ABCC1, an ATP-binding Cassette Protein from Grape Berry, Transports Anthocyanidin 3-*O*- Glucosides

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Supplemental Figure 1. Expression analyses of the closest homologous of ABCC1/2

Standard RT-PCR was performed with 0.5 µg of total RNA isolated from berry exocarps during different fruit developmental/ripening stages (49, 68, 81 and 97 days after flowering). PCR analyses for analyzing the expression of *ABCC2*, *ABCC 14*, *ABCC16*, *ABCC18* and *ABCC19* were performed with gene-specific primers. PCR products with the actin primers were used as a loading control. PCR products were visualized on ethidium bromide-containing agarose gels. No amplification was observed for *ABC2*, *ABCC14* and *ABCC16*.



Supplemental Figure 2. Assessment of physiological intactness of yeast microsomes

To assess the physiological intactness of the isolated vesicles, we chose the lumen acidification method. The acidification is the result of activity of various ATPases. The ATP-dependent quenching of the fluorescent dye 9-amino-6-chloro-2-methoxyacridin (ACMA) indicates that the vesicles are sealed and intact, and the pH gradient is generated. Addition of $(NH_4)_2SO_4$, restored the basic fluorescence, indicating that the proton gradient formed across the membranes collapsed, proof that the vesicles were intact. In **A**) results for the vector control-pNEV, in **B**) the results for pNEV-VvABCC1 are presented. **C**) To test whether both vacuolar and plasma membrane vesicles are present, and to what extent are they sealed, we performed the ACMA quenching experiment in the presence of vanadate (inhibitor of the plasma membrane ATPases), bafilomycin (inhibitor of vacuolar ATPases), and vanadate+bafilomycin. This is a representative figure; the test was performed for each of the used microsome preparation.



Supplemental Figure 3. The effect of BSO on anthocyanin concentration and profile in hairy roots from Portan and Syrah cultivars,

Anthocyanin-producing Portan (**A**,**B**) and Syrah (**C**,**D**) hairy roots were grown on increasing concentrations of buthionine sulfoximine (BSO), a compound that inhibits glutamyl-cysteine synthetase, the enzyme responsible for the first step in glutathione synthesis. Root samples were harvested 14 days post BSO treatment. Anthocyanin content was determined using HPLC. **A**, **C**) Increasing BSO concentration led to a decrease in the total anthocyanin content. The anthocyanin content in roots grown on media without BSO was considered as 100%. **B**, **D**) Analysis of the anthocyanin profile in the root samples described in **A**, **C**) shows that BSO preferentially affects the proportions of the glycosylated fraction, and its effects are stronger in cultivars rich in glycosylated anthocyanins. Three independent experiments were performed. Here, the most representative data of three independent experiments are presented. G, glucosylated-, A, acylated-, and C, coumaroylated anthocyanins.



С



D



Supplemental Table 1. Vitis vinifera ABCC protein inventory

Summary of the *Vitis vinifera* ABCC proteins with their NCBI RefSeq IDs, GENOSCOPE IDs and chromosomal locations. Remarks regarding gene models and annotations are detailed in the Methods section below. Chromosomal locations are given for the GENOSCOPE gene models. (*) The protein and coding sequence of VvABCC1 were experimentally determined in this work (sequence submitted to GenBank under the accession number: JX245004) and deviated from sequences of corresponding gene models identified in the NCBI and GENOSCOPE databases (in brackets).

Name	NCBI ID	GENOSCOPE ID	Location	Start (bp)	End (bp)	Orient.	Length (aa	a) Sequence based on
VvABCC1 *	(XP_002267650.2)*	(GSVIVT01028722001)*	(GENOSCOPE_chr16	19447213	19454986	+)*	1480	This work
VvABCC2	XP_002266842.1	GSVIVT01028744001	GENOSCOPE_chr16	19218947	19224345	-	1525	NCBI model
VvABCC3	XP_002266601.1	GSVIVG01010326001	GENOSCOPE_chr1	19526696	19532390	+	1462	NCBI model
VvABCC4	XP_002265012.1	GSVIVG01027990001	GENOSCOPE_chr7	3032722	3040092	+	1509	NCBI model
VvABCC5	XP_002269589.1	GSVIVG01028440001	GENOSCOPE_chr7	7535201	7546064	-	1540	NCBI model
VvABCC6	XP_002280819.1	GSVIVG01021589001	GENOSCOPE_chr10	7565358	7609701	+	1623	NCBI model
VvABCC7	XP_002281070.1	GSVIVG01021595001	GENOSCOPE_chr10	7765400	7821944	+	1624	NCBI model
VvABCC8	XP_003632995.1	GSVIVT01021593001 & GSVIVT01021594001	GENOSCOPE_chr10	7694908	7752675	+	1550	NCBI model
VvABCC9	XP_002265346.2	GSVIVG01018403001	GENOSCOPE_chr15	9661841	9670181	+	1528	NCBI model
VvABCC10	XP_002264313.1	GSVIVG01015960001	GENOSCOPE_chr9	16112767	16273585	-	1305	NCBI model
VvABCC11	XP_002276193.2	GSVIVG01016879001-A	GENOSCOPE_chr9	2205746	2211753	+	1502	NCBI model
VvABCC12	XP_002276212.2	GSVIVG01016879001-B	GENOSCOPE_chr9	2218514	2225094	+	1509	NCBI model
VvABCC13	XP_002276236.2	GSVIVG01016880001	GENOSCOPE_chr9	2225152	2233977	+	1505	NCBI model
VvABCC14	XP_002271828.2	GSVIVG01019467001	GENOSCOPE_chr2	870871	883981	-	1530	NCBI model
VvABCC15	XP_003631374.1	GSVIVG01019469001	GENOSCOPE_chr2	886847	894005	-	1524	NCBI model
VvABCC16	XP_002271761.2	GSVIVG01019471001	GENOSCOPE_chr2	899832	914539	-	1537	NCBI model
VvABCC17	XP_002271657.1	GSVIVG01019476001	GENOSCOPE_chr2	952858	960480	-	1391	NCBI model
VvABCC18	XP_002271728.1	GSVIVG01019473001	GENOSCOPE_chr2	916178	932015	-	1490	Manual annot.
VvABCC19	XP_002271694.2	GSVIVG01019475001	GENOSCOPE_chr2	933100	947137	-	1532	NCBI model
VvABCC20	XP_002265605.2	GSVIVG01037789001	GENOSCOPE_chr19	7910839	7917664	-	1529	NCBI model
VvABCC21	-	GSVIVG01014633001	GENOSCOPE_chr19	8023417	8033145	-	1428	GENOSCOPE model
VvABCC22	-	GSVIVT01014629001	GENOSCOPE_chr19	7936173	7941661	-	1004	Manual annot.
VvABCC23	XP_003634755.1	GSVIVG01014632001	GENOSCOPE_chr19	7977107	7983555	-	1532	NCBI model
VvABCC24	XP_003634753.1	GSVIVG01014628001	GENOSCOPE_chr19	7925931	7935919	-	1530	NCBI model
VvABCC25	-	GSVIVT01014631001	GENOSCOPE_chr19	7967803	7976826	-	1314	Manual annot.
VvABCC26	-	GSVIVG01028459001	GENOSCOPE_chr7	7912161	7916627	+	287	GENOSCOPE model

Supplemental Table 2. Structure and distribution of the five major anthocyanins of grape berries

The table summarizes the general anthocyanin structure; R1 and R2 represent the substitution pattern specific to each anthocyanin. Cultivars are characterized by a distinct pattern of anthocyanins (represented as % of the total anthocyanin content).

HO HO HO HO HO HO HO HO HO HO HO HO HO H	R1	R2	Tempranillo	Cabernet Sauvignon	Syrah
Delphinidin 3-O-glucoside	OH	OH	16.64	9.99	5.2
Cyanidin 3- <i>O</i> -glucoside	OH	Н	6.53	1.33	1
Petudinin 3-O-glucoside	OCH ₃	OH	12.33	6.07	6.1
Peonidin 3- <i>O</i> -glucoside	OCH ₃	Н	12.53	5.27	8.3
Malvidin 3-O-glucoside	OCH₃	OCH_3	36.68	42.57	36.4
Other forms	-	-	15.29	34.77	43

Adapted from Mazza, 1995