

Accessory publication

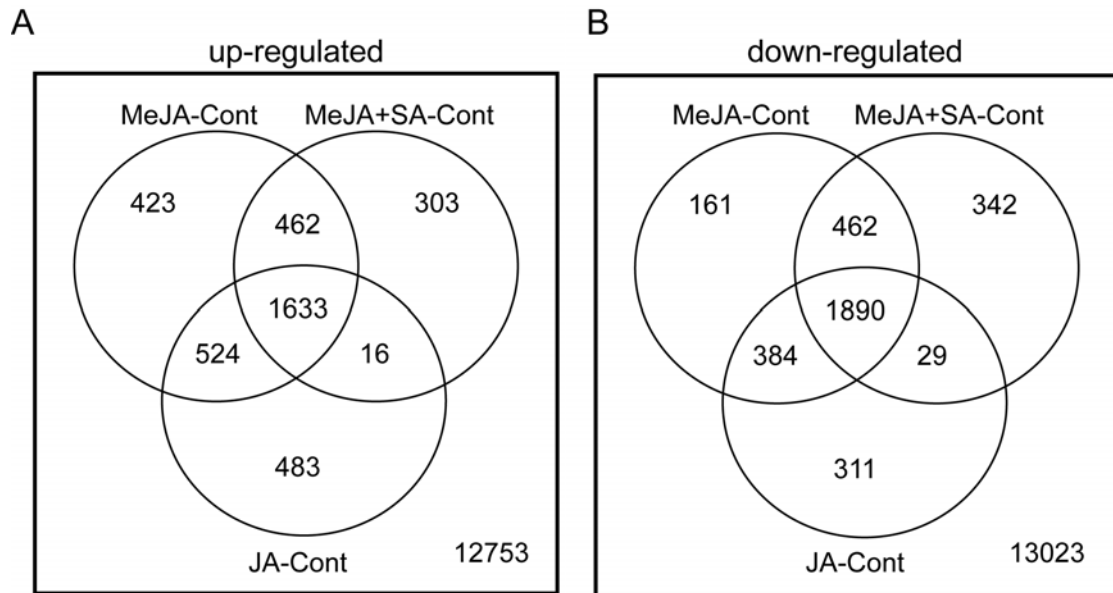


Fig. S1. Global changes in grape cell culture gene expression in response to elicitors. The two Venn diagrams show the number of probe sets (A) up-regulated or (B) down-regulated in response to the three elicitor treatments. The differentially expressed probe sets ($P < 0.001$) were identified using the R package *limma* (Smyth 2004) after empirical Bayes moderated t-statistic P -values were adjusted for multiple testing by Benjamini and Hochberg's method to control false discovery rate (Benjamini and Hochberg 1995).

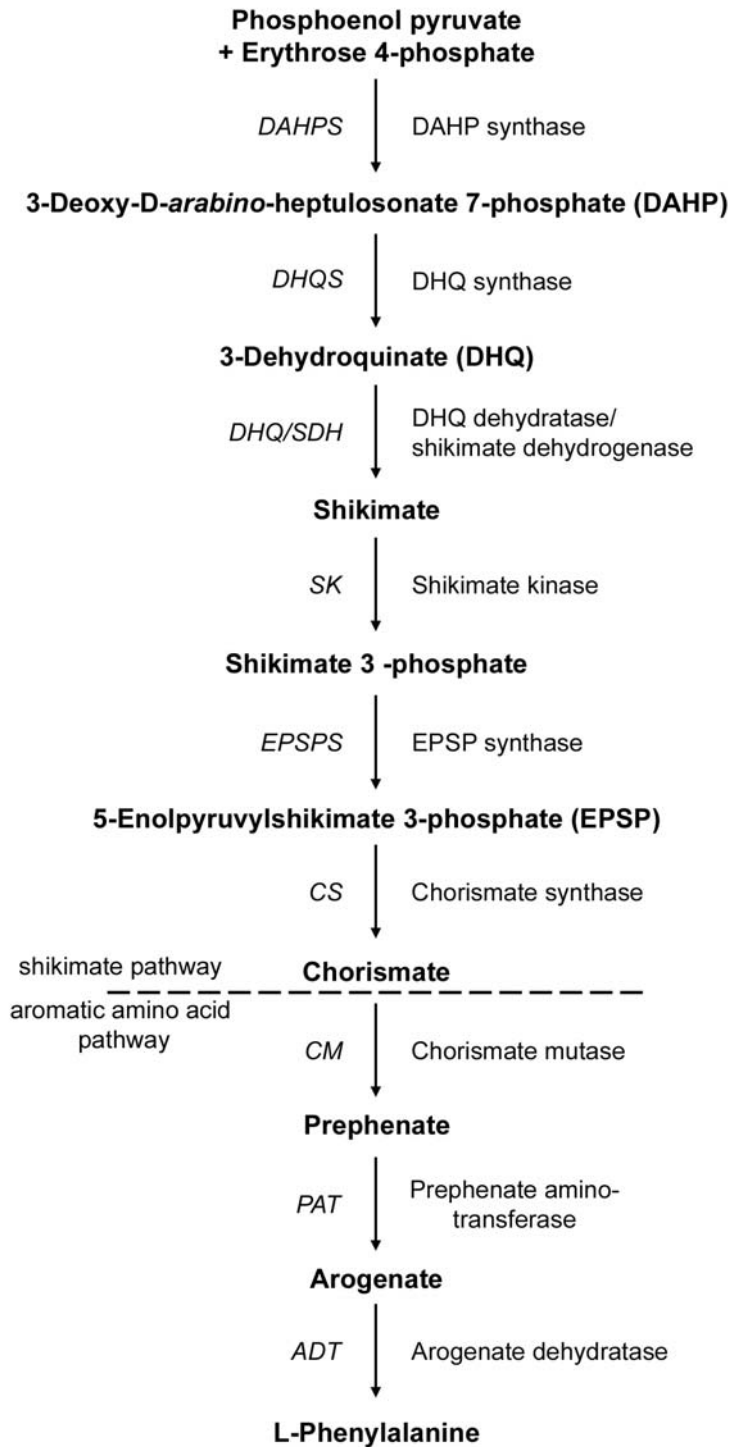


Fig. S2. The shikimate and aromatic amino acid pathways. Simplified schematic of the shikimate and aromatic amino acid pathways. The genes are on the left of the arrows and the enzyme they encode on the right. The dotted line indicates the end of the shikimate pathway.

Table S1. Real-time PCR primers

Sequences of primers used for real-time PCR analysis and the Affymetrix probe identification number from which the sequence data was obtained for primer design, except for the ubiquitin primers which were designed from a GenBank sequence

Gene	Affymetrix probe	Forward primer	Reverse primer
<i>AACT</i>	1610742_at	5'-CTTTCGCCGTTGTAGCTCTT-3'	5'-CCAACTCCATACTCCCATTCT-3'
<i>HMGS</i>	1611853_at	5'-CTCCAGGCACCCACTATCTT-3'	AACATTTTCAGCCAACCTCCT-3'
<i>HMGR</i>	1614923_at	5'-AGAAACCAATCGTGAACAACAA-3'	5'-ACTGGACTCCCCCACTTTAC-3'
<i>MK</i>	1621391_at	5'-TGTTGAGATTTGCGTTGGTAG-3'	5'-TCCATGAACCAGGAAGAATG-3'
<i>PMK</i>	1619480_at	5'-AGGAGCAGGTGGATTTGATG-3'	5'-TGAAGTGAAGAAATGGCTGATG-3'
<i>MPDC</i>	1616679_at	5'-GGAGATGAACCTCAAACTTCAC-3'	5'-CAATAACTGTCTGGGGAAACAA-3'
<i>PAL</i>	1613113_at	5'-TTTGTGAGGGAAGAAGCTGGG-3'	5'-AAGTGTAGGGAAGGGGTGTCT-3'
<i>C4H</i>	1610821_at	5'-GGTGGCTTGCTAACGACTCT-3'	5'-CCAGGGCAGCTTCTTCTTC-3'
<i>4CL</i>	1619320_at	5'-CGAAGAAAAATGGCTACACACA-3'	5'-GTACGACCGCAGCATCAAC-3'
<i>STS</i>	1616575_at	5'-GGGCTTCCTTAGTGACCAGTT-3'	5'-CAATCTGTTGTTCCACTCTTCTTT-3'
<i>CHS</i>	1617019_at	5'-GGGCCTCACCTTTCATTTACT-3'	5'-GCCGAGTTGCTCTCAGTTTC-3'
<i>CHI</i>	1615912_at	5'-TGAAGGAGAGATGGGAAGAA-3'	5'-GCACCAAGAACACTACAAATAAAA-3'
<i>F3H</i>	1607607_s_at	5'-GTGGAAGGAGCATTGTGTGTC-3'	5'-CCACCATCACCGACTTCTCT-3'
<i>DFR</i>	1620675_at	5'-GCGAGAGCGTAGAAATGTCC-3'	5'-CTCAAAGGGAACGAACTCTCA-3'
<i>LDOX</i>	1609765_s_at	5'-CACCTTCATCTCCACAACA-3'	5'-ACTGCCCATGAAATCCTCAC-3'
<i>LAR2</i>	1615174_s_at	5'-TCTCGACATAAATGATGATGTG-3'	5'-TGCAGTTTCTTTGATTGAGTTC-3'
<i>ANR</i>	1612134_at	5'-CAATACCAGTGTCTCTGAGC-3'	5'-AAACTGAACCCCTCTTCAC-3'
<i>UBIQ</i>	CF406001	5'-GAGTATCAAAAACAAAAGC-3'	5'-AGTAGATGACTGCATTGG-3'

Table S2. List comprising those probe sets found to be more than 10-fold up-regulated by MeJA, but not by MeJA+SA or JA treatments

Probe set	Putative function	Closest Arabidopsis match	Fold change		
			MeJA	MeJA+SA	JA
1606663_at	chalcone synthase	AT5G13930	26.93	1.68	3.25
1607607_s_at	flavanone 3-hydroxylase	AT3G51240	20.51	2.43	2.32
1607615_at	D111/G-patch domain-containing protein	AT1G63980	11.10	9.66	9.78
1607732_at	chalcone synthase	AT5G13930	40.94	2.27	5.65
1607739_at	flavanone 3-hydroxylase	AT3G51240	18.44	4.53	3.98
1608039_s_at	unknown	AT4G35190	17.87	8.31	4.46
1608579_at	putative UDP-glucose:indole-3-acetate beta-D-glucosyltransferase	AT3G21560	13.54	-1.28	1.09
1608720_at	protein kinase	AT3G46920	13.96	7.24	7.18
1608791_at	flavonol synthase	AT5G08640	18.20	4.25	9.22
1608930_at	GDSL-motif lipase/hydrolase	AT3G26430	12.39	7.28	8.77
1609765_s_at	leucoanthocyanidin dioxygenase	AT4G22880	23.57	1.02	3.20
1610372_at	jasmonate ZIM-domain protein	AT1G74950	13.07	7.43	8.50
1611091_s_at	VvMYBPA	AT1G22640	18.13	1.17	3.15
1611383_at	inositol transporter	AT1G30220	12.60	2.58	5.62
1612399_at	C2-domain containing protein	AT3G19830	11.93	3.05	8.35
1612804_at	stilbene synthase	AT5G13930	11.02	8.85	9.51
1612836_at	vacuolar invertase	AT1G62660	10.68	4.89	9.75
1613770_s_at	jasmonate ZIM-domain protein	AT1G19180	11.29	6.81	9.75
1614008_at	endo-polygalacturonase	AT3G57510	14.63	1.14	-1.23
1615447_at	chalcone synthase	AT5G13930	27.48	1.46	2.64
1615481_at	cytochrome b5	AT2G32720	14.10	-1.24	1.37
1615789_at	MYB-domain protein	AT3G49690	46.50	2.01	1.64
1616094_at	VvMYBPA	AT1G22640	22.03	1.07	4.03
1616798_s_at	inositol transporter	AT1G30220	13.70	2.37	5.45
1616850_at	serine carboxypeptidase	AT3G12203	20.93	-1.24	2.16
1617019_at	chalcone synthase	AT5G13930	30.36	-1.21	3.02
1617078_at	putative UDP-glucose:indole-3-acetate beta-D-glucosyltransferase	AT3G21560	13.22	-1.28	1.10
1617430_s_at	basic endochitinase	AT3G12500	12.53	9.69	9.69
1618589_s_at	unknown	no match	14.00	3.57	-1.10
1619439_at	pectinesterase	AT2G45220	13.43	5.90	4.46
1619441_at	unknown	AT5G60150	11.27	3.19	9.49
1619642_at	phenylalanine ammonia lyase	AT2G37040	42.06	6.16	8.69
1620305_at	polygalacturonase	AT2G41850	18.12	-1.37	-1.32
1620424_at	chalcone-flavanone isomerase	AT5G05270	20.52	5.69	6.54
1620628_at	neutral invertase	AT3G05820	10.01	6.31	8.94
1620809_at	unknown	AT3G62730	13.89	1.13	1.23
1621101_s_at	unknown	no match	10.85	4.20	4.58
1622131_at	auxin efflux carrier	AT1G20925	11.98	8.20	7.98
1622308_at	unknown	no match	15.86	3.84	9.27
1622638_x_at	stilbene synthase	AT5G13930	11.16	9.27	9.78

Table S3. List comprising those probe sets found to be more than 10-fold up-regulated by MeJA, MeJA+SA and JA treatments of the cell cultures

Probe set	Putative function	Closest Arabidopsis match	Fold change		
			MeJA	MeJA+SA	JA
1607505_s_at	aldehyde dehydrogenase	AT3G48000	10.55	14.20	20.62
1607552_at	unknown	AT1G51920	117.98	69.83	126.89
1608026_at	germin-like protein	AT5G39150	456.98	325.06	459.35
1608306_at	carbonate dehydratase	AT5G14740	175.90	114.43	157.23
1608541_s_at	alcohol dehydrogenase	AT5G06060	53.11	20.79	49.71
1608916_at	NAD+ ADP-ribosyltransferase	AT1G23550	21.79	56.00	34.56
1608981_at	phospholipase	AT2G39420	15.61	11.70	12.85
1609330_at	glutathione S-transferase	AT1G17180	13.46	17.19	22.77
1609696_x_at	stilbene synthase	AT5G13930	12.22	13.87	11.06
1609697_at	stilbene synthase	AT5G13930	14.02	12.10	12.35
1609875_at	protease inhibitor	AT2G38870	130.40	155.65	146.08
1610008_s_at	enoyl-CoA hydratase/isomerase	AT1G06550	30.33	26.29	27.97
1610070_at	stilbene synthase	AT5G13930	14.70	16.76	15.98
1610537_at	unknown	AT1G49000	32.25	23.29	51.00
1610781_at	cytidine/deoxycytidylate deaminase	AT5G28050	11.01	15.06	18.10
1610821_at	cinnamate-4-hydroxylase	AT2G30490	25.14	21.51	23.74
1610850_at	stilbene synthase	AT5G13930	12.33	13.96	10.98
1610962_x_at	unknown	AT1G31130	16.74	12.11	30.18
1610989_at	glutathione S-transferase	AT3G09270	13.64	14.76	15.52
1611027_at	cell-wall invertase	AT1G55120	24.03	22.53	24.78
1611457_at	unknown	AT4G33467	26.93	13.65	31.96
1611611_at	germin-like protein	AT5G20630	258.19	128.95	184.58
1611666_s_at	protease inhibitor	AT2G38870	172.60	188.37	186.56
1611682_at	ACT domain-containing protein	AT5G25320	32.55	14.12	36.59
1612281_at	O-methyltransferase	AT5G54160	86.18	109.84	193.24
1612389_at	glutamate dehydrogenase	AT5G07440	10.96	19.41	12.71
1612439_at	telomere repeat binding protein	AT5G59430	44.63	11.17	31.74
1612464_at	CYP89A6	AT1G64940	11.18	21.27	192.74
1612562_at	unknown	AT5G67370	18.37	48.25	46.88
1612741_at	unknown	AT1G55230	29.99	21.04	53.13
1613113_at	phenylalanine ammonia lyase	AT3G53260	24.54	19.44	24.45
1613136_at	jasmonate ZIM-domain protein	AT2G34600	136.66	144.03	151.82
1613602_at	unknown	AT1G15290	20.08	15.69	30.11
1613763_at	glutathione S-conjugate-transporting ATPase	AT3G59140	15.75	11.53	16.51
1613871_at	class IV chitinase	AT3G54420	13.48	25.78	67.83
1613917_s_at	cytidine/deoxycytidylate deaminase	AT5G28050	10.47	14.47	16.25
1614207_at	asparagine synthetase	AT3G47340	163.63	72.97	84.29
1614441_at	oxidoreductase	AT5G05600	317.85	409.61	473.67
1614528_at	glutamine amidotransferase	AT5G38200	16.96	30.02	33.68
1614673_at	cytidine/deoxycytidylate deaminase	AT5G28050	11.35	14.37	18.94
1614789_at	L-asparaginase	AT3G16150	15.97	16.03	26.74
1614820_at	sodium-dicarboxylate cotransporter	AT5G47560	19.45	11.75	20.33
1615548_at	unknown	AT1G24575	21.96	12.38	21.72
1615595_at	beta-1,3-glucanase	AT4G16260	22.69	17.91	15.84
1615708_s_at	unknown	no match	70.03	70.08	82.76
1615774_at	telomere repeat binding factor	AT1G49950	14.43	27.26	32.22
1615801_at	4-coumarate-CoA ligase	AT1G51680	34.73	21.31	39.44
1615805_at	unknown	AT2G47895	78.70	79.30	82.96
1615950_s_at	poly(A)-binding protein	AT1G49760	69.69	71.70	84.10
1615979_at	alpha/beta fold hydrolase	AT5G53050	18.75	21.94	29.73
1616191_s_at	cinnamate 4-hydroxylase	AT2G30490	23.35	22.23	24.03
1616254_a_at	remorin family	AT2G02170	22.93	26.62	35.75

1616279_at	NAD+ ADP-ribosyltransferase	AT1G23550	19.47	46.26	30.69
1616308_at	unknown	no match	66.68	54.76	86.46
1616312_at	phytosulfokine precursor protein	AT2G22860	38.88	58.87	235.26
1616317_at	trypsin and protease inhibitor	AT1G17860	349.26	477.12	448.19
1616575_at	stilbene synthase	AT5G13930	20.24	26.94	26.98
1616783_at	aldehyde dehydrogenase	AT3G48000	11.98	18.53	29.60
1616944_at	unknown	AT4G24380	36.33	42.60	54.90
1616977_at	2OG-Fe(II) oxygenase	AT4G25310	22.01	10.66	16.09
1617097_at	auxin efflux carrier	AT1G20925	17.48	19.91	18.28
1617116_s_at	unknown	AT1G51920	114.96	64.50	85.69
1617405_at	zinc transporter	AT2G29410	71.23	67.22	80.81
1617507_s_at	unknown	no match	123.28	121.96	129.06
1617589_at	F-box/Kelch-repeat protein	AT1G23390	21.65	14.78	19.17
1617676_at	serine carboxypeptidase	AT2G33530	25.12	15.70	18.40
1618493_s_at	ABC-type multidrug transporter	AT3G59140	14.81	10.57	16.06
1618561_at	short-chain dehydrogenase/reductase	AT4G13180	16.18	16.37	31.94
1618663_s_at	dirigent protein	AT3G13650	56.37	42.97	75.43
1618751_at	serine carboxypeptidase	AT1G28110	32.50	18.00	21.15
1619320_at	4-coumarate-CoA ligase	AT1G65060	32.45	26.94	40.90
1619325_at	CYP72A14	AT3G14690	24.41	12.35	28.42
1619346_at	unknown	AT1G55230	109.07	83.42	182.50
1619610_at	IAA-Ala hydrolase	AT1G51760	221.14	148.36	204.59
1619916_s_at	1,3-beta-glucosidase	AT3G57240	314.92	26.10	155.13
1620065_at	sulfate transporter	AT5G19600	75.25	28.40	53.00
1620276_at	embryo-abundant protein-related	AT2G41380	36.01	25.37	47.25
1620319_s_at	MYB transcription factor	AT2G31180	67.79	122.02	101.53
1620588_at	blue copper protein	AT3G27200	13.96	15.47	17.50
1620785_at	unknown	AT1G31130	20.06	14.12	35.36
1620964_s_at	stilbene synthase	AT5G13930	11.96	13.94	12.64
1621068_at	enoyl-CoA hydratase/isomerase	AT1G06550	24.55	20.03	21.49
1621102_at	acidic endochitinase	AT5G24090	246.63	72.30	202.76
1621244_s_at	short-chain alcohol dehydrogenase	AT4G13180	13.29	13.91	26.25
1621261_at	exocyst complex subunit	AT3G09520	30.34	24.40	40.18
1621649_at	Na+-driven multidrug efflux pump	AT1G33090	22.42	12.55	18.33
1621789_s_at	hydrolase, alpha/beta fold family protein	AT5G53050	17.99	20.36	26.55
1622064_at	MYB transcription factor	AT2G31180	35.74	107.68	67.48
1622203_at	trypsin and protease inhibitor	AT1G17860	29.72	26.26	15.83
1622544_a_at	serine/threonine protein kinase	AT5G57630	10.34	21.90	22.93
1622549_at	NADP-dependent oxidoreductases	AT1G26320	61.36	28.69	79.81

Table S4. Concentration of sesquiterpenes and compounds with sesquiterpene like mass-spectra in the cell cultures

Peak numbers are listed in relation to Fig. 1. The retention index is based on a series of n-alkanes (C₁₀–C₂₆) on ZB-Wax + (30 m, 0.25 mm, 0.25 μm). Method of identification: A, identities confirmed by comparison of mass spectra and retention index with those of authentic standards; B, identities tentatively assigned based on the comparison with those from either the NIST05 and Wiley Registry 7th edition mass spectral library or literature; C, unidentified compound with a mass spectral match to known sesquiterpenes. Concentrations were quantified relative to a (*E,E*)-farnesol standard using the area of the total ion chromatograph (TIC) peak. nd, not detected

Peak number	Retention index	Compound	Control	MeJA (μg g ⁻¹)	MeJA + SA (μg g ⁻¹)	JA (μg g ⁻¹)
1	1416	α-Cubebene (A)	nd	4.54	0.07	28.93
2	1456	α-Copaene (A)	nd	5.05	0.06	27.76
3	1498	α-Gurjunene (A)	nd	0.73	0.03	7.65
4	1509	β-Gurjunene (B)	nd	2.28	nd	4.10
5	1584	α-Bergamotene (B)	nd	0.10	nd	0.46
6	1599	β-Caryophyllene (A)	nd	28.40	0.58	29.25
7	1637	(+)-Epi-bicyclosesquiphellandrene (B)	nd	nd	nd	0.46
8	1645	Alloaromadendrene (A)	nd	0.82	0.01	4.63
9	1658	Epizonarene (B)	nd	nd	nd	1.61
10	1670	α-Caryophyllene (A)	nd	3.06	0.16	4.19
11	1690	Valencene (A)	nd	0.20	nd	1.65
12	1703	2-Isopropyl-5-methyl-9-methylene-bicyclo[4.4.0]dec-1-ene (B)	nd	0.31	nd	2.53
13	1720	α-Muurolene (B)	nd	0.55	nd	3.59

14	1752	δ -Cadinene (B)	nd	4.98	0.04	26.01
15	1778	1,2,3,4,4a,7-hexahydro-1,6-dimethyl-4-(1-methylethyl)- naphthalene (B)	nd	0.07	nd	1.81
16	1827	(-)-Calamenene (B)	nd	2.55	nd	8.27
17	1877	τ -Cadinene (B)	nd	0.93	nd	5.06
18	1927	τ -Muurolene (B)	nd	0.92	0.03	5.28
19	1976	Caryophyllene oxide (B)	nd	3.35	nd	0.53
20	2048	Cubenol (B)	nd	0.50	nd	2.31
21	2055	δ -Cadinol (B)	nd	0.52	nd	2.57
22	2162	Unidentified sesquiterpene (C)	nd	0.04	nd	0.31
23	2178	τ -Muurolol (B)	nd	0.12	nd	0.68
24	2185	τ -Cadinol (B)	nd	0.04	nd	0.27
25	2225	α -Cadinol (B)	nd	0.08	nd	0.27
