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Published in:
Journal of Experimental Botany

DOI:
10.1093/jxb/erv491

Publication date:
2016

Document version
Publisher's PDF, also known as Version of record

Citation for published version (APA):
Drew, D. P., Andersen, T. B., Sweetman, C., Møller, B. L., Ford, C., & Simonsen, H. T. (2016). Two key polymorphisms in a newly discovered allele of the Vitis vinifera TPS24 gene are responsible for the production of the rotundone precursor -guaiene. Journal of Experimental Botany, 67(3), 799-808. https://doi.org/10.1093/jxb/erv491
Two key polymorphisms in a newly discovered allele of the *Vitis vinifera* TPS24 gene are responsible for the production of the rotundone precursor α-guaiene

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Received 2 September 2015; Revised 13 October 2015; Accepted 26 October 2015

Editor: Robert Hancock, The James Hutton Institute

Abstract

Rotundone was initially identified as a grape-derived compound responsible for the peppery aroma of Shiraz wine varieties. It has subsequently been found in black and white pepper and several other spices. Because of its potent aroma, the molecular basis for rotundone formation is of particular relevance to grape and wine scientists and industry. We have identified and functionally characterized in planta a sesquiterpene synthase, VvGuaS, from developing grape berries, and have demonstrated that it produces the precursor of rotundone, α-guaiene, as its main product. The VvGuaS enzyme is a novel allele of the sesquiterpene synthase gene, *VvTPS24*, which has previously been reported to encode VvPNSeInt, an enzyme that produces a variety of selinene-type sesquiterpenes. This newly discovered VvTPS24 allele encodes an enzyme 99.5% identical to VvPNSeInt, with the differences comprising just 6 out of the 561 amino acid residues. Molecular modelling of the enzymes revealed that two of these residues, T414 and V530, are located in the active site of VvGuaS within 4 Å of the binding-site of the substrate, farnesyl pyrophosphate. Mutation of these two residues of VvGuaS into the corresponding polymorphisms in VvPNSeInt results in a complete functional conversion of one enzyme into the other, while mutation of each residue individually produces an intermediate change in the product profile. We have therefore demonstrated that VvGuaS, an enzyme responsible for production of the rotundone precursor, α-guaiene, is encoded by a novel allele of the previously characterized grapevine gene VvTPS24 and that two specific polymorphisms are responsible for functional differences between VvTPS24 alleles.

Key words: Pinot Noir, rotundone, sesquiterpene synthase, sesquiterpenoids, Shiraz, wine aroma.

Introduction

Terpenoids are one of the most diverse and abundant classes of specialized metabolites in the plant kingdom and perform a variety of functions, including defence against insects and microbes (Pare and Tumlinson, 1999) or the attraction of pollinators (Martin et al., 2009). Many terpenoids are volatile and therefore have the potential to act as aroma compounds,
a function that is particularly relevant in the cultivated grapevine *Vitis vinifera* L., owing to the use of its berries in wine making (Lund and Bohlmann, 2006; Dunlevy et al., 2009). There have been several studies into the effect of 10-carbon monoterpenoids, such as linalool, nerol, and geraniol, on the muscat aroma of white wine varieties (Sanchez-Palomo et al., 2005; Vilanova and Sietro, 2006; Dziadas and Jelen, 2010), and into the genetic basis for monoterpenoid biosynthesis in grapes (Martin and Bohlmann, 2004; Battilana et al., 2011; Martin et al., 2012). In recent studies, the presence of 15-carbon sesquiterpenoids in grapes has been investigated (Coelho et al., 2006; Kalua and Boss, 2010; May and Wust, 2012; Matarese et al., 2013; Matarese et al., 2014), although their presence in wine and the individual and collective effect of sesquiterpenes on wine aroma are poorly understood (Robinson et al., 2014b).

In 2007, the sesquiterpene ylangene was identified as a ‘marker compound’ for the peppery aroma in Shiraz wine, although the chemical itself was not found to have a significant aroma (Parker et al., 2007). A different bicyclic sesquiterpene, rotundone, was subsequently identified as the compound responsible for the peppery aroma (Wood et al., 2008). Rotundone exhibits extremely low detection thresholds of 8 ng/L in water and 16 ng/L in wine (Siebert et al., 2008). This specialized plant metabolite is a stable sesquiterpenoid composed of a guaiene carbon skeleton with a single ketone group in the carbon 2 position. Its identification in Shiraz represented the first demonstration of a specific sesquiterpene directly linked to an aroma characteristic in wine. Given the potent effect of this single volatile metabolite, an understanding of the gene or genes responsible for rotundone biosynthesis in grapes will provide a platform to select for desired levels of rotundone in different grape varieties. This could include utilizing techniques such as marker-assisted selection or metabolic engineering for the purpose of producing wines with increased or less peppery character. Such options have previously been outlined with respect to grape monoterpenoid content following the discovery of a polymorphism within 1-deoxy-D-xylulose 5-phosphate synthase responsible for increased linalool, nerol, and geraniol content in berries of some varieties (Battilana et al., 2011).

The precise mechanism of rotundone biosynthesis is unknown. Based on its structure, the direct precursor is likely to be α-guaiene, which can be formed in a single step from farnesyI pyrophosphate (FPP) by a terpene synthase (TPS) (Kumeta and Ito, 2010). This hypothesis is further supported by recent evidence that α-guaiene can be converted to rotundone via a non-specific oxidation reaction mediated by a fungal laccase enzyme in the presence of chemical mediators (Schilling et al., 2013) or by direct oxidation (Huang et al., 2014). Furthermore, rotundone is found in plants that also contain α-guaiene and other guaiene-type sesquiterpenes (bicyclic compounds comprising 5-carbon and 7-carbon rings), including pepper (*Piper* spp.; Jirovetz et al., 2002), agarwood (*Aquilaria* spp.; Ishihara et al., 1991), and some *Cyperus* spp. (Ishihara et al., 1991; Olawore et al., 2006; Kumeta and Ito, 2010). α-Guaiene has been identified in numerous plants and in essential oils (Pandey et al., 2003; Wei and Shibamoto, 2007; Sundaresan et al., 2009; Pripdeevech et al., 2011) and has thus been more widely detected in comparison to rotundone. This may, however, be due to differences in concentration and ease of detection. Following the initial identification of rotundone in Shiraz grapes and wine, it has been found in a number of other red and white wine varieties, demonstrating that it is not unique to a single grapevine cultivar (Caputi et al., 2011; Mattivi et al., 2011; Matarese et al., 2014; Scarlett et al., 2014). Nevertheless, the absence of rotundone in many varieties could suggest that genes responsible for its biosynthesis, or for the biosynthesis of its precursor, may be absent or differentially expressed in some varieties.

In plants, TPSs are encoded by a multigene family with up to 150 members in some species (Chen et al., 2011). The TPS family has been relatively well defined in grapevine, with 69 full-length TPS genes identified on the published genomic scaffold based on an inbred Pinot Noir genome, PN40024 (Jaillon et al., 2007; Martin et al., 2010). These included 30 potential genes of the TPS-a subfamily, generally considered responsible for sesquiterpene biosynthesis, which were found to exist in two clusters on chromosomes 18 and 19. Of these, 13 of the encoded enzymes were functionally characterized by Martin et al. (2010) using *Escherichia coli* engineered to produce and accumulate the substrate FPP. Other grape-derived TPSs have previously been functionally characterized in other studies (Lucker et al., 2004; Martin et al., 2009; Martin et al., 2012; Matarese et al., 2014). While there is no clear candidate for the gene responsible for the biosynthesis of a rotundone precursor, a recombinantly expressed protein from Pinot Noir named VvPNSelInt, whose main products were selinene and intermedeol, also produced α-guaiene as a minor product (3.5%) (Martin et al., 2010).

In order to investigate the possibility that polymorphic differences in TPS genes could alter their function, we amplified a number of TPS cDNAs from developing grape berries of the Shiraz variety, a variety known to produce rotundone. Here we report the functional characterization and mutagenic analysis of one of the encoded enzymes by transient expression in *Nicotiana benthamiana* leaves. We demonstrate that a novel allele of *VvTPS24*, the gene expected to encode VvPNSelInt, actually encodes VvGuaS, an enzyme with predominantly α-guaiene synthase activity. Furthermore, we show that two specific nucleotide substitutions in the *VvTPS24* gene can change its encoded product from VvGuaS into VvPNSelInt, and thus relate two grapevine polymorphisms with a physiologically relevant functional outcome.

**Materials and Methods**

*Plant material and nucleic acid isolation and amplification*

Total RNA was isolated from *Vitis vinifera* cv. Shiraz grown in the Nuriootpa Research vineyard, Barossa Valley, South Australia, and harvested at various times of the 2013 season. Harvested grapes were frozen immediately in liquid nitrogen and stored at −80°C until required. RNA extractions were carried out as described (Sweetman et al., 2012) and cDNA was synthesized using the iScript™ Select cDNA Synthesis Kit (Bio-Rad) as per the manufacturer’s instructions. *VvTPS24* was amplified from cDNA using Phusion® High-Fidelity DNA Polymerase (NEB) with the primer
pair 5′- CACCATGCTGTTCCACTACTAGTCTCAG-3′ and 5′-TTACATTGGCACAGGATCTATG-3′ under standard PCR conditions. In the first instance, amplicons were ligated into pENTR/D-TOPO (Invitrogen) and at least three clones were sequenced (AGRF, Adelaide).

Site-directed mutagenesis

Mutations were carried out on cDNAs in the pENTR/D-TOPO vector using an adaptation of the QuikChange Site Directed Mutagenesis kit (Stratagene) essentially as described (Drew et al., 2011). In short, the complete T414S mutant was amplified, complete with plasmid, using the mutagenesis primer 5′-GCAACGCGTCGTAAAAGC TCTGCCGTCTATG-3′ and its reverse complement pair (non-complementary nucleotide shown in bold). The V530M mutant was made with the 5′-CTGAATTTTAGCCGATGA TGGACGCTCTGTACAA-3′ primer and its reverse complement pair. The double mutant T414S/V530M was created in a two-step process by carrying out the V530M mutation using the T414S mutant as a template. All products were confirmed via sequencing.

Homology modelling

The coordinates of 5-epi-aristolochene synthase (TEAS; Protein Data Bank accession 5EAT) (Starks et al., 1997) were used as a template structure for homology modelling of the VvGuaS sequence. This template structure included a structural analogue of FPP bound within the active site for determination of its proximity to residues forming the surface of the binding cavity. Homology modelling was performed using satisfaction of spatial restraints of all non-hydrogen atoms using MODELLER version 7.2 (Eswar et al., 2003). All figures were generated using PyMOL (DeLano Scientific LLC, San Francisco, CA, USA) and modelling of mutated amino acid residues was carried out within the VvGuaS model using the PyMOL residue mutation function.

Heterologous expression in Nicotiana benthamiana and solid-phase micro-extraction

Forward and reverse primers were designed with USER-overhangs to enable cloning into a USER-compatible version of the pEAG-HT vector. USER cloning was performed as previously described (Nour-Eldin et al., 2006). The pEAG-HT plasmid (kindly provided by George Lomonossoff, John Innes Research Centre, Norwich, UK) harbouring the viral suppressor p19 was modified to harbour a USER cassette. N. benthamiana plants were grown from seeds at 24°C day/19°C night cycles for 5 weeks before infiltration. Transformation of Agrobacterium tumefaciens and subsequent expression of N. benthamiana were performed as described previously (Yang et al., 2012; Bach et al., 2014). A whole leaf from infiltrated N. benthamiana was inserted into a 20 ml glass vial and the volatiles extracted at 60°C for 20 min using a Supelco 57298-U, 30/30 μm divinylbenzene/carboxen/polydimethylsiloxane StableFlex/SS (1 cm) fibre (Supelco Sigma-Aldrich, Denmark). Fibres were reconditioned for 20 min at 240°C. Analysis was performed in triplicate for each sample and N. benthamiana leaves expressing p19 from the pEAG-HT vector were used as controls for comparison.

GC-MS method and data analysis

Samples were analysed on a Shimadzu GCMS-QP2010 Plus using an Agilent HP-5ms Ultra Inert fused Silica capillary column of 29 m length × 0.25 mm diameter × 0.25 μm film thickness, inserted directly into the ion source of the MS (Simonsen et al., 2009; Drew et al., 2013). The pressure was kept at 16 kPa, giving a column flow of 1.25 mL/min. The injection port temperature was set to 250°C, and lower injection port temperatures were investigated to confirm that a significant degree of thermal degradation did not occur (Andersen et al., 2015). The oven temperature was set to 60°C for 3 min, and increased to 160°C at a rate of 7°C/min, before a further increase to 300°C at a rate of 50°C/min. This temperature was held for 5 min and finally increased to 320°C at a rate of 50°C/min, where it was maintained for 5 min. The carrier gas was H2 and the ionization electron energy was 70 eV. The ion source temperature was 230°C with an interface temperature of 280°C. The total run time was 28.49 min. A C7-C30 standard series (Sigma-Aldrich, Denmark) was used to calculate retention indices (I). All data were analysed using the Shimadzu software Lab Solutions. GCMS Solutions version 2.50 SU3. NIST and Wiley 2008 libraries were used in conjunction with the NIST Standard Reference Database for compound identification. Putative compound assignment was made based on a combination of retention index (RI) and mass spectrum similarity, and by comparison to authentic standards for α-guaiene, α-bulnesene, α-copaene, δ-cadinene, α-humulene and β-caryophyllene.

Results

Identification of a novel Vitis vinifera guaiene synthase

Recent work investigated the global expression of mRNA transcripts in Shiraz grapes and identified a number of potential members of the TPS-a subfamily expected to produce sesquiterpenes, and actively transcribed in developing Shiraz berries (Sweetman et al., 2012). The products of these enzymes included a number of monocyclic and bicyclic sesquiterpenes, some of which have previously been identified as products of grape enzymes (Martin et al., 2010). However, one of the TPSs we investigated, encoded by VvTPS24 (National Center for Biotechnology Information [NCBI] accession XM_002282452), was of particular interest owing to the high proportion of guaiene-type sesquiterpenes produced. The activity of the encoded enzyme was investigated through Agrobacterium-mediated transient expression of VvTPS24 cDNA into N. benthamiana leaves, followed by analysis of volatile products produced using solid phase micro-extraction (SPME) GC-MS. Comparison of RIs and mass spectra to those of authentic standards from appropriate GC-MS libraries enabled identification of the major products as α-guaiene (44%) and α-bulnesene (35%), also known as δ-guaiene). A number of minor products were also produced, putatively annotated as epiglobulol, γ-gurjunene, and pogostol, that also exhibit the characteristic guaiene-type 5,7 bicyclic carbon skeleton of the peppery aroma compound rotundone (Fig. 1). Based on this analysis, we named this VvTPS24 gene product VvGuaS, despite the expectation that it should encode the selinene-producing VvPNSeInt (Martin et al., 2010). GC-MS data for VvGuaS products are presented in the Supplementary data.

VvGuaS is a polymorphic variant of the VvTPS24 gene

The array of products detected following expression of this protein was somewhat unexpected given that VvPNSeInt, an enzyme apparently encoded by the VvTPS24 gene, was previously functionally characterized and found to produce a completely different array of sesquiterpene products. BLAST searches utilizing the nucleic acid sequence of our isolated cDNA, as well as the amino acid sequence of VvGuaS, demonstrated that it was 99.5% identical to a sesquiterpene synthase transcript (NCBI accession...
XM_002282452). It is on this sequence that the synthetic terpene synthase construct VvPNSelnt (Martin et al., 2010). No sequences from the NCBI reference sequence genome, based on the Pinot Noir-derived variety PN40024, matched our variant. However, contig VV78X107636.8 (NCBI accession AM459143), produced as part of the whole genome shotgun sequencing of Pinot Noir (Velasco et al., 2007), contained a predicted protein-encoding region that contained ambiguous nucleotide calls at four out of six positions corresponding to differences between VvGuaS and VvPNSelnt. Specifically, the VvGuaS and VvPNSelnt amino acid sequences differed at positions 403, 405, 414, 431, 499, and 530, and the predicted protein product of contig VV78X107636.8 showed ambiguous residues at all but the first two positions. The presence of these ambiguous base calls at these sites strongly indicates that the VvTPS24 gene is heterozygous and that alleles encoding both VvGuaS and VvPNSelnt exist in the Pinot Noir genome. Meanwhile, the absence of any sequence corresponding to VvGuaS in the NCBI reference genome suggests that it may have been bred to homozygosity during the development of the PN40024 inbred variety, with only the allele encoding VvPNSelnt remaining.

Structural comparison of VvGuaS and VvPNSelnt

To investigate the reasons for the dramatic functional differences observed between these two enzymes, a comparison of the structural location of the amino acid difference between VvGuaS and VvPNSelnt was undertaken. Molecular modeling of the two enzymes based on the TEAS template structure revealed that two of the varying amino acid positions were directly located in the active site, proximal to the location of FPP binding and subsequent catalysis, while the other four amino acid differences were located more peripherally (Fig. 2A). The two polymorphisms within the active site of VvGuaS compared to VvPNSelnt corresponded to T414S and V530M substitutions. In both cases, modeling of the electrostatic surface of the active site of VvGuaS demonstrated that the T414 and V530 residues both contribute to the internal binding site of FPP (Fig. 2B, C) and are located on separate alpha-helices that contribute to the formation of the internal cavity comprising the FPP substrate-binding site. The estimated distances from the most proximal atoms of the side-chains of T414 and V530 to FPP in the molecular model of VvGuaS were approximately 4 Å. The remaining four residue differences between VvGuaS and VvPNSelnt, namely T403R, E405D, M431I, and V499F, were located a minimum...
of 10 Å from the FPP binding site and did not contribute to the molecular surface of the internal cavity (Fig. 2A).

It has previously been demonstrated that amino acid residues located near the site of FPP binding within enzymes of the sesquiterpene synthase family can have profound effects on the metabolites produced, with the observed effects decreasing with decreasing proximity (Greenhagen et al., 2006). To investigate whether the two amino acid residue polymorphisms located at the FPP binding site of VvGuaS could be responsible for the different products generated compared with the previously characterized isoform VvPNSeInt, we carried out site-directed mutagenesis of the VvTPS24 cDNA to produce versions with either individual (T414S and V530M) or double (T414S/V530M) mutations. Agrobacterium-mediated transient transformation of N. benthamiana leaves was carried out with these mutated versions of VvGuaS and the volatile metabolites were analysed via SPME GC-MS (Table 1).

**Effect of site-directed mutagenesis of selected VvGuaS residues**

Compared with wild-type (WT) VvGuaS, the T414S mutant exhibited a relatively minor change in product profile, with the two major volatile metabolites continuing to be α-guaiene (41%) and α-bulnesene (18%). The relatively small decrease in the total proportion of α-bulnesene was replaced by the new products selina-4,11-diene (4%) and α-selinene (7%). These new products were observed at retention times where no trace sesquiterpene ions were visible in the WT VvGuaS enzyme. Additionally, the proportion of epi-α-selinene increased from 1% to 4% of the total ion chromatogram (TIC). Thus, the T414S mutant had 12 identifiable products, compared to nine for the WT enzyme, with each of the new products consisting of sesquiterpenes with a 6,6 bicyclic carbon backbone similar to products of VvPNSeInt (Table 1 and Supplementary data). In the case of VvGuaS-V530M, a more significant change in the range of products was observed, with the overall theme again being a shift towards the product profile reported for VvPNSeInt. The proportions of the 5,7 bicyclic α-guaiene (24%) and α-bulnesene (12%) significantly decreased compared to WT, and substantially higher amounts of the 6,6 bicyclic compounds putatively identified as selina-4,11-diene (24%), α-selinene (16%), and epi-α-selinene (8%) were produced. Pogostol (a hydroxy-guaiene) was no longer present, while a hydroxy-selinene compound, likely intermedeol, now comprised 8% of the TIC. Analysis of the double mutant VvGuaS-T414S/V530M demonstrated that its guaiene synthase activity was almost completely compromised, with only 5% of the volatile products comprising α-guaiene, and α-bulnesene not detectable. Instead, the major products were predominantly the 6,6 bicyclic sesquiterpenes selina-4,11-diene (40%), α-selinene (23%), epi-α-selinene (12%), and a hydroxylated selinene (9%) with the same reported RI as intermedeol.

**Discussion**

Following the widespread and relatively rapid domestication and cultivation of grapevines over the past several thousand years (This et al., 2006), there are now up to 10 000 acknowledged varieties of V. vinifera (Alleweldt and Dettweiler, 1994). While several hundred of these varieties are commonly used for the production of wine, much remains to be discovered concerning the precise content of aroma-active compounds.

### Table 1. Volatile metabolic products of VvGuaS expressed in N. benthamiana

| Compound          | TIC%   | WT | T414S | V530M | T414S/V530M | VvPNSeInt |
|-------------------|--------|----|-------|-------|-------------|-----------|
| α-copaenea        | 1373   | 1372–1376 | 2     | 3     | 1           | 1         |
| α-gurjunene       | 1407   | 1402–1411 | 1     | 1     | 0           | 0         |
| α-guaiene         | 1437   | 1428–1437 | 44    | 41    | 24          | 5         |
| Unknown           | 1440   | n/a | 0     | 0     | 0           | 1         |
| γ-gurjunene       | 1478   | 1479 | 4     | 3     | trace       | 0         |
| Selina-4(14),11-diene | 1482 | 1472–1488 | 0     | 4     | 24          | 40        |
| Epiglobulol       | 1488   | 1463–1497 | 6     | 12    | 2           | 2         |
| α-selinene        | 1492   | 1478–1497 | 0     | 7     | 16          | 23        |
| Unknown           | 1498   | n/a | 5     | 5     | 4           | 4         |
| α-bulnesene       | 1506   | 1500–1515 | 35    | 18    | 12          | 0         |
| Epi-α-selinene    | 1517   | 1518 | 1     | 4     | 8           | 12        |
| a-cadinene        | 1524   | 1519–1530 | 0     | 0     | 3           | 2         |
| Pogostol          | 1653   | 1637–1656 | 3     | 2     | 0           | 0         |
| Intermedeol       | 1660   | 1654–1667 | 0     | 2     | 8           | 9         |

TIC percentages are semi-quantitative because they depend on each compound’s affinity for the SPME fibre. Compound identities reported based on comparison to authentic standards (a) or putatively annotated based on mass spectrum similarity (>90% as calculated by Shimadzu GCMS Solution 2.50 software against compounds in NIST08 and Wiley08 libraries) and RI within the range of reported references, except for epi-α-selinene and intermedeol, which are based on RI alone. b Ranges of reported retention indices for DB5 and similar columns as compiled in the NIST Standard Reference Database 69: NIST Chemistry WebBook. c Products previously reported for VvPNSeInt shown for comparison (Martin et al., 2010).
in most of them. Nevertheless, it is apparent that white wine varieties tend to have a higher relative content of monoter-
pene compounds, while sesquiterpenes have so far been pre-
dominantly found in red wine varieties (Coelho et al., 2006; 
Vilanova and Sieiro, 2006; Coelho et al., 2007; Kalua and 
Boss, 2009, 2010; May and Wust, 2012; Matarese et al., 2013; 
Matarese et al., 2014; Robinson et al., 2014a). While this may, 
in part, be a result of the localization of sesquiterpene com-
pounds in berry exocarp, and thus heavily influenced by the 
involveinent of berry skin in the winemaking process, studies 
focusing on berries have shown similar results. This suggests 
that a complete molecular understanding of the enzymatic 
pathways involved in sesquiterpene biosynthesis in grapes 
could provide valuable information regarding the origins of 
biochemicals present in wine.

The bicyclic sesquiterpene rotundone, first identified in 
Shiraz wine, is an extraordinarily potent aroma compound 
with an extremely low detection threshold (Siebert et al., 
2008; Wood et al., 2008). Conflerring a distinct peppy or 
spicy note to wine, rotundone is also the first sesquiterpene 
conclusively shown to have a significant effect on wine char-
acter, and has been described as one of the most important 
aroma compounds in wine (Geffroy et al., 2014). Following 
its initial identification in Shiraz, a variety that is famous for 
its peppy character, rotundone has been found in several 
other cultivars, including Duras, Durif, Graciano, Grüner 
Veltliner, Schioppettino, and Vespoldina (Caputi et al., 2011; 
Qian and Shellhammer, 2012; Geffroy et al., 2014). Owing 
to the importance of this compound as a chemical deter-
mnant of wine aroma, several studies have investigated the 
location and timing of rotundone biosynthesis in grapes, and 
the environmental factors and viticultural practices that may 
influence final concentrations. Rotundone has been found in 
exocarp and skin, but is absent from pulp or seeds (Caputi 
et al., 2011). Absolute levels were shown to increase late in 
berry ripening and were generally higher in cooler vintages 
(Caputi et al., 2011; Geffroy et al., 2014). These data add to 
physiological studies investigating the production of other 
grape specialized metabolites, whose results have demon-
strated that their biosynthesis can be influenced by biotic fac-
tors such as insect attack (D’Onofrio et al., 2009), or abiotic 
factors such as light exposure, crop load, and nitrogen levels 
(Chapman et al., 2004; des Gachons et al., 2005; Chone et al., 
2006).

Given the direct line between rotundone and the pep-
erry aroma of wine, the elucidation of the metabolic path-
way of its biosynthesis, and the enzymes responsible for 
catalytic steps within this pathway, would open up possibili-
ties for investigating grapevine varieties for their potential 
to produce a pepper aroma. Additionally, techniques such 
as quantitative mRNA transcript analysis could enable the 
real-time monitoring of environmental or agronomic fac-
tors that affect the expression of the genes responsible. As 
a sesquiterpene ketone, the most likely biosynthetic pathway 
of rotundone is via a guaione intermediate, that is, a bicyclic 
5,7 ring carbon skeleton (see Fig. 1), that would be directly 
generated from FPP by a terpene synthase (Kumeta and 
Ito, 2010). Indeed, the oxidation of α-guainese by a fungal 
lacase has been shown to result in the production of rotun-
done (Schilling et al., 2013), and rotundone accumulates over 
time in commercial samples of guaione that are exposed to 
the environment (unpublished observation). Recently, Huang 
et al. (2014) demonstrated that rotundone is one of the main 
products of the auto-oxidation of α-guainese. Their data sug-

gest that α-guainese can slowly oxidize to rotundone over a 
number of weeks at room temperature. This process is dra-
matically increased at temperatures of 40–50ºC (Huang et al., 
2014). If spontaneous conversion of α-guainese to rotundone 
plays a role physiologically, this could potentially explain the 
increased levels of rotundone in grapes that are harvested sig-
nificantly later than usual (Geffroy et al., 2014; Davies et al., 
2015). In contrast, two separate studies have indicated that increased temperature actually correlates with lower rotun-
done concentrations (Zhang et al., 2013; Scarlett et al., 2014). 
This suggests that small increases in ambient temperature do 
not have a significant effect on the rate of any non-enzymatic 
α-guainese oxidation that may be occurring.

While it has been shown that α-guainese can be oxidized 
to rotundone spontaneously (Huang et al., 2014), there is 
also the possibility that the final step in rotundone produc-
tion is carried out enzymatically. The oxidation of sesqui-
terpene hydrocarbons into more specialized products has been 
well described in a number of plant species. This would likely 
be carried out by a member of the cytochrome P450 fam-
ily. The oxidation of valencene into nootkatone is a specific 
example of a sesquiterpene hydrocarbon being converted to a 
ketone in a single step by a cytochrome P450 (Cankar et al., 
2011). Numerous other examples exist of sesquiterpene oxida-
tion being carried out by this family of enzymes, predomin-
antly from the diverse CYP71 subfamily (Ro et al., 2006; 
Pickel et al., 2012). In summary, although there is currently 
no biochemical evidence that rotundone is enzymatically 
produced from α-guainese in grapes, structurally similar com-
pounds have been shown to be produced from the combined 
action of a terpene synthase and cytochrome P450 in other 
plants. Therefore, whether it is the non-enzymatic oxidation 
of α-guainese that leads to the accumulation of rotundone in 
some wines, or whether an enzyme exists that can specifically 
catalyse the formation of rotundone from α-guainese, is yet 
to be determined. Sweetman et al. (2012) previously reported 
that transcripts corresponding to VvTPS24 were present in 
Shiraz berries during veraison, but were not detected at signif-
icant levels at harvest. Although this work reported data from 
only a single season, if their results prove to be representative 
of VvGuaS expression, this could suggest that downstream 
modification of α-guainese after veraison is crucial in deter-
mining rotundone levels.

The findings presented here demonstrate that a newly 
identified allele of the VvTPS24 gene encodes VvGuaS, a 
sesquiterpene synthase whose main product is the rotun-
done precursor α-guainese (Fig. 3). We showed that as few as 
one or two polymorphisms in VvTPS24 determine whether 
it will produce α-guainese (Fig. 3). A previously character-
ized enzyme, VvPNSeInt, also encoded by VvTPS24, was 
shown to produce selina-4,11-diene (34%) and interme-
deol (30%), and only 3.5% α-guainese (Martin et al., 2010).
Two key polymorphisms in a newly discovered allele of the grapevine TPS24 gene

Both selina-4,11-diene and intermedeol differ structurally from the products of the allele identified in this report, in that they have a 6,6 bicyclic carbon skeleton rather than the 5,7 carbon skeleton of guaiene-type sesquiterpenes. Other than α-guaiene, the only product of VvGuaS that was also reported to be a product of VvPNSeInt was putatively identified as epi-α-selinene, which accounted for 1% of the TIC of VvGuaS compared with 15% for VvPNSeInt (Martin et al., 2010). These data suggest that although the enzymes encoded by the two VvTPS24 alleles share 99.5% identity at the amino acid level, they clearly have different catalytic functions. Furthermore, analysis of the available sequence data indicates that VvTPS24 is heterozygotic for the two alleles in the variety Pinot Noir, while the inbred variety PN40024 is likely homozygotic for VvPNSeInt.

In VvGuaS, the double mutation of T414S and V530M, and to a lesser extent the V530M mutation alone, caused a change in the conformation of the active site that resulted in the formation of the second ring favouring a 7,2 closure rather than the 6,2 closure favoured by the WT VvGuaS enzyme (Fig. 4). The products of the double mutant therefore consisted predominantly of sesquiterpenes with a 6,6 bicyclic carbon skeleton, in contrast to WT VvGuaS, which produces a range of guaiene-like sesquiterpenes with a 5,7 bicyclic skeleton (Fig. 3). In other words, the VvGuaS-T414S/V530M double mutant enzyme produced a product profile equivalent to the alternative VvTPS24 allele, VvPNSeInt. This change in product profile was partially achieved with both of the single mutations T414S and V530M, with the latter having a greater effect. The four major products of the WT VvGuaS enzyme (α-guaiene, α-bulnesene, epiglobulol, and γ-gurjunene) were responsible for 89% of the TIC, while the major four products for the double mutant made up 84% of the TIC, indicating there was no significant decrease in catalytic specificity resulting from the functional change. Similarly, notwithstanding the semi-quantitative nature of SPME GC-MS, no significant differences were observed in the absolute quantities of products produced by the respective enzymes.

Differences in the functionality exhibited by the two highly similar enzymes can potentially be explained by the existence of lone-pair electrons on the sulfur atom of methionine (present in VvPNSeInt), which could be involved in the stabilization of the carbocation intermediate. While the lone-pair on the sulfur is the most likely new interaction partner, differences to the preferred bond closure of the carbocation could be the result of steric changes associated with the relatively minor size differences between the substituted residues (Fig. 2). Although the crystal structure of the WT and mutant enzymes would be required to answer such mechanistic speculation, it has previously been reported that very minor changes to the active site of TPSs can have a significant impact on their products (Greenhagen et al., 2006; O’Maille et al., 2008). In the present study, we used protein-encoding sequences from two alleles of the same gene to direct our mutational analyses and demonstrated that a maximum of
two specific residue changes were necessary and sufficient to change the nature of the second ring closure.

In summary, at least two alleles of the VvTPS24 gene exist in grapevine, both of which encode functional sesquiterpene synthases (VvGuaS and VvPNSeInt). Despite only minor differences in amino acid sequence, we demonstrated that one allele encodes an α-guaiene synthase (VvGuaS), in contrast to the previously investigated version that encodes a selinene synthase (VvPNSeInt). Furthermore, the functional differences between these enzymes can be traced back to two specific polymorphisms in the active site of the protein. The heterozygosity of Pinot Noir for both versions of this enzyme, as evidenced by the existence of contig VV78X107636.8, suggests that it is not only the presence of the α-guaiene-producing allele that is responsible for rotundone accumulation. Nevertheless, the fact that the VvGuaS-producing allele has been discovered in the Shiraz variety, famous for its peppery aroma, could suggest that further investigation into the expression of these two highly similar, but functionally distinct, alleles is warranted.

The identification of a grapevine enzyme that produces α-guaiene as its main product is a vital step in determining the molecular basis for rotundone accumulation in grapes, and opens up the possibility for further studies into the factors that influence the peppery aroma of wine.

Supplementary Data

Supplementary materials are available at JXB online. Supplementary data. Gas chromatogram and mass spectral data for VvGuaS products.

Acknowledgements

The authors would like to thank the reviewer of a previous version of this manuscript, who drew our attention to the presence of contig VV78X107636.8, thus demonstrating that VvTPS24 is heterozygous in Pinot Noir. The pEAQ-HT plasmid was kindly provided by George Lomonosonoff (John Innes Research Centre, Norwich, UK). CS was supported by grants from the Grape and Wine Research and Development Corporation, and the University of the Adelaide and Wine 2030 programme. DPD received funding from the European Union Seventh Framework Programme (FP7/2007–2013) under grant agreement 275422, which supported a Marie Curie International Outgoing Fellowship. The Danish Strategic Research Council Grant “SPOTLight” supported the work of TBA and HTS. The research work was supported by a grant from the VILLUM Research Center for Plant Plasticity, by the Center for Synthetic Biology “bioSYNergy” supported by the UCPH Excellence Programme for Interdisciplinary Research, and by an ERC Advanced Grant to BLM (ERC-2012-ADG_20120314, Project No: 323034).

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