Genetic relationships of some local and introduced grapes (Vitis vinifera L.) by microsatellite markers

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ABSTRACT
In this study, the genetic relationships of 29 grape genotypes were defined with six SSR (simple sequence repeat) markers, and 65 polymorphic bands were identified, with matrix correlation (r) of 0.79. The expected heterozygosity (He) ranged from 0.783 (VrZAG62) to 0.869 (VVM7D) and the observed heterozygosity (Ho) from 0.483 (VrZAG62) to 0.897 (VVS2). According to the results, the smaller main cluster included only one ancient cultivar, ‘Buca Razakı’. Foça Karası, an ancient cultivar in the large main group, was separated from other grapes varieties. The first sub-cluster (S1) formed by mainly introduced cultivars included three cultivars, ‘Cabernet Sauvignon’, ‘Cabernet Franc’ and ‘Merlot’. The second sub-cluster (S2) was the largest group, and included 19 cultivars, ‘Semillion’, ‘Alicante Bouschet’, ‘Delbele’, ‘Çeşme Pembe’, ‘Grenache’, ‘Oküzgözü’, Petit Syrah’, ‘Papaz Karası’, ‘Colombard’, ‘Harsleleh’, ‘Moisylative’, ‘Şıka’, ‘Müşküle’, ‘Öhannes’, ‘Çinsaut’, ‘Kirmızı Şam’, ‘Kozak Gemresi’, ‘Siyah Gemre’ and ‘Yuvarlak Razakı’. The third sub-cluster (S3) included four cultivars, ‘Cardinal’, ‘Italia’, ‘Hafızali’ and ‘Malbee’. ‘Hafızali’ is an ancient cultivar and is included in this group. The fourth sub-cluster included only one ancient cultivar, ‘Pek Uzümü’. Based on the rates of similarities of the cultivars included in this study, the highest rate was recorded for ‘Oküzgözü-Petit Syrah’ (93%) in the second sub-cluster. The results reported here are important as the first steps towards better characterization of these grape genotypes and will aid future germplasm management and breeding efforts.

Introduction
The domestication of grape (Vitis vinifera L.) is believed to have occurred around 4000 BC from a perennial wild grape originally classified as V. sylvestris in Afghanistan, Black Sea and the Caspian Sea, however a recent archaeological finding suggested 5400–5000 BC as the probable period of domestication of the grape in the mountains of Iran [1,2]. Turkey, which is located in two main floristic regions (Near-East and Mediterranean), has a rich genetic diversity potential for grapevines because of its strategic position in the Mediterranean Sea and the heterozygotic hereditary structure of the grapevines have led to the emergence of greatly diversified varieties, types and species [3–5]. According to De Andrés et al. [6], the time when wild grapevines spread over Southern Europe and Western and Central Asia was during the Neolithic period. Archaeological and historical evidence indicates that grapevines were semi-domesticated in the Near East. Several studies have shown evidence supporting that secondary domestication events existed along the Mediterranean basin [7]. The viticulture practices in Turkey date back to 3500 BC, providing a deep-rooted history in Anatolia [8]. There are 1500 grape varieties in a germplasm collection of The National Germplasm Repository Vineyard of the Viticulture Research Institute in Turkey [9].

V. vinifera originated in the Middle East and some of today’s varieties could be more than a 1000 years old, and although these varieties generated most of the remaining cultivars over the centuries, it could be impossible to trace back their origin [10]. The domesticated grapevine spread over to European and North African Mediterranean countries and it is well documented that the diversity of grape varieties is very high around the world. A large number of grapevine varieties are reported in the literature. V. vinifera belongs to Family Vitaceae and genus Vitis with 60 species, including 10,000 varieties, many of which are synonyms.

The conventional methods of identification rely on ampelography based on the morphological differences between the varieties [11–13], i.e. leaf shape and
contours, growing shoots characteristics, flower sex, grape cluster shape and grape colour. Traditionally, morphological data have been used to characterize cultivars and to define relationships between them, but now, molecular markers and especially SSRs (simple sequence repeats) have become an essential tool for the cultivar identification of grape varieties and for clonal discrimination. Microsatellite markers are multi-allelic and highly polymorphic and accurate means of detecting genetic polymorphism [10,14–25].

The most important indigenous grapevine varieties in Turkey are the white ‘Sultani Çekirdeksiz’ (‘Sultanina’ or ‘Thompson Seedless’, particularly for table grape production), ‘Emir’, ‘Narince’ and ‘Misket’ and the red ‘Öküzgözü’ and ‘Boğazkere’ [2,26–28]. Over the last two decades, many researchers have performed studies on identification, characterization and conservation of germplasm in different countries from national to regional and local levels. Preserving grapevine biodiversity, especially autochthonous grapevines is very important for the production of new varieties [18,29–36]. It is of particular importance to study the grapevine gene potential in Turkey and to prepare a catalogue for this potential to validate it in international contexts [37]. The classification of Turkish grapevine cultivars is traditionally based on classical ampelographic characteristics according to OIV descriptors [38]. However, the common morphological identification has different limitations and sometimes does not provide enough evidence for the correct identification of the accessions. Driven by the current requirements for cultivar improvement, investigating genetic relationships is of great importance for germplasm conservation, evaluation and utilization information, which are essential for future grape breeding programmes. This study was carried out to perform genetic characterization of 29 local and introduced grape genotypes in an ex situ collection of the experimental field of Horticulture Department at Agriculture Faculty, Ege University. The grape genotypes were analysed by six SSRs markers required by the ‘European Project GENRES CT96 No 08’ [21], since different methods of SSR analysis may result in small deviations (1–2 bp) in allele size. In this study, the grape genotypes, including some ancient cultivars, were identified by SSR markers and their genetic relationships were analysed.

Materials and methods

Plant material

In this study, a total of 29 grapevine genotypes collected from the vineyard of the Horticulture Department at the Agriculture Faculty, in an ex situ collection of the experimental field of Ege University in Turkey, ’38°27’32” N and 27°13’21” S’, were analysed. The soil was a well-drained sandy loam. The vines were approximately 12 years old and all cultivars were subjected to standard pruning, fertilization and spraying. Grape cultivars were grafted on the rootstock 41B (Millardet et de Grasset) and each vine was given a 2.5 × 3-m (vixenrow). The accession names and the basic ampelographic characteristics of grape varieties used in this study are listed in Table 1.

Microsatellite analysis and grapevine microsatellite databases consulted

Six SSR markers were employed in the ‘European Project GENRES CT96 No 08’, and ‘2nd Edition of the OIV Descriptor list for grape varieties and Vitis species’ ([https://www.genres.de/, http://www.oiv.int/]) were used in polymerase chain reaction (PCR) studies [21,39]. A total of six sequence-tagged microsatellite site loci, fully characterized in earlier studies, were used as follows: VVS2 locus [36], VVMD5, VVMD7, VVMD27 loci [37], VrZAG79, VrZAG62 loci [38].

DNA extraction

DNA analysis was performed on 29 grapevine genotypes. Young leaf tissues of these genotypes were harvested in the spring. Genomic DNA was extracted using the cetyl trimethylammonium bromide (CTAB) method modified by Lodhi et al. [39] and stored at −80°C. An RNase treatment was performed on the eluted DNA samples. The concentrations and purity of DNA were calculated using NanoDrop® ND-1000 [28].

Genomic DNA was amplified by the PCR according to the following conditions: 5–10 ng of DNA template, 1 × PCR buffer (Fermentas, Life Sciences), 1.5 mmol/L MgCl2 (Fermentas, Life Science), 0.2 mmol/L for each dNTP, 0.5 μmol/L forward and reverse primer, 0.25 Unit Taq DNA polymerase (Fermentas, Life Sciences, Burlington, CA) and milliQ water to 25 μL PCR final volume. Negative controls consisting of reactions without a DNA template were included. PTC-100TM (MJ Research Inc.) was used for amplification. PCR thermocycling reactions were performed with a 2-min initial denaturation/activation step, followed by 40 cycles at 92°C for 30 s, annealing temperature (T_m = 52–56°C) for 1 min, and 72°C for 2 min, with a final extension step of 7 min at 72°C [28].

A DNA marker (100 bp) was used for the approximate quantification of the bands. Amplification products were...
observed on a 6% (w/v) polyacrylamide gel (Promega Silver Staining kit) stained using silver staining. The gel images of the bands were scanned and scored. The genetic profile of the accessions was compared to international databases in order to match each genotype to the corresponding variety when possible [40].

### Results and discussion

#### Genetic analysis and evaluation

The number of alleles, allele frequencies, expected (He) and observed (Ho) heterozygosity and probability of identity were calculated using Cervus© 3.0.7 (Tristan Marshall 1998–2014) software [41]. For cluster analysis, dendrograms for genotypes according to UPGMA (unweighted pair-group method with arithmetic average) grouping were obtained by using NTSYS-version 2.0 (Numerical Taxonomy and Multivariate Analysis System) [40] statistical package program. Total gene diversity was distributed hierarchically according to differentiation observed in the UPGMA tree. Principal component analysis (PCA) was performed based on the genotypic data from the SSR markers.

### Table 1. Basic ampelographic characteristics of the grape cultivars used in this study.

| Cultivar         | Cluster form | Berry form | Berry colour | Flavour    | Seed    |
|------------------|--------------|------------|--------------|------------|---------|
| Cabernet Sauvignon | Very dense   | Round      | Blue-black   | Little flavour | Present |
| Merlot           | Very dense   | Round      | Blue-black   | Little aromatic | Present |
| Sémillon         | Dense        | Round      | Green-yellow | Neutral    | Present |
| Alicante Boushet | Very dense   | Slightly flat | Blue-black  | Little flavour | Present |
| Buca Razाकsi    | Loose        | Long elliptic | Green-yellow | Little flavour | Present |
| Cabernet Franc   | Dense        | Round      | Blue-black   | Neutral    | Present |
| Cardinal         | Loose        | Round      | Blue-black   | Little aromatic | Present |
| Cinsaut          | Dense        | Long elliptic | Blue-black  | Neutral    | Present |
| Conlonbart       | Medium       | Obtuse-ovate | Green-yellow | Neutral    | Present |
| Çeşme Pembeși     | Loose        | Ovate      | Rose         | Neutral    | Present |
| Delbele          | Medium       | Obovate    | Blue-black   | Neutral    | Present |
| Foça Karası      | Very dense   | Round      | Blue-black   | Neutral    | Present |
| Grenache         | Medium       | Round      | Blue-black   | Little flavour | Present |
| Hafızali         | Loose        | Obtuse-ovate | Blue-black  | Neutral    | Present |
| Harselehe        | Dense        | Long elliptic | Dark red-violet | Neutral | Present |
| Italia           | Loose        | Round      | Red          | Little flavour | Present |
| Kırmızı Sam      | Very loose   | Round      | Red          | Little flavour | Present |
| Kozak Gemresi    | Loose        | Round      | Red          | Neutral    | Present |
| Malbe            | Dense        | Round      | Blue-black   | Neutral    | Present |
| Moiseyelative    | Medium       | Obtuse-ovate | Blue-black  | Little flavour | Present |
| Muşkül           | Loose        | Round      | Dark red-violet | Neutral | Present |
| Öhannes          | Loose        | Round      | Green-yellow | Little flavour | Present |
| Oküzgozü        | Loose        | Slightly flat | Rose        | Little flavour | Present |
| Papazkarass      | Very dense   | Round      | Red          | Little flavour | Absent |
| Pek Uziumüi      | Medium       | Obtuse-ovate | Blue-black  | Little flavour | Present |
| Petit Syrah      | Dense        | Round      | Blue-black   | Neutral    | Present |
| Siyah Gemre      | Loose        | Round      | Red          | Neutral    | Present |
| Şika             | Loose        | Ovate      | Dark red-violet | Neutral | Present |
| Yuvarlak Razākı  | Loose        | Round      | Green-yellow | Neutral    | Present |

### Table 2. Genetic parameters for SSR loci in some local accessions and introduced grapes (V. vinifera).

| Loci   | Number of alleles (n) | Expected heterozygosity (He) | Observed heterozygosity (Ho) | PIC      | Null allele frequencies |
|--------|-----------------------|------------------------------|------------------------------|----------|-------------------------|
| VVS2   | 13                    | 0.846                        | 0.897                        | 0.814    | -0.0467                 |
| VWM05  | 9                     | 0.785                        | 0.655                        | 0.738    | 0.0844                  |
| VWM07  | 10                    | 0.869                        | 0.621                        | 0.837    | 0.1610                  |
| VWM27  | 10                    | 0.792                        | 0.586                        | 0.749    | 0.1358                  |
| VrZAG62| 11                    | 0.783                        | 0.483                        | 0.736    | 0.2346                  |
| VrZAG79| 12                    | 0.785                        | 0.552                        | 0.746    | 0.1476                  |
| Total  | 65                    | 4.861                        | 3.794                        | 4.620    | –                       |
| Mean   | 10.833                | 0.810                        | 0.632                        | 0.770    | –                       |
allele frequencies for 29 grape cultivars analysed at 6 SSR markers. The total number of alleles for the analysed six SSR loci was 65. Based on the number of alleles, the highest allele number was obtained from VVS2 (13 alleles), followed by VrZAG79 (12 alleles), VrZAG62 (11 alleles), VVMD7 (10 alleles), VVMD27 (10 alleles) loci and VVMD5 locus with 9 alleles. The results obtained in our study corroborated the findings of similar previous studies [2,38, 43–46]. The most informative loci were VVMD7 (0.869), VVS2 (0.846), with a PIC value of 0.837 and 0.814, respectively. In our research, the mean PIC values (0.769) were lower than the values of expected heterozygosity (0.810). The expected heterozygosity of the investigated cultivars ranged from 0.783 (VrZAG62) to 0.869 (VVMD7) with a mean of 0.810, and the null allele frequencies were generally found to be close to zero or negative. The lowest observed heterozygosity (0.483) was detected at the VrZAG62 locus and the highest at the VVS2 loci (0.846). The average $He$ value was 0.810; this value is nearly similarly the one reported by Martinez et al. [47] (0.810) and Martin et al. [48] (0.806) and the mean PIC value was 0.769.

Microsatellites have been widely used for cultivar identification [49–51] and analysis of genetic relationships [52]. Microsatellite technology has been used in grapevine genetics because they have high degree of polymorphism [1].

The PIC value was calculated for each locus to evaluate the effectiveness of each marker. Table 3 shows the allele sizes, heterozygotes, homozygotes, locus frequencies and null allele frequencies for 29 grape cultivars analysed using SSR markers. The allele frequency was as follows: 130–187 in VVS2, 222–268 in VVMD5, 236–257 in VVMD7, 172–247 in VVMD27, 184–206 in VrZAG62 and 184–206 in VrZAG79. The most frequent alleles at each locus and their frequencies are presented in Table 4. The frequency of alleles

### Table 3. SSR loci, allele, heterozygotes (Het.), homozygotes (Hom.), frequency (Freq.) and null allele frequencies for 29 grape cultivars analysed by six SSR markers.

| Locus | Allele | Count | Het. | Hom. | Freq. | Freq. with null |
|-------|--------|-------|------|------|-------|----------------|
| VVS2  | 130    | 3     | 3    | 0    | 0.0517 | 0.0530        |
|       | 131    | 2     | 2    | 0    | 0.0345 | 0.0350        |
|       | 133    | 17    | 15   | 1    | 0.2931 | 0.3296        |
|       | 137    | 13    | 13   | 0    | 0.2241 | 0.2566        |
|       | 138    | 1     | 1    | 0    | 0.0172 | 0.0174        |
|       | 139    | 4     | 4    | 0    | 0.0690 | 0.0714        |
|       | 140    | 1     | 1    | 0    | 0.0172 | 0.0174        |
|       | 149    | 1     | 1    | 0    | 0.0172 | 0.0174        |
|       | 151    | 1     | 1    | 0    | 0.0172 | 0.0174        |
|       | 177    | 4     | 4    | 0    | 0.0690 | 0.0714        |
|       | 178    | 7     | 3    | 2    | 0.1207 | 0.0901        |
|       | 179    | 3     | 3    | 0    | 0.0517 | 0.0530        |
|       | 187    | 1     | 1    | 0    | 0.0172 | 0.0174        |
|       | 222    | 3     | 3    | 0    | 0.0517 | 0.0527        |
|       | 228    | 13    | 9    | 2    | 0.2241 | 0.2104        |
|       | 230    | 20    | 10   | 5    | 0.3448 | 0.3025        |
|       | 232    | 13    | 9    | 2    | 0.2241 | 0.2104        |
|       | 234    | 1     | 1    | 0    | 0.0172 | 0.0173        |
|       | 236    | 2     | 2    | 0    | 0.0345 | 0.0348        |
|       | 238    | 4     | 2    | 1    | 0.0690 | 0.0527        |
|       | 239    | 1     | 1    | 0    | 0.0172 | 0.0173        |
|       | 268    | 1     | 1    | 0    | 0.0172 | 0.0173        |
|       | 236    | 1     | 1    | 0    | 0.0172 | 0.0169        |
|       | 238    | 11    | 5    | 3    | 0.1897 | 0.1448        |
|       | 239    | 7     | 7    | 0    | 0.1207 | 0.1254        |
|       | 243    | 10    | 4    | 3    | 0.1724 | 0.1254        |
|       | 244    | 4     | 2    | 1    | 0.0690 | 0.0517        |
|       | 246    | 1     | 1    | 0    | 0.0172 | 0.0169        |
|       | 247    | 11    | 7    | 2    | 0.1897 | 0.1647        |
|       | 248    | 4     | 4    | 0    | 0.0690 | 0.0696        |
|       | 250    | 1     | 1    | 0    | 0.0172 | 0.0169        |
|       | 257    | 8     | 4    | 2    | 0.1379 | 0.1064        |

### Table 4. The most frequent alleles per locus and their frequency.

| SSR-marker | VVS2 | VVMD5 | VVMD7 | VVMD27 | VrZAG62 | VrZAG79 |
|------------|------|-------|-------|--------|---------|---------|
| Most frequent allele | 133 | 220 | 238–247 | 243 | 195 | 255 |
| Major allele frequency, % | 30.31 | 35.48 | 18.97 | 35.48 | 32.76 | 39.66 |
was registered for VrZAG79 – 255 (39.66%), VVMD27 – 243 (35.48%), VVMD5 – 230 (35.48%), VrZAG62 – 195 (32.76%), VVS2 – 133 (30.31%) and VVMD7 – 238–247 (18.97%).

Genetic relatedness

The dendrogram shown in Figure 1 was constructed using UPGMA for the evaluation of the genetic diversity and relatedness between the investigated cultivars. In the dendrogram, the investigated cultivars were separated into two main clusters. The smaller main cluster included only one ancient cultivar, ‘Buca Razakı’, which is a razaki grape variety. ‘Buca Razakı’ is completely separated from the other grape varieties. The Turkish genetic pool was formed during thousands of years of folk selection and later was enriched by hybridizations and mutations. Local varieties are an important resource of genes for viticulture. Their genotypes may be of interest in viticulture in addition to the advantage of their adaptation to local conditions.

The large cluster exhibited four distinct sub-clusters labelled S1, S2, S3 and S4. ‘Foça Karası’, an ancient cultivar in this group, is separated from other grapes varieties. The first sub-cluster (S1) formed by mainly introduced cultivars and included three ones: ‘Cabernet Sauvignon’, ‘Cabarnet Franc’ and ‘Merlot’. The second sub-cluster (S2) is the largest group, including 19 cultivars: ‘Semillion’, ‘Alicante Bouschet’, ‘Delbele’, ‘Çeşme Pembesi’, ‘Grenache’, ‘Öküzgözü’, ‘Petit Syrah’, ‘Papaz Karası’, ‘Colombard’, ‘Harsleleh’,

Figure 1. Dendrogram of hierarchical cluster analysis based on SSR markers. Note: 1: Cabernet Sauvignon; 2: Merlot; 3: Semillion; 4: Alicante Bouschet; 5: Buca Razakı; 6: Cabarnet Franc; 7: Cardinal; 8: Cinsaut; 9: Colombard; 10: Çeşme Pembesi; 11: Delbele; 12: Foça Karası; 13: Grenache; 14: Hafzali; 15: Harsleleh; 16: Italia; 17: Kirmızı Şam; 18: Kozak Genresi; 19: Malbe; 20: Moiseylative; 21: Müsküle; 22: Ohannes; 23: Öküzgözü; 24: Papaz Karası; 25: Pek Üzümü; 26: Petit Syrah; 27: Siyah Gemre; 28: Şika; 29: Yuvarlak Razakı.
Figure 2. Biplot based on PCA for some local and introduced grapes based on SSR markers. Note: 1: Cabernet Sauvignon; 2: Merlot; 3: Semillion; 4: Alicante Bouschet; 5: Buca Razakısı; 6: Cabernet Franc; 7: Cardinal; 8: Cinsaut; 9: Colombard; 10: Çeşme Pembesi; 11: Delbele; 12: Foça Karası; 13: Grenache; 14: Hafızalı; 15: Harslele; 16: Italia; 17: Kırmızı Şam; 18: Kozak Gemresi; 19: Malbe; 20: Moiseylative; 21: Müslüman; 22: Ohannes; 23: Öküzgözü; 24: Papaz Karası; 25: Pek Üzümü; 26: Petit Syrah; 27: Siyah Gemre; 28: Şıka; 29: Yuvarlaç Razaki.

‘Moiseylative’, ‘Şıka’, ‘Musulman’, ‘Ohannes’, ‘Cinsault’, ‘Kırmızı Şam’, ‘Kozak Gemresi’, ‘Siyaş Gemre’ and ‘Yuvarlaç Razak’. The matrix correlation ’r’ found at 0.79 and above showed reliability of the dendogram. Based on the rates of similarities of cultivars included in the study, the highest rate was recorded for ‘Öküzgözü–Petit Syrah’ (93%) in the second sub-cluster (S2). Very close relationships with high similarity were determined for ‘Öküzgözü’ and ‘Petit Syrah’ with the same pedigree or origin. ‘Öküzgözü’ (an ancient grape variety having a little flavour, a loose cluster form and a rose berry colour) and ‘Petit Syrah’ (an introduced variety having a neutral flavour, a dense cluster form and a blue-black berry colour) have different ampelographic features, but had high similarity ratios (93%), which may be associated with the gene flow that naturally occurred in ancient times. Since *V. vinifera* has been cultivated in the Mediterranean and Middle East areas since very old times, some varieties may be very ancient: Pinot noir, Muscat Blanc à Petits Grains, and Sultanina, for example, date back probably to one or two thousands of years ago [10,14,25].

The third sub-cluster (S3) included four cultivars: ‘Cardinal’, ‘Italia’, ‘Hafızalı’ and ‘Malbe’. ‘Hafızalı’ is an ancient cultivar. The fourth sub-cluster (S4) included only one ancient cultivar, ‘Pek Üzümü’. *V. vinifera* growing practice spread with historic migrations of people and progression of civilization; the same flow might be assumed for cultivated varieties [10]. The true origins of cultivated grape varieties can be masked because of migrations and heavy reduction of diversity [10]. Special care should be taken to conserve these cultivars in Turkey for the purpose of grape breeding and production of new varieties with new potential (i.e. resistance to disease) [2,53]. As previously acknowledged by Bergamini et al. [10], the origin assessment and pedigree reconstruction in grapevine varieties is even more difficult owing to synonymy and homonymy. In such cases, SSRs are often the markers of choice, since they can identify varieties despite changes of plant phenotype in different environments. Scientists also view SSR fingerprinting as suitable for studies into genetic relations and pedigrees, because SSR markers have co-dominant, neutral behaviour and Mendelien segregation [10,54,55].

The PCA based on the genotypic data from the SSR markers (Figure 2) showed that dim-1, dim-2 and dim-3 account for 28.57%, 7.95%, and 6.36% of the overall variation, respectively. The PCA results were nearly consistent with those of the UPGMA analysis, which had very small difference between ‘Öküzgözü’ and ‘Petit Syrah’. This close genetic relationship is also shown in Figure 1, and is supported by clear overlapped in the PCA (Figure 2). However, there were some differences between the dendogram and the PCA plot. The PCA results separated ‘Merlot’ from group S1, which may be due to differences in the calculation methods used in the methods.

In our genetic research, mainly ancient cultivars and introduced cultivars were divided into different groups. The obtained findings uncover the intricate nature of Turkish grape cultivars, considered peculiar to the area, but possibly being the remains of ancient varieties. Therefore, the application of modern techniques like SSRs to determine the genetic relationship between the studied genotypes has been extremely important.

**Conclusions**

Turkey has many indigenous grapevine varieties and the genetic analysis of their cultivars is essential for the correct description of genetic resources and the ascertainment of genetic relationships between grapevine genotypes and their pedigrees. The molecular characterization and analysis of the genetic structure in the Turkish grape germplasm based on allele frequencies and heterozygosity contributes to the knowledge about the levels and the distribution of genetic diversity of the investigated cultivars. Our results
confirmed the high effectiveness of using SSR-based genetic analysis of the grapevine germplasm and provide reliable information about genetic diversity and genetic relations between accessions.

Disclosure statement
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