

Hormonal and transcriptional profiles highlight common and differential host responses to two arbuscular mycorrhizal fungi and the regulation of the oxylipin pathway. JA Lopez-Raez, A Verhage, I Fernandez, JM Garcia, C Azcon-Aguilar, V Flors, and MJ Pozo

SUPPLEMENTARY DATA

Table S1. Primer sequences used in the real time qPCR analysis.

ID	Gene	Primers (5'-3')
U09026	Lipoxygenase A (LOXA) ¹	GGTTACCTCCCAAATCGTCC TGTTTGTAAGTGCCTGTG
U37840	Lipoxygenase D (LOXD) ²	GACTGGTCCAAGTTCACGATCC ATGTGCTGCCAATATAAATGGTTCC
AJ271093	Allene oxide synthase 1 (AOS1) ¹	CACCTGTAAACAAGCGAAAC GACCTGGTGGCATGTTCGT
AF230371	Allene oxide synthase 2 (AOS2) ²	AGATTTTCTCCCGAATATGCTGAA ATACTACTGATTTTCATCAACGGCAT
AF454634	Allene oxide synthase 3 (AOS3) ¹	GCGGAGGAGTTCAATCCAG CGCATGAAAACTCCACAACC
AF384374	Allene oxide cyclase (AOC) ²	GCACGAAGAAGAGAAGAAAGGAGAT CGGTGACGGCTAGGTAAGTTTC
AJ278332	12-oxophytodienoate 3 reductase (OPR3) ²	TTGGCTTAGCAGTTGTTGAAAG TACGTATCGTGGCTGTGTTACA
AF317515	Divinyl ether synthase (DES) ¹	CCGGATGAGTTTGTACCTGA ATCTTTGCCTGGACATTGCT
AF083253	Multicystatin ²	GAGAATTTCAAGGAAGTTCAA GGCTTTATTTACACAGAGATA
K03291	Proteinase inhibitor II ²	GAAAATCGTTAATTTATCCCAC ACATACAAACTTTCCATCTTTA
BI933750	1-deoxy-D-xylulose 5-phosphate 2 (DXS-2) ¹	AGACGGTCCAACGCATTGT CCTCTAGGAAATCGGAAACA
U30465	Class II chitinase (Chi2;1) ¹	TGCTGCTTGTGGTGCAGAAAG TGCCCATCCACCCGTAG
CN384809	1-aminocyclopropane-1-carboxylic acid oxidase 1 (ACO1) ¹	GGACTCCGCGCTCATAACAGA ATAGAGTGGCGCATGGG
X58885	Ethylene forming enzyme (EFE) ¹	CGCAGGAGGCATCATACTTC CTTCCCGTTGGTAATCAC
AY394002	CTR1-like protein kinase (CTR4) ¹	CATCCTCTTTCTTACTGTGAGAAAATTTAGA CATTTCCCTGTATAAAAACGTTTCAGTT
Z97215	9-cis-epoxycarotenoid (NCED) ¹	ACCCACGAGTCCAGATTTTC GGTTCAAAAAGAGGGTTAGC
AY885651	Phosphate transporter LePT4 ³	GAAGGGGAGCCATTTAATGTGG ATCGCGGCTTGTTTAGCATTTTC
M69247	Pathogenesis related protein PR1a ¹	ATGTGTGTGTTGGGGTTGGT ACTTTGGCACATCCAAGACG
Y15846	Pathogenesis protein PR10-like ¹	CCAAGGCTGTAGAAGCATACC CGTCTCTCATTGAGCGTTT
X51904	Le4 ¹	ACTCAAGGCATGGGTACTGG CCTTCTTTCTCCTCCACCT
X14449	Elongation factor 1 (SIEF) ⁴	GATTGGTGGTATTGGAAGTGC AGCTTCGTGGTGCATCTC
DQ282611	GintEF ⁵	GCTATTTTGATCATTGCCGCC TCATTAACGTTCTTCCGACC

¹This work; ²Uppalapati *et al.*, 2005; ³Balestrini *et al.*, 2007; ⁴Rotenberg *et al.*, 2006; ⁵Benabdellah *et al.*, 2009

Table S2. Mycorrhization, root and shoot fresh weights, and phosphorus content in tomato plants colonized by *G. mosseae* (Gm) or *G. intraradices* (Gi). Nm indicates control non-mycorrhizal plants.

	Mycorrhization (%)	Root weight (g)	Shoot weight (g)	Shoot P content (%)
Nm	0	1.95 ± 0.35 ^a	5.84 ± 0.68 ^a	0.19 ± 0.02 ^a
Gm	23 ± 4 ^a	1.91 ± 0.43 ^a	5.58 ± 1.02 ^a	0.16 ± 0.01 ^a
Gi	41 ± 7 ^b	1.70 ± 0.62 ^a	5.44 ± 1.66 ^a	0.17 ± 0.01 ^a

Numbers represent the average of 3 independent replicates ± SD. Different superscript letters indicate statistically significant differences between means ($P < 0.05$).

Table S3. Expression level of genes involved in hormone metabolism in roots colonized by *G. mosseae* (Gm) or *G. intraradices* (Gi).

ID	Annotation	Roots	
		Gm	Gi
	Jasmonates		
U09026	Lipoxygenase A (LoxA)	6.59	2.78
U09025	Lipoxygenase B (LoxB)	<i>nd</i>	<i>nd</i>
U37839	Lipoxygenase C (LoxC)	<i>nd</i>	<i>nd</i>
U37840	Lipoxygenase D (LoxD)	1.27	2.17
AJ271093	Allene oxide synthase (AOS1)	2.14	2.52
AF230371	Allene oxide synthase (AOS2)	0.97	0.89
AF454634	Allene oxide synthase (AOS3)	8.49	3.42
AF384374	Allene oxide cyclase (AOC)	1.34	1.29
AJ278332	12-oxophytodienoate 3 reductase (OPR3)	0.94	1.05
BG628687	Jasmonic acid carboxyl methyl transferase (JMT)	1.53	1.62
BT013697	Jasmonate-amino synthetase (JAR1)	1.03	1.10
AY455313	Methyl jasmonate esterase (JAME)	2.16	2.82
BG628191	Jasmonate ZIM domain 2 (JAZ2)	2.23	2.49
	ABA		
Z97215	9- <i>cis</i> -epoxycarotenoid (NCED1)	0.96	0.69
AF258808	Aldehyde oxidase 1 (AO1)	0.97	0.93
AF258809	Aldehyde oxidase 2 (AO2)	0.89	0.92
AF258810	Aldehyde oxidase 3 (AO3)	1.13	1.16
AF258811	Aldehyde oxidase 4 (AO4)	<i>nd</i>	<i>nd</i>
AY074788	Moco sulfurase (FLACCA)	1.29	0.99
AW034203	ABA 8'-hydroxylase	0.62	1.66
Y14809	Beta-carotene hydroxylase (CrtR-b1)	0.63	0.79
BG734834	Zeaxanthin epoxydase	0.78	0.89
AF385366	Violaxanthin epoxydase	<i>nd</i>	<i>nd</i>
AW219893	ABA-induced protein	0.84	0.99
	ET		
M34289	ACC synthase 2 (ACS2)	<i>nd</i>	<i>nd</i>
U17972	ACC synthase 3 (ACS3)	<i>nd</i>	<i>nd</i>
X58885	Ethylene forming enzyme (ACO)	0.69	1.13
CN384809	ACC oxidase 1 (ACO1)	2.35	2.27
AB013101	ACC oxidase 4 (ACO4)	0.64	0.65
AJ715790	ACC oxidase 5 (ACO5)	<i>nd</i>	<i>nd</i>
AY394002	CTR1-like protein kinase (CTR4)	1.11	1.13
AF110518	CTR1-like protein kinase (ethylene-inducible)	1.12	0.99
	SA		
BG626517	S-adenosyl-L-methionine:salicylic acid carboxyl methyltransferase (SAMT)	<i>nd</i>	<i>nd</i>

Genes involved in the metabolism and signaling of jasmonates, abscisic acid (ABA), ethylene (ET) and salicylic acid (SA) and present in the Affymetrix GeneChip Tomato Genome Array are shown. Data are expressed as fold-change in expression levels compared to the non-mycorrhizal control roots according to the microarray analysis. *nd* indicates non-detected expression.

Table S4. Genes specifically induced or repressed in tomato roots colonized by *G. intraradices* (Gi). Fold-change in their expression level compared to non mycorrhizal plants or upon methyl jasmonate (MeJA) treatment.

ID	Annotation	Gi	MeJA
AI771939	Class III alcohol dehydrogenase 5	5.04	2.89
AF243040	Receptor-like protein kinase (PRK3)	4.85	0.99
AI899070	Ent-kaurene oxidase (CYP701A)	4.27	0.99
AW030757	Gibberellin 2-oxidase (SIGA2ox3)	4.26	5.49
BI204920	Zinc finger (C3HC4-type RING finger)	4.19	26.42
BI922195	Class III alcohol dehydrogenase 5	3.85	1.44
M80604	Beta-1,3-glucanase	3.31	0.07
BM409727	N-hydroxycinnamoyl/benzoyltransferase	3.26	4.83
BT012691	2-oxoglutarate-dependent dioxygenase	3.16	15.39
AF254793	Lycopene beta-cyclase (CrtL-b)	3.02	0.64
CN385777	Zinc finger (C2HC2)	2.87	9.10
AW035980	Amino acid binding (ACR8)	2.81	2.09
BG631850	Phytoene desaturase (PDS)	2.75	0.76
AW625888	1-aminocyclopropane-1-carboxylic acid oxidase (ACO)	2.70	1.63
BG628645	Chitinase	2.65	1.69
BT014289	1-phosphatidylinositol phosphodiesterase-related	2.64	8.45
BG627506	Carbonic anhydrase	2.63	276.72
BT012812	Elongation factor-like	2.60	4.59
BI932691	Unknown	2.57	1.02
AF096246	Ethylene-responsive transcriptional coactivator	2.55	3.31
AW928514	Peroxidase	2.49	0.17
BT013303	4-amino-4-deoxychorismate lyase	2.48	0.30
BI210904	Purine transmembrane transporter (AtPUP3)	2.44	1.77
BG627658	Unknown	2.43	2.42
BE353179	N-acetyltransferase	2.32	4.84
U89256	DNA-binding protein Pti5	2.31	4.70
AW219676	Unknown	2.29	3.53
BT013913	L-lactate dehydrogenase	2.26	1.60
BG643871	Enoyl-[acyl-carrier-protein] reductase	2.24	0.16
CN385420	Calcium binding protein	2.24	5.90
U37840	Lipoxygenase D (LOXD)	2.17	10.79
AI777697	Unknown	2.16	0.91
BT013211	Cystathionine beta-synthase	2.15	0.45
AF195507	Zeta-carotene desaturase (ZDS)	2.13	1.51
BT014379	Histidine decarboxylase	2.11	0.36
AW092785	Unknown	2.11	1.38
BI928506	Annexin	2.11	4.48
BT013586	Heat shock protein 70 kD (Hsc-1)	2.11	3.56
AW223067	Calmodulin	2.09	1.07
AI775872	2-oxoglutarate-dependent dioxygenase	2.07	1.12
BG628954	Unknown	2.02	1.35
BM410464	Sodium symporter-related	2.02	0.78
AI485696	Calmodulin	1.99	0.97
BG628875	Unknown	1.99	0.31
BG627003	S-adenosylmethionine decarboxylase 2	1.97	3.58

BT014384	2-oxoglutarate-dependent dioxygenase	1.96	4.77
AJ784458	Heat shock protein cognate 70	1.95	1.68
AF331705	1-deoxy-D-xylulose-5-phosphate reductoisomerase (DXR)	1.94	2.42
AY368906	Heat shock protein 90	1.89	1.60
BG630651	Unknown	1.88	1.33
BG735346	Kinesin	1.87	0.67
BG627878	Unknown	1.79	0.41
BT014625	Replication factor C	1.79	0.55
BT013273	Unknown	1.73	1.21
AW092917	Xyloglucan:xyloglucosyl transferase	0.59	0.18
CK715113	Unknown	0.59	0.73
AF218774	Aquaporin PIP1	0.59	0.30
CK720557	Acid phosphatase class B	0.58	0.15
BG628504	Germin-like protein	0.58	1.41
BT014421	Isoflavone reductase	0.58	1.11
AW429117	Unknown	0.58	2.35
CN385091	Peroxidase	0.57	0.56
CK715831	Zinc-binding protein	0.56	0.95
BE451719	Aquaporin PIP2	0.56	0.06
AI898522	2-nitropropane dioxygenase	0.56	3.52
AI490099	Endonuclease (tbn1)	0.56	1.13
CN385508	Proline dehydrogenase	0.55	0.82
BG630440	Unknown	0.55	0.38
CN384666	Germin-like protein	0.55	1.72
AF193439	Glutathione S-transferase/oxidase	0.54	3.02
BF050423	GDP-mannose 3,5-epimerase	0.54	0.25
CN385367	Glutaredoxin	0.54	4.30
AW737374	MYB transcription factor (AIM1)	0.53	5.77
BT014260	Unknown	0.53	0.16
BI925563	Auxin efflux carrier protein	0.53	5.55
AY324397	Alternative oxidase 1c	0.52	0.92
BG627815	LIM domain protein WLIM1	0.52	0.39
AW625684	Asparagine synthetase (AS1)	0.52	2.64
CN385091	Peroxidase	0.51	0.44
AW217188	Germin-like protein	0.51	1.89
CK715555	Dopamine beta-monoxygenase	0.51	1.40
AY497477	Xyloglucan endotransglucosylase-hydrolase XTH6	0.50	0.39
U18678	Isocitrate lyase	0.50	2.07
BF098450	Pectinesterase inhibitor	0.50	2.25
BI208081	Medium-chain acyl CoA synthetase	0.49	3.72
BG643520	Fasciclin-like arabinogalactan-protein 12	0.49	1.26
BG133955	Cysteine-type peptidase	0.49	0.47
BT013407	Lactoylglutathione lyase	0.49	0.91
CK714985	(1-4)-beta-mannan endohydrolase	0.48	0.87
CN384849	Calmodulin	0.48	1.27
AW033570	Amino acid binding protein	0.48	0.28
AW625370	LOB domain-containing protein	0.46	1.82
AW626006	Unknown	0.46	1.38
AI490099	Putative endonuclease precursor	0.45	1.45
AJ011914	bZIP transcription factor THY5	0.44	0.47
CN385880	Fasciclin-like arabinogalactan protein	0.44	1.06

AW218741	60S ribosomal protein L6	0.43	1.32
CK575023	Nam-like protein	0.43	5.96
BG126009	Unknown	0.43	1.02
BG734719	Unknown	0.43	0.33
AW649367	Carbohydrate transporter	0.43	20.75
AW738551	Carbohydrate transporter	0.43	24.15
BG626715	Apyrase-like protein	0.43	1.26
BT013228	Transcription factor Y	0.42	0.14
BT013477	Glycolate oxidase	0.42	2.37
Z68309	Metallothionein-like protein	0.42	0.93
BM408981	Copper-binding protein	0.41	1.29
BG127578	60S ribosomal protein L6	0.39	1.17
AJ417830	Extensin-like protein	0.36	0.13
AW626016	Cationic peroxidase	0.36	0.09
AY344540	Alpha-dioxygenase DOX-2	0.35	0.33

Table S5. Genes specifically induced or repressed in tomato roots colonized by *G. mosseae* (Gm). Fold change in their expression level compared to non-mycorrhizal plants or upon methyl jasmonate (MeJA) treatment.

ID	Annotation	Gm	MeJA
BG630425	Proteinase inhibitor I	30.86	159.77
AJ133600	Extensin-like protein	14.15	3.49
BG631444	Proteinase inhibitor I	13.86	165.58
BI931127	Putative miraculin	13.09	928.35
AF083253	Multicystatin	9.27	291.27
BG631366	Unknown	9.10	321.97
BG628187	Proteinase inhibitor I	8.27	3.51
BG625870	Polyphenol oxidase (PPO)	6.68	20.19
BG628643	Threonine deaminase	6.43	111.68
K03291	Proteinase inhibitor II	5.92	425.73
BG626001	Serin protease/subtilisin-like	5.71	30.52
BT013249	Inducible plastid-lipid associated protein	4.00	170.19
AF242849	Wound-inducible carboxypeptidase	3.95	9.47
BG629245	Unknown	3.95	0.52
AF146690	Pto-responsive gene 1 protein	3.86	231.96
X77373	Glycine rich protein	3.42	3.94
AJ133601	Gamma-thionin	3.40	1.36
BI203812	Phosphatase (psi14A)	3.39	41.71
Y10149	Subtilisin-like protease	3.16	0.47
CN385118	Unknown	3.07	3.04
BG130169	Extensin-like	2.78	9.48
AJ459816	Phosphatase (psi14B)	2.75	5.49
AJ459817	Phosphatase (psi14A)	2.57	3.11
BI210284	Unknown	2.55	5.94
X71593	Peroxidase CEVI-1	2.53	0.75
AJ635324	Polyphenol oxidase	2.44	1.47
AW648097	Unkonwn	2.35	7.95
AI773917	Arogenate dehydrogenase	2.33	20.60
AW649666	1-aminocyclopropane-1-carboxylate oxidase (ACO)	2.32	0.72
AY026343	Non-symbiotic hemoglobin class 1 (Glb1)	2.27	1.10
BG629220	1-aminocyclopropane-1-carboxylic acid oxidase (ACO6)	2.20	0.43
AW622064	LOB domain 37 (LBD37)	2.15	1.74
BG734632	Unknown	2.13	0.63
BF112635	1-aminocyclopropane-1-carboxylate oxidase (ACO)	2.09	0.60
X94944	Lipid desaturase-like protein (cevi19)	2.08	0.52
CN384955	Unknown	2.08	2.93
AW649659	Gibberellic acid-induced gene (gasa4)	2.07	0.08
AI779060	LOB domain	2.05	1.59
BG127217	Gamma-thionin/defensin	2.04	1.28
BI206094	NIP2	2.02	1.27
L76632	Osmotin-like protein	1.97	1.56
AW625586	Xyloglucan-specific fungal endoglucanase inhibitor protein precursor (Xegip)	1.90	0.32
BG131634	Lipase	1.86	0.91
CN385868	Auxin-responsive protein	1.85	8.45
BG629316	Unknown	1.84	1.54
BE460442	Phosphopyruvate hydratase	1.83	0.16

BG627786	Proline rich protein	1.82	0.90
AF022874	Phosphate transporter 2 (LePT2)	1.78	0.07
AY568721	Wound/stress protein	1.77	0.56
AI782210	Unknown	1.73	0.29
BG629955	Arginine decarboxylase (adc1)	1.73	1.96
CN384480	Peroxidase CEVI-16	1.71	1.25
BF097029	Unknown	0.60	0.37
BI207106	NADPH:quinone oxidoreductase	0.58	4.31
BT013653	Protein serine/threonine kinase	0.58	1.10
AF022020	IAA9	0.58	1.26
AW035650	Serine/threonine phosphatase	0.58	1.13
AI895632	Auxin-inducible SAUR protein	0.57	0.67
BT013320	Nodulin MtN3	0.57	0.72
AI899248	Transcription factor APETALA 2	0.57	0.92
BM535315	Carboxylesterase	0.56	1.29
CK715114	UDP-glucosyltransferase	0.56	2.82
BF112381	Cytochrome c oxidase	0.55	1.86
AF204783	Unknown	0.55	1.23
BE460421	Carboxylesterase	0.55	1.09
AB026983	Small heat shock protein (leer-sHSP)	0.54	1.17
BT014402	Cohesin	0.54	1.48
AI772299	Cytochrome P450 (CYP76C1)	0.54	0.64
AI898501	DNAJ heat shock protein	0.54	1.83
BM412737	Protein binding/transcription regulator (BT1)	0.52	6.52
AF146691	Eli3 protein	0.52	24.52
BI933005	Short-chain dehydrogenase/reductase (SDR)	0.52	6.02
BT014359	Purine transmembrane transporter	0.50	0.75
BG631327	Unknown	0.50	0.34
AY007562	Glutathione S-transferase	0.50	10.69
AW929113	Class I small heat shock protein (HSP15.7-CI)	0.49	1.13
BM410870	Class I small heat shock protein (HSP26.5-P)	0.49	0.92
AJ606077	Spermine synthase (spe4)	0.49	0.48
AI779519	Unknown	0.47	0.66
BI210938	Unknown	0.46	0.38
BT012739	ADP-ribose pyrophosphohydrolase	0.46	0.66
X92855	Mannitol dehydrogenase	0.45	3.44
BM410706	L-ascorbate peroxidase	0.45	1.18
BT013685	Zinc finger	0.44	11.81
BG132890	Dihydroneopterin triphosphate pyrophosphohydrolase (NUDIX1)	0.44	0.83
BM410261	3-ketoacyl-CoA synthase 6	0.42	0.74
AI771544	Homeobox-leucine zipper protein HAT5	0.42	0.92
BT014212	Non-phosphorylating glyceraldehyde dehydrogenase	0.38	1.09
BT014113	Phosphosulfolactate synthase-related protein	0.36	1.17
BM412443	Calcium-binding EF hand family protein	0.36	0.58
BT014414	Flavonoid glucosyltransferase	0.36	20.43
BM535201	Nodulin ENOD18	0.35	2.49
AI773696	Lipid transfer protein (LTP2)	0.35	0.86
AW648171	Urease accessory protein G (ureG)	0.35	0.88
BG126449	Calcium:hydrogen antiporter (CAX3)	0.33	1.10
BM409988	Flavonoid glucosyltransferase	0.31	1.44
BM536272	Oxidoreductase 2OG-Fe(II) oxygenase	0.30	0.77
AF123256	Class II small heat shock protein Le-HSP17.6	0.30	1.13

AW624885	Unknown	0.28	2.09
AW223624	UDP-glycosyltransferase	0.28	1.55
U72396	Class II small heat shock protein Le-HSP17.6	0.11	1.34