GENETICS OF CULTIVATED PLANTS AND THEIR WILD RELATIVES

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Genetic diversity analysis of apricots from Dagestan using SSR markers

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Background. This publication presents the results of a study into the genetic structure of apricot genotypes from Dagestan using the SSR genotyping technique. The importance of the study is seen in the still underexplored gene pool of Dagestani apricot at the genetic level. With this in view, an assessment of the Dagestani apricot genetic diversity, followed by an analysis of its genetic structure, is of theoretical and practical interest.
Materials and methods. The study included 27 apricot genotypes of Dagestani origin: 9 advanced contemporary cultivars and hybrids, 15 seed selections and landraces, and 3 wild forms. Eight SSR markers were used for the genetic diversity analysis: H1-3, A1-91, H2-79, H1-26-2, H2-16, A1-17, RPPG1-032, and RPPG3-026.
Results. The UPGMA and NJ dendrogram construction techniques revealed the genetic similarity among the Dagestani apricots, confirmed by a low level of cluster significance. The tendency towards setting apart the genotypes of hybrid origin (obtained from free pollination of introduced cultivars) from the locally selected cultivars was observed by comparing the results of Bayesian analysis and the K-means approach using the Structure and Statistica software. Such isolation is partial, being obviously affected by constant integration of new apricot genotypes into the local gene pool and its enrichment with new alleles at the genetic level.
Conclusion. The contemporary assortment of apricots in Dagestan was formed on the basis of both the local autochthonous gene pool and Central Asian and European cultivars introduced into this area. The obtained data will enrich the knowledge about the genetic diversity of apricots in Dagestan and serve as the platform for further studies into the florigenetic links of the North Caucasus with other regions.

Keywords: *Prunus armeniaca* L., genetic polymorphism, SSR markers, PCR

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ГЕНЕТИКА КУЛЬТУРНЫХ РАСТЕНИЙ И ИХ ДИКИХ РОДИЧЕЙ

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Анализ генетического разнообразия абрикосов из Дагестана по SSR-маркерам

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Актуальность. В настоящей работе представлены результаты изучения генетической структуры сортов абрикоса дагестанского происхождения с помощью метода SSR-генотипирования. Ценность исследования обусловлена малоизученностью генофонда абрикоса Дагестана на генетическом уровне. В этой связи оценка генетического разнообразия дагестанского абрикоса с последующим анализом генетической структуры представляет теоретический и практический интерес.

Материалы и методы. В исследовании проанализировано 27 образцов абрикоса дагестанского происхождения: 9 современных сортов и гибридов, 15 семенных отборов и стародавних сортов, а также 3 дикие формы. Для анализа генетического разнообразия использовали 8 SSR-маркеров: H1-3, A1-91, H2-79, H1-26-2, H2-16, A1-17, RPPG1-032, RPPG3-026.

Результаты. Методами UPGMA и NJ при построении дендрограмм была установлена генетическая близость сортов абрикоса дагестанского происхождения, подтвержденная низким уровнем достоверности кластеров. При сопоставлении результатов, полученных на основе байесовского анализа и метода K-средних в программах Structure и Statistica, установлена тенденция к обособлению сортов гибридного происхождения (получены от свободного опыления интродуцированных сортов) от сортов из местных отборов. Это обособление имеет частичный характер, что связано, очевидно, с постоянным процессом интеграции новых генотипов абрикоса в местный генофонд и его обогащением новыми аллелями на генетическом уровне.

Заключение. Современный сортимент абрикоса в Дагестане сложился при участии как местного автохтонного генофонда, так и среднеазиатских и европейских сортов, интродуцированных в данную местность. Полученные сведения позволят обогатить знания о генетическом разнообразии сортов абрикоса Дагестана и послужат основой для последующего изучения флорогенетических связей Северного Кавказа с другими регионами.

Ключевые слова: *Prunus armeniaca* L., генетический полиморфизм, SSR-маркеры, ПЦР

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Introduction

Apricot (*Prunus armeniaca* L.) is among the most important fruit crops. K. F. Kostina (Kostina, 1936) identified the following ecogeographic groups for common apricot: Chinese, Central Asian, European, and Irano-Caucasian, based on the principles of ecogeographic classification of cultivated plants developed by N. I. Vavilov. Some adjustments were made in the years to follow (Kostina, 1964). Foreign experts traditionally recognize four main groups: Central Asian, Irano-Caucasian, European, and Dzungar-Trans-Ili, which, in their turn, are represented by local subgroups corresponding to a particular area of origin (Mehlenbacher et al., 1990). Two more groups were later identified: North Chinese and East Chinese (Layne et al. 1996). Different apricot groups are differing in the prevailing crown type, the shape of fruits, leaves and flowers, and a number of physiological characters, such as winter and frost resistance, heat and drought tolerance, flowering schedule, self-fertility, and disease resistance. There are transitional plant forms identified between the groups and subgroups. China and Central Asia are believed to be the primary centers of apricot domestication. It was from these regions that apricot spread to the territories of Western Asia, the Caucasus, the Middle East, and North Africa, shaping its secondary centers of morphogenesis, from where the apricot came to Europe and further over the world (Kostina, 1936; Vavilov, 1931; Bailey, Hough, 1975; Faust et al., 1998; Pedryc et al., 2009).

Dagestan, located on the trade routes of the Great Silk Road, which passed through the North Caucasus in ancient times and the Middle Ages, was also among the secondary centers of apricot morphogenesis.

According to the ecogeographic classification, the apricots in Dagestan are singled out as a separate regional Dagestani subgroup, part of the Irano-Caucasian ecogeographic group (Kostina, 1936; Mehlenbacher et al., 1990).

The present-day Dagestan is rich in fruit plant genetic resources, including apricots, which are still poorly studied and insufficiently involved in breeding practice. More than 120 local cultivars and forms have been identified. It was shown by the results of Dagestani gene pool testing that local cultivars are characterized by early flowering schedule, rounded leaf shapes, drought resistance, poor winter hardiness, and low resistance to brown rot and *Clasterosporium*. Natural populations of Dagestani apricot demonstrated high morphological diversity and breeding potential (Anatov, 2019; Asadulaev et al. 2020).

SSR markers have proven to be an effective molecular genetic tool for studying fruit crop gene pools. The initial research phase employed the SSR markers (Hormaza, 2002; Zhebentyayeva et al., 2003; Romero et al., 2003) earlier developed and tested on peach and other cultivated *Prunus* L. spp. (Cipriani et al., 1999; Testolin et al., 2000; Aranzana et al., 2002). Such approach made it possible to obtain good results. For example, primers of the SSR markers developed for peach produced PCR amplifications in 50–60% of cases with apricot genotypes (Cipriani et al., 1999; Zhebentyayeva et al., 2003). Those markers showed a high level of allelic polymorphism in various collections of apricot accessions (Hormaza, 2002; Romero et al., 2003; Zhebentyayeva et al., 2003; Sánchez-Perez et al., 2005). Subsequently, taking into account the apricot genome, SSR markers for this crop were developed on the basis of the apricot genome sequences (Lopes et al., 2002; Messina et al., 2004).

The first large-scale study of the apricot gene pool using this method (SSR markers) was performed in 2005 (Maghuly et al., 2005). Ten polymorphic SSR markers were selected to genotype a collection of 133 apricot cultivars. Their effectiveness was also demonstrated in a number of subsequent works (Yilmaz et al., 2012b; Raji et al., 2014; Krichena et al., 2014). In 2020, the results of an extensive study of the worldwide apricot germplasm were published (Bourguiba et al, 2020): 890 apricot accessions were genotyped with 25 SSR markers. The work with a large set of genotypes made it possible to trace the main routes along which the apricot crop had spread. A detailed genetic assessment of local germplasms emphasized the relevance of research aimed at understanding general patterns of apricot distribution over the world. Such local germplasms include the Dagestani apricot gene pool, which was not presented in the abovementioned publications.

Meanwhile, the study of the local apricot gene pool in Dagestan using DNA marker techniques is now at an early stage. For the time being, the results of the SSR analysis performed on a number of old-time apricot varieties compared with cultivars from nearby regions have been published. The resulting data attested to the complex origin of the Dagestani apricot gene pool and the impact of various sources on the formation of its germplasm (Stepanov et al, 2019).

The purpose of this study was to assess the genetic diversity of a part of Dagestani apricot genotypes using the SSR genotyping method and subsequent analysis of its genetic structure. The gene pool of Dagestani apricots was replenished applying various approaches: hybridization of introduced cultivars with local forms, selection of the best genotypes from traditional apricot plantations, etc. Dagestani apricots of diverse origin were compared in the framework of this study to find common patterns in the formation of the studied germplasm.

Materials and methods

The CTAB method was applied to extract DNA samples from leaf tissues in the unfolding phase (Murray, Thompson, 1980). The breeding material selected for genotyping is presented in Table 1. The study included 27 apricot genotypes of Dagestani origin, including 9 advanced modern cultivars and hybrids, 15 seed selections and the landraces 'Bukhara', 'Shindakhlan' and 'Khonobakh' collected in various villages of Dagestan and their environs, and 3 wild forms. Selections were carried out in the following villages: Gergebil (Gergebilskiy Avgustovskiy), Salta (Kakhab Aik, Isin Bakhsan, Salta 1, Salta 2, Salta 7, Salta 9, and Salta 10), Goor (Karandalaevskiy, and Khibil Bakvaleb), Zirani (Kakhab), and Nizhneye Inkho (Kachasul). Nothing is known about the origin of these genotypes, except the collection site. Both old-time landraces and cultivars introduced from Central Asia, the Caucasus and Europe could participate in their development, as well as wild forms from neighboring apricot groves. Three genotypes in the studied set were considered to be old-time Dagestani landraces: 'Bukhara', 'Shindakhlan', and 'Khonobakh'. 'Khonobakh' was represented by two forms: Korodinskaya and Buynakskaya, the latter probably being a seedling from free pollination of 'Khonobakh'. Cvs. 'Tamasha', 'Untsukulskiy pozdniy', 'Esdelik' and 'Uzden' were seedlings from free pollination of plants of the Central Asian varietal types: Kursadyk and Supkhany. Two hybrids were obtained from crossing local varieties with European ones: Khibil Bakvaleb × Krasnochekiy and Medunets × Khonobakh, while two forms from the village of Chugli resulted from crossing the famous Armenian cultivar 'Shalakh' ('Yerevani') with local varieties.

Optimal parameters (the concentration of components, and the temperature regime of the reaction) were selected for the implementation of PCR. The following optimal protocol

Table 1. List of Dagestan apricot genotypes used in the study

Таблица 1. Перечень использованных дагестанских образцов абрикоса

Apricot genotypes	Conditional groups	Subgroup of Dagestan	Origin
1. Bukhara-1	old	Dagestan	Landrace
2. Gergebilskiy Avgustovskiy	new	Dagestan	Selection
3. Isin bakhsan	old	Dagestan	Selection
4. Karandalaevskiy	old	Dagestan	Selection
5. Kakhab	old	Dagestan	Selection
6. Kakhab Aik	old	Dagestan	Selection
7. Kachasul	old	Dagestan	Selection
8. Salta 1	old	Dagestan	Selection
9. Salta 10	old	Dagestan	Selection
10. Salta 2	wild	Dagestan	Selection
11. Salta 7	old	Dagestan	Selection
12. Salta 9	old	Dagestan	Selection
13. Uzden	new	Dagestan / Central Asia	Hybridization
14. Khibil Bakvaleb	old	Dagestan	Selection
15. Khonobakh Buynakskiy	old	Dagestan	Landrace
16. Khonobakh Korodinskiy	old	Dagestan	Landrace
17. Khukumat kurek	old	Dagestan	Selection
18. TSEB 1	wild	Dagestan	Selection
19. TSEB 4	wild	Dagestan	Selection
20. Chugli-293	new	Dagestan / Irano-Caucasian	Hybridization
21. Chugli-295	new	Dagestan / Irano-Caucasian	Hybridization
22. Shindakhlan	old	Dagestan	Landrace
23. Khibil Bakvaleb × Krasnoschekiy	new	Dagestan / Europe	Hybridization
24. Tamasha	new	Dagestan / Central Asia	Hybridization
25. Untsukulskiy pozdniy	new	Dagestan / Central Asia	Hybridization
26. Esdelik	new	Dagestan / Central Asia	Hybridization
27. Medunets × Khonobakh	new	Dagestan / Europe	Hybridization

was accepted: the total 25 µL volume of the PCR mixture included 50 ng of DNA, 0.25 mM of dNTPs, 0.2 µM of each primer; plus 2.5 µL of 10x buffer and 1 u of Taq polymerase. PCR was carried out according to the following program: initial denaturation for 3 minutes at 94°C, then 35 cycles: denaturation at 94°C for 45 seconds, annealing stage at 58°C for 45 seconds, elongation at 72°C for 45 seconds; the final stage was elongation for 4 minutes 30 seconds at 72ºC. An ABI prism 3130 instrument was used to assess the size of PCR products. The results were processed in the Gene Mapper 4.1 program. We analyzed 8 SSR markers: H1-3, A1-91, H2-79, H1-26-2, H2-16, A1-17 (Wang et al, 2014), RPPG1-032, and RPPG3-026 (Dettori, 2016).

A macro for Microsoft Office Excel 2007, GenAlEx 6.503, was employed. Principal coordinates analysis (PCoA) was performed using PAST v. 2.17c. Bayesian analysis was carried out in the STRUCTURE 2.3.4 program. Calculation of K-means values was made using the Statistica v.13.3 program.

Results

Eight SSR markers were used to analyze 27 apricot genotypes. The number of alleles (Na) identified with 8 tested markers ranged from two (marker RPPG1-032) to ten (marker H1-3), averaged to 5.375 alleles per locus. A total of 43 alleles were recognized for all markers used in the study. A number of genetic parameters characterizing the polymorphism of the selected markers in the studied group of apricot genotypes were calculated (Table 2).

Such parameters as the effective number of alleles (Ne) and the Shannon index (I) make it possible to assess not only the number of alleles, but also the uniformity of their frequency. The H1-3 marker (Ne = 4.215; I = 1.812) had the highest parameter values, while the RPPG1-032 marker had the lowest values (Ne = 1.113; I = 0.209).

The highest value of observed heterozygosity (Ho) was found for the H1-26-2 marker, which had three alleles, while

Table 2. **Parameters used to assess SSR markers**

Таблица 2. **Параметры, использованные для оценки SSR-маркеров**

Markers	Na	Ne	I	Ho	He	F
RPPG1-032	2	1.113	0.209	0.107	0.101	-0.057
RPPG3-026	5	2.920	1.229	0.036	0.658	0.946
H1-3	10	4.215	1.812	0.607	0.763	0.204
A1-91	6	3.751	1.508	0.393	0.733	0.464
H2-79	5	1.725	0.896	0.393	0.420	0.065
H1-26-2	3	2.815	1.063	0.750	0.645	-0.163
H2-16	6	2.454	1.095	0.643	0.592	-0.085
A1-17	6	3.336	1.402	0.393	0.700	0.439
Mean	5.375	2.791	1.152	0.415	0.577	0.227
SE	0.844	0.362	0.169	0.089	0.077	0.132

Note: Na – number of alleles; Ne – effective number of alleles; I – Shannon information index; Ho – observed heterozygosity; He – expected heterozygosity; F – fixation index

Примечание: Na – число аллелей; Ne – эффективное число аллелей; I – индекс информативности Шеннона; Ho – наблюдаемая гетерозиготность; He – ожидаемая гетерозиготность; F – индекс фиксации

the minimum value was recorded for the RPPG3-026 marker. The highest value of expected heterozygosity (He) was identified for the H1-3 marker, and the lowest for RPPG1-032. For three markers, the observed heterozygosity was higher than the expected one, attesting to high hybridization efficiency, which contributed to the saturation of the gene pool with heterozygous forms. Low values of the fixation index (F) also pointed to the panmicticity of the Dagestani apricot gene pool.

Genetic similarity among apricots of Dagestani origin was confirmed by the low statistical significance levels of the clusters when constructing dendrograms using the UPGMA and NJ methods. Besides, Bayesian analysis was carried out in the Structure program, and K-means analysis in the Statistica program. The results of both techniques were compared with each other. The Past program was employed to make the PCoA that confirmed the general genotype distribution patterns.

Discussion

Apricot varieties were categorized into two clusters in the Structure 2.3.4 and Statistica 13.3 programs, using Bayesian analysis (Fig. 1) and K-means (Table 3), respectively.

The distribution of genotypes into clusters differed depending on the method applied. When comparing the two techniques, the genotypes were divided into four groups

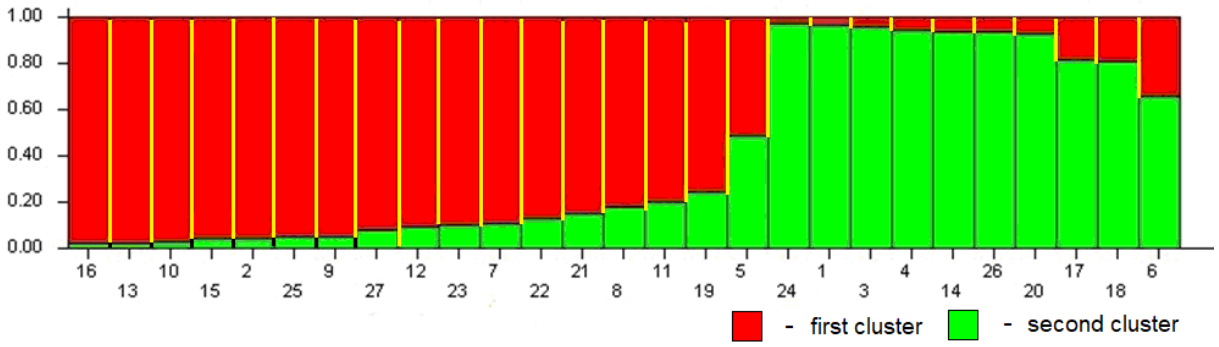

Fig. 1. **Graph of Bayesian analysis of 27 Dagestani apricot genotypes in the Structure program**

Рис. 1. **График байесовского анализа 27 дагестанских образцов абрикоса в программе Structure**

Note: **1** – Bukhara-1, **2** – Gergebilskiy Avgustovskiy, **3** – Isin Bakhsan, **4** – Karandalaevskiy, **5** – Kakhab, **6** – Kakhab Aik, **7** – Kachasul, **8** – Salta 1, **9** – Salta 10, **10** – Salta 2, **11** – Salta 7, **12** – Salta 9, **13** – 'Uzden', **14** – Khibil Bakvaleb, **15** – Khonobakh Buynakskiy, **16** – Khonobakh Korodinskiy, **17** – Khukumat kurek, **18** – TSEB 1, **19** – TSEB 4, **20** – Chugli-293, **21** – Chugli-295, **22** – 'Shindakhlan', **23** – Khibil Bakvaleb × Krasnoschekiy, **24** – 'Tamasha', **25** – 'Untsukulskiy posdniy', **26** – 'Esdelik', **27** – Medunets × Khonobakh

Примечание: **1** – Бухара-1, **2** – Гергебильский Августовский, **3** – Исин Бахсан, **4** –Карандалаевский, **5** – Кахаб, **6** – Кахаб Аик, **7** – Качасул, **8** – Салта 1, **9** – Салта 10, **10** – Салта 2, **11** – Салта 7, **12** – Салта 9, **13** – 'Уздень', **14** – Хибил Баквалеб, **15** – Хонобах Буйнакский, **16** – Хонобах Кородинский, **17** – Хукумат курек, **18** – ЦЭБ 1, **19** – ЦЭБ 4, **20** – Чугли-293, **21** – Чугли-295, **22** – 'Шиндахлан', **23** – Хибил Баквалеб × Краснощекий, **24** – 'Тамаша', **25** – 'Унцукульский поздний', **26** – 'Эсделик', **27** – Медунец × Хонобах

Table 3. **Comparison of the results of Bayesian analysis and K-means for 27 apricot genotypes of Dagestani origin**

Таблица 3. **Сопоставление результатов байесовского анализа и К-средних на 27 образцах абрикоса дагестанского происхождения**

Название сортов	K-means*	Distance*	K = 2**	Cluster
Khonobakh Korodinskiy	1	0.29	1	1
Uzden	1	0.38	1	1
Salta 2	1	0.41	1	1
Gergebilskiy Avgustovskiy	1	0.37	1	1
Untsukulskiy pozdniy	1	0.33	1	1
Medunets × Khonobakh	1	0.30	1	1
Khibil Bakvaleb × Krasnoschekiy	1	0.34	1	1
Chugli-295	1	0.32	1	1
TSEB 4	1	0.30	1	1
Khonobakh Buinakskiy	2	0.45	1	2
Salta 10	2	0.42	1	2
Salta 9	2	0.36	1	2
Kachasul	2	0.37	1	2
Shindakhlan	2	0.30	1	2
Salta 1	2	0.28	1	2
Salta 7	2	0.28	1	2
Kakhab	2	0.36	1	2
Tamasha	2	0.26	2	3
Bukhara-1	2	0.25	2	3
Isin bakhsan	2	0.32	2	3
Karandalaevskiy	2	0.30	2	3
Khibil Bakvaleb	2	0.28	2	3
Chugli-293	2	0.28	2	3
Kakhab Aik	2	0.42	2	3
Esdelik	1	0.31	2	4
Khukumat kurek	1	0.34	2	4
TSEB 1	1	0.36	2	4

* – results of clustering in the Statistica program; ** – results of clustering in the Structure program

* – результаты кластеризации в программе Statistica; ** – результаты кластеризации в программе Structure

(see Table 3). The first group included genotypes assigned to the first cluster, matching on the basis of both methods. The second group included those assigned to the first cluster in Structure and the second cluster in Statistica. The third group contained genotypes that matched the second cluster in both programs. The fourth group incorporated genotypes assigned to the second cluster in Structure and the first cluster according to K-means.

The first group consisted of one old-time landrace, Khonobakh Korodinskiy, and a number of modern forms of hybrid origin (Khibil Bakvaleb × Krasnoschekiy, Chugli-295, and Medunets × Khonobakh), including those with Central Asian genotypes as parents ('Uzden', and 'Untsukulskiy pozdniy'). The three genotypes selected by collecting missions were TSEB 4, Salta 2, and Gergebilskiy Avgustovskiy. In general, the main part of modern cultivars had a parent of non-Dagestani origin.

The second group included the 'Shindakhlan' landrace, genotypes selected in the village of Salta (1, 9, 7, and 10) as well as the Kachasul and Kakhab selections found by collecting teams. The Khonobakh Buynakskiy genotype also entered this group. Most of the apricot forms within the group were selections collected by plant explorers, mainly from the village of Salta.

The third group comprised the 'Bukhara' landrace, and two genotypes of hybrid origin: 'Tamasha', and Chugli-293. Four apricot forms were local selections.

The fourth group was represented by three genotypes: two local selections and one with Central Asian roots.

The abovementioned leads to an assumption that contrasting division of the genotypes in the selected set occurred between local genotype selections growing in mountain villages and new cultivars of hybrid origin, in which European or Asian apricots were found among maternal parents. According to the ratio of hybrid cultivars to local varieties, the first group (5 cultivars of hybrid origin and 3 genotypes from selections) and the second one (6 genotypes from selections, with no new hybrid cultivars in the group) can be regarded as contrasting to each other. It is noteworthy that the first group contained the 'Khonobakh' landrace, possessing a number of features characteristic of Central Asian genotypes (drought resistance, and productivity), while 'Shindakhlan' from the second group was, in its turn, a typical apricot cultivar from the Irano-Caucasian ecogeographic group (large fruit size, light fruit color, medium height, weak winter hardiness, and poor resistance to fungal diseases).

The third and fourth groups demonstrated a mixed composition of genotypes, without a pronounced predominance of hybrid forms or those selected by collecting missions. The presence of mixed groups pointed to the influence of apricots differing in their origin on the local germplasm. In its turn, the revealed isolation of selected local forms of apricot, especially in the village of Salta, confirmed the presence of a unique gene pool of this fruit crop, formed in the mountainous regions of Dagestan. The emergence of this gene pool could be facilitated by both geographic isolation, provoked by the inaccessibility of the mountain settlements in Dagestan, and specific features of folk breeding, which contributed to the selection of apricots with specific characteristics.

Three landraces were distributed among three groups: Khonobakh Korodinskiy (first group), 'Shindakhlan' (second group), and 'Bukhara' (third group). It can be assumed that the three Dagestani landraces had significant genetic differences among themselves. Each of these landraces in different times was widespread in the Dagestani horticultural practice and strongly influenced the gene pool of apricots cultivated in Dagestan. This can be evidenced by the even distribution of cultivars selected from local apricot forms among the three main groups. Khonobakh Korodinskiy is genetically different from Khonobakh Buynakskiy, thus making doubtful the relationship between these genotypes. It is also worth noting that the Structure program made it possible to establish two intermediate genotypes (the graph shows a significant contribution of two clusters), Kakhab and Kakhab Aik.

The principal coordinates analysis also confirmed the pattern with four groups of genotypes (Fig. 2). Each group occupies its own position in the coordinate space. The first group is located in the upper right corner, the second group in the upper left corner, the third group in the central part of the left side, and the fourth group in the center of the graph.

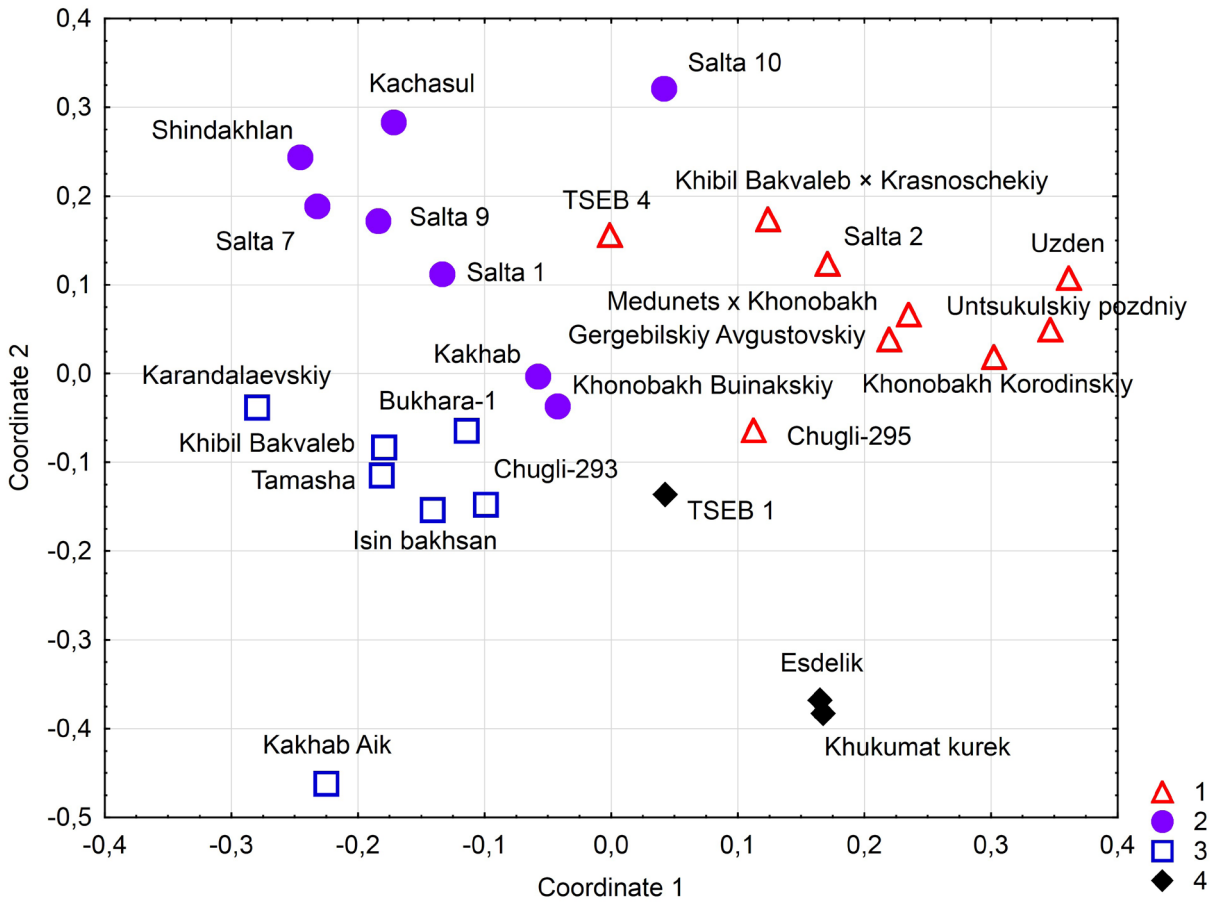

Fig. 2. PCoA distribution of apricot genotypes

Рис. 2. Распределение генотипов абрикоса методом PCoA

Note: the numbers indicate the groups from Table 3

Примечание: цифрами обозначены группы из таблицы 3

Conclusion

Thus, the use of SSR markers for the analysis of polymorphism in apricot genotypes from the Dagestani gene pool demonstrated its effectiveness. Markers made it possible to assess the genetic diversity of apricots of Dagestani origin. The data obtained during genotyping served as the basis for assessing the genetic diversity of the studied breeding material. A number of regularities in the distribution of the main genotype groups were found, while the landraces were evenly distributed among the entire set of apricot genotypes, without forming a separate group. It may attest to the heterogeneous origin of these genotypes, which largely contributed to the shaping of the contemporary apricot gene pool in Dagestan. A tendency towards isolation was revealed among some genotypes selected by collecting missions compared to new cultivars with parents of non-Dagestani origin. The data obtained during this study lead to the conclusion that the main sources of the Dagestani apricot gene pool formation were old-time landraces of different origin.

References / Литература

Anatov D.M. Phenetic analysis of natural apricot populations in the Mountainous Dagestan for endocarp (stone) features. *Proceedings on Applied Botany, Genetics and Breeding*. 2019;180(1):89-94. [in Russian] (Анатов Д.М. Фенетический анализ природных популяций абрикоса Горного Дагестана по признакам эндокарпия (косточки). *Труды по прикладной ботанике, генетике и селекции*. 2019;180(1):89-94). DOI: 10.30901/2227-8834-2019-1-89-94

Aranzana M.J., Garcia-Màs J., Carbó J., Arús P. Development and variability analysis of microsatellite markers in peach. *Plant Breeding*. 2002;121(1):87-92. DOI: 10.1046/j.1439-0523.2002.00656.x

Asadulaev Z.M., Anatov D.M., Osmanov R.M. Apricot in Dagestan (Abrikos v Dagestane). Makhachkala; 2020. [in Russian] (Асадулаев З.М., Анатов Д.М., Османов Р.М. Абрикос в Дагестане. Махачкала; 2020).

Bailey C.H., Hough L.F. Apricots. In: J. Janick, J.N. Moore (eds). *Advances in Fruit Breeding*. West Lafayette, IN: Purdue University Press; 1975. p.367-383.

Bourguiba H., Scotti I., Sauvage C., Zhebentyayeva T., Ledbetter C., Krška B. et al. Genetic structure of a worldwide germplasm collection of *Prunus armeniaca* L. reveals three major diffusion routes for varieties coming from the species' center of origin. *Frontiers in Plant Science*. 2020;11:638. DOI: 10.3389/fpls.2020.00638

Cipriani G., Lot G., Huang W.G., Marrazzo M.T., Peterlunger E., Testolin R. AC/GT and AG/CT microsatellite repeats in peach [*Prunus persica* (L.) Batsch] isolation, characterization and cross-species amplification in *Prunus*. *Theoretical and Applied Genetics*. 1999;99(1):65-72. DOI: 10.1007/s001220051209

Dettori M.T., Micali S., Giovinazzi J., Scalabrin S., Verde I., Cipriani G. Mining microsatellites in the peach genome: development of new long-core SSR markers for genetic analyses in five *Prunus* species. *SpringerPlus*. 2015;4:337. DOI: 10.1186/s40064-015-1098-0

Faust M., Suranyi D., Nyujto F. Origin and dissemination of apricot. *Horticultural Reviews*. 1998;22:225-266.

Hormaza J.I. Molecular characterization and similarity relationships among apricot (*Prunus armeniaca* L.) genotypes using simple sequence repeats. *Theoretical and Applied Genetics*. 2002;104(2-3):321-328. DOI: 10.1007/s001220100684

Kostina K.F. Application of the botanico-geographic method to the classification of apricot (Primeneniye botaniko-geograficheskogo metoda v klassifikatsii abrikosa). In: *150 years to the Nikita State Botanical Gardens. 1812–1962: collection of scientific papers. Vol. 37 (150 let Gosudarstvennomu Nikitskomu botanicheskomu sadu. 1812–1962: sbornik nauchnykh trudov. T. 37)*. Moscow: Kolos; 1964. p.170-183. [in Russian] (Костина К.Ф. Применение ботанико-географического метода в классификации абрикоса. В кн.: *150 лет Государственному Никитскому ботаническому саду. 1812–1962 : сборник научных трудов. Т. 37.* Москва: Колос; 1964. С.170-183).

Kostina K.F. Apricot. *Proceedings on Applied Botany, Genetics and Breeding*, 1936; Suppl 83:290 p. [in Russian] (Костина К.Ф. Абрикос. *Труды по прикладной ботанике, генетике и селекции*. 1936; Приложение 83: 290 с.).

Krichen L., Audergon J.M., Trifi-Farah N. Assessing the genetic diversity and population structure of Tunisian apricot germplasm. *Scientia Horticulturae*. 2014;172(5):86-100. DOI: 10.1016/j.scienta.2014.03.038

Layne R.E.C., Bailey C.H., Hough L.F. Apricots. In: J. Janick, J. Moore (eds). *Fruit Breeding, Vol. 1: Tree and Tropical Fruits*. New York, NY: John Wiley & Sons, Inc.: 1996. p.79-111.

Lopes M.S., Sefc K.M., Laimer M. Da Câmara Machado A. Identification of microsatellite loci in apricot. *Molecular Ecology Notes*. 2002;2(1):24-26. DOI: 10.1046/j.1471-8286.2002.00132.x

Maghuly F., Fernandez E.B., Ruthner Sz. Pedryc A., Laimer M. Microsatellite variability in apricots (*Prunus armeniaca* L.) reflects their geographic origin and breeding history. *Tree Genetics and Genomes*. 2005;1(4):151-165. DOI: 10.1007/s11295-005-0018-9

Mehlenbacher S.A., Cociu V., Hough L.F. Apricots (*Prunus*). In: J.N. Moore, J.R. Ballington (eds). *Acta Hotticulturae. Vol. 290. Genetic Resources of Temperate Fruit and Nut Crops*. 1991. p.63-109. DOI: 10.17660/ ActaHortic.1991.290.3

Messina R., Lain O., Marrazzo M.T. Cipriani G., Testolin R. New set of microsatellite loci isolated in apricot. *Molecular Ecology Notes*. 2004;4(3):432-434. DOI: 10.1111/j.1471-8286.2004.00674.x

Murray M.G., Thompson W.F. Rapid isolation of high molecular weight plant DNA. *Nucleic Acids Research*. 1980;8(19):4321-4325. DOI: 10.1093/nar/8.19.4321

Pedryc A., Herman R., Halász J., Gutermuth A., Hegedus A. Apricot breeding – aims and results: 'GNT – 5/47' hybrid. *Hungarian Agricultural Research*. 2009; 2:16-18.

Raji R., Jannatizadeh A., Fattahi R., Esfahlani M.A. Investigation of variability of apricot (*Prunus armeniaca* L.) using morphological traits and microsatellite markers. *Scientia Horticulturae*. 2014;176:225-231. DOI: 10.1016/j.scienta.2014.06.033

Romero C., Pedryc A., Muñoz V. Llacer G., Badenes M.L. Genetic diversity of different apricot geographical groups determined by SSR markers. *Genome*. 2003;46(2):244-252. DOI: 10.1139/g02-128

Sánchez-Pérez R., Ruiz D., Dicenta F. Egea J., Martínez-Gómez P. Application of simple sequence repeat (SSR) markers in apricot breeding: molecular characterization, protection, and genetic relationships. *Scientia Horticulturae*. 2005;103(3):305-315. DOI: 10.1016/j.scienta.2004.06.009

Stepanov I.V., Suprun I.I., Anatov D.M., Lobodina E.V., Osmanov R.M. SSR-analysis of some apricot varieties (*Prunus armeniaca* L.) of the Dagestan eco-geographical subgroup. *Horticulture and Viticulture*. 2019;(4):16-20. [in

Russian] (Степанов И.В., Супрун И.И., Анатов Д.М., Лобо-дина Е.В., Османов Р.М. SSR-анализ некоторых сортов абрикоса (*Prunus armeniaca* L.) дагестанской эколо-го-географической подгруппы. *Садоводство и виноградарство*. 2019;(4):16-20). DOI: 10.31676/0235-2591-2019-4-16-20

Testolin R., Marrazzo M.T., Cipriani G. Quarta R., Verde I., Dettori M.T. et al. Microsatellite DNA in peach (*Prunus persica* (L.) Batsch) and its use in fingerprinting and testing the genetic origin of cultivars. *Genome*. 2000;43(3):512-520. DOI: 10.1139/g00-010

Vavilov N.I. Wild relatives of fruit trees in the Asian part of the USSR and the Caucasus and the problem of the origin of fruit trees (Dikiye rodichi plodovykh derevyev aziatskoy chasti SSSR i Kavkaza i problema proiskhozhdeniya plodovykh derevyev). *Bulletin of Applied Botany, of Genetics and Plant Breeding*. 1931;26:85-107. [in Russian] (Вавилов Н.И. Дикие родичи плодовых деревьев азиатской части СССР и Кавказа и проблема происхождения плодовых деревьев. *Труды по прикладной ботанике, генетике и селекции*. 1931;26:85-107).

Wang Z., Liu H., Liu J., Li Y., Wu R., Pang X. Mining new microsatellite markers for Siberian apricot (*Prunus sibirica* L.) from SSR-enriched genomic library. *Scientia Horticulturae*. 2014;166:65-69. DOI: 10.1016/j.scienta.2013.12.004

Yilmaz K.U., Paydas S., Dogan S., Kafkas S. Genetic diversity analysis based on ISSR, RAPD and SSR among Turkish apricot germplasms in Iran Caucasian eco-geographical group. *Scientia Horticulturae*. 2012;138:138-143. DOI: 10.1016/j.scienta.2012.02.017

Zhebentyayeva T.N., Reighard G.L., Gorina V.M., Abbott A.G. Simple sequence repeat (SSR) analysis for assessment of genetic similarity in apricot germplasm. *Theoretical and Applied Genetics*. 2003;106(3):435-444. DOI: 10.1007/s00122-002-1069-z

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