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ORIGINAL ARTICLE / ORIGINALBEITRAG

Genetic Characterization and Conservation of Grapevine Germplasms in Kayseri Province of Turkey

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Abstract
Turkey is within the region where the viticulture has been traditionally practiced since ancient times. The Cappadocia location, including the province of Kayseri, is an important grape production area with its autochthonous grape cultivars and unique tradition in history. Due to viticulture history, this region is rich in vine genetic resources. This survey study was carried out in vineyards areas and residential gardens in 23 different regions of Kayseri province between 2017 and 2019. A total of 174 local genotypes from different locations were determined and were further examined through molecular characterization with SSR markers. A total of 112 bands were amplified by 12 SSR primers, all of which were polymorphic with a 100% polymorphism. The highest number of polymorphic bands (18) was produced by the primer Scu8vv, while the lowest number of polymorphic bands (3) was found in VMC8D3 and VMC8E6. An UPGMA dendrogram was created via scoring the bands and the genetic similarity between the genotypes was determined between 0.63–1.0. In conclusion, a wide range of genetic diversity was determined in grapes of Kayseri indicating an ancient residential germplasm collection that could be used for breeding studies.

Keywords Genetic Resources · Grapevine · SSR marker · Kayseri

Genetische Charakterisierung und Erhaltung genetischer Ressourcen von Weinreben in der türkischen Provinz Kayseri

Schlüsselwörter Genetische Ressourcen · Weinrebe · SSR-Marker · Kayseri

Introduction

Turkey, as a cradle and domestication ecosystem of many plants (Tan 2010), also has a rich grapevine germplasm (Sabir 2008). Local varieties and populations are valuable because they are highly adaptable to their ecological conditions, resist diseases and pests, and carry much quality feature such as taste, color, odor, and size. By using plant genetic materials, new genotypes with high quality and resistance to many adverse conditions such as diseases and pests, salinity, drought, and current biotic-abiotic stress factors can be developed (Yılmaz et al. 2012). Plant genetic resources are indispensable for the breeding of new varieties that can adapt to increasing human population, changing climate and environmental conditions (Karagöz et al. 2020).

Turkey with its unique autochthonous grape varieties and types offer a wealth of genetic resources that can be used in breeding programs in terms of viticulture (Sabir 2008). Identification of grapevine genetic resources first started with using ampelographic descriptors. Today, with the investment of molecular marker techniques, plant genetic resources have been characterized at the genetic level, and both methods are used to complement each other. SSR markers have come to the forefront due to their robust features in identification of varieties, determination of kinship relations, identifying parental statutes, revealing the homonymous or synonymous genotypes and enabling

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comparison of international information (Tekdal and Sarlar 2016).

Located in the middle of Turkey, Kayseri is a famous city possessing a long history of traditional viticulture with authentic "Gesi Vineyards" and "Erkilet Vineyards". As a micro gene center for grapevines, the city has a wide range of grape genetic diversity with autochthonous hybrids and mutants that have gained well adaptation over many years. However, due to environmental and social adversities such as climate changes, urbanization, especially the old vineyards close to the settlement centers are dismantled. Many viticulture areas have been damaged with housing and industrial constructions. Therefore, the cultivation of local grape varieties belonging to Kayseri is decreasing day by day and it will be inevitable that these valuable genetic resources will be lost in the near future if they are not protected. Today, it has been imperative to determine the genetic resources we have using correct and reliable methods and to nomenclature and protect them correctly.

The aim of this study was the molecular characterization of local grape gene sources grown in Kayseri province, Turkey and their relationships with some standard varieties.

Material and Methods

Plant Materials

In this study, 174 local grape genotypes were collected from 23 different locations (Garipçe, Bedir, Hamurcu, Süksün, Develi, Yeşilhisar, Yahyalı, Özvatan, Bünyan, Sarıoğlan, Pınarbaşı, Sarız, Talas, Hacılar and Tomarza, Yuvalı, Yüceyar, Erkilet, Gesi, Hisarcık, Kızıltepe, Eğribucak and Mimsin) including the villages of Kayseri. In addition, 8 standard grape cultivars ('Sultani', 'Akdimrit', 'Tarsus Beyazı', Karadimrit', 'Trakya İlkeren', Alphonse Lavelle', '41B'-rootstock-, 'Wild' -collected from Turkey-) were used for logical comparison. Cluster and fruit variations of some grape genotypes are presented in Fig. 1, and the studied

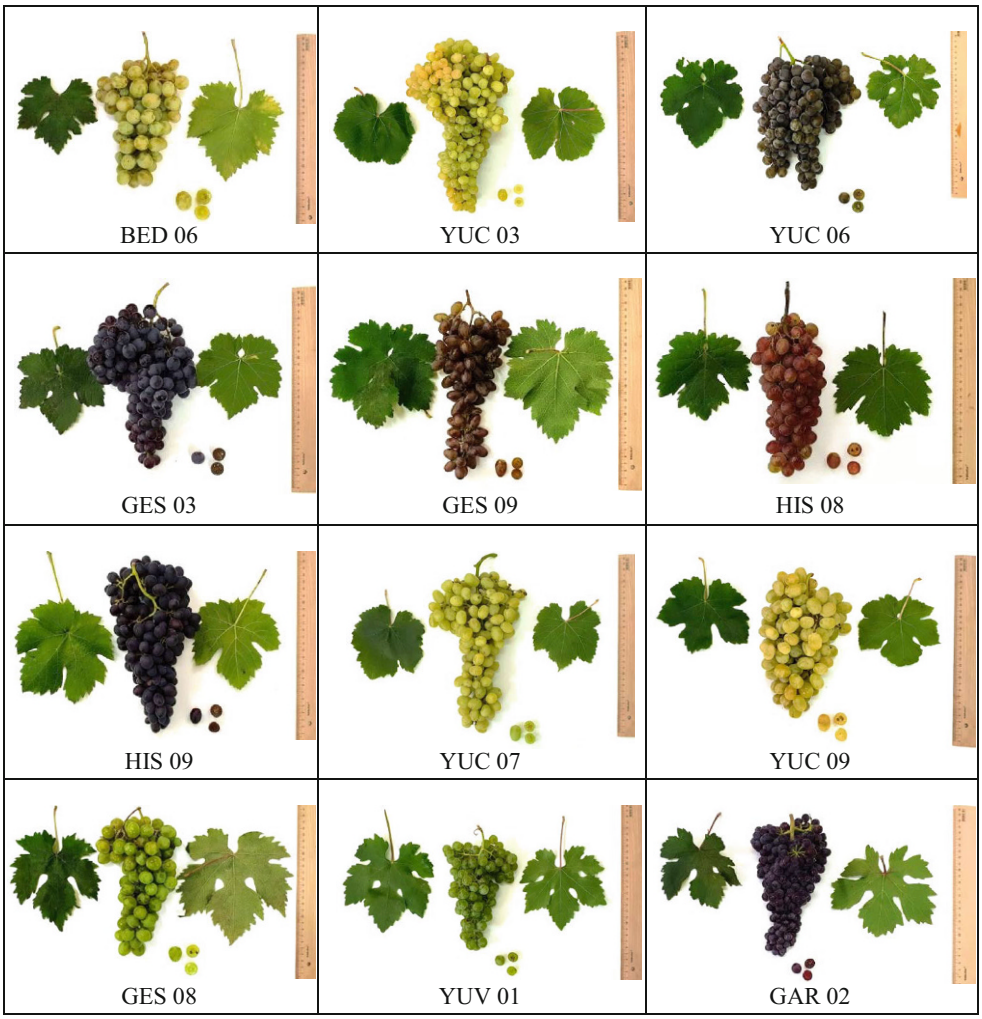

Fig. 1 Cluster and berry variations in some grapevine genotypes

Table 1 The studied genotypes and their geographical origins

Origin	Genotype	Origin	Genotype	Origin	Genotype	Origin	Genotype	Origin	Genotype
Bedir	(1)BED 01	*Garipçe*	(39)GAR 01	*Hamurcu*	(168)HAM 01	*Mimsin*	(96)MIM 01	*Yüceyar*	(147)YUC 01
	(2)BED 02		(40)GAR 02		(169)HAM 02		(97)MIM 02		(148)YUC 02
	(3)BED 03		(41)GAR 03		(170)HAM 03	*Özvatan*	(98)OZV 01		(149)YUC 03
	(4)BED 04		(42)GAR 04		(65)HAM 04		(99)OZV 02		(150)YUC 04
	(5)BED 05		(43)GAR 05		(66)HAM 05		(100)OZV 03		(151)YUC 05
	(6)BED 06		(165)GAR 06		(67)HAM 06		(101)OZV 04		(152)YUC 06
	(7)BED 07	*Gesi*	(44)GES 01		(68)HAM 07		(102)OZV 05		(153)YUC 07
	(8)BED 08		(45)GES 02		(69)HAM 08		(103)OZV 06		(154)YUC 08
Bünyan	(9)BUN 01		(46)GES 03		(70)HAM 09		(104)OZV 07		(155)YUC 09
	(10)BUN 02		(47)GES 04		(71)HAM 10		(105)OZV 08		(156)YUC 10
Develi	(11)DEV 02		(48)GES 05		(171)HAM 11		(106)OZV 10		(157)YUC 11
	(12)DEV 03		(49)GES 06		(72)HAM 12		(107)OZV 11		(158)YUC 12
	(13)DEV 04		(50)GES 07		(73)HAM 13		(108)OZV 12		(159)YUC 13
	(14)DEV 06		(51)GES 08		(74)HAM 14		(109)OZV 13		(160)YUC 14
	(15)DEV 07		(52)GES 09		(75)HAM 15		(110)OZV 14		(161)YUC 15
	(16)DEV 08	*Hacılar*	(53)HAC 01		(76)HAM 16		(111)OZV 15		(162)YUC 16
	(17)DEV 09		(54)HAC 02		(77)HAM 17	*P.başı*	(112)PIN 01		(163)YUC 17
	(18)DEV 10		(55)HAC 03	*Hisarcık*	(78)HIS 01	*Süksün*	(115)SUK 01		(164)YUC 18
	(19)DEV 11		(56)HAC 04		(79)HIS 02		(116)SUK 02	*S.oğlan*	(166)SAR 01
	(20)DEV 12		(57)HAC 05		(80)HIS 03		(117)SUK 03		(167)SAR 04
E.Bucak	(21)EG 01		(58)HAC 06		(81)HIS 04		(118)SUK 04	*Sarız*	(113)SRZ 01
	(22)EG 05		(59)HAC 07		(82)HIS 05		(119)SUK 05		(114)SRZ 02
	(23)EG 06		(60)HAC 08		(83)HIS 06		(120)SUK 07	*Control*	(173)'Sultani'
	(24)EG 07		(61)HAC 09		(84)HIS 07		(!21)SUK 08		(174)'Akdimrit'
	(25)EG 08		(181)HAC 10		(85)HIS 08		(122)SUK 09		(175)'T.Beyazı'
	(26)EG 09		(62)HAC 11		(86)HIS 09		(123)SUK 10		(176')K.dimrit'
	(27)EG 10		(182)HAC 12	*Kızıltepe*	(87)KIZ 01		(124)SUK 11		(177)'T.Ilkeren'
Erkilet	(28)ERK 01		(172)HAC 13		(88)KIZ 02		(125)SUK 12		(178)'Alfonse'
	(29)ERK 02		(63)HAC 14		(89)KIZ 04		(126)SUK 13		(179)'Wild'
	(30)ERK 03		(64)HAC 15		(90)KIZ 05		(127)SUK 14		(180)'41B'
	(31)ERK 04	*Yahyalı*	(134)YAH 01		(91)KIZ 06	*Talas*	(128)TAL 01		
	(32)ERK 05		(135)YAH 02		(92)KIZ 07		(129)TAL 02		
	(33)ERK 06		(136)YAH 03		(93)KIZ 08		(130)TAL 03		
	(34)ERK 07		(137)YAH 04		(94)KIZ 10	*Yuvalı*	(142)YUV 01		
	(35)ERK 08		(138)YAH 05		(95)KIZ 11		(143)YUV 02		
	(36)ERK 09	*Y.Hisar*	(139)YES 02	*Tomarza*	(131)TOM 01		(144)YUV 03		
	(37)ERK 10		(140)YES 03		(132)TOM 02		(145)YUV 04		
	(38)ERK 11		(141)YES 04		(133)TOM 03		(146)YUV 05		

genotypes and their geographical origins are listed in Table 1.

DNA Isolation

The method called "minipreparation" modified from Doyle and Doyle (1990) was performed using young leaves of genotypes. For DNA isolation, CTAB buffer solution (100 mM Tris-HCl, 1.4 M NaCl, 20 mM EDTA, 2% CTAB, 2% PVP, 0.1% Na_2SO4), chloroform: isoamyl alcohol (24: 1) mixture, cold isopropanol, ammonium acetate and TBE solution (10 mM Tris, 1 mM EDTA, pH: 8.0) was used.

PCR Conditions

PCR components and cycle were programmed according to the protocol modified from Uzun (2009), (1.5 µl 10X PCR buffer, 1.33 mM forward and reverse primer, 200 µM each dNTP (dATP, dGTP, dCTP and dTTP), 2.5 mM $MgCl_2$, 0.2 µg/µl BSA (Bovine serum albumin), 1 unit of taq DNA polymerase enzyme, 20 ng DNA, 4.3 µl ddH_2O).

Table 2 SSR primer pairs and their sequences used in the study

No	Primer Code	Forward (F) and reverse (R) primers
1	Scu8vv	F: CGAGACCCAGCATCGTTTCAAG R: GCAAAATCCTCCCCGTACAAGTC
2	Scu10vv	F: TACCCCCACAACCCTTTT R: TTCTCCGCCACCTCCTTTTCAC
3	VVMD21	F: GGTTGTCTATGGAGTTGATGTTGC R: GCTTCAGTAAAAAGGGATTGCG
4	VVMD36	F: GAAAATTAATAATAGGGGGACACGGG R: GCAACTGTAAAGGTAAGACACAGTCC
5	VrZAG64	F: TATGAAAGAAACCCAACYCGGCACG R: TGCAATGTGGTCAGCCTTTGTGGG
6	VrZAG79	F: AGATTGTGGAGGAGGGAACAAACCGR R: TGCCCCCATTTTCAAACTCCCTCCC
7	VMC8A4	F: TCATGAATAGCCCCTGGAAGAG R: TGAAGGATGGAGATGGGAAGAG
8	VMC8B5	F: AAAGGAGACATCTGCATCAT R: GCCTTGATCTTCCTTCTAAT
9	VMC8C2	F: AAGGAATTTGGATACTGAAGGT R: TGAAGACATCTACGTAGGTGAA
10	VMC8D3	F: TGGCAAGACACAATAAAACAGA R: ATAGAGTCCTGCAAATCCAAGA
11	VMC8E6	F: AAGGGGTTCATTTGATTGAGAG R: CTTCATCCATCCTTACAGCTTAGA
12	VMC8G6	F: TCAGTAATCACGAGCTTCCCG R: TGGAGTGGGGATATGGAAATG

Amplification protocol was 1 cycle of denaturation for 2 min at 94 °C; 1 min at 94 °C; 1 min at 48 °C; 1 min at 72 °C; for an extension of total 38 cycles; and the final extension at 72 °C for 7 min. PCR products were loaded to 2% agarose gel stained with ethidium bromide (EtBr) in 1 X TBE (89 mM Tris, 89 mM Boric acid, 2 mM EDTA) and electrophoresed under 110 volts for 4–5 h. In electrophoresis processes, 100 bp DNA ladder was used as standard and the bands were visualized under UV light.

SSR Analysis

PCR-based SSR molecular marker technique was used to determine genetic similarities between local grape genotypes. Six SSR primers reported by Halasz et al. (2005) (Scu8vv, Scu10vv, VVMD21, VVMD36, VrZAG64, VrZAG79) and 6 standard SSR primers (VMC8A4, VMC8B5, VMC8C2, VMC8D3, VMC8D3, VMC8D3) reported by This et al. (2004) were used (Table 2).

Statistical Analysis

Electrophoresis gel bands were evaluated by giving the number in the band presence (1), band absence (0) and amplification absence (9). These data were analyzed in NTSYS [Numerical Taxonomy Multivariate Analysis System, NTSYS-pc version 2.1, Exeter Software, Setauket, N.Y., USA], (Rohlf 2000) computer package program. Similarity indices were calculated according to the Dice (1945) method and dendrograms were created according to the UPGMA (Unweighted Pair-Group Method with Arithmetic Average) method. The principal components analysis (PCA) of the original binary data matrix was also performed using NTSYS-pc version 2.1. The GenAlEx ver. 6.5 program was employed to determine allele frequency (p and q), no of effective alleles (Ne), Shannon's information index (I), expected (He) and unbiased expected heterozygosity (uHe) (Peakall and Smouse 2012).

Results

A total of 112 bands were obtained from 12 SSR primers among 184 grape genotypes, comprising 174 local genotypes and 10 reference varieties. A high level of genetic variation was revealed among the studied genotypes. All the genotypes were necessarily distinguished from each other with a 100% polymorphism rate. The highest number of polymorphic bands (18 bands) was obtained from the primer Scu8vv, while the lowest number of polymorphic bands (3 bands) was generated from the primers VMC8D3 and VMC8E6, with the average band number of 9.33 (Table 3). The genetic similarity between the genotypes ranged from 0.63 (GES 09) to 1.0 (HIS 06 and OZV 02).

Table 3 Polymorphism table of SSR primers in the study

Primers	Total number of bands	Number of polymorphic bands	Polymorphism rate
Scu8vv	18	18	100
Scu10vv	10	10	100
VVMD21	6	6	100
VVMD36	12	12	100
VrZAG64	7	7	100
VrZAG79	9	9	100
VMC8A4	11	11	100
VMC8B5	10	10	100
VMC8C2	13	13	100
VMC8D3	3	3	100
VMC8E6	3	3	100
VMC8G6	10	10	100
Total	*112*	*112*	*100*
Average	*9.33*	*9.33*	*100*

Table 4 SSR primers studied, their estimated allele frequency (*p* & q), no of effective alleles (Ne), Shannon's information index (I), expected (He) and unbiased expected heterozygosity (uHe)

Primers	*p*	q	Ne	I	He	uHe
VMC8A4	0.183	0.817	1.369	0.362	0.228	0.230
VVMD36	0.224	0.776	1.270	0.323	0.192	0.193
VVMD21	0.320	0.680	1.139	0.207	0.110	0.110
VMC8E6	0.663	0.337	1.336	0.400	0.242	0.244
VrZAG64	0.314	0.686	1.354	0.332	0.212	0.213
Scu8vv	0.142	0.858	1.264	0.298	0.177	0.178
VMC8D3	0.456	0.544	1.323	0.312	0.194	0.195
VrZAG79	0.220	0.780	1.285	0.309	0.187	0.188
VMC8G6	0.176	0.824	1.268	0.293	0.177	0.178
Scu10vv	0.338	0.662	1.408	0.392	0.251	0.253
VMC8B5	0.183	0.817	1.293	0.280	0.176	0.177
VMC8C2	0.311	0.689	1.298	0.306	0.190	0.191
Average	*0.294*	*0.706*	*1.300*	*0.317*	*0.194*	*0.195*

Values for effective alleles (Ne) ranged from 1.139 (VVMD21) to 1.408 (Scu8vv) (average 1.30), for Shannon's information index (I) from 0.207 (VVMD21) to 0.392 (Scu8vv) (0.317), for expected heterozygosity (He) from 0.110 (VVMD21) to 0.251 (Scu10vv) and for unbiased expected heterozygosity (uHe) from 0.110 (VVMD2) to 0.253 (Scu10vv) (average 0.195) (Table 3). For all these parameters, Scu10vv primer had the highest value whereas VVMD21 had the lowest value. (Table 4).

In the dendrogram obtained, 2 groups were formed, and the first group included the GES 09 (Parmak Buludu collected from Gesi) genotype alone, while the second group included other genotypes (Fig. 2). Again, the 2nd group was further divided into 2 subgroups, there are many subgroups in the second subgroup that covers the majority of the genotypes, and some genotypes are distributed throughout the dendrogram. Since the reference genotypes in the study are of Turkish origin, it was determined that they did not form a separate group from the local genotypes. According to the dendrogram, the genetically most distant genotype was GES 09 (Parmak Buludu collected from Gesi) genotype, while the closest genotypes were HIS 06 (Siyah Keçimemesi collected from Hisarcik) and OZV 02 (Beyaz Keçimemesi collected from Ozvatan).

On the dendrogram, there were close groupings according to the berry colors, berry shape and local names. It has been determined that the broadest groupings are among the green-yellow colored genotypes according to the berry skin color. Genotypes with white berries such as Devedisi, Gogcek, Karaburcu, Karabekir, Beyaz Sıralık, Eldas and Sungurlu were located in close groups. Another reason for such genotypic closeness might also be associated with their round shaped berries. It was determined that local genotypes named Buludu, which have three different colors (black, white and gray), form a wide grouping in the dendogram, but this grouping is based on grain shape rather than grain color.

Another important grouping was seen in genotypes known by villagers with the local same name Buludu. It is noteworthy that the Buludu genotypes collected from different regions (YUC 06, HAC 06, OZV 01, HAM 06, KIZ 02, ERK 01, and EG 10) constructed close groups in

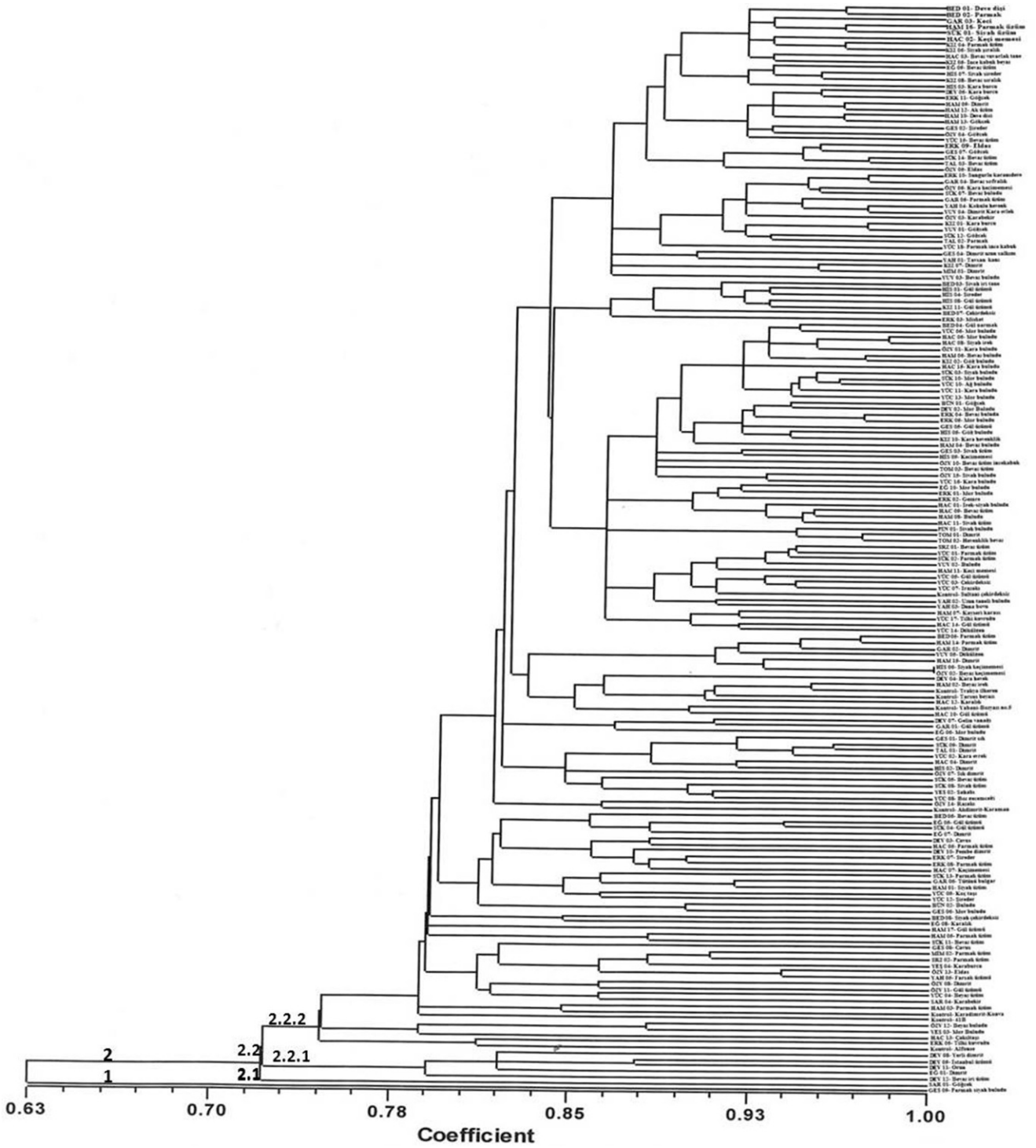

Fig. 2 Dendrogram of Kayseri local grapevine genotypes obtained from SSR data

dendrogram, indicating their associate genetic background. It has been suggested that the unique clustering structure of Buludu genotypes could be emerging from their spherical berry shape. On the other hand, the genotypes HAC 08 and HAC 01 called as Siyah Irek by distinct growers could also be a synonymous one of the Buludu group according to their clustering results on dendrogram and certain associate amphelographic attributes.

Close groupings were also found among the Dimrit genotypes gathered from different regions such as GES 01, SUK 09, TAL 01, HAC 04, HIS 02, and OZV 07 in the study. Similarly, Gül Üzümü established close clustering

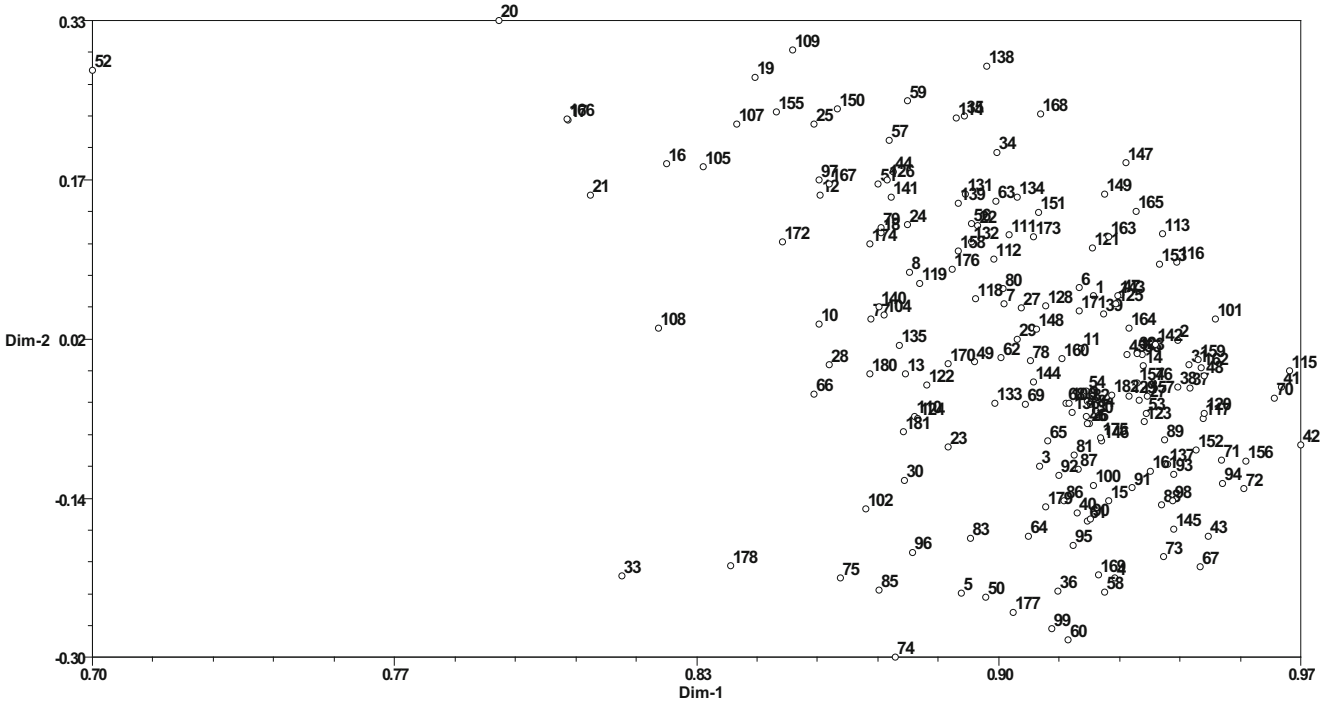

Fig. 3 Two-dimensional plot of the principal components analysis of SSR data

to HIS 01, HIS 08, KIZ 11 and HAC 10, GAR 01. Genotypes with the local name Tavsan Kanı (YAH 01) and Gelin Yanağı (DEV 07) are also believed to be synonyms of the Gül Üzümü when the amphelographic characteristics, especially the pink berry color and dendrogram results are considered.

Among the Parmak grape genotypes, YUC 01, SUK 02, SRZ 01 genotypes were found close, while TAL 02 and YUC 18 genotypes, BED 05 and HAM 14 genotypes were found close. Sultani Çekirdeksiz variety used as a standard in the study, displayed remarkable association with YUC 03 (Çekirdeksiz collected from Yüceyar) and YUC 07 (Irazakı collected from Yüceyar), BED 07 (Çekirdeksiz collected from Bedir) and ERK 03 (Misket collected from Erkilet) genotypes were on the other side of the branching. As a result of the research conducted by Yüksel (2008, p. 59), it was determined that the seedless cultivars used did not show a specific branching and were genetically related to other cultivars.

YUC 07 (Irazakı collected from Yüceyar) and OZV 14 (Razakı collected from Ozvatan) genotypes, which are similar in terms of their local names, are phenotypically different from each other and can be evaluated as homonymous, considering the berry characteristics, the similarity of the OZV 14 (Razakı collected from Ozvatan) genotype to the Akdimrit genotype used as a control in the study was also seen in the dendrogram.

In the study, it was observed that YUC 17 (Tilki Kuyruğu collected from Yüceyar) and ERK 06 (Tilki Kuyruğu collected from Erkilet) genotypes with the same local names in two different regions were different from each other when the cluster and grain shape were examined, and the dendrogram results supported this.

ERK 09 (Eldaş from Erkilet) and OZV 05 (Eldaş collected from Ozvatan) genotypes in the white grape group are located close to each other. GES 07 (Gögcek collected from Gesi) and TAL 03 (Beyaz collected from Talas) genotypes are similar to Eldaş genotypes in terms of their phenotype features, and this situation is also reflected in the dendrogram results. Besides, YAH 05 (Farsak collected from Yahyalı) and OZV 13 (Eldaş collected from Ozvatan) genotypes were found to be similar in terms of both phenotype and genetics.

The principal components analysis (PCA) was performed for better demonstration of relations among the genotypes used in present study. The results of PCA are provided in Fig. 3. PCA-1 and PCA-2 represented 81.6% and 1.9% of the variation in the binary data matrix, respectively. It implies that 93.4% of the total variation in the original dimensions could be represented by just two dimensions defined by the first two PCs. Two-dimensional dispersion showed that some genotypes were nested clearly apart from others. GES 09 (52), DEV 12 (20), SAR 01 (166), SAR 04 (167), EG 01 (21), ERK 06 (33), OZV 12 (108) and Alfonse (178) were positioned away from other genotypes.

Discussion

According to the results of our study, it has been determined as a result of many previous studies that the synonym and homonym status among the local grape genotypes are common and that this situation may be caused by no name as well as the emergence of different clones (Dilli 2008; Aslantaş 2010; Yıldırım 2010; Boz et al. 2011).

Overall results of this study indicated that SSR (Simple Sequence Repeats) molecular markers in molecular characterization of local grape genotypes are a useful method in distinguishing genotypes and determining genetic similarities. In parallel with this view, Dilli (2008) determined that SSRs were suitable for genetic identification of grape genotypes, and reported that VVMD28 and VrZAG79 markers were the most informative markers among the studied microsatellite markers. Sabir et al. (2018), studying on the autochthonous grape genotypes of mountainous regions of Konya, Karaman and Mersin provinces, indicated that SSR and SRAP data were capable of the revealing a wide genetic variability among local grape varieties that have been cultivated for many years, and the molecular data produced in their study are of great benefit for conducting the future breeding strategies. Similarly, Dong et al. (2018) emphasized that SSR marker system is a useful method in the analysis and differentiation of grape varieties, and that SSR markers can be used to differentiate and analyze genetic resources between cultivars.

Many researchers have proven the usefulness of SSRs in identification of genetically close grapevine genotypes. In the study carried out by Sabir (2008), 59 grape varieties from a grapevine germplasm in Adana province and 20 American grape rootstocks were identified ampelographic descriptors and molecular marker methods. The researcher determined that the geographical origins and their parental background were effective on clustering on dendrogram. Muganu et al. (2009), in their study for the ampelographic and molecular characterization of some old vine genotypes in the Tuscia region of Italy, emphasized that genotyping or DNA fingerprinting of clonally replicated types is extremely valuable in the management of genetic resources. They further underlined the necessity of combining DNA analysis with ampelographic definitions in planning the selection of clones. Garcia-Muñoz et al. (2011), emphasized that ampelography is an excellent preliminary technique for the identification of varieties and that it can be confirmed with SSR marker analysis results. Benito et al. (2016) indicated that ampelographic characterization supported by molecular screening can be suggested to identify wild grape genotypes. Knezovic et al. (2017) reported that both methods are essential method in identifying similarities and differences between varieties in the study where they used 16 OIV characters and 9 SSR markers in the definition of 10 native vine genotypes with the same name in Bosnia and Herzegovina. Popescu et al. (2017) concluded that both the ampelographic and SSR marker method were effective in identifying the genetic types of grapevine and misnamed genotypes in the grapevine gene banks in identifying grapevine genetic resources in Romania. Ferlito et al. (2018) reported that SSR markers also help differentiate varieties. The researchers emphasized that analysis based on both identification methods provided more reliable information about the variety of grapes and contributed to the development of gene resource conservation strategies.

The classical principal components analysis (PCA) results are generally consistent with the results obtained in the dendrogram. While some of the genotypes were distinctly located separately in the two-dimensional plot, some of them formed groups. PCA is likely an example of dimensionality reduction. Therefore, it is important that the required information is strongly related to the variance in the data (Scholz and Selbig 2006). Marak and Laskar (2010) argued, that the PCA revealed some aspects of interrelations among the studied materials that were not discernable by the cluster analysis.

Conclusion

The results of the present and previous studies have proven that SSR markers are highly polymorphic and could be successfully used in identification of genetically close local grapevine genotypes. Molecular investigations revealed that Kayseri Province has a significant ancient grape diversity. However, this diversity is threatened by different adversities such as diseases, misuse of agricultural lands, urbanization, industrialization, monovarietal modern vineyard establishment etc. In order to protect this richness from genetic erosion, genotypes representing unique diversity should be propagated and transferred to a germplasm plot. It is also a great priority to decipher the pioneering features of each genotype to improve well-adapted sustainable grapevine breeding studies.

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Conflict of interest G. Yılmaz, A. Uzun, A. Sabır and H. Pınar declare that they have no competing interests.

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