

## Supplemental Information

**Diet of Arbuscular Mycorrhizal Fungi: Bread and Butter?**Mélanie K. Rich\*, Eva Nouri\*, Pierre-Emmanuel Courty<sup>1</sup>, and Didier Reinhardt<sup>2</sup>

Dept. of Biology, University of Fribourg, Rte Albert-Gockel 3, 1700 Fribourg, Switzerland

<sup>1</sup>Present address: Agroécologie, AgroSupDijon, CNRS, INRA, Université de Bourgogne Franche-Comté, 21000 Dijon, France.<sup>2</sup>Correspondence: [didier.reinhardt@unifr.ch](mailto:didier.reinhardt@unifr.ch) (D. Reinhardt)

\*These authors contributed equally

**Table S1. Lipid-Related Transcripts Induced in AM Symbiosis**

Host plant species	<i>Medicago truncatula</i>	<i>Medicago truncatula</i>	<i>Medicago truncatula</i>	<i>Medicago truncatula</i>	<i>Medicago truncatula</i>	<i>Medicago truncatula</i>	<i>Medicago truncatula</i>	<i>Lotus japonicus</i>	<i>Oryza sativa</i>	<i>Petunia hybrida</i>	<i>Solanum lycopersicum</i>	<i>Casuarina glauca</i>
AM fungal species	<i>Rhizophagus irregularis</i>	<i>Simiglomus mosseae</i>	<i>Rhizophagus irregularis</i>	<i>Gigaspora margarita</i>	<i>Rhizophagus irregularis</i>	<i>Rhizophagus irregularis</i>	<i>Gigaspora margarita</i>	<i>Rhizophagus irregularis</i>				
Refs.	[S1]	[S1]	[S2]	[S3]	[S4]	[S5]	[S6]	[S7]	[S8]	[S9]	[S10]	
<b>Fatty acid biosynthesis</b>												
Glycerol-3-phosphate dehydrogenase (G3PD)	n.d.	n.d.	Mtr.13234.1.S1_at	TC96455	medtr6g022550.1	n.d.	Ljwgs_01550 8.0.1_at	Os01g74000	cn5471	n.d.	n.d.	
Acyl carrier protein (ACP)	n.d.	MT007363	Mtr.12210.1.S1_at	n.d.	n.d.	medtr2g025430	n.d.	Os03g63930	cn4070	n.d.	CG-GI1f_003_I12	
Acetyl-coenzyme A carboxylase (ACCase)	n.d.	n.d.	n.d.	n.d.	medtr4g161110.1	medtr4g161110	chr4.CM000 4.51_at	Os05g22940	n.d.	SGN-U230893	n.d.	
Biotin carboxyl carrier protein subunit (BC)	MT001915 <sup>a</sup>	n.d.	Mtr.43125.1.S1_at	n.d.	Medtr6g015070.1	medtr6g015070	Ljwgs_02486 8.1_at	n.d.	n.d.	SGN-U218181	CG-N02f_034_P18	
Malonyl CoA-ACP transacylase	MT004004	MT004004	Mtr.37706.1.S1_at	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.	
β-Ketoacyl-ACP synthase I (KAS I)	n.d.	MT008820	Mtr.12584.1.S1_at	n.d.	medtr4g165920.1	medtr4g165430	chr4.CM002 5.55_x_at	Os06g09630	n.d.	n.d.	n.d.	
β-Ketoacyl-ACP reductase	MT007771	n.d.	Msa.958.1.S1_at	n.d.	medtr3g103330.1	medtr3g103330	n.d.	n.d.	n.d.	n.d.	n.d.	CG-N02f_007_J20
β-Hydroxyacyl-ACP dehydratase	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.	Os08g12840	n.d.	SGN-U219066	n.d.	
Enoyl-ACP reductase	MT002087	n.d.	Mtr.43890.1.S1_at	n.d.	n.d.	medtr4g101180	n.d.	Os08g23810	n.d.	SGN-U215147	n.d.	
Palmitoyl-acyl carrier protein thioesterase	n.d.	n.d.	n.d.	TC99271	n.d.	n.d.	chr5.CM032 8.85_at		n.d.	n.d.	n.d.	
Oleoyl-acyl carrier protein thioesterase	n.d.	n.d.	Mtr.35910.1.S1_at	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.	
<b>Fatty acid and lipid processing</b>												
Stearoyl-acyl-carrier protein desaturase	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.	Os01g69080	n.d.	n.d.	n.d.	n.d.
Acyl-ACP desaturase	n.d.	n.d.	Mtr.8836.1.S1_at	n.d.	Medtr5g024070.1	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.
Oleate desaturase	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.	Os07g23410	n.d.	SGN-U218869	n.d.	
Ω-3 fatty acid desaturase	MT001133	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.
Ω-6 fatty acid desaturase	MT015305	MT015305	n.d.	n.d.	medtr8g145530.1	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.
δ-8 sphingolipid desaturase	n.d.	n.d.	Mtr.20014.1.S1_at	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.
Acyl-CoA binding protein	n.d.	n.d.	Mtr.42250.1.S1_at	n.d.	medtr7g138990.1	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.
Acyl-CoA oxidase (ACX3)	n.d.	n.d.	n.d.	TC97009	n.d.	n.d.	n.d.	Os01g44950	n.d.	n.d.	CG-R01f_016_H07	

Acyl-CoA ligase / Acyl-CoA synthetase	n.d.	n.d.	Mtr.1923.1.S1_s_at	n.d.	n.d.	n.d.	n.d.	Os12g04990	n.d.	n.d.	n.d.
Acyl-CoA dehydrogenase	n.d.	n.d.	Mtr.38936.1.S1_at	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.
Acetyl-coenzyme A acyltransferase	n.d.	n.d.	Mtr.38560.1.S1_at	AL383672	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.
Long chain acyl-CoA synthetase 6 (LACS)	n.d.	n.d.	n.d.	n.d.	Medtr8g151250_1	n.d.	n.d.	n.d.	cn5749	n.d.	n.d.
Long fatty acid hydroxylase (CYP 704)	n.d.	n.d.	Mtr.42853.1.S1_at	n.d.	ac233669_10.1	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.
Glycerol-3-phosphate acyl transferase (GPAT)	n.d.	n.d.	Mtr.36944.1.S1_at	n.d.	medtr1g059560_1	n.d.	n.d.	n.d.	drpoolB-CL5253Contig1	n.d.	n.d.
Lipid transfer protein (LTP) non-specific	MT000718	n.d.	Mtr.35447.1.S1_at	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.
ABC transporter, subfamily G (ABCG) (STR1)	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.	TM0445.17_at	Os09g23640	drpoolB-CL8456Contig1	n.d.	n.d.
ABC transporter, subfamily G (STR2)	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.	TM0445.31_s_at	n.d.	n.d.	n.d.	n.d.
GDSL Lipase / hydrolase	MT013025	n.d.	Mtr.29623.1.S1_at	TC108660	n.d.	medtr8g088830	Ljwgs_039202_2_at	Os03g38350	n.d.	n.d.	CGCL373Contig1
TAG lipase	MT007472	MT006317	n.d.	TC110731	medtr7g092600_1	n.d.	n.d.	n.d.	drpoolB-CL2127Contig1	n.d.	n.d.
Phospholipase C	MT005857	MT005857	Mtr.42267.1.S1_at	n.d.	medtr5g090070_1	n.d.	n.d.	Os01g72520	drpoolB-CL3666Contig1	n.d.	n.d.

<sup>a</sup>Gene IDs with an induction ratio >2-fold are listed.

## Supplemental References

- S1** Hohnjec, N., et al. (2005) Overlaps in the transcriptional profiles of *Medicago truncatula* roots inoculated with two different *Glomus* fungi provide insights into the genetic program activated during arbuscular mycorrhiza. *Plant Physiol.* 137, 1283-1301
- S2** Hogekamp, C. and Küster, H. (2013) A roadmap of cell-type specific gene expression during sequential stages of the arbuscular mycorrhiza symbiosis. *BMC Genomics* 14, 306
- S3** Gomez, S.K., et al. (2009) *Medicago truncatula* and *Glomus intraradices* gene expression in cortical cells harboring arbuscules in the arbuscular mycorrhizal symbiosis. *BMC Plant Biology* 9, 10
- S4** Gaude, N., et al. (2012) Arbuscule-containing and non-colonized cortical cells of mycorrhizal roots undergo extensive and specific reprogramming during arbuscular mycorrhizal development. *Plant J.* 69, 510-528
- S5** Gaude, N., et al. (2012) Cell type-specific protein and transcription profiles implicate periarbuscular membrane synthesis as an important carbon sink in the mycorrhizal symbiosis. *Plant Signaling and Behavior* 7, 461-464
- S6** Guether, M., et al. (2009) Genome-wide reprogramming of regulatory networks, cell wall and membrane biogenesis during arbuscular-mycorrhizal symbiosis in *Lotus japonicus*. *New Phytol.* 182, 200-212
- S7** Gümil, S., et al. (2005) Comparative transcriptomics of rice reveals an ancient pattern of response to microbial colonization. *Proc. Natl. Acad. Sci. U. S. A.* 102, 8066-8070
- S8** Breuillin, F., et al. (2010) Phosphate systemically inhibits development of arbuscular mycorrhiza in *Petunia hybrida* and represses genes involved in mycorrhizal functioning. *Plant J.* 64, 1002-1017
- S9** Fiorilli, V., et al. (2009) Global and cell-type gene expression profiles in tomato plants colonized by an arbuscular mycorrhizal fungus. *New Phytol.* 184, 975-987
- S10** Tromas, A., et al. (2012) Heart of endosymbioses: Transcriptomics reveals a conserved genetic program among arbuscular mycorrhizal, actinorhizal and legume-rhizobial symbioses. *Plos One* 7, e44742