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Ectopic Expression of VvMybPA2 Promotes Proanthocyanidin Biosynthesis in Grapevine and Suggests Additional Targets in the Pathway\textsuperscript{1}[W][OA]

Nancy Terrier*, Laurent Torregrosa, Agnès Ageorges, Sandrine Viala, Clotilde Verriers, Véronique Cheynier, and Charles Romieu

UMR SPO 1083 (N.T., A.A., S.V., C.V., V.C.) and UMR DIAPC 1097 (L.T., C.R.), Campus SupAgro-INRA, F-34060 Montpellier, France

Grapevine (\textit{Vitis vinifera}) proanthocyanidins contribute to plant defense mechanisms against biotic stress and also play a critical role in organoleptic properties of wine. In grapevine berry, these compounds are mainly accumulated in exocarps and seeds in the very early stages of development. A previous study has already identified VvMybPA1 as the first transcription factor involved in the regulation of the proanthocyanidin pathway during seed development in grapevine. A novel Myb factor, VvMybPA2, which is described in this study, is in contrast mainly expressed in the exocarp of young berries and in the leaves. This transcription factor shows very high protein sequence homology with other plant Myb factors, which regulate flavonoid biosynthesis. Ectopic expression of either VvMybPA1 or VvMybPA2 in grapevine hairy roots induced qualitative and quantitative changes of the proanthocyanidin profiles. High-throughput transcriptomic analyses of transformed grapevine organs identified a large set of putative targets of the VvMybPA1 and VvMybPA2 transcription factors. Both genes significantly activated enzymes of the flavonoid pathway, including anthocyanidin reductase and leucoanthocyanidin reductase 1, the specific terminal steps in the biosynthesis of epicatechin and catechin, respectively, but not leucoanthocyanidin reductase 2. The functional annotation of the genes whose expression was modified revealed putative new actors of the proanthocyanidin pathway, such as glucosyltransferases and transporters.

Flavonoids are a family of plant secondary metabolites that comprise several groups of compounds (e.g. anthocyanins, flavonols, and flavan 3-ols) and accumulate in a wide variety of plant tissues, where they are involved in diverse functions. In particular, flavonols play a role in protection against UV radiation (Winkel-Shirley, 2002), proanthocyanidins (PAs; i.e. flavan 3-ol oligomers and polymers) protect plants against microbial attacks and fungal growth (Dixon et al., 2005), and anthocyanins of flowers and fruits attract pollinators and help to disseminate seeds (Grotewold, 2006).

Grapevine (\textit{Vitis vinifera}) flavonoids are also of particular importance for wine quality: anthocyanins of red-skinned cultivars are responsible for the red wine color, while PAs or so-called “condensed tannins” confer its astringency to the wine.

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\item\textsuperscript{*} Corresponding author; e-mail terrier@supagro.inra.fr.
\item The author responsible for distribution of materials integral to the findings presented in this article in accordance with the policy described in the Instructions for Authors (www.plantphysiol.org) is: Nancy Terrier (terrier@supagro.inra.fr).
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\end{itemize}
the synthesis of epicatechin and catechin as monomer (Devic et al., 1999; Tanner et al., 2003). In grapevine, two isogenes of LAR (LAR1 and LAR2) and one gene of ANR have been identified (Bogs et al., 2005). Production of a LAR1 *Escherichia coli* recombinant protein confirmed its role in catechin synthesis (Bogs et al., 2005). A LAR2 yeast recombinant protein accepts the three leucoanthocyanidins (mono-, di-, and trihydroxylated on the B ring) as substrates (Pfeiffer et al., 2006). The expression of both ANR and LAR genes is high in young berries and then constantly decreases during fruit development. LAR1 expression was almost restricted to seeds, whereas LAR2 was expressed in both skin and seeds (Bogs et al., 2005). ANR transcripts and, to a lesser extent, LAR2 transcripts were also detected in the pulp of green berries (Verriès et al., 2008). In vegetative organs, ANR was expressed at high levels throughout leaf development; LAR2 expression was only detected in mature leaves, and LAR1 was hardly expressed in leaves (Bogs et al., 2005).

Despite this recent progress in the knowledge of PA unit synthesis, the mechanisms involved in either polymerization or galloylation of units and the fine regulation of the spatiotemporal PA composition remain to be elucidated. At least six transcription factors, regulating different branches of the flavonoid pathway (Fig. 2), of other plant Myb factors involved in the regulation of the phenylpropanoid and flavonoid pathways (Fig. 2), like phenylpropanoid volatiles (PhODO1; Verdonk et al., 2005), flavonols (AtMyb112, AtMyb11, and AtMyb12; Stracke et al., 2007), anthocyanins (VvMybPA1 and VvMybPA2 [Bogs et al., 2007], MdMyb10 [Espley et al., 2007], AtPAP1 and AtPAP2 [Borevitz et al., 2000], LeANT1 [Mathews et al., 2003], MdMyb10 [Espley et al., 2007], and MdMyb1 [Takos et al., 2006]), PAs (VvMybPA1 [Bogs et al., 2007] and AtTT2 [Nesi et al., 2001]), vacuolar pH (PH4; Quattrocchio et al., 2006), or Myb whose function is still undetermined (OsMyb3, PmMBF1). This tree reveals that VvMybPA2 is very distinct from regulators of the anthocyanin pathway and appears to be more closely related to AtTT2 than the other grapevine Myb factors identified so far. Analyses of the primary structure (motif 1; Fig. 1) revealed that the R2R3 repeat region of VvMybPA2 is highly homologous to other plant MYB factors and contains the residues of a conserved signature sequence, [D/E]Lx2[R/K]x3Lx6Lx3R, for interaction with bHLH proteins (Grotewold et al., 2000). The nine-residue consensus sequence V(I/V)R(T/P)(K/R) A(I/L)/V(R/K)/C is present in both AtTT2 and OsMYB3 in the highly variable C-terminal region

**RESULTS**

**VvMybPA2 Encodes a Myb Domain Protein**

Three ESTs, named EC939601, EC993595, and EC950762, were obtained by BLAST search in the *Vitis* database using AtTT2 as a query sequence. The sequences were assembled in a contig, and the full-length cDNA was amplified from cDNA of 3-week-postflowering Shiraz berries, a developmental stage corresponding to the maximum rate of PA biosynthesis. The sequence recovered, called *VvMybPA2* (accession no. EU919682), encodes a protein of 284 amino acid residues (Fig. 1) with a predicted molecular mass of 31.8 kD and a calculated pI of 5.45. In the grapevine PN 40024 genome sequence, this gene is located on chromosome 11 (Jaillon et al., 2007). In this region, gene GSVIVT00016470001 was predicted. However, the in silico predicted coding region of GSVIVT00016470001 is shorter than the *VvMybPA2* actual one experimentally observed. This difference is due to a failure in the automatic detection procedure of intron/exon boundaries used for the annotation of the whole genome.

A phylogenetic tree was constructed using the neighbor-joining method with the protein sequences of other plant Myb factors involved in the regulation of the phenylpropanoid and flavonoid pathways (Fig. 2), like phenylpropanoid volatiles (PhODO1; Verdonk et al., 2005), flavonols (AtMyb112, AtMyb11, and AtMyb12; Stracke et al., 2007), anthocyanins (VvMybPA1 and VvMybPA2 [Kobayashi et al., 2002], AtPAP1 and AtPAP2 [Borevitz et al., 2000], LeANT1 [Mathews et al., 2003], MdMyb10 [Espley et al., 2007], and MdMyb1 [Takos et al., 2006]), PAs (VvMybPA1 [Bogs et al., 2007] and AtTT2 [Nesi et al., 2001]), vacuolar pH (PH4; Quattrocchio et al., 2006), or Myb whose function is still undetermined (OsMyb3, PmMBF1). This tree reveals that VvMybPA2 is very distinct from regulators of the anthocyanin pathway and appears to be more closely related to AtTT2 than the other grapevine Myb factors identified so far. Analyses of the primary structure (motif 1; Fig. 1) revealed that the R2R3 repeat region of VvMybPA2 is highly homologous to other plant MYB factors and contains the residues of a conserved signature sequence, [D/E]Lx2[R/K]x3Lx6Lx3R, for interaction with bHLH proteins (Grotewold et al., 2000). The nine-residue consensus sequence V(I/V)R(T/P)(K/R) A(I/L)/V(R/K)/C is present in both AtTT2 and OsMYB3 in the highly variable C-terminal region.
Expression Profiling of VvMybPA2

The spatiotemporal expression of VvMybPA2 was evaluated by real-time PCR with RNA isolated from several vegetative tissues and berries sampled at different stages of development. Figure 3A shows that VvMybPA2 was highly expressed in very young berries shortly after anthesis. Then, transcript abundance decreased to a very low level after véraison. When berries were divided into exocarp, mesocarp, and seed at three stages of development, VvMybPA2 expression was mostly restricted to the exocarp of very young berries (Fig. 3B). In vegetative organs, the maximum expression of VvMybPA2 was detected in leaves, especially in younger ones (Fig. 3C).

Functional Characterization of VvMybPA1 and VvMybPA2

In order to establish the function of VvMybPA1 and VvMybPA2, each full-length cDNA driven by the 35S promoter was separately introduced into grapevine hairy roots. Hairy roots were screened by PCR for the presence of the hygromycin phosphotransferase gene from the pH2GW7 backbone, yielding seven positive independent transgenic lines from the 10 plants inoculated with each construct. Ectopic expression of VvMybPA1 and VvMybPA2 transcription factor led to PA accumulation. For each gene, the two lines with the highest PA content were selected as independent biological duplicates for more detailed phenotypic and transcriptomic analysis. Hairy roots without the VvMybPA1/2 transgene were used as a wild-type control.

Flavonoid and Lignin Content in Grapevine Organs Overexpressing VvMybPA1 and VvMybPA2

VvMybPA1- and VvMybPA2-expressing hairy roots contained around 8 mg PA g⁻¹ fresh weight, which represents a 5-fold greater accumulation than the levels found in control lines (Fig. 4). Whereas PAs of wild-type roots do not contain any B-ring trihydroxylated units, the percentage of epigallocatechin reached 4% and 5% in roots expressing VvMybPA1 and VvMybPA2, respectively. The mDP exhibited a slight increase in VvMybPA2-expressing lines, with mean values of 16.7 (wild type = 11.6). The high heterogeneity between the two analyzed control lines prevents us from drawing any conclusion concerning the possible influence of the Myb factors on the galloylation level. Neither anthocyanin nor flavonol was detected.
the sectors accumulating high level of PAs, epidermis, endoderm, and vascular bundles were found to be the richest. Pericycle was less marked by the DMACA, and almost no coloration could be observed in the cortical parenchyma cells whatever the type of roots.

With the objective to evaluate whether the transformation induced some redirection in the phenolic metabolism, preliminary analyses of lignin content and composition of the hairy root samples were performed by thioacidolysis (Lapierre et al., 1995) and are presented in Supplemental Table S1. The total yields of lignin-derived thioacidolysis guaiacyl and syringyl monomers were similarly low, whatever the samples (ranging between 8 and 14 μmol g⁻¹ dry weight), and the nonmethoxylated H monomers were recovered as trace components. This yield suggests that all of the hairy root samples have a similarly low lignin content.

Figure 2. Phylogenetic tree showing selected plant MYB transcription factors retrieved from public databases. The phylogenetic tree was constructed from the Clustal alignment using the neighbor-joining method in the MEGA4 package. The scale bar represents 0.05 substitutions per site. The GenBank accession numbers of the MYB proteins are as follows: AtMYB12 (NP_182268), AtMYB11 (NP_191820), AtMYB111 (NP_199744), ZmP (P27898), PhPH4 (AAV52377), VvMyb5b (AAX51291), VvMyb5a (AAS68190), VvMybPA1 (CAJ98331), PmMBF1 (AAA82943), ZmC1 (AAA33482), ZmPL (AAA19821), VvMybPA2 (EU919682), OsMYB3 (AA223339), AtTT2 (Q9FA2), BnTT2-1 (AB113038), BnTT2-2 (AB113039), BnTT2-3 (AB113040), FaMYB1 (AAK84064), AmMIXTA (CAA55725), AtMYB2 (BAA21619), PhODO1 (AAV98200), AtGL1 (NP_189430), AtWER (AAF18939), MdMYB1 (ABK58136), MdMYB10 (ABB67537), AtPAP2 (NP_176813), AtPAP1 (NP_176057), LeANT1 (AAQ55181), VvMYBA1 (BAD18977), and VvMYBA2 (BAD18978).

VvMybPA2 Regulates the Proanthocyanidin Pathway in Grapevine

Figure 3. Transcript levels of VvMybPA2 during berry pericarp development (A), in different berry tissues at three developmental stages (B), and in different organs of vine plants (C). Veraison (V) is marked with the arrows. Gene expression was determined by real-time PCR and normalized with the expression of EF1α. All data are means of three replicates, with error bars indicating SD.
By contrast, the molar frequency of the monomethoxy-
ated guaiacyl thioacidolysis monomers was found to be increased, particularly in the hairy roots of the VvMybPA2-expressing lines. This result suggests that the formation of the guaiacyl lignin units might be affected by the transformation, whereas the total lignin content is not changed.

Expression Analysis of Putative Targets

In order to decipher the mechanisms that underlie the phenotypic changes observed in grapevine ectopically expressing VvMybPA1 and VvMybA2, we first performed real-time PCR experiments on previously known genes of grapevine PA metabolism (Fig. 6A). Overexpression of VvMybPA1 and VvMybPA2 transgenes was confirmed in the respective transformed lines. Some direct or indirect activation was found, as endogenous VvMybPA1 was slightly induced by 35S:: VvMybPA2, while the converse was not true concerning VvMybPA2.

ANR transcripts were significantly increased by VvMybPA1 and VvMybPA2 overexpression. Similar results were observed with LAR1, except that its induction by VvMybPA2 was slightly lower (+65% compared with wild-type organs) and not significant. LAR2 expression was not significantly modified upon overexpression of the VvMybPA factors when compared with controls.

Global Transcriptome Response Analysis Induced by VvMybPA1/2 Overexpression

Transcriptome analysis was performed with a 14 K microarray to identify new genes involved in PA biosynthesis and particularly the putative targets of VvMybPA1 and VvMybPA2. The design corresponded to a comparison analysis of two couples of independent biological replicates of wild-type/overexpressing organs for both VvMybPA1 and VvMybPA2 (comprehensive data are available as Supplemental Materials and Methods S1).

A t test (P < 0.01 based on permutation) revealed that only 2% to 3% of the total number of oligonucleotides spotted on the array presented significant variations due to VvMybPA1 and VvMybPA2 overexpression (510 and 371, respectively). For VvMybPA1, 305 oligonucleotides presented an increase in their hybridization signal and 205 presented a decrease. In the case of VvMybPA2, the respective increase and decrease were 158 and 213 (Supplemental Materials and Methods S1). Among the transcripts whose abundance increased, 55 are common to the VvMybPA1- and VvMybPA2-overexpressing organs (Table I). Further analysis revealed that this set of 55 genes corresponds to only 51 unigenes, as four couples of oligonucleotides may hybridize the same transcript. Although significant, the induction ratios in organs ectopically expressing VvMybPA were rather low, as they ranged from 1.1 to 3.7.

Among the genes induced in common by VvMybPA1 and VvMybPA2, 10 are linked to the PA pathway, including nine genes previously identified in grape-
vine: Phe ammonia lyase, 4-coumarate:CoA ligase, chalcone synthase, two genes of flavanone-3-hydroxylase, flavonoid-3′-hydroxylase (F3′H), dihydroflavonol-4-reductase, leucoanthocyanidin dioxygenase (LDOX), ANR, and a multidrug and toxic compound extrusion (MATE) transporter (GSVIVP00018839001) exhibiting homology with TT12 (Debeaujon et al., 2001) that represents a new putative actor in the PA pathway in grapevine. Two isogenes encoding cinnamoyl-CoA reductase of the phenylpropanoid pathway were also identified. Both transcription factors led to the induction of four genes linked to the metabolism of aromatic amino acids and shikimate (shikimate kinase, shikimate dehydrogenase, 3-deoxy-D-arabino-heptulosonate 7-phosphate synthase, and prephenate dehydratase), precursors of the flavonoid pathway. In addition to genes encoding enzymes already annotated as actors in the flavonoid pathway, the experiments revealed several genes linked with sugar metabolism: two glucosyltransferases (GSVIVT00036656001 and GSVIVT00036670001), one Glc acyltransferase (GSVIVT00038626001), two sugar

**Figure 5.** Phenotype of grapevine hairy roots stained with DMACA. A, Wild-type hairy roots showing the distribution of blue dye formed with PA on main and secondary organs. Bar = 2 mm. B, Wild-type hairy root section. Bar = 250 μm. C, VvMybPA1-expressing hairy root. Bar = 250 μm. D, VvMybPA2-expressing hairy root. Bar = 250 μm. DZ, Division zone; EZ, elongation zone; SR, secondary roots.

**Figure 6.** Transcript levels of putative targets (A) and validation of microarray results (B) in grapevine organs overexpressing VvMybPA1 (lines PA1-2A and PA1-7A) or VvMybPA2 (lines PA2-1A and PA2-7A) versus the wild type (lines control-1 and control-2). Gene expression was determined by real-time PCR and normalized with the expression of EF1α. All data are means ± SD of three replicates. Stars indicate that expression levels are significantly different between wild-type and transformed hairy roots (P < 0.01).

VvMybPA2 Regulates the Proanthocyanidin Pathway in Grapevine
Table I. List of transcripts whose expression is induced after both VvMybPA1 and VvMybPA2 overexpression

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<th>PA1/Wild-Type Ratio</th>
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(Table continues on following page.)
transporters, and a Fru-1,6-bisphosphatase. Another striking category contains seven genes related to signaling mechanisms, including a Myb factor, a calcineurin B-like (CBL) protein, and a CBL-interacting protein kinase. All of these genes represent the most induced genes, and for some of them this induction was confirmed by real-time PCR (Fig. 6B). Genes induced to a lower extent have miscellaneous or unknown functions, and some of them do not even exhibit homologies with other genes of the plant kingdom.

A total of 828 genes were found significantly differentially expressed between hairy roots overexpressing VvMybPA1 and VvMybPA2. Among them, 59 are specifically induced in 35S::VvMybPA1 transformants, such as a chalcone synthase isogene, another MATE transporter, while 21 are more specific for VvMybPA2, such as another glucosyltransferase, GSVIVT00013771001 (Fig. 6B; Supplemental Materials and Methods S1).

**DISCUSSION**

VvMybPA1 and VvMybPA2 Regulate the PA Pathway in Grapevine Berries

PA synthesis in grapevine berries is restricted to the early stages of development in skin and seed and in pulp to a certain extent (Verrie`rs et al., 2008). Moreover, PAs of these different tissues exhibit noticeable structural differences whose biological determinism is unknown, although it is probably linked to the differential regulation of F3'H, flavonoid 3',5'-hydroxylase (F3'5'H), ANR, LAR1, and LAR2 isoforms in a precise time- and tissue-specific manner. The data presented here indicate that at least two transcription factors belonging to the Myb family are involved in the control of PA content in grapevine. VvMybPA1 was previously identified by Bogs et al. (2007). VvMybPA2, which was identified here, appears to be the closest ortholog of AtTT2 identified so...
far in grapevine. R2R3 Myb factors share very limited homology in their C-terminal regions, which could be related to their target specificity. A sequence conserved between AtTT2 and OsMYB3 and more recently confirmed in Brassica napus putative orthologs of TT2 was identified in this highly variable C-terminal region (Nesi et al., 2001; Stracke et al., 2001; Wei et al., 2007). This motif is also present in VvMybPA2 but is not strictly conserved in the VvMybPA1 sequence (Bogs et al., 2007).

We demonstrated here that the spatiotemporal expression of VvMybPA2, restricted to the skin of young berries and leaves, is compatible with a putative role in the regulation of PA biosynthesis. The VvMybPA2 expression pattern argues in favor of a preferential role in PA synthesis and accumulation in berry skins when compared with VvMybPA1. VvMybPA1 is expressed before véraison and actually correlates with PA accumulation in seeds (Bogs et al., 2007). Its involvement in the accumulation of PA accumulation in skin was ruled out, on the basis of its very low expression level in this tissue. Moreover, according to some authors, VvMybPA1 showed an unexpected maximum of expression 2 weeks after véraison when PA accumulation was stopped (Bogs et al., 2007; Deluc et al., 2007). Conversely, the profile of VvMybPA2 is consistent with a critical function in the accumulation of PAs in berry skin. It was hypothesized that the different branches of the flavonoid and phenylpropanoid pathways are specified by Myb proteins inside the activating complex (Zhang et al., 2003). However, Deluc et al. (2006), expressing VvMyb5a transcription factor in tobacco (Nicotiana tabacum), showed that the activation of diverse branches of the flavonoid and phenylpropanoid pathways in the different parts of the transgenic plants could also be modulated by bHLH and WD40 as members of the transcriptional machinery. Nevertheless, this transcription factor did not trigger anthocyanin accumulation in natural circumstances, being expressed in berries at green stage, and its actual function in grapevine remains to be clarified. We show here that both VvMybPA1 and the new VvMybPA2 actually act as specific positive regulators of PA biosynthesis when stably expressed in grapevine, alleviating the hazard of artifacts upon ectopic expression in heterologous plants, as suspected for VvMyb5a (Deluc et al., 2006). Both transcription factors described here appeared as extremely specific to the PA pathway, since no shift toward lignin, anthocyanin, and flavonol production appeared in long-term experiments.

VvMybPA1 and VvMybPA2 Overexpression Give Similar Results

In order to clarify the specific roles of VvMybPA1 and VvMybPA2, we observed the respective pheno-typic and transcriptomic variations induced by their ectopic overexpression in grapevine. Both genes were able to modify PA contents and their subunit composition. When overexpressed in hairy roots, VvMybPA1 and VvMybPA2 actually triggered de novo B ring trihydroxylation, and a slightly increased mDP was observed in the case of VvMybPA2-expressing lines, which is consistent with the composition of skin PAs. The level of trihydroxylation of transgenic hairy root PAs was similar to that of Maccabeo berry skin (3.5%) and higher than in seeds (0%; Souquet et al., 2006). In this respect, the increase of trihydroxylated units observed here upon the overexpression of VvMybPA1 is consistent with its ability to activate the promoter of F3’5’H (Bogs et al., 2007). However grapevine seed PAs do not contain any (epi)gallocatechin unit, which may suggest a pretranscriptional or posttranscriptional negative regulation of F3’5’H in the seeds. Despite exhibiting an increase upon ectopic expression of VvMybPA2, the PA chain length remained three times lower than the mDP of approximately 50 encountered inside the skin of Maccabeo plants from the field (Souquet et al., 2006). More generally, we did not succeed in reproducing the large structural differences among seed and skin tannins upon differential ectopic expression of VvMybPA1 and VvMybPA2.

This PA accumulation was found restricted to some tissues despite the use of a 35S promoter. At the transcription level, several causes could explain the deficit in PA accumulation in some tissues and cells: (1) lack of members of the activating complex, (2) absence of transcription factors in the role of activators, or (3) expression of inhibitors. In Arabidopsis, Nesi et al. (2001), observing that ectopic expression of TT2 activated TT8, BAN, or TT12 without subsequent PA accumulation, hypothesized the lack of activation of earlier genes of the pathway. In grapevine cell suspensions, cotransformation with a bHLH factor was found mandatory for the transient activation of the LDOX promoter by VvMybPA1 (Bogs et al., 2007). In our experiments, the sole overexpression of VvMybPA1 or VvMybPA2 proved to be sufficient to enhance the LDOX expression. This means that either the partners forming the PA regulatory complex were already present in the tissues of the roots accumulating PAs or that long-term overexpression is necessary to induce all partners required for full activation of the PA pathway. The latter hypothesis appears rather unlikely, since no induction of any bHLH or WD40 transcription factors was found associated with the ectopic accumulation of PAs in grapevine. However, it must be kept in mind that the 14 K oligoarray used in this study may probe only half of the Vitis transcriptome, according to Jaillon et al. (2007).

As the phenotypes of transgenic grapevine organs expressing VvMybPA1 or VvMybPA2 are quite similar, the reason for the existence of two distinct transcription factors with apparent redundant function can be questioned. A similar functional redundancy was described in Arabidopsis, in which three different Myb factors controlling the flavonol pathway were identified, each of them exhibiting a specific tissue expression pattern (Stracke et al., 2007). Recently, Matus et al. (2008) classified the 108 members of the grape R2R3
Myb family in terms of their genomic structures and similarity to their putative Arabidopsis orthologues. Eight genes, including *VvMybPA2* but neither *VvMybPA1* nor *VvMyb5a*, were designated as putative candidates for PA pathway regulators. Further work is needed to better understand the putative functions of these regulators in the tissue-specific regulation of the PA pathway.

Despite the phenotype similarities, the high-throughput transcriptomic analysis presented here revealed that several targets were specifically induced by each Myb factor. However, either the genes identified were isogenes of already identified targets, like the identified glucosyltransferase specifically induced in *VvMybPA2* transgenic lines, suggesting here again functional redundancy (or very subtle differences in their catalytic properties), or the level of induction for these genes was remarkably low.

This experiment also raises the question of the interactions between transcription factors. A first result emerged from this study, where overexpression of *VvMybPA2* resulted in the accumulation of *VvMybPA1* transcripts, suggesting that *VvMybPA2* signal acts upstream of *VvMybPA1*.

**Expected and Unexpected Targets, and Absence of Expected Targets**

**Enzymes of the Flavonoid Pathway**

Being the final result of a transcriptomic screening after overexpression of two different transcription factors inducing PA accumulation, the list of the 51 induced transcripts is very likely to contain specific isogenes involved in the PA pathway. Microarray analysis revealed the induction of genes from Phe ammonia lyase to ANR. Rather low expression ratios were observed after overexpression of both Myb factors. This could result from the preactivation of the PA pathway in wild-type hairy roots, which already contain significant amounts of PAs. In addition, we observed that despite the use of a constitutive promotor, only specific tissues were able to ectopically accumulate PAs. Consequently, the sensibility of the analysis is probably hampered by the low number of cells inside the organs affected by PA accumulation. Some genes belonging to this pathway were not detected. For example, the only copy of chalcone isomerase in the genome is induced in both types of transformants, but its induction reaches a significant threshold only under *VvMybPA1* overexpression. In addition, some genes could not be monitored due to the absence of a probe, like F3’5’H. The induction of F3’5’H seems necessary to synthesize the trihydroxylated units observed in transgenic roots. Unfortunately, the grapevine genome contain 10 genes coding for putative F3’5’H (Jaillon et al., 2007; Velasco et al., 2007), which precluded the design of isogene-specific 70-mer-long probes.

Neither the overexpression of *VvMybPA1* nor that of *VvMybPA2* resulted in a significant induction of LAR2. Bogs et al. (2007) reported that *VvMybPA1* was able to activate the promoters of LAR1, as confirmed here, but they did not address LAR2 activation. The proportion of catechin as TU or free monomer was not impaired when compared with the wild type, probably due to the activity of LAR1 (data not shown). Disturbing results concerning particular LAR isogenes are reported in the literature on other plants (Pang et al., 2007; Paolocci et al., 2007). Similarly, ectopic expression of the maize (*Zea mays*) bHLH flavonoid regulator *Sn* in *Lotus corniculatus* resulted in an increase of PA content and induction of ANR and LAR1 transcripts, while LAR2 transcription remained unaffected (Paolocci et al., 2007). They failed to detect any catechin synthesis after the heterologous production of the LAR2 enzyme (Paolocci et al., 2007). PAs of *Medicago truncatula* seed coat contain insignificant amounts of catechin as TU or EU, despite the presence of LAR transcript in this tissue and the ability of the heterologous LAR protein to synthesize catechin in vitro (Pang et al., 2007). These authors also reported that transgenic tobacco plants overexpressing *MiLAR* did not exhibit changes in their PA or catechin content. Taken together, these results indicate that LAR isogenes occupy a particular place in the PA pathway, from the functional and transcriptional regulation points of view, and the precise role of LAR2 remains to be elucidated.

In addition to the induction of genes previously shown to be involved in sensu stricto PA biosynthesis, screenings revealed the induction of one (GSVIVT00018839001) of the 65 MATE-type transporters of the grapevine genome (C. Gomez, personal communication). With 70% amino acid homology, this gene appears to be the closest homolog of TT12, which was shown to be critical for PA accumulation in the Arabidopsis seed testa (Debeaujon et al., 2001). The protein encoded by TT12 was found located on the tonoplast, and in vitro experiments showed that TT12 transports the anthocyanin cyanidin-3-O-glucoside (Marinova et al., 2007). A glutathione S-transferase (Kitamura et al., 2004) and a AHA10-like H+-ATPase (Baxter et al., 2005) have been reported to be involved in PA storage, but no grapevine homolog of these transcripts has been identified in our microarray screening.

Several genes were described as systemically expressed concomitantly with anthocyanin accumulation, like UDP-Glc:flavonoid 3-O-glucosyltransferase (Boss et al., 1996) or a putative methyl transferase and a particular isogene of glutathione S-transferase (Ageorges et al., 2006). Other experiments were performed by our group with the aim to ectopically activate anthocyanin accumulation in hairy roots with the *VvMybA1* gene identified by Kobayashi et al. (2002). It resulted in anthocyanin accumulation and the induction of a set of genes specific for the anthocyanin pathway, without any modification of their PA content or of the expression level of the PA biosynthetic genes, ANR, LAR1, and LAR2 (Cutanda-Perez et al., 2007).
et al., 2009). On the other hand, neither the anthocy-
atin biosynthetic genes nor flavonol synthase were
induced in the hairy roots overexpressing VvMybPA1
and VvMybPA2 genes, confirming their specific role in
the regulation of the PA pathway and an activation
spectrum different from that of VIMybA1.

**Signal Transduction**

Overexpression of both VvMybPA1 and VvMybPA2
also induced the expression of a set of genes associated
with signaling. A homolog of Arabidopsis Myb4 was
ectopically induced in grapevine organs. AtMyb4 was
shown to act as a repressor of the phenylpropanoid
pathway (Jin et al., 2000). Its induction as a conse-
quence of VvMybPA1 and VvMybPA2 overexpression
could be considered as a way to counterbalance their
attempt to avoid the bolting of the PA pathway.

CBL proteins and their target kinases, CBL-interacting
protein kinases, have often been described as function-
ing in complex in the response to abiotic stresses
(Batistic and Kudla, 2004). The simultaneous induction
of these genes may result from the stress experienced
by the plant after ectopic expression of the VvMybPA or
from a sudden increase of intracellular PA concentra-

**Genes Linked to Sugar Metabolism**

Several genes related to sugar metabolism appeared
as potentially driven by VvMybPA factors. Among
them, the induction of a hexose transporter called
VvHT2 (Fillion et al., 1999) was unexpected. Fillion
et al. (1999) described its expression maximum 1 week
after véraison, whereas Hayes et al. (2007) reported a
constant decrease of expression during berry devel-
opment. However, the in planta role of VvHT2 remains
to be characterized. Incidentally, a protein from Lotus
japonica annotated as “Suc transporter” and located at
the tonoplast proved to be capable of transporting
phenyl glucosides (Reinders et al., 2008). A possible
involvement of genes annotated as “sugar trans-
porter” in the transport of a glycosylated intermediate
of the pathway cannot be excluded.

The two closest identified homologs of
GSVIVT00038626001, a putative Glc acyltransferase,
are (1) DkSCPL1, a gene of persimmon (Diospyros kaki)
identified through a suppression subtractive hybrid-
ization between fruits differing in their PA content
(Ikegami et al., 2007), and (2) a Solanum pennellii
acyltransferase catalyzing the formation of diacylglu-
cose (Li and Steffens, 2000). These proteins could act as
Glc acyltransferases that use 1-O-β-acetyl Glc esters as
acyl donors (Milkowski and Strack, 2004).

Several glucosyltransferases were also identified.
Two of them (GSVIVT00036670001 and GSVIV-
T000386656001) are induced by both transcription fac-
tors, whereas another one (GTGSVIVT00013771001)
appears more specifically driven by VvMybPA2.
GSVIVT00036656001 was already identified as a

**MATERIALS AND METHODS**

**Plant Material and Nucleic Acid Extraction**

Organs (berries, leaves, tendrils, and roots) from grapevine (Vitis vinifera ‘Shiraz’) plants grown in the SupAgro-INRA vineyard in Montpellier, France,
were collected at several developmental stages. Young leaves corresponded to
leaves explanted from the third node below the shoot tips, with a mean weight
of 0.3 g. Old leaves corresponded to fully expanded leaves sampled from the
mature shoot part, with a mean weight of 2.8 g. Eight- to 10-week-old plantlets
of cv. Maccabeu grapevine propagated onto half-strength Murashige and
Skoog medium were used for transformation procedures.

After sampling, hairy roots and plant organs were rapidly frozen in liquid
nitrogen and then ground to a fine powder with a Dangoumau blender
(Dangoumill 300) and stored at –80°C until use.

DNA was extracted from 50 mg of frozen tissue using the DNA Plant Mini
kit (Qiagen). Total RNA was extracted using the RNeasy Plant Mini kit
(Qiagen) following the manufacturer’s instructions, starting from 200 mg of
tissue.

**Cloning and Vectors**

The coding regions of VvMybPA1 and VvMybPA2 were amplified from
young Shiraz pericarp cDNA with high-fidelity Taq polymerase (Advantage-
VvMybP2A regulates the proanthocyanidin pathway in grapevine

HF 2 PCR kit; Clontech) using the forward primers 5′-CACCATGGGCA-
GAGCACCCTGGTG3′ and 5′-CACCAGGAAAGACATCTGTTG3′ and the reverse primers 5′-TAAATGGATGATACTGGC-3′ and 5′-CTATGACGATTGATTTTC-3′ for VvMybPA1 and VvMybPA2, respectively. The amplicons were directionally cloned in pENTR/D-TOPO (Invitrogen Life Technologies) according to the manufacturer’s instructions. The sequences of the positive clones were confirmed following transformation of One Shot competent Escherichia coli (Invitrogen Life Technologies) and LR recombination in the binary vector pH2G7v7 (Karimi et al., 2002) to yield the 3SS
VvMybPA constructs. The sequence of VvMybPA2 was deposited in GenBank under accession number EU919682.

Sequence Analysis

Full-length amino acid sequences of Myb factors from several species were retrieved from public databases. Alignments were performed with the ClustalW2 algorithm with default parameters (Thompson et al., 1994). The phylogenetic tree was constructed from the Clustal alignment using the neighbor-joining method in the MEGA4 package (Kumar et al., 2004).

Real-Time PCR

The RNA was accurately quantified with Ribogreen reagent (Molecular Probes). A triplicate reverse transcription was performed on 500 ng of total RNA from each developmental stage using the SuperScript II reverse transcriptase kit (Invitrogen Life Technologies) and LR recombination in the binary vector pH2G7v7 (Karimi et al., 2002) to yield the 3SS VvMybPA constructs. The sequence of VvMybPA2 was deposited in GenBank under accession number EU919682.

Recombinant plasmids were electroporated into Agrobacterium rhizogenes strain A4 introduced from Collection Francaise de Bacteries Phytopathogenes (http://www-intranet.angers.inra.fr/cfbp/).

Sequence Analysis

Full-length amino acid sequences of Myb factors from several species were retrieved from public databases. Alignments were performed with the ClustalW2 algorithm with default parameters (Thompson et al., 1994). The phylogenetic tree was constructed from the Clustal alignment using the neighbor-joining method in the MEGA4 package (Kumar et al., 2004).

Real-Time PCR

The RNA was accurately quantified with Ribogreen reagent (Molecular Probes). A triplicate reverse transcription was performed on 500 ng of total RNA from each developmental stage using the SuperScript II reverse transcription kit (Invitrogen) according to the manufacturer’s instructions. Triplicate reverse transcriptions for PCR were pooled to minimize the heterogeneity of the reverse transcription reaction efficiency. Specific oligonucleotide primer pairs were designed with Primer3 software except for DLOX (Bogs et al., 2005) and for dihydroflavonol-4-reductase (Jeong et al., 2005).

Microarray Experiments

We used the Quagen Operon Array-Ready Oligo Set for the Grape Genome Version 1.0 containing 14,562 70-mer probes representing 14,562 transcripts from The Institute for Genomic Research (TIGR) Grape Gene Index, release 3. Oligonucleotides were reamplified using the DFCI Grape Gene Index, release 3. Oligonucleotides were spotted on mirror slides, and the probes were labeled with Cy3 and Cy5 dyes with the Alumino Allyl MessageAmp II aRNA kit (Ambion). The experiment was performed using eight slides (two biological replicates for each condition and a dye swap, detailed in Supplemental Materials and Methods S1). Hybridized microarrays were simultaneously scanned for Cy3- and Cy5-labeled probes with an Axon Genepix 4000B scanner.

Statistical Treatments

Regarding microarray experiments, data from both channels corresponding to Cy3- and Cy5-labeled probes were normalized using the Lowess algorithm in the Microarray Data Analysis System at TIGR. Data from all of the slides were log2 transformed and normalized (centered on 0, variance equalized to 1); those data are available in Supplemental Materials and Methods S1. The significance was calculated at the 0.01 level by permutation test in Multiexperiment Viewer from TIGR.

Supplemental Data

The following materials are available in the online version of this article.

Supplemental Table S1. Lignin content, subunit composition, and proportion (guaiaeryl and syringyl lignin-derived monomers) in grapevine organs overexpressing VomYbPA1 or VomYbPA2 compared with controls.

Supplemental Table S2. Primers used for real-time PCR and expected sizes of the amplified fragments.
**Supplemental Materials and Methods S1. terriresupS2.xls contains experimental design ("design"); sheet 1), complete hybridization results log-transformed and normalized ("totlognorm"); sheet 2), list of genes for which transcript accumulation is significantly affected by ectopic overexpression of VvMybPA1 ("PA1signif"); sheet 3) or VvMybPA2 ("PA2signif"); sheet 4), list of genes for which transcript accumulation is significantly different between ectopic overexpression of VvMybPA1 and VvMybPA2 ("PA2difPA1"); sheet 5), list of genes specifically induced by ectopic overexpression of VvMybPA1 ("PA1spec"); sheet 6), and list of genes specifically induced by ectopic overexpression of VvMybPA2 ("PA2spec"); sheet 6).

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**LITERATURE CITED**


VvMybPA2 Regulates the Proanthocyanidin Pathway in Grapevine

Activation tagging in tomato identifies a transcriptional regulator of anthocyanin biosynthesis, modification, and transport. Plant Cell 15: 1697–1703


