculture, Erzurum

Gürcan, K., Öcal, N., Yılmaz, K. U., Ullah, S., Erdoğan, A. & Zengin, Y. (2015). Evaluation of Turkish apricot germplasm using SSR markers: Genetic diversity assessment and search for Plum pox virus resistance alleles. Scientia Horticulturae, 193

Hegedũs, A., Engel, R., Abrankó, L., Balogh, E., Blázovics, A., Hermán, R., Halász, J., Ercisli, S., Pedryc, A. & Stefanovitsbányai, É. (2010). Antioxidant and antiradical capacities in apricot (*Prunus armeniaca* L.) fruits: Variations from genotypes, years, and analytical methods. J Food Sci 75(9):C722-C730.

Hormaza, J.I. (2002). Molecular characterization and similarity relationships among apricot genotypes using simple sequence repeats. Theor. Appl. Genet. 104, 321–328

IPGRI, CEC. (1984). Revised descriptor list for apricot (*Prunus Armeniaca*). Editors: Guerriero R., Watkins R. International Board for Plant Genetic Resources Commission of European Communities, Committee on Disease Resistance Breeding and use of Genebanks. Rome, Italy.

Karimi, H. R, Zamani, Z., Ebadi, A. & Fatahi, M. R. (2008). Morphological diversity of pistacia species in Iran. Genetic Resources and Crop Evolution 44: 76–81.

Khush, G.S. (2002). Molecular genetics-plant breeder's perspective. (In) Molecular Techniques in Crop Improvement, Jain S M, Brar D S, and B S Ahloowalia (Eds.). pp 1–8 Kluwer.

Kostina, K. F. (1964). "Application the phytogeographical method to apricot classification (in Russian)," in Proceedings (Trudi) of the Nikita Botanical Gardens Vol 24, Moscow.

Krichen, L., Audergon, J. M. & Trifi-Farah, N. (2014). Variability of morphological characters among Tunisian apricot germplasm. Scientia Horticulturae, 179, 328–339.

Lo Bianco, R., Farina, V., Indelicato, S. G, Filizzola F. & Agozzino P. (2010). Fruit physical, chemical and aromatic attributes of early, intermediate and late apricot cultivars. J Sci Food Agric 90(6):1008-1019.

Lopes, M. S., Sefc, K. M., Laimer, M. & da Camara Machado, A. (2002). Identification of microsatellite loci in apricot. Mol. Ecol. Notes 2, 24–26.

Mratinić, E., Popovski, B., Milošević, T. & Popovska M. (2011). Analysis of Morphological and Pomological Characteristics of Apricot Germplasm in FYR Macedonia E. J. Agr. Sci. Tech. Vol. 13: 1121-1134

Ogasanovic, D., Plazinic, R., Rankovic, M., Stamenkovic, S. & Milinkovic, V. (2007). Pomological characteristics of new plum cultivars developed in Cacak. Acta Horticulturae 734: 165–8.

Perez-Gonzales, S. (1992). Associations among morphological and phenological characters representing apricot germplasm in Central Mexico. J. Am. Soc. Hort. Sci. 117, 486–490.

Perrier, X. & Jacquemoud-Collet, J. P. (2006). DARwin Software. Available online at: http://darwin.cirad.fr/darwin.

Raji, R., Abbasali, J., Reza, F. & Mohammad Abedini, E. (2014). Investigation of variability of apricot (*Prunus armeniaca* L.) using morphological traits and microsatellite markers. Scientia Horticulturae, 176, 225–231.

Ruiz, D. & Egea, J. (2008). Phenotypic diversity and relationships of fruit quality traits in apricot (*Prunus armeniaca* L.) germplasm. Euphytica, 163:143-158.

Ruml, M., Vuković, A. & Milatović, D. (2010). Evaluation of different methods for determining growing degree-day thresholds in apricot cultivars. Int J Biometerol 54:411-422.

Sanchez-Perez, R., Ruiz, D., Dicenta, F., Egea, J. & Martinez-Gomez, P. (2005). Application of simple sequence repeat (SSR) markers in apricot breeding: molecular characterization, protection, and genetic relationships. Sci. Hortic. 103, 305–315

Schuelke, M. (2000). An economic method for the fluorescent labeling of PCR fragments A poor man's approach to genotyping for research and high-throughput diagnostics. Nature Biotechnology 18:1-2.

Soriano, J. M., Domingo, M. L., Zuriaga, E., Romero, C., Zhebentyayeva, T., Abbott, A. & Badenes, M. L. (2012). Identification of simple sequence repeat markers tightly linked to Plum pox virus resistance in apricot. Mol. Breed. 30, 1017–1026.

Unal, M. S., Sahin, M., Olmez, H., Celik, B., Asma, B. M. & Bas, M. (1999). The Breeding of Late Flowering and Resistance to Late Spring Frosts Apricots through Crossing (First Phase). Tagem/IY/96–06–02–014, Fruit Research Institute, Malatya.

Vavilov, N. I. (1951). The origin, variation, immunity and breeding of cultivated plants. Soil Sci. 72:482.

Vera-Ruiz, E. M., Soriano, J. M., Romero, C., Zhebentyayeva, T., Terol, J., Zuriaga, E., Llácer, G., Abbott, A.G. & Badenes, M.L. (2011). Narrowing down the apricot Plum pox virus resistance locus and comparative analy. Mol. Plant Pathol. 12, 535–547

Wani A. A., Zargar, S. A.; Malik, A. H., Kashtwari, M., Nazir, M., Khuroo, A. A., Ahmad, F. D. & Tanveer A. (2017). Assessment of variability in morphological characters of apricot germplasm of Kashmir, India. Scientia Horticulturae, 225, 630–637.

Yilmaz, K. U., Paydas Kargi, S. & Kafkas, S. (2012). Morphological diversity of the Turkish apricot (*Prunus armeniaca* L.) germplasm in the Iran of Caucasian eco-geographical group. Turk. J. Agric. For. 36, 688–694.

Zhang, Q. P., Liu, D. C., Liu, S., Liu, N., Wei, X., Zhang, A. M., & Liu, W.S. (2013). Genetic diversity and relationships of common apricot (*Prunus armeniaca* L.) in China based on simple sequence repeat (SSR) markers. Genetic Resources and Crop Evolution, 61(2),

Zhebentyayeva, T. N., Ledbetter, C., Burgos, L. & Llácer, G. (2012). "Apricots," in Handbook of Plant Breeding. Fruit Breeding, Vol. 8, eds M. L. Badenes and D. H. Byrne (New York, NY: Springer), 415–458.