SUPPLEMENTARY DATA
Cluzet, S., Corio-Costet, M.-F., Burdziej, A., Da Costa , G., Le Mao, I., Laurens, M., Béllée, A., & Bodin, E. (2024). Effects of three elicitors on primary metabolism six days after treatment in healthy *Vitis vinifera* leaves and eight days after treatment in healthy and downy mildew-inoculated leaves. *OENO One, 58*(4).
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Supplementary data

TABLE S1. Genes used for *Vitis vinifera* leaf analysis with "Biostim"96" chips (Bodin *et al.,* 2020). Primer sets are available on request to authors.

Function	Gene Name		GenBank No.	PCR primer efficiencies
Reference Gene	*VvTIP41*	TIP41-like protein	XM_019219016.1	1.05
	VvTHIORYLS8	Thioredoxin-like protein YLS8	XM_002283586	1.14
	VvGADPH	Glyceraldehyde 3-phosphate dehydrogenase	XM_002263109.1	0.83
PHYTOHORMONES				
Auxin	*VvABCB19*	ABC transporter B family member 19	XM_002283015.4	0.92
	VvABCB11	ABC transporter B family member 11	XM_002273951	1.01
	VvABCB9	ABC transporter B family member 9	XM_010657312	1.05
	VvILR1	IAA-amino acid hydrolase	XM_002269190.3	1.03
	VvIGPS	Indole-3-glycerol phosphate synthase, chloroplastic	XM_002265239.4	0.97
	VvLax2	Auxin transporter-like protein 2	XM_002268889	0.94
Abscissic acid	*VvAAO1*	Abscisic aldehyde oxidase 1	XM_002273593.3	0.88
	VvHYD2	Abscisic acid 8'-hydroxylase	NM_001281052.1	0.95
	VvABCG25	ABC transporter G family member 25	XM_002268337.3	1.01
	VvABCG40	Pleiotropic drug resistance protein 1	XM_010656420.2	0.87
	VvBGLU	Beta glucosidase 18	XM_002276015.4	0.85
	VvUTG71B6	UDP-glucosyltransferase 71B	XM_002263625.3	0.95
Gibberellin	*VvKAO*	Ent-kaurenoic acid oxidase 1	XM_002264179	0.99
	VvGAI	DELLA protein gibberellin insensitive	XM_002284612	0.98
	VvGA20ox	Gibberellin 20-oxidase	NM_001280982.1	0.94
	VvGA2Ox	Gibberellin 2-beta-dioxygenase	XM_002269181.4	0.96
Cytokinin	*VvIPT*	Adenylate isopentenyltransferase 3, chloroplastic	XM_002271926.3	0.92
	VvCKX3	Cytokinin dehydrogenase 3	XM_002279483.3	0.9
	VvCKX7	Cytokinin dehydrogenase 7	XM_002279924.3	0.95
STRESS RESPONSES				
Pathogenesis-related proteins	*VvPR2-Glu**	Beta-1,3-glucanase, PR protein class 2	NM_001280967.2	1.18
	*VvPR8-Chit3**	Acidic endochitinase-like, PR protein class 8	NM_001281119.1	0.98
Stilbene	*VvROMT**	Resveratrol *O*-methyl-transferase	FM178870	0.96
Oxido-reduction	*VvCAT*	Catalase	NM_001281169.1	0.92
Heat shock	*VvDnaJ*	Chaperone protein DnaJ	XM_003633561.3	0.96
	VvHSP	Class I heat shock protein	XM_002281249.4	1.02
Other	*VvALDH**	Aldehyde dehydrogenase family 3 member F1	XM_002273322	1.03
PRIMARY METABOLISM				
Krebs Cycle	*VvMDH*	Malate Dehydrogenase, cytoplasmic	XM_002278676.3	1.28
	VvIDH41	Isocitrate Dehydrogenase	XM_002281790.3	1.08
	VvIDH42	Isocitrate Dehydrogenase	XM_002270581.3	1.08
	VvCS	Citrate synthase, mitochondrial	XM_002271415.2	0.97

Nitrogen metabolism	*VvNR*	Nitrate Reductase	NM_001281120.1	1.02
	VvNiR	Nitrite Reductase	NM_001281265.1	1.01
	VvNrT1	Nitrate/nitrite transporter	KF649633.1	1.18
Sugar metabolism - Glycolysis	*VvPlast*	Fructose-bisphosphate aldolase	XM_003631825	0.97
	VvHT5	Hexose transporter	NM_001281278	0.97
HOMEOSTASIS				
Aquaporin	*VvXIP1*	Probable aquaporin tonoplast intrinsic protein 3-2	XM_010649040	0.87
	VvTIP1-1	Tonoplast intrinsic protein 1-1	NM_001280994.1	1.02
	VvTIP2-1	Tonoplast intrinsic protein 2-1	NM_001281029.1	1.17
	VvPIP1-1	Plasma membrane Intrinsic Protein 1-1	NM_001280989.1	0.95
	VvPIP1-2	Plasma membrane Intrinsic Protein 1-2	NM_001281020.1	0.87
	VvPIP1-3	Plasma membrane Intrinsic Protein 1-3	NM_001280992.1	1.15
	VvPIP2-1	Plasma membrane Intrinsic Protein 2-1	NM_001280993.1	0.80
	VvPIP2-2	Plasma membrane Intrinsic Protein 2-2	NM_001281028.1	0.99
	VvPIP2-3	Plasma membrane Intrinsic Protein 2-3	NM_001281129.1	0.99
	VvPIP2-4	Plasma membrane Intrinsic Protein 2-4	EF364438.1	0.81
Copper	*VvCTR1*	Copper transporter 1	HQ108185	0.97
	VvCTR2	Copper transporter 2	HQ108186	0.99
	VvCTR8	Copper transporter 8	HQ108192	0.87
	VvPAA1	Putative copper-transporting ATPase, chloroplastic	XM_002274461.4	0.77
	VvCSD1	Cu/Zn-superoxide dismutase	JQ692111	0.95
	VvCSD2	Cu/Zn-superoxide dismutase	JQ692112	0.96
	VvATX1	Copper transport protein	XM_002264296.4	0.92
	VvATOX1	Cytochrome c oxidase copper chaperone 2	XM_002284967.4	0.86
Iron	*VvIRT*	Probable iron transporter 10	XM_002273143.3	0.95
	VvFER	Ferritin-4, chloroplastic	XM_002268018.4	0.82
	VvBTS	Zinc finger protein BRUTUS	XM_002279499.4	0.71
	VvPYE	Transcription factor bHLH47	XM_010665082.2	0.86
	VvFSD1	Superoxide dismutase [Fe], chloroplastic	XM_002280486.4	0.79
	VvYSL1	Metal-nicotianamine transporter, yellow stripe 1	AY538258.1	0.90
	VvYSL6	Metal-nicotianamine transporter Yellow stripe 6	XM_002274523.4	0.95
	VvYSL7	Metal-nicotianamine transporter Yellow stripe 7	XM_002266621.4	1.00
Zinc	*VvZIP2*	Zinc transporter 2	XM_002283203.3	0.98
	VvZIP4	Zinc transporter 4, chloroplastic	XM_010650054.2	0.90
	VvCAX3	Cation/proton exchanger 3	XM_002274755.4	1.05
Calcium	*VvTPC1*	Two pore channel 1	NM_001281096.1	0.93
	VvGLR3-4	Glutamate receptor 3.4, mitochondrial	XM_002273708.4	0.89
DIVISION				
Cell division	*VvAPC10*	Anaphase-promoting complex subunit 10	XM_002266036.4	0.94
Plastid division	*VvPDV1*	Plastid division protein	XM_002276562.4	0.87

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gènes	UT-6dpt	Tri-6dpt	MeJA-6dpt	PHOS-6dpt	ASM-6dpt
VvIRT	0,00	2,61	4,59	5,71	7,40
VvFER	0,00	0,80	-0,83	0,85	0,78
VvBTS	0,00				
VvPYE	0,00		-1,01		
VvFSD1	0,00	0,49		0,77	
VvYSL1	0,00				0,43
VvYSL6	0,00				
VvYSL7	0,00	0,48			1,03
VvZIP2	0,00	0,72		0,70	0,93
VvZIP4	0,00	-0,36		-0,51	
VvCTR1	0,00	0,43		0,82	0,81
VvCTR2	0,00				-1,11
VvCTR8	0,00	0,72		0,71	0,83
VvPAA1	0,00	0,47		0,49	0,47
VvCSD1	0,00				
VvCSD2	0,00		0,94		
VvATX1	0,00			-0,55	
VvATOX1	0,00		-0,31		
VvCAX3	0,00				
VvTPC1	0,00				
VvGLR3-4	0,00				
VvALDH	0,00				-1,15
VvXIP1	0,00				
VvTIP1-1	0,00	0,67			-0,87
VvTIP2-1	0,00				
VvPIP1-1	0,00		0,71		0,64
VvPIP1-2	0,00		0,78		-1,06
VvPIP1-3	0,00			-0,49	
VvPIP2-1	0,00	0,76	1,49		
VvPIP2-2	0,00	-0,10		-0,50	
VvPIP2-3	0,00			0,37	-0,60
VvPIP2-4	0,00	0,99	1,57		
VvAAO1	0,00				1,59
VvABCG25	0,00				
VvABCG40	0,00				1,25
VvHYD2	0,00	0,86			1,84
VvUTG71B6	0,00	-1,99			
VvBGLU	0,00				
VvKAO	0,00			-1,29	
VvGA2OX	0,00				-0,74
VvGA20ox	0,00	-0,55	-1,23		-1,79
VvGAI	0,00			0,57	
VvABCB19	0,00				-1,34
VvABCB11	0,00				0,39
VvABCB9	0,00				
VvILR1	0,00				0,38
VvIGPS	0,00			0,61	
VvLax2	0,00				-0,81
VvIPT	0,00				-0,78
VvCKX3	0,00				
VvCKX7	0,00	-0,51	-0,84		
VvAPC10	0,00		-0,37		
VvPDV1	0,00				
VvMDH	0,00			-0,28	
VvIDH42	0,00				
VvCS	0,00				
VvNR	0,00	-0,45	-0,84	-1,03	-0,54
VvNiR	0,00		-0,74		-0,97
VvNrT1	0,00				1,64
VvHT5	0,00	0,50			2,06
VvPlast	0,00				
VvCAT	0,00			-0,50	0,34
VvGlu/PR2	0,00	2,47	2,78		3,07
VvCHIT3/PR8	0,00	0,92	1,13		4,10
VvROMT	0,00	1,09			2,31
VvDnaJ	0,00				
VvHSP	0,00	-0,68	-1,90		

FIGURE S1. Heatmap of relative expression (RE) of genes (fold change in Log2) in grapevine leaves treated with Triton (Tri), MeJA, PHOS or ASM, at 6 dpt. Gene expression of untreated leaves were used as reference to calculate the relative expression. Values are means ± SD of three independent biological replicates. Genes up-regulated in shades of red (log2(RE) > 0), with expression level higher than 5 in bright red. Genes down-regulated in shades of blue (log2(RE) < 0), with intensity lower than −5 in dark blue. Numbers in boxes represent significant gene modulation compared to control (Dunnett test, $p < 0.05$).

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TABLE S2. Relative abundance of the identified compounds by ^{1}H-NMR spectroscopy at 6 dpt in untreated and treated leaves with Triton, methyl jasmonate (MeJA), potassium phosphonate (PHOS) or acibenzolar-*S*-methyl (ASM). Values are expressed as means of three replicates with standard deviation. Letters indicate significant differences ($p < 0.05$, Tukey's test) among all modalities.

Compound	Untreated		Triton		MeJA		PHOS		ASM	
Organic acids										
Fumaric acid	0.65	± 0.02 ^{b}	0.38	± 0.05 ^{ab}	0.09	± 0.01 ^{a}	0.51	± 0.02 ^{ab}	1.34	± 0.40 ^{c}
Pyruvic acid	1.26	± 0.05 ^{a}	1.82	± 0.11 ^{b}	2.90	± 0.23 ^{c}	1.78	± 0.10 ^{b}	2.51	± 0.18 ^{c}
Acetic acid	3.64	± 0.08 ^{a}	5.51	± 0.12 ^{cd}	6.35	± 0.37 ^{d}	4.90	± 0.53 ^{bc}	4.28	± 0.51 ^{ab}
Succinic acid	6.67	± 1.29 ^{a}	13.50	± 0.49 ^{bc}	11.77	± 1.08 ^{b}	14.00	± 0.50 ^{bc}	15.49	± 0.03 ^{c}
Malic acid	119.80	± 0.01 ^{a}	446.15	± 30.08 ^{c}	267.15	± 26.92 ^{b}	508.28	± 12.88 ^{c}	640.58	± 29.31 ^{d}
Tartaric acid	226.21	± 5.45 ^{a}	387.17	± 13.52 ^{b}	348.83	± 10.52 ^{b}	373.14	± 35.10 ^{b}	518.73	± 59.96 ^{c}
Sugars										
alpha-Glucose	71.83	± 7.50 ^{ab}	95.58	± 25.35 ^{b}	52.75	± 4.41 ^{a}	67.09	± 2.80 ^{ab}	76.33	± 10.52 ^{ab}
beta-Glucose	158.34	± 23.86 ^{a}	160.86	± 40.36 ^{a}	123.66	± 17.37 ^{a}	151.95	± 16.36 ^{a}	160.79	± 16.31 ^{a}
Fructose	60.25	± 2.49 ^{c}	54.26	± 0.03 ^{bc}	44.39	± 2.12 ^{ab}	42.86	± 4.14 ^{a}	57.83	± 4.61 ^{c}
Sucrose	1870.68	± 164.47 ^{bc}	1800.25	± 8.95 ^{bc}	1276.53	± 30.93 ^{a}	1557.10	± 94.31 ^{ab}	2192.65	± 220.89 ^{c}
Myo-inositol	448.74	± 5.46 ^{a}	534.63	± 24.47 ^{ab}	486.73	± 9.47 ^{b}	540.74	± 38.56 ^{ab}	503.11	± 54.52 ^{b}
Amino acids										
Alanine	28.25	± 0.91 ^{b}	23.16	± 7.19 ^{ab}	22.03	± 0.97 ^{ab}	24.76	± 3.41 ^{ab}	15.28	± 1.80 ^{a}
GABA	0.51	± 0.04 ^{a}	2.16	± 0.53 ^{a}	5.32	± 1.13 ^{b}	6.52	± 0.33 ^{b}	1.60	± 0.45 ^{a}
Glutamic acid	81.19	± 10.56 ^{a}	106.04	± 10.70 ^{b}	95.33	± 9.97 ^{ab}	146.65	± 7.78 ^{c}	91.00	± 2.99 ^{ab}
Glutamine	8.75	± 1.79 ^{a}	22.53	± 3.36 ^{a}	22.36	± 7.51 ^{a}	50.90	± 0.16 ^{b}	14.76	± 1.70 ^{b}
Proline	163.67	± 1.29 ^{a}	173.84	± 25.53 ^{a}	238.58	± 37.85 ^{b}	189.84	± 22.74 ^{ab}	161.55	± 16.05 ^{a}
Threonine	16.46	± 1.44 ^{a}	29.57	± 3.96 ^{b}	49.23	± 1.01 ^{c}	22.36	± 4.53 ^{ab}	27.43	± 3.18 ^{b}
Tyrosine	3.71	± 0.56 ^{a}	8.85	± 0.69 ^{cd}	11.71	± 1.09 ^{d}	5.23	± 1.63 ^{ab}	7.08	± 1.14 ^{bc}
Valine	1.84	± 0.32 ^{ab}	1.93	± 0.01 ^{ab}	3.16	± 0.12 ^{c}	2.01	± 0.20 ^{b}	1.44	± 0.09 ^{a}
Amines										
Trigonelline	0.34	± 0.03 ^{a}	1.22	± 0.00 ^{b}	2.07	± 0.15 ^{c}	1.51	± 0.26 ^{b}	0.00	± 0.00 ^{a}
Choline	10.98	± 0.87 ^{a}	15.14	± 0.14 ^{ab}	17.54	± 1.25 ^{b}	12.26	± 1.39 ^{a}	15.10	± 2.82 ^{ab}
Adenine	1.12	± 0.01 ^{ab}	0.46	± 0.16 ^{a}	0.65	± 0.00 ^{ab}	1.48	± 0.35 ^{b}	0.42	± 0.16 ^{a}
Polyphenols										
trans-Feruloyl derivative	95.86	± 0.01 ^{a}	190.76	± 3.65 ^{d}	195.67	± 6.84 ^{d}	125.24	± 9.55 ^{b}	151.19	± 3.16 ^{c}
Quercetin-3-*O*-glucoside	8.68	± 1.28 ^{a}	30.71	± 1.90 ^{d}	13.91	± 1.83 ^{b}	21.65	± 2.04 ^{c}	18.00	± 1.39 ^{bc}
Shikimic acid	21.32	± 0.33 ^{a}	30.25	± 0.71 ^{b}	33.32	± 2.40 ^{b}	17.86	± 2.42 ^{a}	46.53	± 0.35 ^{c}
Syringic acid	7.96	± 0.37 ^{a}	8.58	± 2.03 ^{a}	7.42	± 0.92 ^{a}	6.96	± 0.36 ^{a}	8.66	± 1.70 ^{a}
(+)-Catechin	11.35	± 0.70 ^{a}	24.69	± 0.21 ^{c}	35.48	± 1.88 ^{d}	17.91	± 1.41 ^{b}	13.88	± 1.89 ^{a}

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gènes	UT-8dpt-2dpi	Tri-8dpt-2dpi	MeJA-8dpt-2dpi	PHOS-8dpt-2dpi	ASM-8dpt-2dpi
VvIRT	0,00			3,18	
VvFER	0,00		1,77	2,28	
VvBTS	0,00	-3,48	2,83		4,11
VvPYE	0,00	-3,53		1,70	
VvFSD1	0,00				
VvYSL1	0,00				
VvYSL6	0,00				
VvYSL7	0,00	0,72		1,47	
VvZIP2	0,00	2,42			
VvZIP4	0,00				
VvCTR1	0,00				
VvCTR2	0,00				
VvCTR8	0,00	2,73			
VvPAA1	0,00				
VvCSD1	0,00				
VvCSD2	0,00		3,36		
VvATX1	0,00	2,50	1,83		
VvATOX1	0,00				
VvCAX3	0,00				
VvTPC1	0,00			2,83	
VvGLR3-4	0,00			1,50	
VvALDH	0,00			2,79	
VvXIP1	0,00				
VvTIP1-1	0,00				
VvTIP2-1	0,00	1,46	1,37		
VvPIP1-1	0,00	1,11	1,16		
VvPIP1-2	0,00	0,97	1,07		
VvPIP1-3	0,00	1,20	1,40	0,94	
VvPIP2-1	0,00				
VvPIP2-2	0,00				
VvPIP2-3	0,00	-0,61	-1,91		-2,82
VvPIP2-4	0,00				
VvAAO1	0,00		2,24	3,16	
VvABCG25	0,00		2,42	2,86	4,44
VvABCG40	0,00		1,27	1,37	
VvHYD2	0,00				3,89
VvUTG71B6	0,00			1,87	
VvBGLU	0,00	0,71	1,14	1,65	
VvKAO	0,00				
VvGA2OX	0,00		1,22	1,17	
VvGA20ox	0,00	0,79	1,48	1,48	0,98
VvGAI	0,00		1,05	1,36	0,86
VvABCB19	0,00			2,24	
VvABCB11	0,00	2,78	2,83	3,33	
VvABCB9	0,00				
VvILR1	0,00	0,85	0,97	0,88	0,81
VvIGPS	0,00				
VvLax2	0,00	2,03		2,46	
VvIPT	0,00		0,51		
VvCKX3	0,00			2,24	
VvCKX7	0,00				
VvAPC10	0,00				
VvPDV1	0,00	-1,02			
VvMDH	0,00		1,68		
VvIDH42	0,00				
VvCS	0,00				
VvNR	0,00				
VvNiR	0,00				
VvNrT1	0,00		3,13	3,60	
VvHT5	0,00		0,55		0,71
VvPlast	0,00			1,19	
VvCAT	0,00				
VvGlu/PR2	0,00	0,92	0,78		1,21
VvCHIT3/PR8	0,00		2,78		
VvROMT	0,00				
VvDnaJ	0,00			1,68	
VvHSP	0,00			2,33	

FIGURE S2. Heatmap of relative expression (RE) of genes (fold change in Log2) in grapevine leaves treated with TRI, MeJA, PHOS or ASM, at 8dpt-2dpi. Gene expression of untreated leaves were used as reference to calculate the relative expression. Values are means ± SD of three independent biological replicates. Genes up-regulated in shades of red (log2(RE) > 0), with expression level higher than 5 in bright red. Genes down-regulated in shades of blue (log2(RE) < 0), with intensity lower than −5 in dark blue. Numbers in boxes represent significant gene modulation compared to control (Dunnett test, $p < 0.05$).

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TABLE S3. Relative abundance of the identified compounds by ^{1}H-NMR spectroscopy at 6 dpt in untreated and treated leaves with Triton, methyl jasmonate (MeJA), potassium phosphonate (PHOS) or acibenzolar-*S*-methyl (ASM). Values are expressed as means of three replicates with standard deviation. Letters indicate significant differences ($p < 0.05$, Tukey's test) among all modalities.

Compound	**Untreated**		**Triton**		**MeJA**		**PHOS**		**ASM**	
Organic acids										
Fumaric acid	0.97	± 0.24 ^{c}	0.61	± 0.12 ^{bc}	0.00	± 0.00 ^{a}	0.45	± 0.12 ^{ab}	0.56	± 0.04 ^{bc}
Pyruvic acid	1.52	± 0.20 ^{a}	2.44	± 1.03 ^{a}	2.81	± 0.17 ^{a}	2.28	± 0.10 ^{a}	1.71	± 0.17 ^{a}
Acetic acid	5.90	± 1.22 ^{a}	5.50	± 0.32 ^{a}	8.88	± 0.37 ^{b}	7.15	± 0.58 ^{ab}	6.52	± 0.65 ^{a}
Succinic acid	15.78	± 0.47 ^{bc}	11.03	± 1.26 ^{a}	11.32	± 0.66 ^{a}	17.62	± 0.44 ^{c}	15.33	± 0.74 ^{b}
Malic acid	545.24	± 26.10 ^{b}	603.23	± 33.36 ^{b}	363.00	± 32.25 ^{a}	893.55	± 61.77 ^{d}	746.69	± 10.37 ^{c}
Tartaric acid	269.98	± 56.58 ^{a}	464.87	± 32.09 ^{b}	260.73	± 33.74 ^{a}	457.34	± 82.28 ^{b}	460.20	± 73.09 ^{b}
Sugars										
alpha-Glucose	77.62	± 9.10 ^{b}	73.42	± 8.49 ^{b}	47.79	± 3.01 ^{a}	54.69	± 2.78 ^{a}	83.34	± 7.77 ^{b}
beta-Glucose	169.94	± 28.02 ^{ab}	190.73	± 18.91 ^{b}	123.88	± 1.78 ^{a}	128.98	± 14.94 ^{a}	183.56	± 25.82 ^{b}
Fructose	77.14	± 8.20 ^{a}	74.34	± 2.40 ^{a}	64.60	± 2.75 ^{a}	65.12	± 4.63 ^{a}	77.68	± 7.74 ^{a}
Sucrose	1527.77	± 379.92 ^{b}	1440.71	± 175.86 ^{ab}	925.67	± 114.41 ^{a}	1122.14	± 63.28 ^{ab}	1617.88	± 113.69 ^{b}
Myo-inositol	499.38	± 49.61 ^{a}	527.65	± 28.30 ^{a}	513.92	± 26.34 ^{a}	724.35	± 16.75 ^{b}	558.53	± 17.72 ^{a}
Amino acids										
Alanine	25.58	± 2.77 ^{c}	22.35	± 0.00 ^{ac}	16.09	± 0.86 ^{a}	19.83	± 2.10 ^{ab}	22.68	± 1.95 ^{bc}
GABA	15.33	± 2.27 ^{a}	18.12	± 0.00 ^{a}	10.16	± 1.33 ^{a}	19.13	± 1.32 ^{a}	22.38	± 6.64 ^{a}
Glutamic acid	177.52	± 14.77 ^{c}	151.30	± 0.00 ^{bc}	138.00	± 8.13 ^{b}	144.25	± 1.74 ^{b}	113.96	± 5.11 ^{a}
Glutamine	31.07	± 8.46 ^{a}	45.13	± 0.00 ^{ab}	27.84	± 4.44 ^{a}	32.08	± 5.04 ^{a}	54.35	± 5.77 ^{b}
Proline	179.06	± 3.52 ^{a}	213.13	± 0.00 ^{a}	211.88	± 50.27 ^{a}	185.25	± 39.53 ^{a}	255.47	± 9.33 ^{a}
Threonine	19.86	± 2.26 ^{ab}	24.47	± 0.00 ^{bc}	27.51	± 1.00 ^{c}	20.72	± 2.40 ^{ab}	15.84	± 1.28 ^{a}
Tyrosine	5.22	± 1.53 ^{a}	8.16	± 0.00 ^{ab}	16.70	± 0.42 ^{c}	8.30	± 0.22 ^{b}	14.68	± 1.08 ^{c}
Valine	8.28	± 0.91 ^{a}	7.50	± 0.00 ^{a}	6.83	± 1.49 ^{a}	6.39	± 1.21 ^{a}	6.77	± 0.38 ^{a}
Amines										
Trigonelline	0.00	± 0.00 ^{a}	0.58	± 0.08 ^{c}	1.37	± 0.03 ^{d}	0.16	± 0.01 ^{b}	0.00	± 0.00 ^{a}
Choline	12.46	± 2.27 ^{a}	13.13	± 1.40 ^{a}	11.47	± 1.47 ^{a}	14.46	± 1.35 ^{a}	14.39	± 2.36 ^{a}
Adenine	1.17	± 0.62 ^{a}	0.40	± 0.22 ^{a}	0.63	± 0.43 ^{a}	0.45	± 0.14 ^{a}	0.34	± 0.26 ^{a}
Polyphenols										
trans-Feruloyl derivative	128.62	± 29.32 ^{a}	150.35	± 6.67 ^{a}	222.75	± 13.60 ^{b}	135.81	± 7.55 ^{a}	140.78	± 3.49 ^{a}
Quercetin-3-O-glucoside	13.06	± 3.20 ^{a}	21.72	± 1.25 ^{b}	19.72	± 3.01 ^{b}	18.38	± 0.97 ^{ab}	18.54	± 1.66 ^{ab}
Shikimic acid	30.06	± 7.42 ^{ab}	34.04	± 3.80 ^{b}	19.57	± 1.37 ^{a}	28.61	± 5.49 ^{ab}	40.35	± 3.62 ^{b}
Syringic acid	8.29	± 0.77 ^{ab}	9.13	± 0.83 ^{ab}	7.91	± 0.76 ^{a}	8.16	± 0.24 ^{ab}	9.63	± 0.14 ^{b}
(+)-Catechin	11.79	± 0.66 ^{a}	17.91	± 1.29 ^{b}	37.81	± 1.36 ^{d}	41.48	± 2.69 ^{d}	23.35	± 2.14 ^{c}

SUPPLEMENTARY DATA
Cluzet, S., Corio-Costet, M.-F., Burdziej, A., Da Costa , G., Le Mao, I., Laurens, M., Béllée, A., & Bodin, E. (2024). Effects of three elicitors on primary metabolism six days after treatment in healthy *Vitis vinifera* leaves and eight days after treatment in healthy and downy mildew-inoculated leaves. *OENO One, 58*(4).
https://doi.org/10.20870/oeno-one.2024.58.4.8163

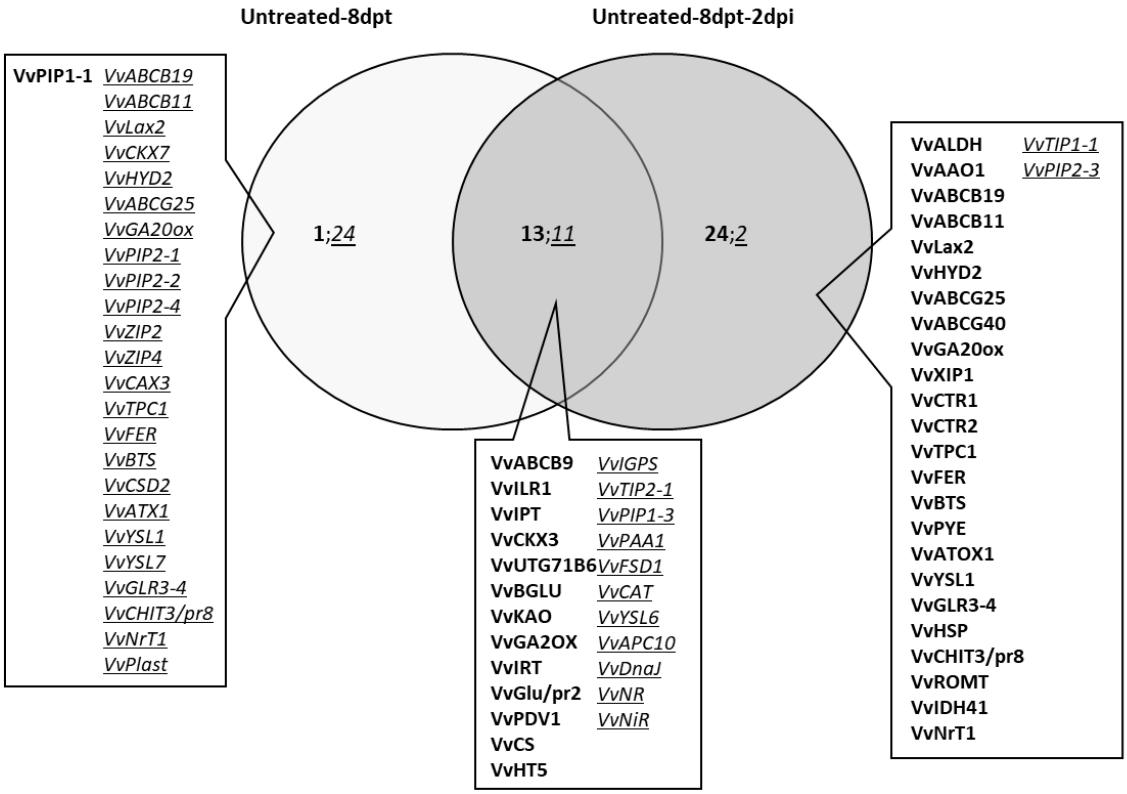


FIGURE S3. Venn diagramm of modulated genes in untreated grapevine leaves at 8 days, two days after or not *P. viticola* inoculation. Values are means ± SD of three independent biological replicates. Genes in bold correspond to significantly up-regulated genes (log2(RE) > 0), and the surligned ones to down-regulated genes (log2(RE) < 0).