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Genetic diversity of wild and cultivated grapevine accessions from southeast Turkey

DILEK DEĞIRMENCİ KARATAŞ1, HÜSEYİN KARATAŞ1, VALÉRIE LAUCOU2, GÖLGE SARIKAMIŞ1, LEILA RIAHI4, ROBERTO BACILIERI2 and PATRICE THIS2

1Department of Horticulture, Faculty of Agriculture, Dicle University, Diyarbakır, Turkey
2TGU 1334, AGAP, INRA, Equipe DAAV 2, Montpellier, France
3Department of Horticulture, Faculty of Agriculture, Ankara University, Ankara, Turkey
4Laboratoire de Physiologie Moléculaire des Plantes, Centre de Biotechnologie Borj Cedria, Hammam-Lif, Tunisia

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Wild grapevine genetic diversity in southeast Turkey has not been documented to date. In the present work, in order to clarify the relationships between wild and cultivated grape accessions from southeastern Turkey, 22 nuclear and three chloroplast microsatellite loci were used on 21 wild grapevine Vitis vinifera L. ssp. sylvestris (Gmelin) and 13 cultivated grapevine Vitis vinifera ssp. sativa accessions. The number of alleles per SSR locus ranged from 4 (VVIn16) to 20 (VVV67) and the mean allele number per locus was 10.09. Expected locus heterozygosity ranged from 0.586 (locus VVIB01) to 0.898 (locus VVIV67). The three cpSSR molecular markers presented variation in size both in cultivars and in wild Turkish accessions. Two size variants were detected for cpSSR3 (106 and 107 bp) for cpSSR5 (104 and 105 bp), and for cpSSR10 (115 and 116 bp). The six alleles in wild grapevines fell into three haplotypes B, C and D. A genetic structure according to accessions taxonomic status (wild or cultivated) was revealed by UPGMA analysis. This highlighted a clear separation between domesticated and wild accessions in Turkish germplasm. The results pointed out the need to further collect and characterize this wild and cultivated grapevine germplasm.

Dilek Değirmenci Karataş, Dept of Horticulture, Faculty of Agriculture, Dicle Univ., TR-21280 Diyarbakır, Turkey. E-mail: degrimenci@yahoo.com

Grape is unique, not only as a major global horticultural crop but also because of its ancient historical connections with human culture development. McGovern (2003) suggested that human beings encountered wild grapes for the first time in the upland regions of eastern Turkey. Indeed, seeds of domesticated grapes dated circa 8000 BP were found in Georgia and in Turkey (This et al. 2006), while the oldest wild grape (Vitis vinifera ssp. sylvestris) seeds known (dated 8400 years BP) were excavated in Turkey on the slope of Euphrates side valley (Hauptmann 1997; Pasternak 1998).

Wild grapevines (Vitis vinifera L. ssp. sylvestris) are heavily threatened in their natural habitats and high priority is given to the collection and preservation of this germplasm (Forneck et al. 2003). Indeed, the preservation of wild populations of V. v. ssp. sylvestris is considered essential for the maintenance of genetic variability and the resistance to genetic erosion (Cunha et al. 2009).

Turkey is an important center of origin both for cultivated Vitis vinifera ssp. sativa and wild Vitis vinifera ssp. sylvestris (Arroyo Garcia et al. 2006). Correspondingly, Turkey is rich in wild grapevines and grape cultivars (approx. 1200 accessions) which offers to grape breeders a valuable gene pool from which to extract genes of interest (Üzun and Bayır 2010). More specifically, Anatolia has long been linked with grapevine, especially in its eastern and southeastern regions to which earlier authors commonly ascribe the origin of viticulture and wine making (Ağaoğlu and Čelik 1987; Ağaoğlu et al. 1998). With this long-standing history, southeast Anatolia can boast both significant wild grapevine populations and a rich panel of local cultivars (Karataş et al. 2007). Analysing genetic diversity and relationships between wild (Vitis vinifera ssp. sylvestris) and cultivated (Vitis vinifera ssp. sativa) populations in this unique grapevine diversity ‘hotspot’ could help us understand the process of grapevine domestication.

SSR markers were useful as a complementary tool to traditional ampelography for cultivar identification. Wild grape populations have recently been studied using molecular markers (De Mattia et al. 2008; Bodor et al. 2010; García Muñoz et al. 2011; Laucou et al. 2011; Ergül et al. 2011; De Andres et al. 2012).

Southeastern Turkish wild grape V. v. ssp. sylvestris populations and their relationship with cultivated grape genotypes have however not been studied yet and the present work aims to analyse genetic relationships between

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wild and cultivated grape accessions in this area of particular significance in grapevine domestication history.

MATERIAL AND METHODS

Plant material

In total 34 samples were analyzed on this study with 21 wild grapevines samples and 11 cultivated grape accessions collected from three different locations (Diyarbakır, Elazığ, Siirt) in southeast Turkey (Fig. 1, Table 1); Cabernet Sauvignon and Merlot were used as reference (outgroup) cultivars. In this study, the wild populations collected were usually located along river banks in both hilly areas and on the sides of valleys, natural expanses which have not been markedly altered for a long time and remote from agricultural and residential areas. All wild samples were ampelographically characterized on the collecting sites (DEĞIRMENCI Karatas et al. 2014) and further grown in greenhouse conditions. From these samples shoot tips were collected later for DNA analyses.

DNA isolation and PCR amplification

DNA was extracted from spring young leaves as described by LAUCOU et al. (2011). Microsatellite analyses were performed on 22 microsatellite markers (nSSRs) well distributed across the 19 grape chromosomes (DOLIGEZ et al. 2006) as previously described (LAUCÔBE et al. 2007), two of the VMC series (VMC1b11, VMC4f3; Vitis Microsatellite Consortium, (ADAM-BLONDON et al. 2004)), nine of the VVI series (VVIn01, VVIn16, VVIn54, VVIn73, VVIp31, VVIp60, VVIp37, VVIp67, VVIp52, (MERDINOĞLU et al. 2005)), eight of the VVMD series (VVMD5, VVMD7, VVMD21, VVMD24, VVMD25, VVMD28, VVMD32, VVMD32 (BOWERS et al. 1996, 1999)), VVS2 (THOMAS and SCOTT 1993; THOMAS et al. 1994), VrZAG62 and VrZAG79 (SEFC et al. 1999). We also used the three chloroplast loci (ccmp3, ccmp5 and ccmp10 (POWELL et al. 1995)) found to be polymorphic in Vitis vinifera samples (ARROYO-GARCÍA et al. 2002).

Amplifications were performed using a TC412 (Techne) thermocycler as described by LAUCOU et al. (2011). Reactions were performed on a mixture (20 µl final volume) containing 10 ng µl⁻¹ genomic DNA, 2 µl buffer 10× (Qiagen), 200 µM deoxynucleoside triphosphate, 2.5 mM MgCl₂, 0.08 µl Taq polymerase (Qiagen), 0.32 pM of unlabelled primer and a variable quantity of the labelled primer depending on the marker. Amplification conditions included an initial denaturation step of 4 min at 95°C followed by 35 cycles of 1 min at 94°C, 1 min at 56°C for all loci (except for locus VMC1b11 and VMC4f3 at 60°C), 2 min at 72°C, with a final extension step (6 min at 72°C). Multiplexes were planned with a maximum of three colours, taking into account the size of the amplified fragments and up to seven markers per sequencing run were mixed as previously described by DiVECCHI STARAZ (2007) and LACOMBE et al. (2007).

Data analysis

The genetic analysis ‘IDENTITY’ 1.0 program (WAGNER and SEFC 1999) according to PAETKAU et al. (1995) was used to calculate allele frequency and number, expected and observed heterozygosity, estimated frequency of null alleles, and probability of identity per locus. Genetic dissimilarity was determined with the ‘MICROSAT’ program, ver. 1.5 (MINCH et al. 1995) using proportion of shared alleles, which was calculated using ps (option 1 – (ps)) as described by BOWCOCK et al. (1994). The results were then converted to a similarity matrix and a dendrogram was constructed with UPGMA (unweighted pair-group method with arithmetic mean, SNEATH and SOKAL 1973), using the NTSYS-pc software (Numerical Taxonomy and Multivariate Analysis System, ver. 2.0, ROHLF 1988).

GENETIX 4.02 computer package (BELKHIR 1999) was used to calculate gene diversity (He) (NEI 1973) and observed heterozygosity (Ho) per population.

For cpSSR analysis, allelic and haplotypic frequencies within each population were directly estimated as the percentage of individuals sharing the same allele or haplotype in each sample of cultivated and wild grapevines. Gene diversity (He) was calculated as in WEIR (1996), where n equals the number of alleles and pi equals the frequency of the allele in the population. Haplotype diversity (Hd) was calculated in the same manner as gene diversity, with n and pi referring to haplotypes.

RESULTS

Genetic diversity of the Turkish grape accessions was measured for nuclear microsatellites by estimating the average number of observed alleles per locus (Na), observed heterozygosity (Ho) and estimated heterozygosity (He).

Genetic diversity within the collection of 34 grapeaccessions were assessed by 22 nuclear and three chloroplast SSR markers. We detected a total of 61 alleles at the 22 nSSRs loci analyzed. The number of alleles per SSR locus ranged from 4 (VVIn16) to 20 (VVlv67) and the mean

Fig. 1. Collection sites of Vitis vinifera ssp. sylvestris from Eastern Turkey.
Table 1. List of grapevine accessions analyzed in this study.

| N  | Population | Location (province) | Location (town) | Main use – genotype          |
|----|------------|---------------------|-----------------|------------------------------|
| 1  | C1         | Diyarbakır          | Çüngüş1         | Wild (V. v. ssp. sylvestris) |
| 2  | C2         | Diyarbakır          | Çüngüş2         | Wild (V. v. ssp. sylvestris) |
| 3  | C3         | Diyarbakır          | Çüngüş3         | Wild (V. v. ssp. sylvestris) |
| 4  | C4         | Diyarbakır          | Çüngüş4         | Wild (V. v. ssp. sylvestris) |
| 5  | D1         | Diyarbakır          | Boğazkere      | Wine (V. v. ssp. sativa)     |
| 6  | D2         | Diyarbakır          | Tahannebi      | Table (V. v. ssp. sativa)    |
| 7  | D4         | Diyarbakır          | Abdullah       | Table (V. v. ssp. sativa)    |
| 8  | D6         | Diyarbakır          | Hatunparmaği   | Table (V. v. ssp. sativa)    |
| 9  | E1         | Elazığ              | Sılfoni        | Table (V. v. ssp. sativa)    |
| 10 | E2         | Elazığ              | Besni          | Table (V. v. ssp. sativa)    |
| 11 | E3         | Elazığ              | Kèsirir        | Table (V. v. ssp. sativa)    |
| 12 | E4         | Elazığ              | Kırmızı Sılfoni| Table (V. v. ssp. sativa)    |
| 13 | E5         | Elazığ              | Agın           | Table (V. v. ssp. sativa)    |
| 14 | E6         | Elazığ              | Kohnu          | Table (V. v. ssp. sativa)    |
| 15 | E7         | Elazığ              | Ergani1        | Wild (V. v. ssp. sylvestris) |
| 16 | ER1        | Diyarbakır          | Ergani2        | Wild (V. v. ssp. sylvestris) |
| 17 | ER2        | Diyarbakır          | Kulp1          | Wild (V. v. ssp. sylvestris) |
| 18 | K1         | Diyarbakır          | Lice1          | Wild (V. v. ssp. sylvestris) |
| 19 | L1         | Diyarbakır          | Lice3          | Wild (V. v. ssp. sylvestris) |
| 20 | L3         | Diyarbakır          | Lice4          | Wild (V. v. ssp. sylvestris) |
| 21 | L4         | Diyarbakır          | Maden1         | Wild (V. v. ssp. sylvestris) |
| 22 | M1         | Elazığ              | Maden2         | Wild (V. v. ssp. sylvestris) |
| 23 | M2         | Elazığ              | Maden3         | Wild (V. v. ssp. sylvestris) |
| 24 | M3         | Elazığ              | Maden4         | Wild (V. v. ssp. sylvestris) |
| 25 | M4         | Elazığ              | Maden5         | Wild (V. v. ssp. sylvestris) |
| 26 | M5         | Elazığ              | Maden6         | Wild (V. v. ssp. sylvestris) |
| 27 | M7         | Elazığ              | Maden7         | Wild (V. v. ssp. sylvestris) |
| 28 | M8         | Elazığ              | Maden8         | Wild (V. v. ssp. sylvestris) |
| 29 | M9         | Elazığ              | Maden9         | Wild (V. v. ssp. sylvestris) |
| 30 | S1         | Siirt               | Pervari1       | Wild (V. v. ssp. sylvestris) |
| 31 | S2         | Siirt               | Pervari2       | Wild (V. v. ssp. sylvestris) |
| 32 | S3         | Siirt               | Pervari3       | Wild (V. v. ssp. sylvestris) |
| 33 | CS         | International       | Cabernet-Sauvignon | Wine (V. v. ssp. sativa)           |
| 34 | M          | International       | Merlot         | Wine (V. v. ssp. sativa)      |

allele number per locus was 10.09 (Table 2). Expected heterozygosity ranged from 0.586 (VVlVb01) to 0.898 (VVlV67). The lowest observed heterozygosity (0.545) was detected at the VVMD21 locus and the highest one (0.906) at the VVMD28 locus. Probability of identity values ranged from 0.030 (VVlV67) to 0.801 (VVlVh54).

The SSR-based dendrogram showing the genetic relationships among Turkish wild and cultivated grapevine accessions is shown in Fig. 2. Southern Turkish grape accessions clustered in four major groups.

The dendrogram revealed four groups labelled G1, G2, G3 and G4. Group 1, included most of Elazığ accessions and only two of Diyarbakır wild accessions, D2 (Tahannebi-standard variety which is grown in Diyarbakır and Elazığ) and S3 (wild sample from Siirt city, very close to Elazığ). It can be noted that wild accession C1 originated from Çüngüş town of Diyarbakır, is also very close to Elazığ city. Most of Diyarbakır accessions were included in group 2 in which local standard grape cultivars were grouped with wild samples. Only three grape cultivars, E4 (local Elazığ sample), M7 (wild sample of Maden town in Elazığ) and Besni (E3 standard cultivar) were classified in this group. The Öküzgözü grape variety, one of the best wine cultivar in Turkey, located in Elazığ, clustered in group 1. Similarly, the Boğazkere grape variety, also one of the best wine cultivar of Diyarbakır city, clustered in group 2. The rest of the wild accessions studied grouped in group 3 and 4. Reference cultivars Cabernet Sauvignon and Merlot presented a subgroup of the group 4.

The closest genetic relationship was observed between the two genotypes D1 (standard cultivar ‘Boğazkere’) - ER2 (V. v. sylvestris) (0.875), followed by E5 (local cultivar) - M9 (V. v. sylvestris) (0.861) and D6 (standard cultivar ‘Hatunparmaği’) - M7 (V. v. sylvestris) (0.750). Our microsatellite-based dendrogram revealed a clear separation between domesticated and wild accessions in
Table 2. Genetic parameters for SSR loci in Turkish accessions.

| Locus     | Allele size range (bp) | N  | He    | Ho    | F    | PI     |
|-----------|------------------------|----|-------|-------|------|--------|
| VMC1b11   | 165–196                | 13 | 0.826 | 0.757 | 0.037| 0.086 |
| VMC4f3    | 162–203                | 15 | 0.869 | 0.748 | 0.068| 0.049 |
| VVlb01    | 290–312                | 5  | 0.586 | 0.781 | −0.123| 0.336 |
| VVlh54    | 139–179                | 13 | 0.839 | 0.848 | −0.005| 0.801 |
| VVln16    | 147–155                | 4  | 0.650 | 0.594 | 0.034| 0.269 |
| VVln73    | 256–269                | 6  | 0.719 | 0.594 | 0.481| 0.219 |
| VVlp31    | 172–190                | 10 | 0.859 | 0.848 | 0.005| 0.065 |
| VVlp60    | 303–330                | 11 | 0.749 | 0.580 | 0.560| 0.139 |
| VVlq52    | 71–83                  | 6  | 0.708 | 0.676 | 0.018| 0.245 |
| VVlv37    | 145–177                | 12 | 0.847 | 0.636 | 0.114| 0.062 |
| VVlv67    | 329–397                | 20 | 0.898 | 0.818 | 0.042| 0.030 |
| VVMD21    | 241–255                | 8  | 0.639 | 0.545 | 0.057| 0.220 |
| VVMD24    | 204–218                | 8  | 0.804 | 0.818 | −0.007| 0.111 |
| VVMD25    | 238–254                | 6  | 0.770 | 0.848 | −0.044| 0.164 |
| VVMD27    | 172–191                | 10 | 0.816 | 0.824 | −0.004| 0.108 |
| VVMD28    | 216–280                | 15 | 0.873 | 0.906 | −0.017| 0.051 |
| VVMD32    | 239–271                | 8  | 0.829 | 0.866 | −0.020| 0.091 |
| VVMD5     | 223–244                | 11 | 0.834 | 0.719 | 0.063| 0.082 |
| VVMD7     | 233–255                | 9  | 0.817 | 0.818 | −0.0005| 0.102 |
| VVS2      | 122–153                | 12 | 0.876 | 0.906 | −0.016| 0.052 |
| VrZAG62   | 188–204                | 8  | 0.817 | 0.710 | 0.059| 0.107 |
| VrZAG79   | 238–270                | 12 | 0.802 | 0.706 | 0.053| 0.117 |
| Mean      |                        | 10.090 | 0.792 | 0.752 | 0.062| 0.159 |

N: Number of alleles, He: Expected heterozygosity, Ho: Observed heterozygosity, PI: Probability of identity, F: Frequency of null alleles

Turkish germplasm (Fig. 2). Except for a few grape accessions, the similarity index value was generally below 0.500. Therefore, for each sample collected from different locations in nature, it can be said that wild vines have acquired a distinct genotype.

Genetic variability within the samples studied: observed and expected heterozygosity (Ho and He), mean number of alleles (MNA), averaged over loci, are presented in Table 3. Gene diversities (He) were high both in wild and cultivated populations. The highest value was obtained for the wild sample (He = 0.7914) and the lowest variation was observed in the cultivated grape germplasm (He = 0.7119). The mean number of alleles per population (MNA) ranged from 8.8 (wild) to 5.6 (cultivated).

A high level of gene diversity was detected in the wild grape population despite its smaller size. This can be correlated with the outbreeding mating system of these dioecious individuals (Grassi et al. 2003).

The three cpSSR molecular markers presented variation in size both for the cultivar sample and in wild accessions (Table 4). Two size variants were detected for cpSSR3 (106 and 107 bp), cpSSR5 (104 and 105 bp), and cpSSR10 (115 and 116 bp). Allelic frequencies for cultivars varied from 0.45 (cpSSR3–107, cpSSR5–104 and cpSSR10–115) to 0.55 (cpSSR3–106, cpSSR5–105 and cpSSR10–116). Allele frequencies in the wild gene pool varied from 0.29 (cpSSR10–116) to 0.71 (cpSSR10–115). The three studied loci presented the same genetic diversity (He) value of 0.495 for cultivar population. Concerning wild accessions,
genetic diversity (He) at these loci ranged from 0.41 (cpSSR10) to 0.5 (cpSSR3, cpSSR5) (Table 4). The six alleles identified at the three chloroplast microsatellite loci in cultivars gene pool fell within the two haplotypes C and D previously described in the cultivated compartment of grapevine (ARRoyo-Garcia et al. 2002, 2006) with haplotype frequencies of 55% and 45% respectively (Table 5). Haplotypic genetic diversity (Hd) for the cultivars was 0.495.

For wild grapevines, the six alleles fell into three haplotypes, B, C and D. Haplotype D was the most frequent (48%) in our sample and with 24% and 28% frequencies respectively for haplotypes B and C (Table 6).

DISCUSSION

Our study is the first genetic diversity analysis of the wild grapevines in the southeast region of Turkey. During our research we observed a large number of wild grapevine populations in this area. However, this first study was performed with few genotypes only to provide an example. The most debated subject is: were these wild vines true *Vitis vinifera* ssp. *sylvestris*? To determine whether these wild genotypes are real *Vitis vinifera* ssp. *sylvestris* or not, clear information can be accessed by relationships studies on larger populations, parentage relationships and phylogenetic studies. Wild vines were collected from mountainous areas and riverbanks 50–60 km away from the city center. As, in the area, traditional viticulture is performed without grafting the likelihood of any rootstock genepool introgression is almost nil. During the field prospection, we also found very small berry clusters on some (M3, L2 and K1) sampled individuals. Ampelographic investigation on leaf and flower showed that some of wild samples showed very similar morphologic characters with *Vitis vinifera* ssp. *sylvestris* (Değirmenci Karataş et al. 2014).

Domesticated plants often have the potential to spontaneously hybridize with their wild relatives that are growing in close proximity (Ellstrand et al. 1999). Such hybridization leads to gene flow “the incorporation of genes into the gene pool of one population from one or more populations” (Futuyma 1998; El Oualkadi 2011). Due to dispersion by birds, cultivated grapevine was able to extend over large territories and often hybridized with native *Vitis sylvestris* plants (Bodor et al. 2010).

### Table 3. Genetic variability within the studied population: observed and expected heterozygosity (Ho and He), mean number of alleles (MNA), averaged over loci. Values in brackets are standard deviations.

| Population      | $H_o$  | $H_e$  | MNA |
|-----------------|--------|--------|-----|
| Wild sample     | 0.7773 (± 0.0829) | 0.7914 (± 0.0807) | 8.8182 |
| Cultivated sample | 0.7200 (± 0.0988) | 0.7119 (± 0.0948) | 5.5909 |

### Table 4. Allele size, allelic frequency and genetic diversity (He) in the analyzed samples.

| Locus | Cultivars | Wild accessions |
|-------|-----------|----------------|
|       | Allele size | Allelic frequency | He | Allelic frequency | He |
| CCMP3 | 106        | 0.55            | 0.52 |
|       | 107        | 0.45            | 0.48 |
|       | 104        | 0.45            | 0.48 |
|       | 105        | 0.55            | 0.52 |
|       | 115        | 0.45            | 0.71 |
|       | 116        | 0.55            | 0.29 |

### Table 5. Chloroplast haplotypes, frequencies and haplotypic diversity (Hd) in the cultivar samples.

| Sample name | cpSSR3 | cpSSR5 | cpSSR10 | Haplotype | Frequency | Hd |
|-------------|--------|--------|---------|-----------|-----------|----|
| D4          | 107    | 104    | 115     | D         |           |    |
| E5          | 107    | 104    | 115     | D         |           |    |
| E6          | 107    | 104    | 115     | D         |           |    |
| E7          | 107    | 104    | 115     | D         | 0.45      |    |
| D1          | 106    | 105    | 116     | C         |           |    |
| D2          | 106    | 105    | 116     | C         |           |    |
| D6          | 106    | 105    | 116     | C         |           |    |
| E2          | 106    | 105    | 116     | C         |           |    |
| E3          | 106    | 105    | 116     | C         | 0.55      | 0.495 |

### Table 6. Chloroplasts haplotypes, frequencies and haplotypic diversity Hd in the wild accessions.

| Sample name | CCMP3 | CCMP5 | CCMP10 | Haplotype | Frequency | Hd |
|-------------|-------|-------|--------|-----------|-----------|----|
| C1          | 107   | 104   | 115    | D         |           |    |
| C2          | 107   | 104   | 115    | D         |           |    |
| ER1         | 107   | 104   | 115    | D         |           |    |
| K1          | 107   | 104   | 115    | D         |           |    |
| L4          | 107   | 104   | 115    | D         |           |    |
| M2          | 107   | 104   | 115    | D         |           |    |
| M5          | 107   | 104   | 115    | D         |           |    |
| M8          | 107   | 104   | 115    | D         |           |    |
| M9          | 107   | 104   | 115    | D         |           |    |
| S1          | 107   | 104   | 115    | D         | 0.48      |    |
| C4          | 106   | 105   | 116    | C         |           |    |
| ER2         | 106   | 105   | 116    | C         |           |    |
| L3          | 106   | 105   | 116    | C         |           |    |
| M7          | 106   | 105   | 116    | C         |           |    |
| S2          | 106   | 105   | 116    | C         |           |    |
| S3          | 106   | 105   | 116    | C         | 0.28      |    |
| M1          | 106   | 105   | 115    | B         |           |    |
| M3          | 106   | 105   | 115    | B         |           |    |
| M4          | 106   | 105   | 115    | B         |           |    |
| C3          | 106   | 105   | 115    | B         |           |    |
| L1          | 106   | 105   | 115    | B         | 0.24      | 0.63 |
The molecular analysis demonstrate that wild and domesticated Turkish grapevine germplasms are genetically divergent. Wild accessions collected from different locations had different genetic profiles. However, it is important to underline that the results of this phenetic analysis cannot be used to draw conclusions with regard to the degree of kinship between the cultivars since clusters illustrates similarity rather than kinship (SeFC et al. 1999; Pellerone et al. 2001).

Various authors have used 22 SSR loci successfully for relationship studies of wild grape accessions (Bodor et al. 2010; Garcia Muñoz et al. 2011; Laucou et al. 2011). As a result of these analyses, the genetic similarity indexes of wild vine are found to be generally low.

The three cpSSR loci studied here were found to be polymorphic in our sample of cultivated and wild Turkish accessions. This is comparable to results of Arroyo-García et al. (2002), Dzhambazova et al. (2009) and Riahi et al. (2011), although Grassi et al. (2003), ImaZio et al. (2006) and DOULATY BANEH et al. (2007), found that only the cpSSR3 and cpSSR10 loci were polymorphic in their conditions.

Comparable levels of genetic diversity (He) were observed among the studied loci either in cultivated or wild samples. He values for cultivars at loci cpSSR3, cpSSR5 were higher than the genetic diversity observed in Tunisian cultivars (Riahi et al. 2011) who cited a value of 0.21, but were similar to results of Arroyo-García et al. (2002) who reported a 0.49 value for these two loci. However, the level of genetic diversity observed at the cpSSR10 locus is lower than the value recorded for other grapevine cultivars i.e. 0.62 in Riahi et al. (2011) an 0.61 in Arroyo-García et al. (2002).

Concerning wild accessions, genetic diversity (He) at loci cpSSR3 and cpSSR5 was comparable to results of Riahi et al. 2011 for Tunisian wild grapevines (0.40) while level of genetic diversity for cpSSR10 was lower than the 0.65 level recorded in Tunisian wild grapevines (Riahi et al. 2011). Haplotypic genetic diversity (Hd) for cultivars was lower than that observed in Tunisian (0.688, Riahi et al. 2011; 0.74, EL Oualkadi et al. 2011), Algerian (0.67, El Oualkadi et al. 2011), Iranian (0.668, DOULATY BANEH et al. 2007), and Moroccan cultivars (0.71, El Oualkadi et al. 2011) as well as in cultivars from Spain and Greece (0.64, Arroyo-García et al. 2002).

The haplotypic genetic diversity was higher in Turkish wild accessions than in cultivars. Comparable levels were recorded in previous reports concerning wild grapevine accessions originating from different areas in the world (Riahi et al. 2011; Grassi et al. 2003). However this diversity level was higher than that observed for Iranian (0.5, DOULATY BANEH et al. 2007), Morrocan (0.32) and French (0.31) wild grapevines (El Oualkadi et al. 2011).

Our results confirm previous studies and highlight that haplotype frequencies of cultivated grapevines seem to depend on the Vitis vinifera sample analyzed. A higher haplotypic genetic diversity which reached 0.63 was recorded for wild accessions. Indeed, haplotypes A and B which are absent from our analysis appear most frequently in the analysis of other samples of cultivars. And in the present study, the putatively ancestral chlorotype B was detected at a low frequency of 0.24. Chlorotype B has been suggested to be an ancestral one since it didn’t show a marked geographical distribution and was represented both homogeneously and at a low frequency in the Eur-Asian Region (Arroyo-García et al. 2006). Consequently, a special importance should be given to chlorotype B analysis in future studies in order to better understand grapevine domestication process.

While haplotype D is reportedly present with low frequency in ’ssp. Sativa’ cultivars, it is present with high frequency in our samples. And its distribution is comparable in both samples. As regards chlorotypes however, chlorotype C is more abundant in the cultivated sample, whereas chlorotype B is totally absent from this sample.

Analyses of chlorotype diversity in sylvestris populations showed that central Mediterranean and eastern populations had higher diversity values than western populations (Arroyo-García et al. 2006), which, based on phenotypic variation (Gökbayrak and Soylemezoğlu 2010) and in agreement with Negru in 1938, suggests that the Anatolian peninsula and Transcaucasian regions are indeed the Vitis vinifera ‘diversity center’.

This et al. (2006) indicated that analysis of wild grapes from eastern countries such as Turkey, Iran or Georgia, the presumed centre of primo-domestication, will be fundamental for understanding the role of Vitis vinifera ssp. sylvestris in the domestication process. The genetic distinction observed between wild and domesticated grapevines suggests that wild germplasm could be used as a source of novel alleles (Zecca et al. 2009). Evaluation of the genetic diversity, differentiation and relationship among wild grape specimens from different areas will contribute to a better understanding of the process of grapevine domestication (El Oualkadi et al. 2011).

This work confirms the usefulness of nSSR and cpSSR markers to provide information on genetic diversity and relationship among wild and cultivated grapes. Our genetic data show that southern Turkish wild and cultivated grape germplasms are an important genetic source for grape breeding. Molecular analysis could help understanding the process of grapevine domestication. The results of the present work could also be the basis for future studies about phylogenetic relationships in the Vitis genus.
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REFERENCES

Adam-Blondon, A. F., Roux, C., Claux, D. et al. 2004. Mapping 245 SSR markers on the Vitis vinifera genome: a tool for grape genetics. – Theor. Appl. Genet. 109: 1017–1027.

Ağaoğlu, Y. S. and Çelik, H. 1987. The work on the conservation of germplasm of the vine in Turkey. – Results of German–Turkish University Partnerships in the Agricultural Sector, Göttingen Symposium (in German), p. 221–230.

Ağaoğlu, Y. S. Söylemezoglu, G., Çalışkan, M. et al. 1998. Identification of some native and foreign grape varieties using isozyme banding patterns by polyacryl-amide gel electrophoresis. – Proc. 4th Vitic Symp., Oct. 1998, Yalova, Turkey, pp. 145–151.

Arroyo-Garcia, R., Lefort, F., Teresa de Andrés, M. et al. 2002. Chloroplast microsatellite polymorphisms in Vitis species. – Genome 45: 1114–1129.

Arroyo-Garcia, R., Ruiz-Garcia, L., Bolling, L. et al. 2006. Multiple origins of cultivated grapevine (Vitis vinifera L. ssp. sattiva) based on chloroplast DNA polymorphisms. – Mol. Ecol. 15: 3707–3714.

Belkhir, K. 1999. GENETIX, ver. 4.02 a windows program for population genetic analysis. – Laboratoire genéome, populations: interactions UPR 9060 du CNRS. Univ. Montpellier 2, Montpellier, France.

Bodor, P., Hohn, M., Pedryc, A. et al. 2010. Conservation value of the native Hungarian wild grape (Vitis sylvestris Gmel.) evaluated by microsatellite markers. – Vitis 49: 23–27.

Bowcock, A. M., Ruiz-Linares, A., Tomfohrde, J. et al. 1994. High resolution of human evolutionary trees with polymorphic microsatellites. – Nature 368: 455–457.

Bowers, J., Boursiquot, J. M. and This, P. 1999. Historical genetics: the parentage of Chardonnay, Gamay, and other wine grapes of northeastern France. – Science 285: 1562–1565.

Bowers, J., Dangl, G. S. and Vignani, R. 1996. Isolation and characterization of endangered wild grapevine Vitis vinifera L. subsp. sylvestris (Gmelin) Hegi in Europe. – Studying wild and cultivated grapevine and building up a regional collection for Italy. – SupAgro, Montpellier, France.

Doligez, A., Adam-Blondon, A. F. and Cipriani, G. 2006. An integrated SSR map of grapevine based on five mapping populations. – Theor. Appl. Genet. 113: 369–382.

Doulaty Baneh, H., Mohammadi, S. A., Labra, M. et al. 2007. Chloroplast microsatellites markers to assess genetic diversity in wild and cultivated grapevines of Iran. – Pakistan J. Biol. Sci. 10: 1855–1859.

Dzhambazova, T., Tsvetkov, I., Atanassov, I. et al. 2009. Genetic diversity in native Bulgarian grapevine germplasm (Vitis vinifera L.) based on nuclear and chloroplast microsatellite polymorphisms. – Vitis 48: 115–121.

El Ouakkadi, A., Ater, M., Laucou, V. et al. 2011. Study of genetic relationships between wild and domesticated grapevine in the north of Morocco. – Int. J. Biodivers. Conserv. 3: 512–526.

Ellstrand, N. C., Prentice, H. C. and Hancock, J. F. 1999. Gene flow and introgression from domesticated plants into their wild relatives. – Annu. Rev. Ecol. Syst. 30: 539–563.

Ergül, A., Perez-Rivera, G., Söylemezoglu, G. et al. 2011. Genetic diversity in Anatolian wild grapes (Vitis vinifera subsp. sylvestris) estimated by SSR markers. – Plant Genetic Resour. 9: 375–383.

Forneck, A., Walker, M., Schreiber, A. et al. 2003. Genetic diversity in Vitis vinifera ssp. sylvestris gmelin from Europe, the middle east and North Africa. – Acta Hort. (ISHS) 603: 549–552.

Futuyma, D. J. 1998. Evolutionary biology, 3rd edn. – Sinauer Press, pp. 447–479.

García Muñoz, S., Lacombe, T. and Teresa de André, M. et al. 2011. Grape varieties (Vitis vinifera L.) from the Balearic Islands: genetic characterization and relationship with Iberian Peninsula and Mediterranean Basin. – Genet. Res. Crop Evol. 59: 589–605.

Gökbayrak, Z. and Söylemezoglu, G. 2010. Grapevine throughout the history of Anatolia. – Int. J. Bot. 6: 465–472.

Grassi, F., Labra, M., Imazio, S. et al. 2003. Evidence of secondary grapevine domestication centre detected by SSR analysis. – Theor. Appl. Genet. 107: 1315–1320.

Hauptmann, H. 1997. Nevali cori. – Oxford Encyclopedia Archaeol. Near East 4: 131–134.

Imazio, S., Labra, M., Grassi, F. et al. 2006. Chloroplast microsatellites to investigate the origin of grapevine. – Genet. Resour. Crop Evol. 53: 1003–1011.

Karataş, H., Değirmenci, D., Velasco, R. et al. 2007. Microsatellite fingerprinting of homonymous grapevine (Vitis vinifera L.) varieties in neighboring regions of southeast Turkey. – Scientia Horticult. 114: 164–169.

Lacombe, T., Boursiquot, J-M., Laucou, V. et al. 2007. Relationships and genetic diversity within the accessions related to Malvasia held in the Domaine de Vassal grape germplasm repository. – Am. J. Enol. Viticult. 58: 124–131.

Laucou, V., Lacombe, T., Dechesne, F. et al. 2011. High throughput analysis of grape genetic diversity as a tool for germplasm collection management. – Theor. Appl. Genet. 122 :1233–1245.

McGovern, P. E. 2003. Ancient wine: the search of the origin of the viniculture. – Princeton Univ. Press.

Merdingo glu, D., Butterlin, G., Bevilacqua, L. et al. 2005. Development and characterization of a large set of microsatellite markers in grapevine (Vitis vinifera L.) suitable for multiplex PCR. – Mol. Breed. 15: 349–366.

Minch, E., Ruiz-Linares, A., Goldstein, D. B. et al. 1995. Microsat (ver. 1.4d): a computer program for calculating various statistics on microsatellite allele data. – Stanford Univ. Medical Center, Stanford, CT.
Nei, M. 1973. Analysis of gene diversity in subdivided populations. – Proc. Natl Acad. Sci. USA 70: 3321–3323.
Paetkau, D., Calvert, W., Stirling, I. et al. 1995. Microsatellite analysis of population structure in Canadian polar bears. – Mol. Ecol. 4: 347–354.
Pasternak, R. 1998. Investigations of botanical remains from Nevali cori PPNB, Turkey. – In: Damania, A., Valkoun, J., Willcox, G. et al. (eds), The origins of agriculture and crop domestication. ICARDA, Syria, pp. 170–177.
Pellerone, F. I., Edwards, J. K. and Thomas, M. R. 2001. Grapevine microsatellite repeats: isolation, characterization and use for grape germplasm from southern Italy. – Vitis 40: 179–186.
Powell, W., Morgante, M. and Andre, C. 1995. Hypervariable microsatellites provide a general source of polymorphic DNA markers for the chloroplast genome. – Curr. Biol. 3: 1023–1029.
Riahi, L., Zoghlamia, N., Laucou, V. et al. 2011. Use of chloroplast microsatellite markers as a tool to elucidate polymorphism classification and origin of Tunisian grapevines. – Scientia Horticult. 130: 781–786.
Rohlf, F. J. 1988. NTSYS-PC numerical taxonomy and multivariate analysis system. – Exeter Publishing, New York, NY.
Sefc, K. M., Regner, F., Turetschek, E. et al. 1999. Identification of microsatellite sequences in Vitis riparia and their applicability for genotyping of different Vitis species. – Genome 42: 1–7.
Sneath, P. H. A. and Sokal, R. R. 1973. Numerical taxonomy. – W. H. Freeman.
This, P., Lacombe, T. and Thomas, M. R. 2006. Historical origins and genetic diversity of wine grapes. – Trends Genet. 22: 511–519.
Thomas, M. R. and Scott, N. S. 1993. Microsatellite repeats in grapevine reveal DNA polymorphisms when analyzed as sequence-tagged sites (Stss). – Theor. Appl. Genet. 86: 985–990.
Thomas, M. R., Cain, P. and Scott, N. S. 1994. DNA typing of grapevine: a universal methodology and database for describing cultivars and evaluating genetic relatedness. – Plant Mol. Biol. 25: 939–949.
Uzun, H. I. and Bayır, A. 2010. Distribution of wild and cultivated grapes in Turkey. – Notulae Sci. Biol. 2: 83–87.
Wagner, H. W. and Sefc, K. M. 1999. Identity1.0. Centre for Applied Genetics. – Univ. of Agricultural Science, Vienna, Austria.
Weir, B. S. 1996. Genetic data analysis II. – Sinauer Ass.
Zecca, G., Mattia, F. De., Lovicu, G. et al. 2009. Wild grapevine: sylvestris, hybrids or cultivars that escaped from vineyards? Molecular evidence in Sardinia. – Plant Biol. ISSN 1435–8603: 1–6.