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Research of Farm Indicators of Sweet Cherry (*Prunus avium* L.) Plant Existed in Azerbaijan and Determination of Genetic Diversity by Means of ISSR Markers

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Abstract**—** *Expeditions have been organized to Guba, Khachmaz, Sheki, Agdash, Tartar districts of Azerbaijan to collect fruit and leaf samples of cherry sorts and forms for research work. Length and width of cherry fruit, length of stalk, mass of fruit, mass of flesh, length and width of stone, leaf parameters were researched. The length of the fruit has varied between 7.7-29.4 (mm) depending on the sorts. The weight of cherry fruit has varied between 1.01-11.2 (g) and has been observed the smallest in Jir gilas sort (Khachmaz) and the highest in the sort Samba. Genetic diversity between cherry samples has been researched through ISSR markers. A total of 68 bands were synthesized on 8 primers in the researched cherry genotypes. The number of polymorphic bands was between 4 - 8. The genetic similarity index between the samples was 0.017 - 0.929.*

Keywords**—** *Fruit, genetic diversity, genetic similarity, ISSR markers, Prunus avium L.*

I. INTRODUCTION

Cherry (*Prunus avium* L.) is an economically significant species of the genus *Prunus*. In order to provide the normal growth of cherries, it is required to implement timely agro-technical work, taking into account the soil and climatic conditions, the pomological features of the variety. During the growth and maturation of fruits, the demand for nutrients of trees increases. During this period, feeding and timely giving of fertilizers leads to a sufficient collection of biochemical substances inside the fruit. This allows for the formation of high quality fruits.

Recently, some studies based on morphological and biochemical analysis have been implemented to identify the degree of polymorphism of local cherry genotypes. Unfortunately, there are very few study work in which the morpho-pomological features of cherry genotypes have been researched in the world. Although morphological features depend on environmental conditions and agro-technical practices, their characterization is the first step that is proposed to be studied before starting biochemical or molecular researches [5].

The genetic characteristics of the genplasm facilitate better management and use of plant collections. Historically, genplasm collections' characterization has been conducted at the taxonomic, biogeographic, morphometric, agronomic, or molecular levels [2]. The increase in variability using molecular markers has allowed genplasm managers, plant breeders and geneticists to resolve import problems related to the genetic resources of agricultural plants [3].

According to the fact that there are not many areas where cherries can be cultivated economically in the world, long-term storage, production of durable, high-quality cherry sorts is implemented in limited regions of certain countries. There are large areas in our country where the ecological conditions are suitable for growing cherries. In our country, which has a great ecological potential in the cultivation of cherries, it has been observed that production has increased rapidly in recent years.

As in the world, our country has been working for many years to create a collection in order to determine the gene resources of fruit sorts and select individuals having superior characteristics.

It is important to determine and protect the plant's gene resources. Rapid developments in biotechnology in recent years have given a direct and great contribution to its use for purposes such as protection, production, renewal, characterization, cultivation and diversity development of genetic resources. Taking into account the methods used for this purpose, it can be observed that they are based on DNA whose genetic structure does not varied.

The identification of cherry by molecular methods has not been researched in our country till today. We have identified by morphological methods of yabani gilas forms and local sorts spread in Azerbaijan and conducted identification by molecular-genetic methods. The study of cherry samples by molecular markers allows to distinguish morphologically similar samples and to estimate the degree of genetic similarity between genotypes.

II. MATERIALS AND METHODS

The economic and biological characteristics of the cherry plant have varied significantly depending on its origin and evolution. The main indicator of each fruit plant is considered sort. As a result of the conducted research, it has been identified that cherry sorts and forms were cultivated 23 in Guba region, 13 in Khachmaz region, 26 in Sheki, 8 in Tartar region and 4 in Agdash region.

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DNA extraction stages

Extraction of nuclear DNA from cherry genotypes was implemented in the Biotechnology Laboratory of the Gen-Stem Cell Center of Erciyes University in Kayseri, Turkey. 2 grams of fresh leaf samples were taken from each genotype, powdered by liquid nitrogen and collected in 2 ml ependorph tubes and used for DNA extraction. DNA extraction was conducted on the basis of the CTAB (cetyltrimethylammonium bromide) protocol proposed by S.O. Rogers (1985) [7].

Quantity of DNA extracted was determined on a spectrophotometer at 260 and 280 nm. The mixture used to determine quantity has consisted of 20 µl of extracted DNA and 1980 µl of ddH_2O or TE buffer. NanoDrop 2000 device was used to measure the quality and quantity of DNA. During dilution of DNA, nuclear DNA was separated, dissolved in water, and diluted to 100 ng, provided that the amount was 200 ml. The dilution was conducted on the basis of the following formula (Table 1).

$C1C2=V1V2$

TABLE 1. Quality of nuclear DNA

№	Samples	DNA/100ng/µl	A260	A280	A260/280
1	Samba (G1)	418.37	10.216	5.907	2.06
2	Lapins (G2)	987.74	21.159	11.241	2.01
3	Ziraat 0900 (G3)	175.67	4.154	2.328	2.08
4	Jir gilas (G4)	192.72	5.453	3.729	1.81
5	Chagrayi Napoleon (G5)	88.81	3.478	2.590	2.00
6	Sari Drogana (G6)	301.50	8.084	5.358	1.83
7	Tezyetishen Kassini (G7)	145.28	3.684	2.268	1.95
8	Ramon Oliva (G8)	454.96	10.490	5.603	2.16
9	Regina (G9)	646.81	13.871	6.759	2.22
10	Sweet heart (G10)	231.62	7.091	4.699	2.07
11	Bianka gozeli (G11)	149.81	3.581	2.020	2.09
12	Sarı Denissema (G12)	120.34	3.362	2.098	2.11
13	Jir gilas-2 (G13)	390.54	9.522	5.493	2.07
14	Biqarro Burlat (G14)	30.31	1.075	0.703	2.59
15	Agh gilas (G15)	522.46	11.145	5.466	2.19
16	Early Lory (G16)	125.85	4.658	3.311	2.15
17	North Vander (G17)	202.97	5.638	3.580	2.03
18	Gara gilas (G18)	415.22	10.629	6.374	2.05
19	May gilasy (G19)	567.96	14.272	8.780	1.97
20	Krim (G20)	219.49	6.600	4.396	2.01
21	Gara Napoleon (G21)	133.11	5.097	3.733	2.05
22	Frans İosif (G22)	124.83	3.886	2.577	2.10
23	Gara jir gilas (G23)	179.06	4.031	2.211	2.03
24	Murebbe agh gilas (S1)	308.61	8.915	5.844	1.99
25	Agh jir gilas (S2)	422.50	23.324	23.324	1.00
26	Gara shabalidi (S3)	422.68	8.595	4.111	2.13
27	Gara gilas (S4)	857.18	19.136	10.093	2.12
28	Ala gilas (S5)	445.67	12.571	8.232	1.95
29	Jir gilas kesikli (S6)	617.14	16.441	9.982	2.10
30	Okuzureyi agh (S7)	860.69	19.956	10.767	2.15
31	Okuzureyi gara (S8)	877.86	18.064	8.604	2.17
32	Gizil gilas (S9)	276.58	8.067	5.351	1.96
33	Kahraba gilas (S10)	297.52	7.880	4.775	2.09
34	Alij gilas (S11)	525.44	13.896	8.526	2.04
35	Agh gilas (S12)	331.57	11.038	7.660	2.04
36	Krim (S13)	160.13	8.513	6.950	1.95
37	Napoleon- Sheki (S14)	536.40	14.552	9.182	2.00
38	Balli gilas (S15)	415.46	16.561	12.292	2.06
39	Jir gilas aji (S16)	96.81	4.012	3.216	1.70
40	Jir gilas-2 (S17)	293.43	7.624	4.693	2.00
41	Mayovka girmizi (S18)	242.19	5.277	2.648	2.19
42	Dum agh gilas (S19)	534.96	13.343	7.420	2.24
43	Albali gilas yumru (S20)	541.93	13.657	7.584	2.27
44	Mayovka chil-chil (S21)	504.72	15.963	11.576	1.77
45	Gara Mayovka (S22)	96.23	4.509	3.690	1.74
46	Sari gilas (S23)	66.76	3.320	2.608	2.14
47	Albali gilas agh (S24)	148.41	4.750	3.393	1.84
48	Sari uzun gilas (S25)	168.94	6.747	6.463	1.09
49	Guzugoren (S26)	217.31	5.046	2.872	2.00
50	Gara okuzureyi (S27)	347.86	11.318	8.524	1.67
51	Zoghali (T1)	50.93	5.574	5.133	1.76
52	Chal Krim (T2)	114.75	3.343	2.170	2.05
53	Gejyetishen okuzureyi (T3)	123.02	3.384	2.177	1.96

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54	Yabani gilas (T4)	215.22	4.576	2.344	2.08
55	Napoleon (T5)	168.13	6.609	5.249	1.68
56	Shampan gilas (T6)	68.88	3.571	2.979	1.75
57	Agh Krim (T7)	198.32	5.249	3.245	2.02
58	May gilasi agh (A1)	94.21	5.207	4.354	1.83
59	Agh gilas (A2)	120.19	8.408	7.697	1.42
60	Ala gilas (A3)	163.88	5.761	4.345	1.76
61	Gara okuzureyi (A4)	150.63	4.290	2.775	2.01
62	Tezyetishen Krim (K1)	132.54	3.065	1.772	1.95
63	Napoleon (K2)	159.05	6.857	5.113	2.21
64	Krim gejyetishen (K3)	116.53	2.545	1.299	2.15
65	Agh gilas (K4)	207.60	6.404	4.644	1.74
66	Xrustal (K5)	76.32	1.701	0.848	2.27
67	Ramon Oliva (K6)	206.35	7.138	4.890	2.20
68	Tezyetishen Krim (K7)	135.75	3.709	2.430	1.89
69	Erken Krasnodar (K8)	157.40	5.600	4.206	1.79
70	Jir gilas (K9)	162.89	4.938	3.293	2.02
71	Alyanag (K10)	99.59	3.874	3.060	1.69
72	En gecyetishen Krim (K11)	252.89	6.575	3.929	2.10
73	Gara Krimson (K12)	73.53	2.550	1.777	2.11
74	Regina (K13)	201.52	10.712	9.279	1.55

ISSR primers and polymerase chain reaction (PCR) amplification

It was used 8 ISSR primers selected from various databases and articles in the current research work. A list of ISSR primers used, their motives, and their combination temperatures are given in Table 2.

TABLE 2. Used ISSR primers and their combination temperature

№	The name of the primer	Repetitions	Tm, S°
1	IS 2	$(GA)_9C$	52
2	IS 3	$G(TG)_9$	52
3	IS 37	$(CA)_8GT$	48
4	IS 47	$(ACC)_6$	46
5	IS 48	$(ATG)_8$	46
6	IS 50	$(GAA)_6$	54
7	IS 54	$(AG)_8C$	52
8	UBC 868	$(GAA)_6$	50

The total reaction's volume at the PCR stage was 20 µl. Each reaction mixture has consisted of 2 µl DNA, 10X buffer 2 µl [10 mMTris – HCl pH 8.0, 50 mM KCl, 1.5 mM MgCl2], 2 µl dNTP (5 mM), 0.5 µl primer, 13.3 µl H_2O, and 0.2 Taq polymerase ferment (Table 3).

After the reaction was accumulated, the tubes were placed in a PCR apparatus (Gene Amp 9700 Applied Biosystems thermocycler). The polymerase chain reaction was initiated by denaturation of DNA at 94 ^{0}S for 3 minutes in an amplifier. It was executed of 35 cycles, consisting of 3 stages - 94 ^{0}S for 1 minute for denaturation, 40-60 ^{0}S for 45 seconds for combination of primer to DNA (it varies according to primer) and 72 ^{0}S for 5 minutes for elongation (Table 4).

TABLE 3. Composition of PCR mixture for ISSR method

PCR mixture	For 1 reaction (µl)	The density of acting solution
ddH_2O	13.3	-
PCR buffer	2.0	-
2 mM dNTP	2.0	2 mM
Primer	0.5	10 pmol/µl
Taq polymerase	0.2	1 U/µl
DNA	2.0	50 ng/µl
Total volume	20	-

TABLE 4. Cycles and duration of polymerase chain reaction

PCR temperature	Duration	Cycle
94 ^{0}S	3 min	1
94 ^{0}S Tm 72 ^{0}S	1 min 45 sec 1 min	35
72 ^{0}S	5 minutes	1

Electrophoretic analysis of PCR products was implemented in 2% agarose gel, the gel was stained with the addition of etidium bromide, and visualized under ultraviolet radiation using the Bio-Rad gel documentation system (Figure 1).

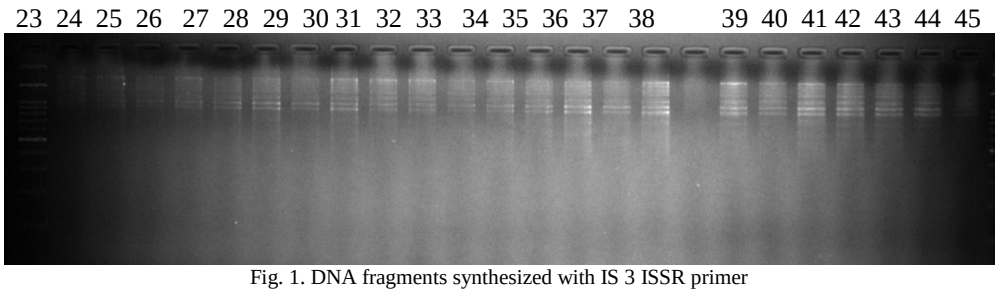

Fig. 1. DNA fragments synthesized with IS 3 ISSR primer

The analysis of the amplified fragments was conducted by the computer program PAST. A number of statistical parameters for the assessment of genetic diversity in the cherry collection, including genetic diversity index (GMI),

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polymorphic information capacity (PIC), effective multiplex coefficient (EMR), marker index (MI), Resolving power (Rp), Mean Resolving power (MRp) was calculated. Assessment of genetic similarity between samples and construction of a dendrogram was implemented on the basis of the Jaccard genetic similarity index, clustering was conducted by the UPGMA method.

III. Results and Discussion

As can be seen from Table 5, the length and width of cherry plant, stalk's length, fruit's weight, flesh's weight, length and width of stone, sugar content, leaf's parameter were researched.

TABLE 5. Biomorphological features and leaf parameters of cherry fruit

Samples	Fruit length (mm)	Fruit width (mm)	Stalk length (mm)	Stone weight(gr)	Flesh weight (gr)	Total sugar %	Stone length (mm)	Stone width (mm)	Mass of one fruit (gr)	Mass of 20 fruit (gr)	Leaf stalk length (mm)	Leaf length (mm)	Leaf width (mm)
G1	24,50	28,60	39,50	0,93	10,12	24,05	10,7	9,7	11,2	223,68	40	82,1	42,3
G2	21,40	25	35,5	0,75	7,13	18,1	8,6	9,7	7,58	151,6	39,8	85	41,6
G3	25,4	26,9	53,5	0,9	8,78	20	11,6	8,7	9,7	193,4	41,1	94,9	48,1
G4	18,3	19,8	44,6	0,56	3,6	25,5	9,4	8,4	4,18	83,76	37,7	89,4	40,5
G5	21,1	24,1	41,9	0,69	6,31	23,45	10	8,6	7,02	140	44	91,7	45,4
G6	21,6	26,1	36	0,75	7,06	19,3	10,1	9,2	7,83	156,76	39,7	90,2	43,5
G7	20,15	22,7	41,5	0,48	5,77	18,05	9,8	8,8	6,25	125	41,15	81	33,1
G8	26,6	24,7	35,8	0,49	6,39	20,35	10	9	6,94	138,8	42,3	94,5	39,8
G9	23,5	24,1	44,3	0,82	7,01	17,7	11,2	8,7	7,86	157,26	42,1	95,2	40,1
G10	21,4	25,2	31,4	0,5	6,78	23,45	8,2	8	7,27	145,4	32,9	74	41
G11	21,6	22,9	43,7	0,49	6,59	16,65	9	9	7,08	141,6	39,2	72,7	31,4
G12	19,9	22,1	42,2	0,66	4,44	19,9	10,4	9,2	5,14	102,7	42,6	99,7	45,1
G13	14	14,5	41,2	0,27	25,2	12,8	5,9	5,9	2,79	55,8	37,2	82,1	31,7
G14	20,9	18,8	35,9	0,57	5,68	13,05	7,9	7,9	6,24	124,8	35,4	84	32
G15	20,6	18,1	54	0,55	6,46	18,45	8,3	7,5	6,99	139,8	49,3	90,1	32,4
G16	18,5	21,1	32,1	0,43	5,14	18,6	7,7	8	5,58	111,6	40	80,6	33,1
G17	21	22,3	45,2	0,66	5,5	20,6	10,3	8,7	6,2	124,12	50,6	103,6	50,6
G18	17,6	16,4	40,9	0,47	5,6	22,75	6,88	6,9	6,07	121,4	37,1	79,5	31,9
G19	17	19	37,4	0,41	4,95	16,2	7,4	6	5,36	107,2	29,7	64,4	27,8
G20	18,4	20,8	38	0,55	6,29	18,85	8,8	8,5	6,82	136,4	34,7	76,7	34,2
G21	21,5	24,3	34,8	0,6	6,39	22,1	9,7	9,5	6,97	139,4	36,2	90,7	38,2
G22	17,8	21	31,7	0,44	5,19	20,15	7,9	7,9	5,62	112,4	37	104,3	34,6
G23	11,5	11,9	51,5	0,3	1,58	13,2	6,8	6,9	1,88	37,6	37,8	76,5	32,3
S1	18,9	19,9	40,5	0,5	5,5	13,5	9,6	6,8	6	119,82	37,4	63,7	44,7
S2	12,1	12,1	46,4	0,22	4,16	12	6,4	5,7	4,46	89,2	37,2	75,2	33,6
S3	19,7	20,6	50,6	0,6	6,05	20,4	9	6	6,5	130	40,6	94	46,6
S4	15,7	23,9	56	0,6	4,2	22,3	8,2	6,3	4,8	96,76	42	120	51,5
S5	15,1	15,8	55,5	0,29	3,08	23,1	7,5	5,8	3,4	67	44	98,5	49,9
S6	16,8	13,8	57,4	0,4	2	23,8	9,5	6	2,4	48,9	32,8	86	54,3
S7	20,7	20,6	37,1	0,68	8,3	21,2	10	9,6	8,98	179,6	36,88	85,1	44
S8	20,8	20,4	51,5	0,4	5,9	18,1	8,7	6,9	6,4	128	46	122	60
S9	19,2	19,7	47,5	0,4	5,3	19	9,1	6	5,72	114,4	37	110,5	49,5
S10	15,6	16,5	52,5	0,43	3,14	11,3	7,9	6,9	3,9	78	38,5	108	40
S11	20,9	23,9	41	0,5	8,9	17,9	7	8,6	9,4	188	39	114	55
S12	17,3	19,5	53	0,5	4,8	14,5	6,6	7,9	5,3	107,1	38,7	114,5	63,5
S13	20,5	19,7	51,5	0,48	6,15	18,1	6,5	9,8	6,6	132,7	33,4	109	42
S14	15,5	18,6	56,8	0,36	3,9	15	8	6,3	4,27	85,4	41,5	121	68,3
S15	18,2	18,4	31	0,5	6,85	25,3	7,9	7,75	7,35	147	30,4	87,9	44,1
S16	16,7	15,6	46,3	0,3	3,3	14,8	6	9,6	3,7	74	52	121	51,5
S17	15,6	16,4	51,2	0,4	3	16,4	7	8,8	3,27	65,4	37,5	71	42,5
S18	22	24,9	55,5	0,5	8,6	18,8	6,9	9,4	9,1	182	31	98,5	52,8
S19	15,2	15,1	52,2	0,42	6,15	18	6,19	6,17	6,57	131,4	36,5	81,8	41,4
S20	15,1	19,5	41	0,45	4,17	15,5	6,7	6,4	5,1	102	33,8	79	52
S21	20,8	18,6	35,3	0,6	4,5	12,3	9,5	7,6	5,07	101,38	43,8	119	65,5
S22	13,8	16	53	0,4	2,9	20,4	6,2	6,5	3,3	66	30	107,5	48,5
S23	14,2	14,4	48,2	0,35	5,62	18,1	6,3	6,2	5,97	119,4	34,7	77,9	41,9
S24	14,7	14,7	41,8	0,42	5,09	12,65	6,1	5,7	5,51	110,2	37,9	90,4	41,2
S25	20,3	16,3	50,1	0,57	7,07	20,3	10,6	8,8	7,62	152,6	33,5	81,4	40,2
S26	18,3	18,2	63,3	0,4	4,4	25,8	6,5	8,5	4,8	95	38,5	98,5	51,5
T1	25,3	27,3	32	0,66	7,62	24,4	9,3	9,7	8,28	165,6	42,1	91,8	33,5
T2	16,4	11,7	51,1	0,56	4,8	15,1	9,3	5,9	5,36	107,2	36,5	75,8	40,1
T3	16,5	16,5	35,4	0,46	5,81	18,65	7,8	6,7	6,27	125,4	33,1	89,8	32,1
T4	25,7	23,7	34,7	0,64	8,41	21,6	10,3	9,6	9,05	181	33,5	90,3	38,6
T5	7,6	7,3	30,2	0,28	1,54	13,6	5,6	5,9	1,82	36,4	33,8	80,9	37,7

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T6	17,4	15,9	50,7	0,45	5,99	18,65	7,9	7,4	6,44	128,8	37,5	80,6	35,3
T7	19,9	21,2	40,4	0,64	6,98	22,3	8,5	8,8	7,6	152	30	86,7	34,1
T8	15,9	15,4	45,8	0,48	6,18	20,8	7,9	7,5	6,7	134	33,6	80,6	36,5
A1	15,1	14,8	40,4	0,14	5,23	15,3	6,5	6,6	5,63	112,6	33	85	37,6
A2	18,4	17,7	51,9	0,56	6,85	21,1	8,1	8,1	7,4	148	37,2	88,5	37,9
A3	16,2	16,7	43,5	0,42	6,07	18,55	8,3	7,9	6,49	129,8	38,2	80,4	39,3
A4	20,5	23,8	29,9	0,63	8,87	22,1	10,4	9,7	9,5	190	39,2	95,7	51,3
K1	22,7	23	44,6	0,73	6,68	15,6	11	8	7,41	148,2	33,8	82,7	38,7
K2	23,8	25,4	47,5	0,77	7,1	15,05	10,8	8,7	7,87	157,4	34,9	93,3	43,7
K3	21	24,1	43,5	0,73	5,18	16,3	11	8,4	5,91	118,2	38,1	98,6	42,7
K4	29,4	21,2	24,3	0,61	6,92	12,05	10,2	8,3	7,53	150,6	40,6	97,3	42,7
K5	20,8	24,7	55	0,77	7,37	12,4	11,1	9,8	7,99	158,8	36,8	92,2	43,4
K6	23,9	25,9	40,5	0,82	7,81	12,9	10,6	8,5	8,63	172,6	42	92,7	46
K7	22	23	50	0,67	7,96	13	10	8	8	172	39,6	92,1	47,9
K8	21,7	22,5	48,1	0,67	8,43	14,4	10,2	9,7	9,1	182	40,2	90,2	41,8
K9	10,7	11,3	42,8	0,21	0,8	26,9	7,9	9,9	1,01	20,2	33,7	71,6	38,1
K10	28,8	18,2	41,1	0,66	3,22	13,2	10,9	7,8	3,85	77	33,4	91	47,3
K11	23,51	22	48,2	0,65	6,25	17	12,6	8,5	6,9	138	39,8	85,7	45,1
K12	21	21	37	0,61	5,54	16	10	8	6	128	42,9	88	50,4
K13	20,2	22,4	54,6	0,74	5,24	11,9	11,7	8,9	5,96	119,2	36	86,3	46,2

The length of the fruit was between 7.6-29.4 mm, depending on the sorts. The highest indicator was observed in Agh gilas (K4) sort, and the lowest indicator was observed in Yabani gilas Antipka sort.

The dimensions of width of the fruit were different. Jir gilas (K9) sort had the lowest index of 11.3 mm, and Samba sort had the highest index of 28.6 mm.

Fruit's stalk. Along with other parameters, the length of the stalk of fruit was also researched. These sizes were 30.2 - 63.3 mm. The shortest stalk has been found in the Yabani gilas Antipka sort, and the longest stalk in the Kuzugoren gilas sort.

The weight of the fruit. The weight of the fruit has been measured with an electronic scale having a sensitivity of 0.01 g. The weight of fruit was between 1.01-11.2 grams. Thus, the smallest weight was observed in the Jir gilas (K9) sort, and the highest weight was observed in the Samba sort.

Total sugar. Along with the productivity of sorts, the study of their quality indicators is of great importance. For this purpose, the percentage of total sugar in the juice was researched to identify the quality of the studied sorts. The amount of sugar in cherry was determined by hand refractometer (Brix, 0-32%). As can be seen in Table 5, the highest sugar content was in the Jir gilas (K9) sort (26.9%) and the lowest in the Kahraba gilas sort (11.3%).

Genetic Analysis

A total of 68 bands were synthesized on 8 primers in the researched cherry genotypes. 47 (69.1%) were polymorphic and 21 (30.9%) were monomorphic. The number of amplified fragments was between 7-10. The length range of the obtained fragments was between 100-1200 n.c. The number of bands for every primer is 8.5.

Maximum number of amplicones (10) has been synthesized with IS 50 and IS 54 primers. Eight of the amplicones synthesized by the IS 50 primer were polymorphic. In the IS 54 primer, 5 of the synthesized bands were polymorphic and the other 5 were monomorphic. The lowest number of amplicons was observed in the IS 3 and IS 48 primers (7 amplicons). Four of the amplicones in the IS 3 primer are polymorphic. In the IS 48 primer, 5 of the synthesized bands were polymorphic. The number of polymorphic bands was between 4-8 and averaged 5.9.

As can be seen from Table 6, the polymorphism index for primers was between 50 to 89%, with an average polymorphism of 69.4%.

The UBC 868 ISSR primer has demonstrated the highest polymorphism in cherry genotypes, being polymorphic in 8 of the 9 amplicons recorded. Polymorphism was 89%. The length of the amplicones was between 400-1200 n.c.

TABLE 6. Dimensions of polymorphism and genetic diversity in cherry genotypes with ISSR primers

Primers	Sequence of primer	Number of synthesized fragments	PFS	Rp	PIC	EMR	MI	MRp	Polymorphism,%	GMİ
IS 2	$(GA)_9C$	9	6	5,56	0,33	6,75	2,2	0,02	70	0,96
IS 3	$G(TG)_9$	7	4	7,46	0,41	4,1	1,6	0,02	57	0,85
IS 37	$(CA)_8GT$	8	6	5,00	0,33	5,6	1,7	0,03	75	0,94
IS 47	$(ACC)_6$	8	5	6,30	0,41	5,6	2,3	0,02	62,5	0,91
IS 48	$(ATG)_8$	7	5	5,16	0,43	4,2	1,7	0,03	71,4	0,93
IS 50	$(GAA)_6$	10	8	7,34	0,45	8,0	3,6	0,01	80	0,97
IS 54	$(AG)_8C$	10	5	8,34	0,41	8,0	3,3	0,01	50	0,93
UBC 868	$(GAA)_6$	9	8	4,46	0,32	6,8	2,0	0,03	89	0,89
Total	-	68	47							
Average value	-	8,5	5,9						69,4	0,92

The genetic diversity index (GMI) was calculated for each ISSR locus during research. The average price of GMI for the collection we studied was 0.92 units. The high indicators were 0.97 and 0.96 units. It was obtained with the IS 50 and IS 2 primers. The high value of GMI indicates the fertile genetic diversity of cherry sorts from different regions of Azerbaijan.

It is known that for dominant markers such as ISSR, the PIC index is between 0-0.5. For the 8 primers used in the

Kh.I. Karimova, "Research of Farm Indicators of Sweet Cherry (Prunus avium L.) Plant Existed in Azerbaijan and Determination of Genetic Diversity by Means of ISSR Markers," *International Research Journal of Advanced Engineering and Science*, Volume 6, Issue 3, pp. 238-244, 2021.

study, the PIC index was 0.32 - 0.45. It averaged 0.39 units. The lowest value of the PIC index for UBC 868 primer, and the highest value for the IS 50 primer were determined. MI and EMR parameters are key indicators of the informativeness of marker systems and are calculated separately for each primer. In the collection, the MI parameter was between 1.6-3.6 and the EMR was between 4.1-8.0, and avarage indicators were 2.3 and 6.1, respectively. Primers with a high number of polymorphic fragments were characterized by higher values of EMR and MI.

Resolving power (Rp) is a parameter that identify the discrimination potential of primers. For all locus studied, Rp has varied between 4.46-8.34. Average value was 6.2. Middle Resolving power (MRp) has varied 0.01 - 0.03.

Ivanovych et al. (2016) It was researched genetic diversity in 24 cherry genotypes of Ukraine using 8 ISSR primers. 193 amplicones were synthesized in the ISSR analysis. The level of polymorphism was 75%. As a result of the study, the highest polymorphism level for the UBC 881 ISSR primer was 91.6% [8].

Ganopoulos et al. It was conducted research work on 19 Greek cherry genotypes using 10 ISSR primers. 91 alleles were synthesized by these primers. UBC 811, 822, 834 and 881 primers has been noticed to be more polymorphic compared to the other 6 primers. The polymorphism level for the UBC 881 primer was 64.2%. For 10 ISSR primers, the polymorphism level was 57.7% [4].

Roghayeh Najafzadeh and others have implemented research work on 12 cherry genotypes cultivated in Iran by using 23 ISSR primers. As a result, 489 amplicones were synthesized. The percentage of middle polymorphism for all genotypes was 98.45%. ISSR has demonstrated the highest polymorphism in 6, 13, 14, 19 primers [6].

Shahi-Gharahlar and others have conducted research work on genotypes of the genus Prunus with 12 ISSR. These primers have synthesized 156 alleles, and polymorphic alleles have varied between 9 - 19. The polymorphism was 96.46% [1].

To determine the relationship between the local cherry sorts and forms of Azerbaijan, a cluster analysis has been implemented on the basis of ISSR profiles and a dendrogram has been compiled. Genotypes have been grouped into 8 main clusters (Figure 2). The genetic similarity index between the samples was 0.017 - 0.929. The largest genetic distance was identified between Ala gilas (Agdash) and Agh gilas (Sheki) sorts, the genetic similarity index between noticed samples was 0.017 units. Minimum genetic similarity was observed between Albalı gilas and Sari gilas cultivated in Sheki, the genetic similarity index between sorts was 0.929 units.

The number of genotypes in the clusters has varied between 1 - 49. The largest 3rd cluster contains 66% of the genotypes. In addition, 2 free clusters were determined in the dendogram. Agh gilas and Ala gilas sorts were formed free clusters. This shows that they are genetically different from all other samples of the collection. In addition, all 4 genotypes included in the 6th cluster were determined organization from Tartar sorts.

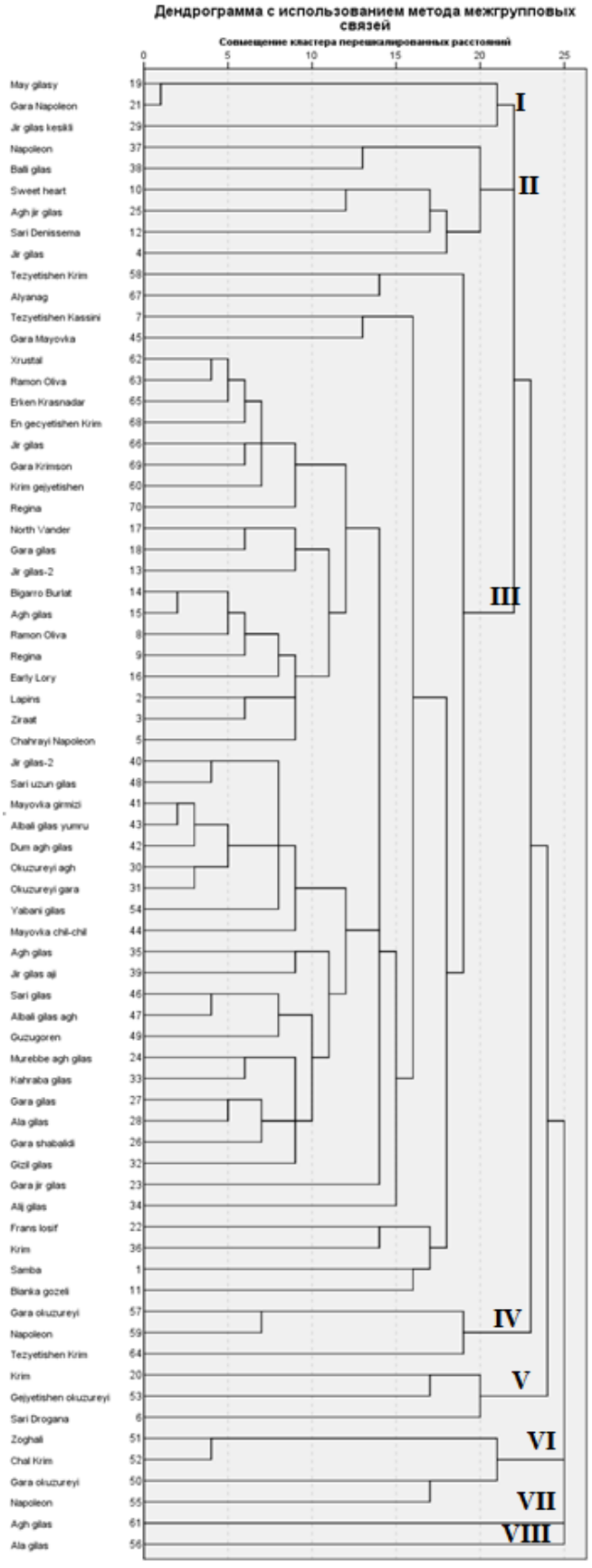

Fig. 2. A dendrogram demonstrating the genetic relationship between cherry genotypes

Kh.I. Karimova, “Research of Farm Indicators of Sweet Cherry (Prunus avium L.) Plant Existed in Azerbaijan and Determination of Genetic Diversity by Means of ISSR Markers,” *International Research Journal of Advanced Engineering and Science*, Volume 6, Issue 3, pp. 238-244, 2021.

The grouping of these sorts in one cluster indicates that they have a similar set of alleles according to intermicrosatellite locus studied. At the same time, genetic diversity were significantly identified between some sorts from the same region. For example, Sari Denissema considered as one of the 3 sorts from the same region is located in the second cluster, and the Regina and Early Lory sorts are located in different subclusters of the same cluster. Genetic distance index between them was 0.609.

IV. CONCLUSION

Thus, as a result of the research of cherry sorts and forms from 5 different regions of Azerbaijan by molecular marker technology, the effectiveness of ISSR markers in the assessment of genetic diversity and genetic relationship was approved. Fertile genetic diversity determined in the collection demonstrates that Azerbaijan is one of the centers of cherry cultivation. The obtained results can be used in planning of research for the accumulation of genetic resources of cherry and in different selection programs.

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