TARIM BİLİMLERİ DERGİSİ 2009, 15(1) 1-8
ANKARA ÜNİVERSİTESİ ZİRAAT FAKÜLTESİ
DOI: 10.1501/Tarimbil_0000001064

Genetic Analysis of Grapevine Cultivars from the Eastern Mediterranean Region of Turkey, Based on SSR Markers

Serpil Gök TANGOLAR[1] Semra SOYDAM[2] Melike BAKIR[3] Eda KARAAĞAÇ[3]
Semih TANGOLAR[4] Ali ERGÜL[3]

Geliş Tarihi: 24.11.2008 Kabul Tarihi: 30.03.2009

Abstract : Turkey is one of the centres for grapevine diversity with many local grapevine cultivars with potentially desirable characteristics are still widely cultivated throughout several regions in the country. One of such regions is the Eastern Mediterranean region of the country. To characterize the grapevine germplasm of this region, we performed a genetic analysis of 59 grapevine cultivars using 14 simple sequence repeat (SSR) loci. The genetic relationships of the cultivars which did not appear to be linked to their ecogeographical distributions within the region were determined. Among the cultivars analyzed in this study, several synonymous and homonymous cultivars were identified, suggesting that some of the grapevine cultivars with different names might be genetically identical while some cultivars with the same names might be genetically different. This study represents a first step toward the genetic characterization of the grapevine genotypes of this region and will help promote more effective germplasm management and breeding programs.

Key Words: *Vitis vinifera* L., SSR, Eastern Mediterranean, synonym, homonym.

Türkiye Doğu Akdeniz Bölgesi Üzüm Çeşitlerinin SSR Markörleri ile Genetik Analizi

Öz: Türkiye, asma genetik kaynaklarının önemli merkezlerinden birisidir. Ülkenin bazı bölgelerinde hala yaygın şekilde yetiştiriciliği yapılan birçok yöresel üzüm çeşidi bulunmaktadır. Bu bölgelerden biri Doğu Akdeniz Bölgesidir. Bu çalışmada, bölgenin asma gen kaynaklarının tanımlanması amacı ile 14 SSR primeri kullanılarak 59 üzüm çeşidinin genetik analizleri yapılmıştır. Çalışma sonucunda çeşitler arasındaki genetik ilişkilerin bölge içindeki ekocoğrafik dağılımları ile bağlantılı olmadığı belirlenmiştir. Çalışmada analiz edilen çeşitler arasında farklı isimlerle anıldığı halde aynı genotip (sinonim) veya aynı isimli ancak farklı genotip özelliği (homonim) gösterenler saptanmıştır. Bölgenin asma genotipleri ile ilgili ilk genetik analiz sonuçlarının sunulduğu bu çalışma, gen kaynaklarının daha etkin kullanımını ve ıslah programlarını destekleyecektir.

Anahtar Kelimeler: *Vitis vinifera* L., SSR, Doğu Akdeniz, sinonim, homonym.

Introduction

Turkey is a center of diversity for grapevines (*Vitis vinifera* L.) and possesses a rich grapevine germplasm (Arroya-Garcia et al. 2006, Ergül et al. 2006). The Mediterranean region of Turkey with suitable climatic conditions possesses the one of the largest areas devoted to grapevine production in the country, second only to the Aegean region. Whereas early maturing cultivars are common in the low-altitude regions (i.e. the region spanning central Adana and İçel, two provinces that are separated by the Tarsus district), late-maturing table grape and wine cultivars are more prevalent at higher altitudes (e.g., the Saimbeyli, Feke and Pozanti districts) of this region.

As expected, viticulture is also a valuable economic activity in most of the country, except for the high altitude regions of East Anatolia and the Eastern Black Sea where unsuitable climatic conditions (e.g. excessive rainfall) largely restrict grapevine cultivation. Grapevine cultivation and wine culture have long been important elements of life in the Eastern Mediterranean region (Oraman 1969) with many local cultivars are still widely cultivated. However, given the relatively large numbers of such cultivars grown in the region, problems related to cultivar identity have recently begun to appear within this germplasm, such that certain cultivars are grown under different names,

---

[1] Ministry of Agriculture and Rural Affairs, Plant Protection Research Institute- Adana
[2] Ankara Univ,, Fac. of Science, Department of Biology-Ankara
[3] Ankara Univ., Biotechnology Institute-Ankara
[4] Çukurova Univ., Faculty of Agriculture, Department of Horticulture- Adana

whereas other, more discrete, cultivars are cultivated under the same name. Consumer preference for certain grape cultivars has increased the possibility that local cultivars which have been widely cultivated for centuries and are well adapted to the region, would eventually disappear.

In this study, we have performed a genetic characterization of grape cultivars grown in the Eastern Mediterranean region (i.e. Adana and the surrounding districts Gülnar, İçel and Tarsus), as well as other Mediterranean cultivars that are well adapted to this region. Specifically, we analyzed 14 simple sequence repeats (SSR) loci from 59 grapevine cultivars and examined allelic data to determine the genetic relationships among these cultivars. Our findings will assist with the conservation of these cultivars and help alleviate problems related to cultivar identity.

Materials and Methods

Plant materials: Plant samples were collected from 15-year-old grapevines maintained at Çukurova University Faculty of Agriculture Collection Vineyard in Adana, as well as from privately owned vineyards (these plants were then included in the collection vineyard in 2008). Grapevine cultivars used in this study and their collection sites are shown in Table 1.

DNA extraction: DNA was extracted using the procedure described by Lefort et al. (1998) and Ağaoğlu et al. (2001). Concentration and purity of the extracted DNA were analyzed using a NanoDrop® ND-1000 spectrophotometer.

Genetic analysis of simple sequence repeats: We analyzed 14 SSR markers, of which 6 belonged to the so-called “core set” (i.e., VVS2, VVMD5, VVMD7, VVMD27, VrZAG62, and VrZAG79) of markers that are recommended for the direct comparison of results from different laboratories (This et al. 2004). PCR amplifications were performed as described by Şelli et al. (2007). PCR products were diluted in sample loading solution (SLS) and standards from the Genomelab DNA Standard Kit-400 were included. The amplified fragments were analyzed at least twice using a CEQ 8800XL capillary DNA analysis system (Beckman Coulter, Fullerton, CA) to ensure reproducibility. Allele sizes were determined for each SSR locus using the Beckman CEQ fragment analysis software. In each run, Cabernet Sauvignon and Merlot were included as reference cultivars.

Table 1. Origin of grape cultivars used in this study

No.	Genotype (synonym)	Collection province (town/city or region)	No.	Genotype	Location (town/city/region)
1	Adana beyazı*	-/Adana	31	Recep	Alpu/Adana
2	Adana beyazı	Gülnar/İçel	32	Recep	Gülnar/İçel
3	Tarsus beyazı *	Tarsus/Adana	33	Horozpaşa*	-/Mediterranean
4	Tarsus beyazı	-/Adana	34	İrengil*	-/Mediterranean
5	Muturu*	Feke/Adana	35	Bağdat siyahı*	-/Mediterranean
6	Muturu	Feke/Adana	36	Bekiroğlu*	-/Mediterranean
7	Muturu	Saimbeyli/Adana	37	Büzgülü*	-/Mediterranean
8	Mücennes*	Saimbeyli/Adana	38	Pafi*	-/ Hatay
9	Mücennes	Saimbeyli/Adana	39	Göküş üzümü	Çiftehan/Pozantı/Adana
10	Kızıl üzüm*	-/Burdur	40	Topkara	Çiftehan/Pozantı/Adana
11	Kızıl üzüm	Saimbeyli/Adana	41	Hatun parmağı*	-/Adana
12	Kuş üzümü (Kişniş)*	Gülnar/İçel	42	İlifkin	Pozantı/Adana
13	Kuş üzümü (Kişniş)	Gülnar/İçel	43	Kokulu miski	Pozantı/ Adana
14	Yerli Dirmit (Dirmit)*	Gülnar/İçel	44	Alpu üzümü	Pozantı/ Adana
15	Burdur Dimriti*	Burdur	45	Koyunoğlu	Pozantı/ Adana
16	Dilmit*	Gülnar/İçel	46	Kıbrıs*	Feke/Adana
17	Kabarcık*	-/Mediterranean	47	Kıbrıs	Feke/Adana
18	Kabarcık	Saimbeyli/Adana	48	Tilki kuyruğu*	-/Adana
19	Siyah Çekirdeksiz*	-/Mediterranean	49	Tilki kuyruğu	Feke/Adana
20	Pembe Çekirdeksiz*	-/Mediterranean	50	Abdülbaki	Feke/Adana
21	Yerel Çekirdeksiz	Gülnar/İçel	51	Akkaya Batmanı	Feke/Adana
22	Adana karası*	-/Adana	52	Akkaya şamı	Feke/Adana
23	Sergi karası*	-/Mediterranean	53	Ağsık	Feke/Adana
24	Horoz karası*	-/Mediterranean	54	Nimelbaki	Saimbeyli/Adana
25	Antep karası	Gülnar/İçel	55	Zeytin üzümü	Saimbeyli/Adana
26	Beyaz Zevük	-/Adana	56	Takkara	Gülnar/İçel
27	Beyaz Zevük	Feke/Adana	57	Gök üzüm	Gülnar/İçel
28	Siyah Zevük	Feke/Adana	58	Pekmez	Gülnar/İçel
29	Tatlı Besni	Pozantı/Adana	59	Ermenek ispitiren	Gülnar/İçel
30	Ekşi Besni	Pozantı/Adana			

*Plant samples were collected from Experimental Vineyard at Çukurova University, Faculty of Agriculture, Adana.
-: information is not available.

The number of alleles (n), allele frequency, expected (H_e) and observed (H_o) heterozygosity, estimated frequency of null alleles (r), probability of identity (PI), and presence of identical genotypes were determined for each locus using IDENTITY version 1.0 software (Wagner and Sefc 1999), as described by Paetkau et al. (1995). Microsat version 1.5 (Minch et al. 1995) was used to calculate the proportion of shared alleles with the ps option [i.e., option 1-(ps)] (Bowcock et al. 1994) selected to assess genetic dissimilarity. Data were then converted to a similarity matrix, and a dendogram was constructed via the unweighted pair-group with arithmetic mean (UPGMA) method (Sneath and Sokal 1973), using the numerical Taxonomy and Multiware Analysis System (NTSYS-pc) software, version 2.0 (Rohlf 1998).

Results and Discussion

SSR analysis: We analyzed 14 SSR markers from 59 grapevine cultivars grown in Adana and neighboring regions (in addition to two reference cultivars) and detected a total of 117 alleles. The average number of alleles was 8.357, consistent with data reported for other grapevines (Dangl et al. 2001, Costantini et al. 2005) (Table 2).

The mean observed heterozygosity (H_o) and expected heterozygosity (H_e) were determined to be 0.743 and 0.749, respectively. The Ho values of the VVMD24, VMC2C3, VVMD28, VVS2, VVIBO1 and VVMD31 loci were high. Previous reports also found relatively high H_es in some other grape loci (Costantini et al. 2005, Santana et al. 2007). In this study, the frequency of null alleles (r) at these VrZAG79, VVMD27, VVMD5, VrZAG62, VMC2H4, VVMD7, VVIH54 and VrZAG83 loci was positive, but these low values suggest the absence of null alleles (Table 2).

The VrZAG83 locus generated the lowest number of alleles (4 alleles), whereas the VVMD28 and VVS2 loci generated the highest number of alleles (12 alleles). Similarly, previous studies have reported that VVS2 (Fatahi et al. 2003, Núñez et al. 2004, Şelli et al. 2007) and VVMD28 generate the highest number of alleles (Vouillamoz et al. 2006, Şelli et al. 2007). Other studies, including ours, have also reported that VrZAG83 generates the lowest number of alleles (Sefc et al. 2000, Snoussi et al. 2004) (Table 2).

The most informative loci, with regards to the probability of identity (PI), were VVMD28 and VVS2, which each generated 12 alleles (PI: 0.132 and 0.084, respectively). The least informative locus was VrZAG83, which generated four alleles (PI: 0.389) (Table 2). Allele sizes (bp) of 59 cultivars from 14 SSR loci are shown in Table 3.

Identification of synonyms and homonyms: Many researchers have used SSR markers to identify synonyms and homonyms of grapevine genotypes (Ibáñez et al. 2003, Martín et al. 2003, This et al. 2004, Vouillamoz et al. 2006, Şelli et al. 2007). Among the grape cultivars analyzed in this study, three cases of identity were found [Muturu (5), Muturu (6) and Muturu (7); Kuş üzümü (Kişniş) (12) and Kuş üzümü (Kişniş) (13); and Kabarcık (17) and Kabarcık (18)] and five cases of synonyms were identified [Adana beyazı (2) and Recep (31); Kuş üzümü (Kişniş) (12 and 13), Dilmit (16) and Topkara (40); Ekşi besni (30) and Tilki kuyruğu (48); Gököş üzümü (39) and Koyunoğlu (45); and Abdülbaki (50) and Nimelbaki (54)].

Our results also indicated that a number of cultivars known by the same names were genetically different, suggesting that they were homonyms. These genotypes are Adana beyazı (1) and Adana beyazı (2); Tarsus beyazı (3) and Tarsus beyazı (4); Mücennes (8) and Mücennes (9); Kızıl üzüm(10) and Kızıl üzüm (11); Beyaz Zevük (26) and Beyaz Zevük (27); Recep (31) and Recep (32); Kıbrıs (46) and Kıbrıs (47); and Tilki kuyruğu (48) and Tilki kuyruğu (49).

SSR-based relationship and ecogeographical distributions: When the genetic similarity of the genotypes was analyzed, the highest similarity ratio (not including the identical and synonym cultivars) was 96.4% between 10 genotypes; however, the rest of the genotypes revealed a similarity index below 92.9%.

The dendrogram shown in Figure 1 reveals that the reference cultivars used in this study are distantly related to the Turkish cultivars studied here. The distribution of cultivars within the dendrogram appears to be independent of their ecogeographical distributions. Among cultivars with similar names, some clustered together (e.g., Muturu, Mücennes, Kuş üzümü, Kabarcık, and Kıbrıs), whereas others [e.g., Adana beyazı, Tarsus beyazı, Kızıl üzüm, Dilmit, Çekirdeksiz, Zevük, Besni, Recep, and Tilki kuyruğu] were more distantly related.

We identified two genotypes of Tarsus beyazı (an early-maturing grape cultivar with a white berry color), which is the most common early grape cultivar native to Adana. These data suggest that genetic variation exists within this cultivar. In contrast, other early-maturing grape cultivars found in the region [Tarsus beyazı (3) and Adana karası (22)] displayed a high similarity index (almost 80%), suggesting that they might have originated from the same genetic background.

Table 2. SSR loci and genetic characteristics of grape cultivars.

SSR loci	n	Ho	He	PI	r
VrZAG79	8	0.721	0.785	0.124	0.0359
VVMD24	7	0.819	0.710	0.212	-0.0635
VVMD27	11	0.770	0.848	0.077	0.0423
VVMD5	8	0.737	0.862	0.065	0.0671
VMC2C3	9	0.803	0.736	0.187	-0.0382
VVMD28	12	0.819	0.772	0.140	-0.0266
VVS2	12	0.901	0.835	0.080	-0.0359
VrZAG62	8	0.639	0.704	0.181	0.0380
VVIBO1	5	0.524	0.478	0.530	-0.0314
VMC2H4	10	0.803	0.846	0.078	0.0233
VVMD7	6	0.754	0.808	0.123	0.0299
VVIH54	9	0.786	0.814	0.093	0.0149
VVMD31	8	0.737	0.681	0.245	-0.0336
VrZAG83	4	0.590	0.601	0.390	0.0073
Total	117				
Average	8.357	0.743	0.749	0.1803	

Abbreviations: N, number of alleles; Ho, observed heterozygosity; He, expected heterozygosity; PI, probability; r, null allele frequencies.

Two genotypes of Adana beyazı (a cultivar with a white berry color), which is also grown extensively in the region, revealed a low similarity index (approximately 35.7%). On the other hand, a high degree of similarity was observed between Adana beyazı (2) and Recep (a cultivar with a white berry color) genotypes 31 and 32 (100% and 64.3%, respectively), suggesting that Adana beyazı (2) was improperly named.

Tilki kuyruğu (48) is thought to be distantly related to Tilki kuyruğu (49). However, our data suggest that Tilki kuyruğu (48) is a synonym of Ekşi besni (30) (a cultivar with a white berry color), suggesting that this cultivar is also improperly named and should be reclassified as Ekşi besni.

Genotypes 16 (Dilmit) and 40 (Topkara) were found to be synonyms of Kuş üzümü (Kişniş) (12 and 13), suggesting that the Dilmit and Topkara cultivars might be in fact Kuş üzümü.

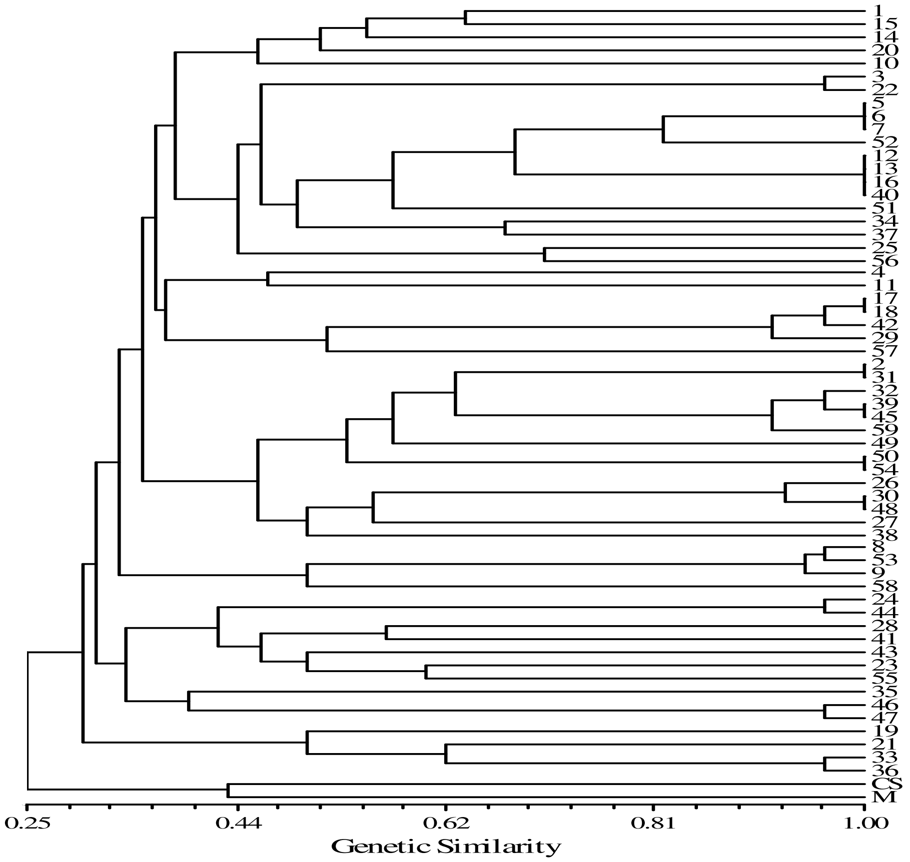

Figure 1 . Genetic relationships among cultivars based on variation detected at 14 SSR loci.

Table 3. Allele sizes (bp) for 59 cultivars from 14 SSR loci

	VrZAG79		VVMD24		VVMD27		VVMD5		VMC2C3		VVMD28		VVS2		VrZAG62		VVIBO1		VMC2H4		VVMD7		VVIH54		VVMD31		VrZAG83	
1	242	250	207	207	185	185	223	229	161	161	233	233	133	135	186	188	292	296	200	214	236	246	164	174	203	211	185	191
2	246	258	207	211	181	183	237	243	167	191	233	257	133	155	188	188	292	296	198	202	246	250	164	176	209	209	185	191
3	246	248	211	215	175	179	225	235	167	177	257	257	135	151	200	204	292	296	202	214	236	236	150	164	209	211	185	185
4	248	248	207	211	187	187	237	243	161	177	235	257	133	153	188	204	292	292	214	214	244	248	138	164	209	213	185	191
5	246	246	211	215	175	179	225	237	161	167	233	257	133	143	188	200	292	296	202	218	240	246	164	164	209	209	185	185
6	246	246	211	215	175	179	225	237	161	167	233	257	133	143	188	200	292	296	202	218	240	246	164	164	209	209	185	185
7	246	246	211	215	175	179	225	237	161	167	233	257	133	143	188	200	292	296	202	218	240	246	164	164	209	209	185	185
8	248	258	205	207	181	183	237	243	161	167	235	239	143	145	202	202	292	296	204	214	244	244	164	174	195	211	187	191
9	248	258	205	207	181	183	237	243	161	167	235	239	143	143	202	202	292	296	204	214	244	246	164	174	195	211	187	191
10	242	258	207	215	181	185	223	237	161	161	247	257	143	143	188	200	292	292	200	214	236	250	164	176	211	211	187	191
11	248	248	207	211	183	183	231	231	161	167	233	233	133	135	188	192	292	296	204	218	240	244	138	164	209	209	191	191
12	246	250	207	215	179	185	233	237	161	167	233	257	137	143	188	200	296	296	198	218	240	246	164	174	209	211	185	185
13	246	250	207	215	179	185	233	237	161	167	233	257	137	143	188	200	296	296	198	218	240	246	164	174	209	211	185	185
14	246	250	207	215	185	185	237	237	161	161	233	247	133	143	200	204	292	296	198	198	236	240	162	162	209	223	185	191
15	242	250	207	207	185	185	235	235	161	161	233	257	133	143	188	200	292	296	200	214	236	240	162	162	209	211	185	185
16	246	250	207	215	179	185	233	237	161	167	233	257	137	143	188	200	296	296	198	218	240	246	164	174	209	211	185	185
17	246	246	207	215	177	179	231	231	161	161	257	257	133	143	192	204	292	296	202	214	244	250	150	176	209	211	187	191
18	246	246	207	215	177	179	231	231	161	161	257	257	133	143	192	204	292	296	202	214	244	250	150	176	209	211	187	191
19	246	254	211	219	179	181	231	231	159	193	217	233	133	151	188	204	292	292	212	212	244	250	162	162	211	215	185	191
20	242	258	207	207	185	195	231	237	167	191	233	243	133	151	186	188	292	296	214	214	236	244	162	162	203	211	185	191
21	246	258	207	215	181	195	231	231	159	191	217	257	145	151	188	188	292	298	204	214	236	250	162	162	211	211	185	191
22	246	248	211	215	175	179	223	235	167	177	257	257	135	151	200	204	292	296	202	214	236	236	150	164	209	211	185	185
23	248	248	207	215	179	195	223	235	161	161	235	279	135	141	196	200	292	292	198	206	244	244	138	166	209	211	191	191
24	246	256	207	215	195	195	225	235	187	191	235	243	135	143	188	200	292	292	204	206	236	246	158	166	203	209	191	191
25	246	246	207	209	187	195	233	233	161	187	243	257	133	137	188	204	292	296	206	218	236	246	138	164	209	211	185	185
26	248	258	207	207	181	183	229	229	161	191	233	243	149	155	188	188	292	292	198	204	240	250	158	176	203	209	185	191
27	258	258	207	215	179	181	233	235	161	177	243	243	143	149	188	188	292	296	198	198	240	250	164	176	203	211	187	191
28	250	256	211	215	179	195	223	231	161	177	233	243	133	135	188	188	292	308	198	206	244	244	164	176	209	213	185	191
29	246	246	207	215	177	179	231	231	161	161	233	243	133	143	192	204	292	296	202	214	244	250	150	176	209	211	187	191
30	248	258	207	207	181	183	229	243	161	191	233	243	149	155	188	188	292	296	198	204	240	250	158	176	203	209	185	191
31	246	258	207	211	181	183	237	243	167	191	233	257	133	155	188	188	292	296	198	202	246	250	164	176	209	209	185	191
32	246	248	205	207	183	183	225	243	167	191	243	257	135	155	188	188	292	292	202	204	246	250	158	164	209	211	185	191
33	242	256	207	215	185	195	225	231	159	167	217	257	131	151	188	188	292	292	204	214	250	250	162	162	211	215	185	185
34	242	250	211	215	181	185	233	233	167	167	257	257	143	143	188	200	296	296	214	218	244	244	150	174	209	209	185	191

Table 3. Allele sizes (bp) for 59 cultivars from 14 SSR loci(Continued)

35	246	256	207	211	179	195	231	235	161	177	239	269	133	143	196	204	296	314	200	206	236	246	158	164	211	215	185	191
36	242	256	207	215	185	195	225	231	159	167	217	257	131	151	188	188	292	292	204	212	250	250	162	162	211	215	185	185
37	242	246	207	207	179	185	233	233	167	195	257	257	137	143	188	200	292	296	214	220	244	244	164	174	209	209	185	191
38	246	256	207	211	175	195	229	243	161	191	233	243	131	143	188	188	292	308	198	198	240	250	138	166	195	203	185	185
39	246	248	205	207	183	183	225	243	167	191	243	257	135	155	188	188	292	292	202	202	246	250	158	164	209	211	185	191
40	246	250	207	215	179	185	233	237	161	167	233	257	137	143	188	200	296	296	198	218	240	246	164	174	209	211	185	185
41	256	256	211	215	195	195	223	223	161	167	233	243	135	143	188	192	292	292	198	198	236	244	166	176	209	209	185	185
42	246	246	207	215	177	179	231	231	161	161	257	257	133	143	192	204	292	296	202	214	244	250	150	176	209	209	187	191
43	248	256	211	215	179	195	233	235	161	161	257	281	135	141	188	192	292	296	206	214	240	244	166	174	209	211	185	191
44	246	256	207	215	195	195	225	235	187	191	235	243	135	143	188	200	292	292	204	204	236	246	158	166	203	209	191	191
45	246	248	205	207	183	183	225	243	167	191	243	257	135	155	188	188	292	292	202	202	246	250	158	164	209	211	185	191
46	250	256	207	207	195	195	229	237	161	191	247	255	145	151	192	204	292	292	200	204	236	248	158	176	211	213	185	191
47	250	256	207	207	195	195	229	237	161	191	247	257	145	151	192	204	292	292	200	204	236	248	158	176	211	213	185	191
48	248	258	207	207	181	183	229	243	161	191	233	243	149	155	188	188	292	296	198	204	240	250	158	176	203	209	185	191
49	246	256	205	207	183	195	237	243	167	167	233	257	133	143	188	188	292	292	198	214	236	246	138	164	209	211	185	185
50	238	258	205	215	179	181	225	243	167	177	243	257	143	155	188	200	292	292	198	204	236	236	158	164	209	211	185	191
51	248	250	207	215	179	185	233	237	161	167	235	257	145	145	188	200	292	292	206	214	240	246	164	164	209	215	185	187
52	246	250	205	215	179	183	237	237	161	167	233	257	133	143	188	200	292	296	198	202	240	246	164	164	209	209	185	185
53	248	258	205	207	181	183	237	243	161	167	235	239	143	143	202	202	292	296	204	214	244	244	164	174	195	211	187	191
54	238	258	205	215	179	181	225	243	167	177	243	257	143	155	188	200	292	292	198	204	236	236	158	164	209	211	185	191
55	250	256	209	209	179	195	223	235	161	187	235	279	135	155	192	200	292	292	206	210	244	244	150	176	209	209	191	191
56	246	246	205	209	175	195	223	233	167	187	243	257	133	155	188	204	292	292	206	214	236	246	138	164	209	209	185	185
57	246	248	205	215	179	193	231	235	167	187	257	257	133	143	204	204	292	292	198	214	244	248	164	176	223	223	187	191
58	242	246	205	207	185	193	233	233	161	167	235	257	143	143	202	202	292	296	214	214	246	246	150	176	211	223	187	187
59	246	246	205	205	183	183	225	243	167	191	243	257	135	155	188	188	292	292	202	202	246	250	158	164	209	211	185	191
CS	246	246	207	217	175	189	229	237	163	177	233	235	139	151	188	194	292	292	212	220	236	236	164	178	205	209	197	197
M	258	258	207	211	189	191	223	233	167	177	227	233	139	151	194	194	292	296	198	212	236	244	164	164	211	215	191	197

Abbreviations:CS, Cabernet Sauvignone; M, Merlot.

Conclusion

Although some plant species from the Mediterranean region of Turkey have been genetically characterized (Bayazit et al. 2007, Ayanoğlu et al. 2007), few studies have explored the genetic diversity within grapevine germplasm of this region. Our findings reported here will assist with future agricultural practices, such as grapevine propagation and breeding and promote better management of regional grapevine cultivars. Importantly, the data reported here can be directly compared with other studies that used these SSR markers on grapes or be integrated into future studies investigating the genetic diversity of grapes from the whole Mediterranean region.

References

Ağaoğlu, Y.S., B. Marasalı ve A. Ergül. 2001. Asmalarda (*Vitis vinifera* L.) farklı dokulardan izole edilen DNA 'ların RAPD (Random Amplified Polymorphic DNA) tekniğinde kullanımı üzerinde bir araştırma. Tarım Bilimleri Dergisi 7(4): 52-56.

Arroyo-Garcia, R., L. Ruiz-Garcia, L. Boulling, R. Ocete, M. A. López, C. Arnold, A. Ergul, G. Söylemezoğlu, H. I. Uzun, F. Cabello, J. Ibáñez, M. K. Aradhya, A. Atanassov, I. Atanassov, S. Balint, J. L. Cenis, L. Costantini, S. Gorislavets, M. S. Grando, B. Y. Klein, P. McGovern, D. Merdinoglu, I. Pejic, F. Pelsy, N. Primikirios, V. Risovannaya, K. A. Roubelakis-Angelakis, H. Snouss, P. Sotiri, S. Tamhankar, P. This, L. Troshin, J. M. Malpica, F. Lefort and J. M. Martinez-Zapater. 2006. Genetic evidence for the existence of independent domestication events in grapevine. Mol. Ecol. 15: 3707-3714.

Ayanoğlu, H., S. Bayazit, G. İnan, M. Bakır, A.E. Akpınar, K. Kazan and A. Ergül. 2007. AFLP and morphological analyses of genetic diversity in Turkish green plum accessions (*Prunus cerasifera* L.) adapted to the Mediterranean Region. Sci. Hortic. 114: 263-267.

Bayazit, S., K. Kazan, S. Gülbitti, V. Cevik, H. Ayanoğlu and A. Ergül. 2007. AFLP analysis of genetic diversity in low chill requiring walnut (*Juglans regia* L.) genotypes from Hatay, Turkey. Scienta Hortic. 111: 394–398.

Bowcook, A. M., A. Ruiz- Linares, J. Tomfohrde, E. Minch, J. R. Kidd and L. L. Cavalli –Sforza. 1994. High resolution of human evolutionary trees with polymorphic microsatellites. Nature 368: 455-457.

Costantini, L., A. Monaco, J. F. Vouillamoz, M. Forlani and M.S. Grando. 2005. Genetic relationships among local *Vitis vinifera* cultivars from Campania (Italy). Vitis 44: 25-34.

Dangl, G. S., M. L. Mendum, B. P. Prins, M. A. Walker, C. P. Meredith and C. J. Simon. 2001. Simple sequence repeat analysis of a clonally propagated species: a tool for managing a grape germplasm collection. Genome 44: 432-438.

Ergül, A., K. Kazan, S. Aras, V. Çevik, H. Çelik and G. Söylemezoğlu. 2006. AFLP analysis of genetic variation within the two economically important Anatolian grapevine (*Vitis vinifera* L.) varietal groups. Genome 49: 467-495.

Fatahi, R., A. Ebadi, N. Bassil, S. A. Mehlenbacher and Z. Zamani. 2003. Characterisation of Iranian grapevine cultivars using microsatellite markers. Vitis 42: 185-192.

Lefort, F., M. Lally, D. Thompson and G. C. Douglas. 1998. Morphological traits microsatellite fingerprinting and genetic relatedness of a stand of elite oaks (*Q.robur* L.) at Tuallynally, Ireland. Silvae Genet. 47: 5-6.

Martín, J. P., J. Borrego, F. Cabello and J. M. Ortiz. 2003. Characterisation of the Spanish diversity grapevine cultivars using sequence-tagged microsatellite site markers. Genome 46: 1-9.

Minch, E., A. Ruiz-Linares, D. B. Goldstein, M. Feldman and L. L. Cavalli-Sforza. 1995. Microsat (version 1.4d): a computer program for calculating various statistics on microsatellite allele data. Stanford, California, Stanford University.

Nuñez, Y., J. Fresno, V. Torres, F. Ponz and F. J. Gallego. 2004. Practical use of microsatellite markers to manage *Vitis vinifera* germplasm: Molecular identification of grapevine samples collected blindly in D.O. “El Bierzo” (Spain). J. Hort. Sci. & Biotech. 79: 437-440.

Oraman, M.N. 1969. Arkeolojik buluntuların ışığı altında Türkiye bağcılığının tarihçesi üzerinde araştırmalar (in Turkish). II.Ankara Üniv.Ziraat Fak.Yıllığı 19: 53-75.

Paetkau, D., W. Calvert, I. Stirling and C. Strobeck. 1995. Microsatellite analysis of population structure in Canadian polar bears. Mol. Ecol. 4: 347-354.

Rohlf, F. J. 1988. Applied Biostatistics Inc., New York.

Santana, J.C., E. Hidalgo, A. I. de Lucas, P. Recio, J. M. Ortiz, J. P. Martin, J. Yuste, C. Arranz and J. A. Rubio. 2007. Identification and relationships of accessions grown in the grapevine (*Vitis vinifera* L.) Germplasm Bank of Castilla y Léon (Spain) and the varieties authorized in the VQPRD areas of the region by SSR-marker analysis. Genet. Resour. Crop. Evol. 55: 573–583.

Sefc, K. M., M. S. Lopes, F. Lefort, R. Botta, K. A. Roubelakis-Angelakis, J. Ibañez, I. Pejic, H.W. Wegner, J. Glössl and H. Steinkellner. 2000. Microsatellite variability in grapevine cultivars from different European regions and evaluation of assignment testing to assess the geographic origin of cultivars. Theor. Appl. Genet. 100: 498-505.

Şelli, F., M. Bakır, G. İnan, H. Aygün, Y. Boz, A.S. Yaşasın, C. Özer, B. Akman, G. Söylemezoğlu, K. Kazan and A. Ergül. 2007. Simple sequence repeat-based assessment of genetic diversity in Dimrit and Gemre grapevine accessions from Turkey. Vitis 46:182-187.

Sneath, P .H. A. and R. R. Sokal. 1973. Numerical taxanomy. San Francisco, CA: Freeman.

Snoussi, H., M. Harbi Ben Slimane, L. Ruiz-Garcia, J. M. Martinez-Zapater and R. Arroyo-Garcia, 2004. Genetic relationship among cultivated and wild grapevine accessions from Tunisia. Genome 47: 1211-1219.

This, P., A. Jung, P. Boccacci, J. Borrego, R. Botta, L. Costantini, M. Crespan, G. S. Dangl, C. Eisenheld, F. Ferreira-Monteiro, S. Grando, J. Ibanez, T. Lacombe, V. Laucou, R. Magalhaes, C. P. Meredith, N. Milani, E. Peterlunger, F. Regner, L. Zulini and E. Maul. 2004. Development of a standard set of microsatellite reference alleles for identification of grape cultivars Theor. Appl. Genet. 109: 1448-1458.

Vouillamoz, J. F., P. E. McGovern, A. Ergül, G. Söylemezoğlu, G. Tevzadze, C. P. Meredith and M. S. Grando. 2006. Genetic characterization and relationships of traditional grape cultivars from Transcaucasia and Anatolia. Plant Genet. Resour. 4: 144-158.

Wagner, H. W. and K. M., Sefc. 1999. Identity 1.0. Centre for Applied Genetics, University of Agricultural Science, Vienna.

Correspendence Address:
Ali ERGÜL
Ankara University, Biotechnology Institute, 06100,
Ankara-Turkey
Tel: 0090 312 2225816
Fax : 0090 312 2225872
E-mail: ergul@agri.ankara.edu.tr