

## Research Note

# Genetic Composition of the Ornamental Grape Roger's Red

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**Abstract:** Roger's Red is an ornamental grape cultivar prized for its scarlet-red fall foliage. It was selected from the wild in Northern California and has been considered a variant of the native *Vitis californica*. Roger's Red has red fruit flesh and juice, traits not characteristic of *V. californica*. Analysis of 11 simple sequence repeat markers showed that Roger's Red is a hybrid of *V. californica* and the *V. vinifera* cultivar Alicante Bouschet. Alicante Bouschet, a teinturier cultivar, has red fruit flesh and juice and has a long history of cultivation in the area where Roger's Red was first selected.

**Key words:** *Vitis californica*, hybrid grape, ornamental grape, microsatellite, SSR, DNA marker, null allele, leafroll virus

Roger's Red is a vigorous grapevine sold as an ornamental cultivar. Its sprawling habit makes it ideal for covering fences and arbors. The primary attraction of the cultivar is its leaves, which turn from dull green to scarlet red in the fall (Supplemental Figure 1). The vines also provide copious fruit; the small seedy berries have flesh and juice of a deep red color and are used for jelly, jams and hobby wines. Although the fruit has no commercial value, it is extremely attractive to birds and other wildlife.

Roger's Red was first selected as a wild vine in fall 1983 by Roger Raiche at the Native Plant Collection at the University of California Botanical Garden, Berkeley (UCBG). The vine was growing with other wild grapes clambering into oaks and redwoods along Palmer Creek Road in rural Sonoma County, ~8 miles west of Healdsburg, California. The one vine had brilliant orange-red leaf coloration, but otherwise had identical leaf sizes and shape when compared to the *Vitis californica* (Benth.) vines growing in the same area. The nearest winegrapes were ~4 miles east in the Dry Creek area (west of Healdsburg).

Cuttings from the wild vine were propagated at the UCBG and planted in the native area of the garden, where in fall 1984 the red leaf color trait had remained stable through

the propagation process. More cuttings were collected from the original wild vine and propagated at the UCBG and at nearby Tilden Botanical Garden. By 1990, commercial nurseries were propagating and selling Roger's Red from UCBG material. It is now grown from San Diego to Seattle and is popular with California native plant enthusiasts.

The cultivar is considered a red fall leaf color variant of native *V. californica* (Benth.). However, since the fruit flesh and juice are deep red, a trait associated with teinturier cultivars of *Vitis vinifera* (L.), the native heritage of Roger's Red has been questioned. For the last decade, many nurseries have sold the cultivar as a suspected hybrid.

Simple sequence repeat (SSR) DNA markers are well established as an effective tool for studying various aspects of European grape, *V. vinifera*, genetics: cultivar identification and germplasm management (Dangl et al. 2001, Thomas et al. 1994), parent/progeny relationships (Bowers and Meredith 1997, Ibáñez et al. 2009) and linkage mapping (Riaz et al. 2004). These markers, mostly cloned from *V. vinifera*, are present and, to varying degrees, polymorphic in other *Vitis* species (Sefc et al. 1999). They have been used to identify (Krivanek et al. 2006) and map (Riaz et al. 2006) markers linked to disease resistance genes in non-*V. vinifera* species and to document hybrid breeding programs (Bautista et al. 2008, Riaz et al. 2007). In this study, we use SSR DNA marker analysis to elucidate the heritage of Roger's Red. Species composition of both parents and cultivar identification of one parent are presented. This is the first report of DNA marker analysis of an ornamental grape cultivar.

## Materials and Methods

Six vines of Roger's Red were analyzed, two of which were from the original collection in the UCBG and the remaining four were from commercial sources. Three of the commercial vines were growing in the University of California, Davis (UCD) Arboretum. Nineteen *V. californica* samples were also tested. Fifteen of these samples were collected from vines growing wild in Northern California

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and four were vines in the National Clonal Germplasm Repository at Davis (NCGR-D). The vines at the NCGR-D were initially collected from several locations in California and Oregon (Table 1).

Young leaves from near the shoot tip were collected and rapidly dried at room temperature (Bautista et al. 2008). Total DNA was extracted and PCR amplifications were performed according to typical protocols (Bautista et al. 2008, Dangl et al. 2005). Eleven SSR markers known to be highly polymorphic in *V. vinifera* were analyzed: VVMD5, VVMD6, VVMD7, VVMD27, VVMD28, VVMD31, VVMD32 (Bowers et al. 1996, 1999), VrZAG62, VrZAG79, VrZAG93 (Sefc et al. 1999) and VVS2 (Thomas and Scott 1993). These 11 markers included the six internationally adopted reference markers (This et al. 2004). Amplified fragments were separated and sized by capillary electrophoresis on an ABI Prism 3100 Genetic Analyzer (Applied Biosystems, Foster City, CA) (Bautista et al. 2008). Each sample was tested at least twice at each marker.

Nei's unbiased gene diversity (Nei 1987), a measure of expected heterozygosity, was calculated separately for each of the 11 markers using the Excel Microsatellite Toolkit (Park 2001). The same tool was used to calculate observed homozygosities for the 11 markers and frequencies for the alleles observed in Roger's Red and *V. californica*.

The allele frequency and expected heterozygosity parameters for *V. californica* were based on the unique profiles obtained in this study. Three hundred profiles of wine and table grape cultivars historically presumed to be pure *V.*

*vinifera* were selected for comparison of allele frequency and expected heterozygosity parameters in *V. vinifera*. These selected profiles include all of the cultivars used for commercial production, past and present, in the area where Roger's Red was initially collected. The profile for Roger's Red and the unique *V. californica* profiles were also compared to the Grape DNA Identification Reference Database (unpublished) at Foundation Plant Services (FPS) to find matches and the parents of Roger's Red. This database has over 1,200 unique grape DNA profiles, including *V. vinifera*, rootstock and hybrid cultivars.

## Results and Discussion

To ascertain the genetic background of Roger's Red, six vines of this ornamental grape cultivar and 19 vines of *V. californica* were analyzed at 11 SSR markers known to be polymorphic in *V. vinifera*, grape rootstock, and hybrid cultivars (Bautista et al. 2008, Bowers et al. 1999, Sefc et al. 1999, This et al. 2004). The multilocus SSR profile was identical for all six Roger's Red samples. While the two vines from the UCBG are closely linked by vegetative propagation to the original wild vine, the four commercial vines, including the three vines at the UCD Arboretum, are likely the result of multiple cycles of propagation. The identical SSR profile of all six samples and the consistently observed phenotype, specifically the red fall leaf color, demonstrate that Roger's Red is a true cultivar, faithfully propagated by cuttings that can be traced back to the original wild vine. The SSR profile shared by all six of the Roger's Red vines did not match any of the *V. californica* samples in this study or any of the over 1,200 grape profiles in the FPS Reference Database.

Nineteen vines of *V. californica* were also tested at the same 11 SSR markers to develop a small database of profiles with which to compare the Roger's Red profile. The *V. californica* vines were assumed to be wild seedlings, each expected to have a unique profile. However, that was true for only 12 of the 19 samples. The remaining seven samples were divided into two groups, Vcal 01 and Vcal 02. Samples within each group were identical to each other at all 11 markers. The end result is 14 unique *V. californica* profiles (Vcal 01-14; Table 1, Table 2).

Both groups of identical profiles, Vcal 01 and 02, were from samples recently collected in Napa County. Wild *V. californica* is a long-lived, sprawling, climbing vine; canes will root given the opportunity. After years of growth, wild vines that appear to be separate individuals may be derived from the same seed, which may account for the identical profile shared by the four Vcal 01 samples, collected within 35 meters of one another. One of the Vcal 02 vines, however, was farther than 160 meters from the other two, making it less likely that all three vines originated from the same seed. There were also several pairs of vines with profiles that differed by only one allele but were geographically distant from each other. For example, Vcal 03 and Vcal 06 were farther than 10 miles apart but differed only at the VrZAG79 marker (Table 1, Table 2). Limited

**Table 1** Sources of the 19 *Vitis californica* samples. Multiple vines within the same profile group have identical SSR marker profiles.

| Profile group                  | Collection site <sup>a</sup>  |
|--------------------------------|-------------------------------|
| <b>California</b>              |                               |
| Vcal 01                        | Southwest Napa Valley         |
|                                | Southwest Napa Valley         |
|                                | Southwest Napa Valley         |
|                                | Southwest Napa Valley         |
| Vcal 02                        | Southwest Napa Valley         |
|                                | Southwest Napa Valley         |
|                                | Southwest Napa Valley         |
| Vcal 03                        | Southwest Napa Valley         |
| Vcal 04                        | Southwest Napa Valley         |
| Vcal 05                        | Southwest Napa Valley         |
| Vcal 06                        | East Napa County Hills        |
| Vcal 07                        | Central Napa Valley           |
| Vcal 08                        | Central Napa Valley           |
| Vcal 09                        | Central Napa Valley           |
| Vcal 10                        | Central Napa Valley           |
| Vcal 11                        | DVIT 1275, Central California |
| <b>Oregon (Jackson County)</b> |                               |
| Vcal 12                        | DVIT 1837, Rogue River Valley |
| Vcal 13                        | DVIT 1838, Rogue River Valley |
| Vcal 14                        | DVIT 1839, Rogue River Valley |

<sup>a</sup>DVITs are accession numbers for the National Clonal Germplasm Repository, Davis; the location given are those of the original source vines. Collection details for DVIT 1275 are unknown.

**Table 2** Genotypes of Roger's Red and 14 *Vitis californica* samples. Allele sizes are reported in base pairs.

| Profile     | VVMD5   | VVMD6   | VVMD7   | VVMD27  | VVMD28  | VVMD31 <sup>a</sup> | VVMD32  | VVMS2   | VrZAG62 | VrZAG79 | VrZAG93 |
|-------------|---------|---------|---------|---------|---------|---------------------|---------|---------|---------|---------|---------|
| Roger's Red | 238 248 | 211 214 | 243 243 | 191 194 | 239 247 | 212 212             | 251 253 | 135 145 | 189 199 | 245 257 | 223 231 |
| Vcal 01     | 248 248 | 214 214 | 241 241 | 191 191 | 239 239 | nd nd               | 253 253 | 135 135 | 199 213 | 245 245 | 227 227 |
| Vcal 02     | 246 248 | 214 214 | 241 241 | 191 191 | 239 239 | nd nd               | 253 253 | 135 155 | 213 213 | 245 257 | 227 227 |
| Vcal 03     | 248 248 | 214 214 | 241 241 | 191 191 | 239 239 | nd nd               | 253 253 | 135 135 | 213 213 | 245 245 | 227 227 |
| Vcal 04     | 246 246 | 214 214 | 241 241 | 191 193 | 239 239 | nd nd               | 253 253 | 135 135 | 199 199 | 245 257 | 223 227 |
| Vcal 05     | 246 246 | 214 214 | 241 241 | 191 191 | 239 239 | nd nd               | 253 253 | 135 135 | 213 213 | 245 261 | 227 227 |
| Vcal 06     | 248 248 | 214 214 | 241 241 | 191 191 | 239 239 | nd nd               | 253 253 | 135 135 | 213 213 | 245 257 | 227 227 |
| Vcal 07     | 246 246 | 214 214 | 255 255 | 191 191 | 239 239 | nd nd               | 253 253 | 135 135 | 199 213 | 245 257 | 227 227 |
| Vcal 08     | 246 248 | 214 214 | 241 241 | 191 191 | 239 239 | nd nd               | 253 253 | 135 135 | 199 213 | 245 245 | 215 227 |
| Vcal 09     | 246 248 | 214 214 | 241 241 | 191 191 | 239 239 | nd nd               | 253 253 | 135 135 | 199 213 | 245 245 | 223 227 |
| Vcal 10     | 248 248 | 214 214 | 241 241 | 191 191 | 231 239 | nd nd               | 253 253 | 135 135 | 213 213 | 245 245 | 227 227 |
| Vcal 11     | 246 246 | 214 214 | 241 241 | 191 193 | 239 239 | nd nd               | 253 253 | 135 135 | 199 213 | 255 257 | 223 227 |
| Vcal 12     | 246 246 | 214 214 | 241 241 | 191 191 | 231 231 | nd nd               | 253 253 | 135 135 | 199 213 | 255 257 | 227 227 |
| Vcal 13     | 246 246 | 214 214 | 241 241 | 191 191 | 231 239 | nd nd               | 253 253 | 135 135 | 213 213 | 255 257 | 209 223 |
| Vcal 14     | 246 246 | 214 214 | 241 241 | 191 191 | 231 239 | nd nd               | 253 253 | 135 135 | 213 213 | 257 257 | 227 227 |

<sup>a</sup>A result of nd (no data) indicates no fragments were amplified.

genetic variability within a population increases the chance that two genetically distinct individuals will randomly have identical or nearly identical SSR marker profiles. Rather than indicating close familial relationships, these identical or extremely similar profiles may be a random result.

The variation within the 14 *V. californica* profiles is limited (Table 3). Expected heterozygosity by locus is between 0 and 0.62 and is 0.23 across all 11 markers. The limited variation is also expressed by high homozygosity and a small number of observed alleles (Table 3, Table 4). The *V. californica* samples in this study are geographically diverse and include three samples from southern Oregon (Table 1), the northern end of the species' range (Munz 1968). Although the sample size is small, given this geographic diversity, the limited observed genetic variability is surprising and may be due to the specific SSR markers used in this study. These markers, chosen from hundreds of available markers, are routinely used by researchers specifically because they are highly polymorphic in *V. vinifera*. Our use of these markers may have introduced a bias ("ascertainment bias"; Goldstein and Pollock 1997), accounting for the limited observed variability within the *V. californica* samples. This bias may also result in the use of markers that have mutations in or have lost priming sites in the alternative species, which may account for the high degree of homozygosity and for the failure to amplify any alleles at VVMD31 from the *V. californica* samples despite repeated attempts.

Roger's Red has been considered a red fall leaf color variant of native *V. californica* based on leaf morphology, growth habit, and the habitat from which it was collected. Although the *V. californica* profile database is small, the Roger's Red profile shares one allele with *V. californica* at 9 of the 11 markers (Table 2), suggesting that it is in part *V. californica*. The exceptions are VVMD7 and VVMD31, where Roger's Red is homozygous. The Roger's Red profile

**Table 3** Expected heterozygosity and observed heterozygosity at 11 SSR markers for two populations. Expected heterozygosity was calculated according to Nei 1987; observed heterozygosity is the number of heterozygous individuals divided by the number of individuals in the population.

| Marker  | Expected heterozygosity            |                                 | Observed heterozygosity            |                                 |
|---------|------------------------------------|---------------------------------|------------------------------------|---------------------------------|
|         | <i>V. californica</i> <sup>a</sup> | <i>V. vinifera</i> <sup>b</sup> | <i>V. californica</i> <sup>a</sup> | <i>V. vinifera</i> <sup>b</sup> |
| VVMD5   | 0.49                               | 0.84                            | 0.11                               | 0.87                            |
| VVMD6   | 0.00                               | 0.79                            | 0.00                               | 0.88                            |
| VVMD7   | 0.14                               | 0.81                            | 0.00                               | 0.84                            |
| VVMD27  | 0.14                               | 0.82                            | 0.09                               | 0.86                            |
| VVMD28  | 0.30                               | 0.89                            | 0.11                               | 0.93                            |
| VVMD31  | 0.00                               | 0.76                            | 0.00                               | 0.79                            |
| VVMD32  | 0.00                               | 0.82                            | 0.00                               | 0.86                            |
| VVMS2   | 0.07                               | 0.79                            | 0.07                               | 0.81                            |
| VrZAG62 | 0.42                               | 0.81                            | 0.13                               | 0.83                            |
| VrZAG79 | 0.62                               | 0.84                            | 0.13                               | 0.84                            |
| VrZAG93 | 0.37                               | 0.63                            | 0.13                               | 0.49                            |
| Average | 0.23                               | 0.80                            | 0.18                               | 0.82                            |

<sup>a</sup>Based on 14 *Vitis californica* vines.

<sup>b</sup>Based on 300 cultivars presumed to be pure *Vitis vinifera*.

also has one allele at 10 of the 11 markers that is not found in the *V. californica* profiles, with VrZAG79 the exception. Each of these 10 "non-*californica*" alleles is found within the profiles of 300 *V. vinifera* wine and table grape cultivars with a frequency of at least 3%; many of these alleles are high frequency in the same set of profiles (Table 5). These results indicate Roger's Red may be a *V. californica* x *V. vinifera* hybrid. The two species readily hybridize (Olmo and Koyama 1980), previously documented using molecular markers (Golman 1996, Wada 2008).

With codominant markers such as SSRs, parent/progeny pairs will share one allele at each locus. For Roger's Red, each of the 10 non-*californica* alleles noted above and one of the VrZAG79 alleles must be present in a putative *V.*

**Table 4** Allele frequencies within *Vitis californica* and *Vitis vinifera* populations for the alleles observed in 14 unique *Vitis californica* SSR profiles. Alleles in bold font are those found in Roger's Red.

| Marker | Allele (bp) | Frequencies (%)                    |                                 |
|--------|-------------|------------------------------------|---------------------------------|
|        |             | <i>V. californica</i> <sup>a</sup> | <i>V. vinifera</i> <sup>b</sup> |
| VVMD5  | 246         | 61                                 | 2                               |
|        | <b>248</b>  | 39                                 | 0                               |
| VVMD6  | <b>214</b>  | 100                                | 28                              |
| VVMD7  | 241         | 93                                 | 0                               |
|        | 255         | 7                                  | 1                               |
| VVMD27 | <b>191</b>  | 93                                 | 4                               |
|        | 193         | 7                                  | 0                               |
| VVMD28 | 231         | 18                                 | 12                              |
|        | <b>239</b>  | 82                                 | 13                              |
| VVMD31 | null        | 100 <sup>c</sup>                   | nd <sup>c</sup>                 |
| VVMD32 | <b>253</b>  | 100                                | 13                              |
| VVMS2  | <b>135</b>  | 96                                 | 5                               |
|        | 155         | 4                                  | 9                               |
| VRIP62 | <b>199</b>  | 29                                 | 0                               |
|        | 213         | 71                                 | 0                               |
| VRIP79 | <b>245</b>  | 53                                 | 10                              |
|        | 255         | 11                                 | 5                               |
|        | 257         | 32                                 | 3                               |
| VRIP93 | 261         | 4                                  | 1                               |
|        | 209         | 4                                  | 0                               |
|        | 215         | 4                                  | 6                               |
|        | <b>223</b>  | 14                                 | 0                               |
|        | 227         | 78                                 | 0                               |

<sup>a</sup>Based on 14 *Vitis californica* vines.

<sup>b</sup>Based on 300 cultivars presumed to be pure *Vitis vinifera*.

<sup>c</sup>The frequency of a specific null allele typically cannot be determined unless the allele is ubiquitous.

*vinifera* parent. Within the set of 300 *V. vinifera* cultivars, only Alicante Bouschet shares one allele at each locus with Roger's Red, accounting for each of the 10 non-*californica* alleles and the 257bp allele at VrZAG79. The same result was found after expanding the search to include over 1,200 profiles in the FPS Reference Database. Alicante Bouschet is a teinturier variety with red flesh and juice, a trait shared with Roger's Red, and has a history of extensive cultivation in California (Johnson 1989). Sharing one allele at each locus does not prove a parent/progeny relationship or indicate the direction of descent (which is the parent). However, using the frequencies calculated from the 300 *V. vinifera* profiles, the chance of sharing these alleles at random is greater than one in 10 billion. Further, Alicante Bouschet was bred in the 1850s in France by Henri Bouschet (Galet 1979), so could not be a progeny of Roger's Red. Hence, Alicante Bouschet is one parent of Roger's Red.

As a first-generation *V. californica* x *V. vinifera* hybrid and given that the non-*californica* alleles are actually *V. vinifera* alleles from Alicante Bouschet, the remaining allele at each marker in the Roger's Red profile must be a *V. californica* allele. At 9 of the 11 markers, the allele not accounted for by Alicante Bouschet was present in the small set of *V. californica* profiles. All nine of these alleles were high frequency in *V. californica* (two had a frequency of

**Table 5** Multilocus profiles, in base pairs, for Roger's Red and Alicante Bouschet are presented followed by the frequencies of the Roger's Red alleles in *Vitis californica* and *Vitis vinifera* populations. Alleles in bold font are those inherited by Roger's Red from Alicante Bouschet.

| Marker  | Alicante Bouschet | Roger's Red | Frequencies (%) of Roger's Red alleles |                                 |
|---------|-------------------|-------------|--|---------------------------------|
|         |                   |             | <i>V. californica</i> <sup>a</sup>     | <i>V. vinifera</i> <sup>b</sup> |
| VVMD5   | 226               | <b>238</b>  | 0                                      | 15                              |
|         | <b>238</b>        | 248         | 39                                     | 0                               |
| VVMD6   | <b>211</b>        | <b>211</b>  | 0                                      | 17                              |
|         | 212               | 214         | 100                                    | 28                              |
| VVMD7   | 239               | <b>243</b>  | 0                                      | 11                              |
|         | <b>243</b>        | null        | nd <sup>c</sup>                        | nd <sup>c</sup>                 |
| VVMD27  | 181               | 191         | 93                                     | 4                               |
|         | <b>194</b>        | <b>194</b>  | 0                                      | 9                               |
| VVMD28  | <b>247</b>        | 239         | 82                                     | 13                              |
|         | 263               | <b>247</b>  | 0                                      | 12                              |
| VVMD31  | <b>212</b>        | <b>212</b>  | 0                                      | 38                              |
|         | 212               | null        | 100 <sup>c</sup>                       | nd <sup>c</sup>                 |
| VVMD32  | <b>251</b>        | <b>251</b>  | 0                                      | 11                              |
|         | 273               | 253         | 100                                    | 13                              |
| VVMS2   | 133               | 135         | 96                                     | 5                               |
|         | <b>145</b>        | <b>145</b>  | 0                                      | 5                               |
| VrZAG62 | 189               | <b>189</b>  | 0                                      | 27                              |
|         | 189               | 199         | 29                                     | 0                               |
| VrZAG79 | 243               | 245         | 53                                     | 7                               |
|         | <b>257</b>        | <b>257</b>  | 35                                     | 3                               |
| VrZAG93 | 215               | 223         | 14                                     | 0                               |
|         | <b>231</b>        | <b>231</b>  | 0                                      | 7                               |

<sup>a</sup>Based on 14 *Vitis californica* vines.

<sup>b</sup>Based on 300 cultivars presumed to be pure *Vitis vinifera*.

<sup>c</sup>The frequency of a specific null allele typically cannot be determined unless the allele is ubiquitous.

100%), and three of these alleles were not found in *V. vinifera* (Table 4, Table 5). VVMD7 and VVMD31 were the two markers at which Roger's Red did not have alleles found in the *V. californica* set. Reliable fragments were not amplified at VVMD31 for any of the 19 *V. californica* despite multiple attempts. At least within this small *V. californica* database, VVMD31 has to be scored a monomorphic null allele with the assumed frequency of 100%. The lack of a "californica" allele in Roger's Red at VVMD7 may also be attributed to the inheritance of a null allele from the presumed *V. californica* parent. Although the small sample size precludes valid statistical estimation of the likelihood of null alleles, at both VVMD7 and VVMD31 Roger's Red appeared homozygous for an Alicante Bouschet allele. This is the expected observed genotype when a null allele is inherited from one parent (Bautista et al. 2008).

Because of the small sample size, we cannot use the frequencies of the 23 alleles observed in the *V. californica* samples to infer the frequencies of these alleles in *V. californica* as a species. However, these alleles are for the most part rare in *V. vinifera* (Table 4). Frequencies for 18 of the 23 alleles are under 10% in *V. vinifera* cultivars; eight of the alleles, including three found in Roger's Red, are not

present at all in *V. vinifera* cultivars. These do not include the two presumed null alleles inherited by Roger's Red for which frequencies within *V. vinifera* cannot be calculated. The sampled *V. californica* vines had typical phenotypes and were sampled within the natural range of *V. californica* and outside the range of *Vitis girdiana*, the only other wild *Vitis* species in California (Munz 1968). The evident conclusion is that these alleles, including the null alleles at VVMD7 and VVMD31, are *V. californica* alleles.

The red fall foliage of Roger's Red is a trait that, to a degree, it shares with its *V. vinifera* parent, Alicante Bouschet. Red fall leaf color is also the main symptom of leafroll disease, a common viral disease wherever grapes are grown. The three Roger's Red vines from the UCD Arboretum were tested for a panel of viruses (Osman et al. 2008) and were found infected with *Grapevine leafroll-associated virus type 2* (GLRaV-2) and *Grapevine virus B* (GVB) (Golino et al. 2009). Both of these viruses cause red leaf symptoms in the fall. GLRaV-2 and GVB are carried in propagation wood; thus if the initial Roger's Red vine were infected, then all of the plants propagated from it would also be infected. The other effects of the virus—reduced fruit yield, reduced sugar and pigmentation, and occasional stunting when grafted—would not necessarily be noticed in an ornamental planting. Therefore, the red fall leaf color of Roger's Red may be due to virus symptoms, the Alicante Bouschet background, or a combination of the two.

In addition, we treated Roger's Red to eliminate virus to determine if the red leaf color is also eliminated. Treatment involves excising a <0.5 mm piece of terminal shoot tip, referred to as a microshoot tip, and growing a new plant from it. Because the virus has often not yet infected the rapidly growing cells in the microshoot tip, the new plant is not virus-infected. This tissue culture treatment has been used successfully on many grape varieties (Golino et al. 2000). The work is still in progress; the result will not be known for several years.

## Conclusions

Using SSR markers, we showed that the ornamental grape cultivar Roger's Red is a first-generation hybrid cross between a wild *V. californica* and the *V. vinifera* teinturier variety, Alicante Bouschet. Roger's Red shared one allele at 11 loci with Alicante Bouschet. Comparison with a small group of *V. californica* profiles showed that nine of the remaining Roger's Red alleles were present in *V. californica* and three of these have not been found in *V. vinifera*. The remaining two alleles were consistent with the presence of null alleles at these loci in the wild *V. californica* parent. Roger's Red is currently being subjected to virus elimination to determine if the red fall leaf color remains stable. This is the first examination of the parentage of an ornamental grapevine cultivar.

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