

Light Microclimate-Driven Changes at Transcriptional Level in Photosynthetic Grape Berry Tissues

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Supplementary Materials

Table S1. Forward (F) and reverse (R) primers used for gene expression analysis by real-time PCR. Sequences accession numbers were obtained through Grape Genome Brower 12x or, for the carotenoid metabolism genes, from Plaza 1.0 (April, 2009; http://bioinformatics.psb.ugent.be/plaza_v1/), or Grape Genome Database (<http://genomes.cribi.unipd.it/grape/>) for *VvLAR2* and *VvRubisCO*.

Gene	Accession number (Genoscope)	Primers
<i>VvACT1</i> (reference gene)	GSVIVT01026580001	F: 5'-GTGCCTGCCATGTATGTTGCC-3'
		R: 5'-GCAAGGTCAAGACGAAGGATA-3'
<i>VvGAPDH</i> (reference gene)	GSVIVT00009717001	F: 5'-CACGGTCAGTGGAAAGCATCAT-3'
		R: 5'-CCTTGTCACTGAACACACCAG-3'
<i>VvPAL1</i>	GSVIVG01025703001	F: 5'-CCGAACCGAATCAAGGACTG-3'
		R: 5'-GTTCCAGCCACTGAGACAAT-3'
<i>VvSTS1</i>	GSVIVT01010590001	F: 5'-CGAACGAACTAGGCATGTGT-3'
		R: 5'-CTCCCCAATCCAATCCTTCA-3'
<i>VvCHS1</i>	GSVIVT01032968001	F: 5'-GTCGGAGGGTTGATTCCAA-3'
		R: 5'-TCTCTTCCTTCAGACCCAGTT-3'
<i>VvCHS3</i>	Lac14-SSH (CX126991)	F: 5'-TCGCATCACAAATAGCGAAC-3'
		R: 5'-CAGGGAAAGCTGCCATGTATT-3'
<i>VvFLS1</i>	GSVIVT01008913001	F: 5'-CAGGGCTTGCAGGTTTTAG-3'
		R: 5'-GGGTCTTCTCCTTGTTCACG-3'
<i>VvMYBPA1</i>	GSVIVT01010590001	F: 5'-AGATCAAATGGTTATGCTTGCT-3'
		R: 5'-AACACAAATGTACATCGCACAC-3'
<i>VvDFR</i>	GSVIVT01009743001	F: 5'-GGTTTCTAGCGAGAGCGTA-3'
		R: 5'-ACTCTCATTTCCGGCACATT-3'
<i>VvANR</i>	GSVIVG01035256001	F: 5'-CAATACCAGTGTCCCTGAGC-3'
		R: 5'-AAACTGAACCCCTTTCAC-3'
<i>VvLAR1</i>	GSVIVT01024419001	F: 5'-CAGGAGGCTATGGAGAAGATAC-3'
		R: 5'-ACGTTCTCTCTGTACATGTTG-3'
<i>VvLAR2</i>	VIT_217s0000g04150	F: 5'-CAAATCGTTCATTCGCCACCTCCC-3'
		R: 5'-GTCATCTTCTCCACGGTTACACGG-3'
<i>VvLDOX</i>	GSVIVT01009743001	F: 5'-ACTTCATCCTCCACAACAT-3'
		R: 5'-AGTAGAGCCTCTGGTCTT-3'
<i>VvChlSyn</i>	GSVIVT01011187001	F: 5'-GCTGAGACTGATGCAAATGAAGCC-3'
		R: 5'-TGCGAGAAGCTGATTGAAGTCG-3'
<i>VvRubisCO</i>	VIT_13s0019g02050	F: 5'-TTCAAAGCTCTGCGCGCTCTAC3'
		R: 5'-TCTCTCAACTTGGATGCCATGAGG-3'
<i>VvSPS1</i>	GSVIVT01012825001	F: 5'-GGTTGCCATTGTTGCCACCAG-3'
		R: 5'-CAAGAAGGCCATTGTCAAGTACCC-3'
<i>VvSuSy1</i>	GSVIVT01015018001	F: 5'-TGTAAAGGCTCTGGATTCAATTAA-3'
		R: 5'-AGCCAAATCTTGGCAAGCA-3'
<i>VvPSY1</i>	VV00G37410	F: 5'-TCGATGTGGTGAAGTTGTGAG-3'
		R: 5'-TCAGGTGTCATCAGCATTGTTCCC-3'
<i>VvLBCY2</i>	VV08G15130	F: 5'-AGGCTGGTGGTGAAGATTGG-3'
		R: 5'-TCCTCAACGACAAACCGAAGTGG-3'
<i>VvLECY1</i>	VV11G01840	F: 5'-TGGATGTGGCAGGGATTCTTGG-3'
		R: 5'-TAGCATGGTTGCTCCAGTAGGG-3'

<i>VvLUT1</i>	VV08G10880	F: 5'-TGCTTGCTAGCAGAGAAGAGGTG-3' R: 5'-ACTGCCATTGAGTGCATCAGTTC-3'
<i>VvVDE1</i>	VV00G14320	F: 5'-GTTGTCTATGGTTGGTGGTTGGC-3' R: 5'-ATGCCAGTGGGTCTCCATTCC-3'
<i>VvZEP1</i>	VV07G11310	F: 5'-AGCGTGCTATTGGTGGAGAGTG-3' R: 5'-CCCGATTATGCAGGGTTGTTCTC-3'

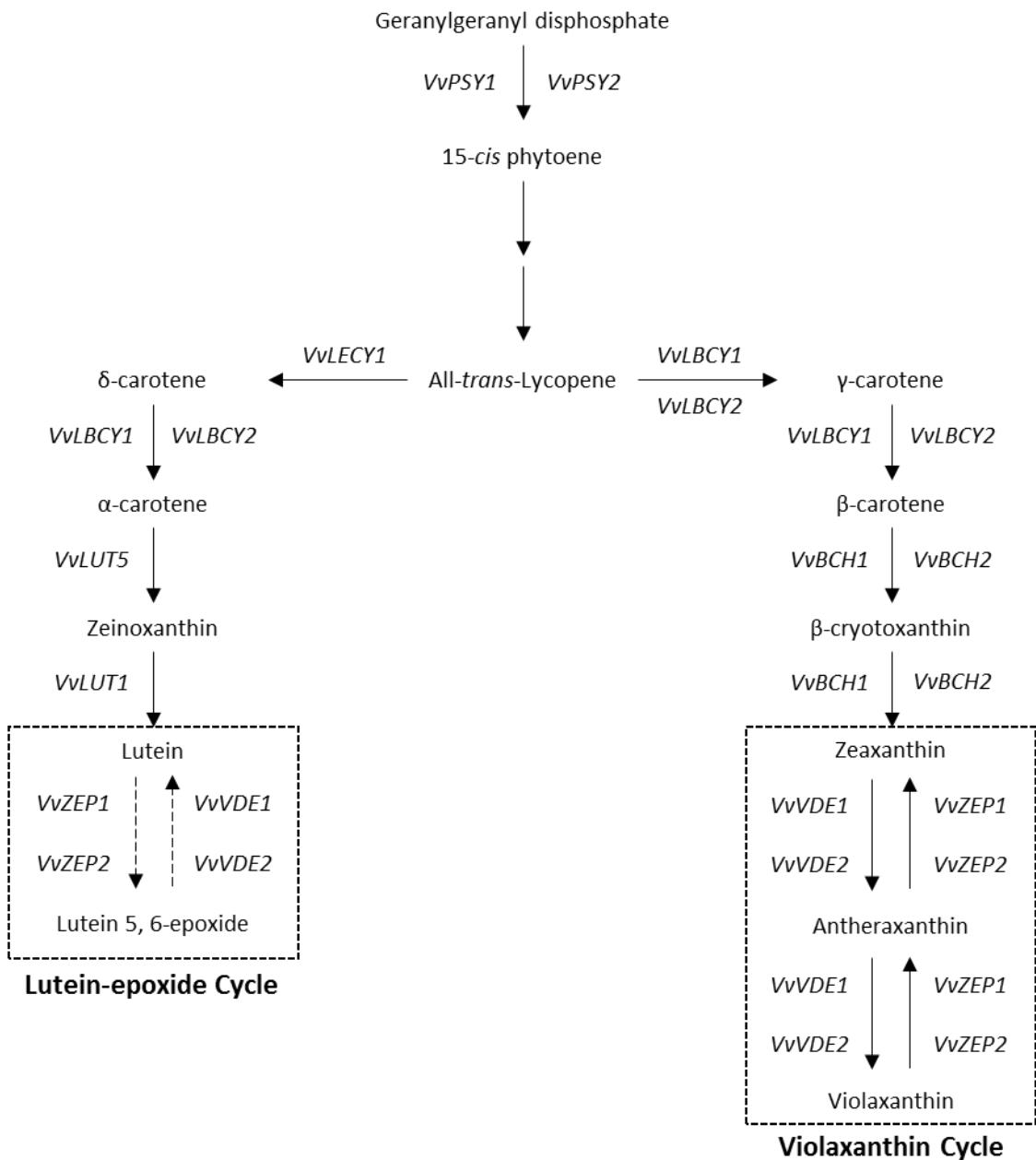


Figure S1. Simplified carotenoid metabolic pathway. *PSY1/PSY2*, phytoene synthase; *LECY1/LECY2*, lycopene epsilon cyclase; *LBCY1/LBCY2*, lycopene β -cyclase; *LUT5/LUT1*, lutein synthase; *BCH1/BCH2*, β -carotene hydroxylase; *VDE1/VDE2*, violaxanthin de-epoxidase; *ZEP1/ZEP2*, zeaxanthin epoxidase. Adapted from Young et al. [39].

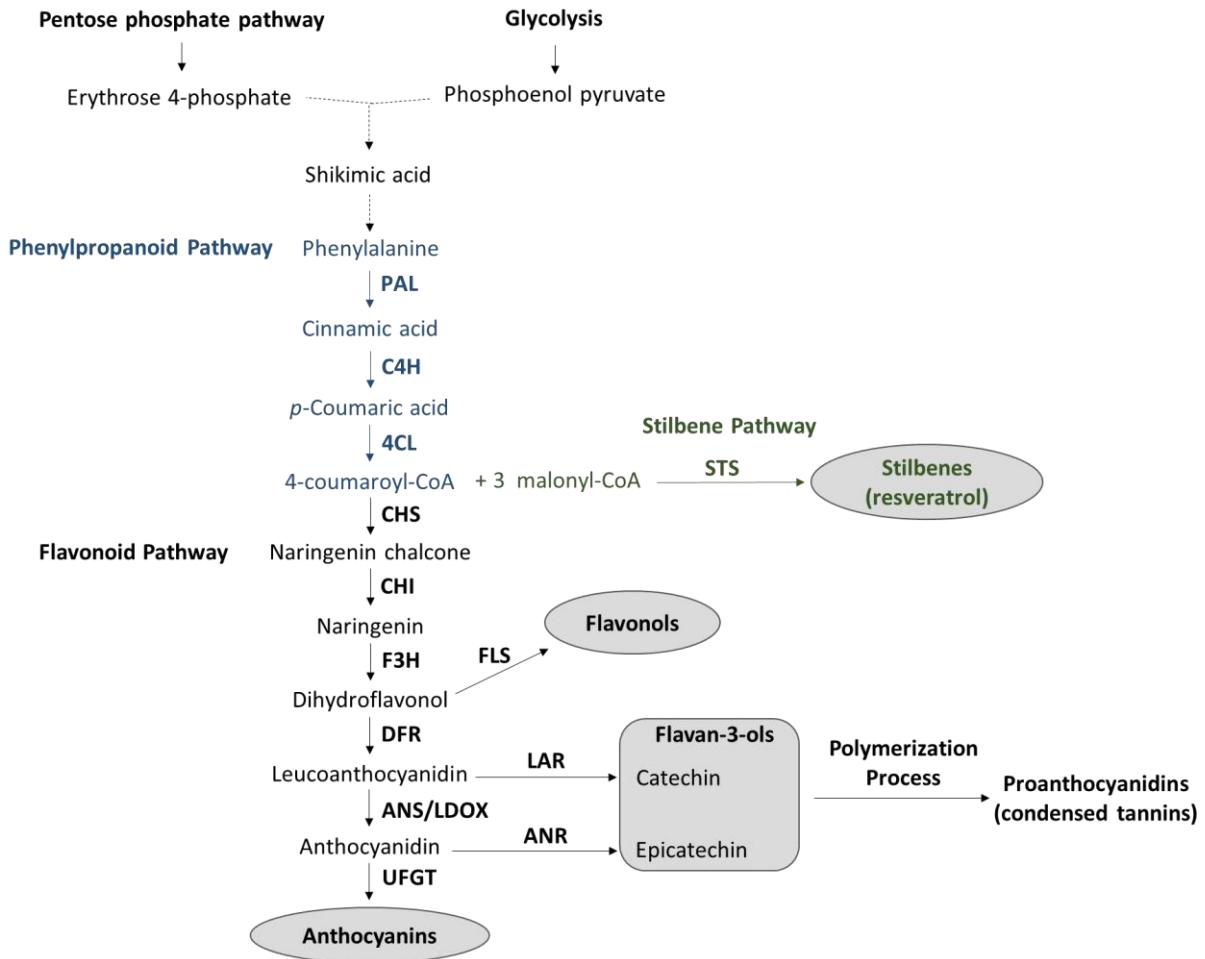


Figure S2. Biosynthetic pathways of phenolic compounds in grape berry. PAL, phenylalanine ammonia lyase; C4H, cinnamate-4-hydroxylase; 4CL, 4-coumaroyl:CoA-ligase; CHS, chalcone synthase; STS, stilbene synthase; CHI, chalcone isomerase; F3H, flavonone 3-hydroxylase; FLS, flavonol synthase; DFR, dihydroflavonol reductase; ANS, anthocyanidin synthase; LDOX, leucoanthocyanidin dioxygenase; LAR, leucoanthocyanidin reductase; ANR, anthocyanidin reductase; UFGT, flavonoid glucosyltransferase. Full lines represent direct enzymatic conversion and dashed lines represent omitted intermediates. Adapted from Ageorges et al. [88] and Teixeira et al. [89].

Table S2. Matrix with Pearson correlation coefficients (r), calculated for selected genes ($VvFLS1$, $VvDFR$, $VvLDOX$, $VvLAR1$, $VvLAR2$, $VvANR$ and $VvMYBPA1$) in the exocarp, considering all samples collected in both light microclimate and developmental stages ($n = 18$). The coefficient values in bold are statistically significant ($p \leq 0.05$).

	$VvFLS1$	$VvDFR$	$VvLDOX$	$VvLAR1$	$VvLAR2$	$VvANR$	$VvMYBPA1$
$VvFLS1$	1.000						
$VvDFR$	-0.770	1.000					
$VvLDOX$	-0.419	-0.104	1.000				
$VvLAR1$	-0.439	0.456	-0.021	1.000			
$VvLAR2$	-0.452	0.842	-0.414	0.567	1.000		
$VvANR$	-0.504	0.845	-0.381	0.567	0.982	1.000	
$VvMYBPA1$	-0.519	0.864	-0.335	0.557	0.962	0.979	1.000

Table S3. Matrix with Pearson correlation coefficients (r), calculated for selected genes ($VvFLS1$, $VvDFR$, $VvLDOX$, $VvLAR1$, $VvLAR2$, $VvANR$ and $VvMYBPA1$) in the seed, considering all samples collected in both light microclimate and developmental stages ($n = 18$). The coefficient values in bold are statistically significant ($p \leq 0.05$).

	$VvFLS1$	$VvDFR$	$VvLDOX$	$VvLAR1$	$VvLAR2$	$VvANR$	$VvMYBPA1$
$VvFLS1$	1.000						
$VvDFR$	-0.379	1.000					
$VvLDOX$	0.877	-0.399	1.000				
$VvLAR1$	-0.239	0.367	-0.342	1.000			
$VvLAR2$	-0.167	0.752	-0.138	0.327	1.000		
$VvANR$	0.556	0.098	0.357	0.420	0.212	1.000	
$VvMYBPA1$	0.125	0.698	0.167	0.215	0.782	0.404	1.000