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Symbiosis-Related Plant Genes Modulate Molecular Responses in an Arbuscular Mycorrhizal Fungus During Early Root Interactions

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To gain further insight into the role of the plant genome in arbuscular mycorrhiza (AM) establishment, we investigated whether symbiosis-related plant genes affect fungal gene expression in germinating spores and at the appressoria stage of root interactions. *Glomus intraradices* genes were identified in expressed sequence tag libraries of mycorrhizal *Medicago truncatula* roots by in silico expression analyses. Transcripts of a subset of genes, with predicted functions in transcription, protein synthesis, primary or secondary metabolism, or of unknown function, were monitored in spores and germinating spores and during interactions with roots of wild-type or mycorrhiza-defective (Myc$^-$) mutants of *M. truncatula.* Not all the fungal genes were active in quiescent spores but all were expressed when *G. intraradices* spores germinated in wild-type *M. truncatula* root exudates or when appressoria or arbuscules were formed in association with wild-type *M. truncatula* roots. Most of the fungal genes were upregulated or induced at the stage of appressorium development. Inactivation of the *M. truncatula* genes *DMI1*, *DMI2/MtSYM2*, or *DMI3/MtSYM13* was associated with altered fungal gene expression (nonactivation or inhibition), modified appressorium structure, and plant cell wall responses, providing first evidence that cell processes modified by symbiosis-related plant genes impact on root interactions by directly modulating AM fungal activity.

Arbuscular mycorrhiza (AM) associations, which have probably existed since the Ordovician/Devonian period (Redecker et al. 2000), today represent a ubiquitous symbiosis between roots of the large majority of land plants and fungi belonging to the division Glomeromycota (Krings et al. 2007; Schüßler et al. 2001). Plants rely on AM fungi to facilitate uptake of mineral nutrients from the soil, especially phosphate, and, in return, the fungal partner receives photosynthetically fixed carbon (Smith and Read 1997). The biotrophic interfaces that are formed between plant and fungal cells must result from coordinated developmental programs in both partners and provide specialized platforms for the exchange not only of metabolites but also of molecular information (Gianinazzi-Pearson 1996; Harrison 1998). An extensive list of plant genes that are predicted to be regulated during AM interactions has become available from high-throughput transcriptome profiling (Feddermann et al. 2008; Frenzel et al. 2005; Gianinazzi-Pearson et al. 2004, 2006; Güimil et al. 2005; Hohnjec et al. 2005; Journet et al. 2002; Küster et al. 2004, 2007; Liu et al. 2003, 2007; Manthey et al. 2004; Massoumou et al. 2007; Siciliano et al. 2007), but comparatively few fungal genes have been identified (Balestrini and Lanfranco 2006; Breuninger and Requena 2004; Ferrol et al. 2004) and little knowledge exists about signaling processes between symbionts in AM, the pathways leading to symbiosis-specific development of AM fungi in root tissues, or mechanisms of subsequent nutrient exchange between them (Balestrini and Lanfranco 2006; Gianinazzi-Pearson et al. 2007; Krajinski and Frenzel 2007; Requena et al. 2007; Séjalon-Delmas et al. 2007).

The life cycle of AM fungi comprises several well-defined developmental stages for which the genetic determinants are still unknown: spore germination, presymbiotic hyphal growth, appressorium formation at the host surface, root penetration, proliferation in internal cortical tissues with differentiation of intracellular arbuscules, and formation of an extraradical mycelium where spores are generated (Harrison 1998; Hause and Fester 2005). Gene expression analyses of these different events is hampered by the fact that AM fungi are obligate biotrophs that cannot be cultured in the absence of root tissues, and by the low abundance of fungal transcripts that can be extracted from colonized root tissues, especially at early time points of mycorrhiza development (Maldonado-Mendoza et al. 2002). In spite of this, there is some evidence for the existence of host plant influences on fungal gene activity both prior to and following root colonization.

Most studies report AM fungal gene activation in intraradical or extraradical mycelium and this relates principally to processes of cell wall synthesis, nutrient metabolism, or membrane transport (Ferrol et al. 2004). For example, two chitin synthase genes of *Gigaspora margarita*, which were not expressed in germinating spores (*GimCHS1* and *GimCHS3*), were found to be induced during mycelium extension in host root tissues (Lanfranco et al. 1999). Isoforms of some genes can vary in

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their expression profiles. This appears to be the case for plasma-membrane H^+-ATPase genes in *Glomus mosseae*, where *GmHA1* is activated in intraradical hyphae, *GmHA2* is expressed in extraradical hyphae (Ferrol et al. 2000), *GmPMA1* is down-regulated in symbiotic tissues, and *GmHA5* is highly induced in both mycorrhizal roots and extraradical hyphae (Requena et al. 2003). On the other hand, expression of the phosphate transporter genes *GvPT* and *GiPT* is only detected in extraradical mycelium of *G. versiforme* (Harrison and van Buuren 1995) and *G. intraradices* (Maldonado-Mendoza et al. 2001), whereas a gene ortholog from *G. mosseae* (*GmosPT*) is significantly expressed in both intraradical and extraradical mycelium (Benedetto et al. 2005). Studying nitrogen transfer in symbiotic tissues, Kaldorf and associates (1998) reported nitrate reductase (*NR*) gene expression in arbuscules while Govindarajulu and associates (2005) showed that a glutamine synthase gene of *G. intraradices* is preferentially expressed in extraradical hyphae, whereas a gene associated with arginine breakdown is more highly expressed in intraradical mycelium. Other genes that have been investigated are, for the most part, constitutively expressed at different developmental stages of the fungal life cycle (Ferrol et al. 2004).

Far less is known about the events prior to root penetration which are controlled by fungal genes involved in plant recognition and signal transduction, or those active in the regulation of hyphal growth arrest and cytoplasm retraction that takes place in the absence of a host root. Host root exudates and strigolactone derivatives induce prolific branching of hyphae developing from germinating spores of AM fungi (Akiyama et al. 2005; Buée et al. 2000; Gianinazzi and Gianinazzi-Pearson 1990; Giovannetti et al. 1996), and upregulation of a number of genes associated with increased cell activity has been detected in *Gigaspora rosea* during this presymbiotic response (Tamasloukht et al. 2003). On the other hand, Requena and associates (2002) have suggested that a gene coding a putative hedgehog protein with GTPase activity (*GmGIN1)* of *Glomus mosseae*, which is mainly expressed during spore germination prior to contact with the plant and completely shut down during symbiosis, could be involved in the signaling cascade controlling growth arrest and further programmed cell death of hyphae in the absence of a signal from the host plant. Development of appressoria is the main host-specific morphogenetic event indicating recognition of a host root surface by fungal hyphae (Giovannetti et al. 1994; Nagahashi and Douds 1997); however, studies of cell processes related to this developmental stage are still very much in their infancy. A recent analysis of transcriptome modifications in germinated sporocarps of *G. mosseae*, triggered in synchrony with appressorium formation on a host root, identified 27 upregulated genes coding proteins with functions in signaling, transduction, general cell metabolism, defense or stress responses, or of unknown function (Breuninger and Requena 2004). Because two of the proteins have a potential role in calcium-based signaling pathways, it was suggested that Ca^{2+} could be involved as a second messenger in the perception of a plant signal leading to appressorium formation.

Plant mutants defective for AM have provided evidence for the existence of a number of genes that control root interactions with symbiotic fungi in *Medicago truncatula*, *Pisum sativum*, *Lotus japonicus*, *Vicia faba*, *Phaseolus vulgaris*, *Melilotus alba*, and *Lycopersicum esculentum* (Borisov et al. 2004; David-Schwartz et al. 2003; Duc et al. 1989; Kistner et al. 2005; Lum et al. 2002; Morandi et al. 2005; Oldroyd and Downie 2004). In *M. truncatula*, three symbiosis-related (SR) genes have been identified: *DMI1* (coding a putative nuclear channel protein) (Ané et al. 2004; Riely et al. 2007), *DMI2/MtSYM2* (coding a receptor like leucine-rich kinase) (Endre et al. 2002; Stracke et al. 2002), and *DMI3/MtSYM13* (coding a nuclear calcium/calmodulin-dependent protein kinase) (Lévy et al. 2004; Mitra et al. 2004; Oldroyd and Downie 2006). Orthologs of these three SR genes are upregulated when calcium responses are elicited in soybean cells by *Gigaspora margarita* (Navazio et al. 2007a). Inactivation of *DMI3/MtSYM13* results in the nonperception of AM fungal signals (Weidmann et al. 2004) and mutation of the pea ortholog *PsSYM9/30* leads to activation of plant defense responses to the symbiotic fungi (Gollotte et al. 1993; Ruiz-Lozano et al. 1999). Furthermore, induction of cytoskeletal endoplasmic reticulum rearrangements in response to appressorium formation is impaired in *M. truncatula* mutated for the genes *DMI2/MtSYM2* or *DMI3/MtSYM13* (Genre et al. 2005). These observations infer that the SR plant genes are involved in fungal recognition and in the implementation of root cell responses essential to mycorrhiza development. However, it cannot be excluded that cell processes modified by SR plant genes may also impact on root interactions by directly modulating AM fungal activity, but this has not so far been investigated.

In order to test this hypothesis and so gain better insight into molecular processes determining compatible interactions essential to AM establishment, we have monitored expression of selected *Glomus intraradices* genes at different stages of the fungal cycle life (quiescent or germinating spores, appressoria, and intraradicular mycelium) and determined how they are influenced by inactivation of *M. truncatula* SR genes. Mutation of *DMI1*, *DMI2/MtSYM2*, or *DMI3/MtSYM13* resulted in cell wall reactions to the AM fungus and in differential nonactivation or repression of fungal genes at the stage of spore germination or appressorium formation on the root surface of *M. truncatula* suggesting that, in addition to fungal signal perception, SR plant genes are involved in symbiotic processes modulating AM fungal activity through the production of stimulatory plant factors or the control of inhibitory plant reactions.

RESULTS

Selection of *G. intraradices* genes potentially active in mycorrhiza.

Blastn comparisons of partial sequences of 5,051 protein-encoding genes from members of Glomeromycota available in public databases against 3,034 expressed sequence tag (EST) clusters from the MtC *M. truncatula* mycorrhizal root library gave 93 sequences with a score of more than 95% similarity over 100 bp. Fourteen of these sequences were selected on the basis of the predicted function of the corresponding genes (Table 1). Fungal identity was confirmed by polymerase chain reaction (PCR) on genomic DNA from *G. intraradices* spores followed by sequencing, and by the absence of amplification using the corresponding gene primer pair in PCR on cDNA from noninoculated *M. truncatula* roots.

Appressorium development on roots of wild-type and mutant *M. truncatula* genotypes.

Alkaline phosphatase staining detected metabolically active appressoria in contact with roots of wild-type J5 *M. truncatula* from 5 to 9 days after inoculation (dai) and of the three symbiosis-defective mutants from 7 to 11 dai. Thereon, the number of appressoria per centimeter of root formed during the first day of *G. intraradices–M. truncatula* contact (5 dai for the wild-type J5 and 7 dai for the three symbiosis-defective mutants) was not significantly different between the *M. truncatula* genotypes (Table 2). *G. intraradices* penetrated wild-type J5 roots 7 dai and, at 28 dai, the fungus had colonized 44.4 ± 3.2% of the root system of wild-type *M. truncatula* and arbuscules were present in 78.3 ± 5.6% of the mycorrhizal tissues. The shape of appressoria was influenced by the plant geno-

type. Elongated lens-shaped appressoria developed at cell junctions on wild-type J5 (Fig. 1A and B) whereas they had a thicker or ill-defined form on *dmi2/Mtsym2* (Fig. 1G and H) or *dmi3/Mtsym13* (Fig. 1J and K) roots and were frequently surrounded by a layer of translucent material (Fig. 1G, H, and J). Typical fork structure of several appressoria were observed when formed on *dmi3/Mtsym13* roots (Fig. 1K). Appressoria forming on roots of the *dmi1* mutant developed irregular outgrowths (Fig. 1D and E) which did not penetrate the root beyond the epidermis. Plant cell wall modifications were observed below the appressoria. Whereas the epidermal cell walls of wild-type J5 remained thin (Fig. 1C), those of the three symbiosis-defective mutants became thickened (Fig. 1F, I, and L), and stratified in the case of *dmi2/Mtsym2* (Fig. 1I) and *dmi3/Mtsym13* (Fig. 1L), where electron-dense material was frequently deposited at the surface of the fungus.

Transcript accumulation during mycorrhiza development.

Transcript accumulation of the 14 *G. intraradices* genes was monitored by reverse-transcription (RT)-PCR in quiescent spores, appressoria (5 dai), and intraradical mycelium (28 dai). *G. intraradices* large-subunit (LSU) rRNA was included in transcript analyses to ensure equivalent levels of fungal RNA at the different developmental stages (Fig. 2). Gel analysis of RT-PCR products of genes encoding the α subunit of translation elongation factor 1 (*TEF*) and the tubulin α chain (*TUB*) indicated similar transcript levels at each stage of *G. intraradices* development whereas all the other protein-encoding genes presented expression profiles which varied between spores, appressoria, or intraradical mycelium (IRM) (Fig. 2). All the 14 fungal genes were clearly active in IRM and, to different extents, in spores or appressoria (Fig. 2). No transcripts for those coding a 26S proteasome regulatory subunit (*26SREG*), a thio-

Table 1. Putative functions of selected genes of *Glomus intraradices*, cluster identity (ID) in MENS, primer sequences, annealing temperature, and amplicon size

		PCR primers[x]			
Category of protein-encoding genes	**ID MENS**	**Name**	**Sequence**	**Temp (°C)[y]**	**Size (bp)[z]**
Signalling, transcription, protein turnover					
Translation elongation factor1, α subunit (*TEF*)	MtD00004.2_GC	TEF for	AGCCGAACGTGAACGTGG		
		TEF rev	GCACAATCGGCCTGAGAAGTAC	55	247
Rho/GDP dissociation inhibitor (*RHO*)	MtC91640_GC	RHO for	GGAATCAGGGTAGATAAAAC		
		RHO rev	AGTAAATTATTAATCCCAATCC	55	214
60S ribosomal protein (*60SRIB*)	MtC30534_GC	60SRIB for	GAATTCGTATCGACTTTGCG		
		60SRIB rev	GTACGGTATCATCAGATCAC	60	376
Peptidylprolyl isomerase (*PEPISOM*)	MtC00626_GC	PEPISOM for	GATGTTCATGCCGGTAAAAG		
		PEPISOM rev	ACTGGATGAACCCAATGTCT	55	235
26S proteasome subunit (*26S*)	MtC91373_GC	26S for	CACGTGTTTTGCCAACGC		
		26S rev	GCTTCTTCTTCTTCAGTAAC	55	183
26S proteasome regulatory subunit (*26SREG*)	MtC91656_GC	26SREG for	CCTACTTTTGACCGACGTCA		
		26SREG rev	CAGCTTTCTTAACATTGGCT	55	231
Carboxypeptidase precursor (*PRECARB*)	MtC91674_GC	PRECARB for	GCAGCAGAAGATACAAAATG		
		PRECARB rev	CTTATGACCAAGCGTCAG	55	129
Lipid metabolism					
Stearoyl-CoA desaturase (*DESAT*)	MtC91345_GC	DESAT for	TCGTGTTCCTGAAAATGAAG		
		DESAT rev	GCTTTAGTGGAGTCTTTACC	55	269
Antioxidative metabolism					
Thioredoxin peroxidase (*THIO*)	MtC91876_GC	THIO for	GGGAAGCTAAGGCAGTTGTT		
		THIO rev	CGCAATATGAGCGTGATGT	60	214
Cu/Zn Superoxide dismutase (*SOD*)	MtD23013_GC	SOD for	CTGGACCTCATTTTAACCCA		
		SOD rev	CCGATAACACCACAAGCAA	55	273
Cytoskeleton					
Tubulin α chain (*TUB*)	MtC50940_GC	TUB for	CGGTGAAGGTATGGAAGAAG		
		TUB rev	GGC CAC CAA GTC ACG AAA A	60	361
Unknown function					
Hypothetical protein (vacuolar import) (*H*)	MtC91226_GC	H for	CGCTCCGAACTTTTATGGAA		
		H rev	CCGAGGACTATCCTGAGTT	55	345
Unknown 1 (*U1*)	MtC00279_GC	U1 for	CGCGTAACCCACTATTTAAGTG		
		U1 rev	CCAACTTTTGCAACTTTA CCG	60	285
Unknown 2 (*U2*)	MtC30486_GC	U2 for	AGGCACCTCATGAAACGCTG		
		U2 rev	GTAATCTCGTCAAAGATCACG	60	521
Ribosomal RNA					
Large subunit rRNA (*LSU rRNA*)		LR1	GCATATCAATAAGCGGAGGA		
		8.24	CGATCAGAGACCAGACAGGT	60	659

[x] PCR = polymerase chain reaction, for = forward, and rev = reverse.
[y] Annealing temperature.
[z] Amplicon size.

Table 2. Number of alkaline phosphatase stained appressoria formed on the four *Medicago truncatula* genotypes between 5 and 11 days after inoculation (dai) with *Glomus intraradices*[z]

***M. truncatula* genotype**	**5 dai**	**6 dai**	**7 dai**	**8 dai**	**9 dai**	**10 dai**	**11 dai**
J5	5.14 a	5.66 a	5.5 a	5.14 a	4.59 a	n.d.	n.d.
dmi1	0	0	5.83 a	6.26 b	9.22 d	7.42 c	7.38 c
dmi2/Mtsym2	0	0	5.61 a	5.65 a	6.17 a	5.92 a	5.74 a
dmi3/Mtsym13	0	0	5.79 a	6 a	6.22 a	4.5 b	3.22 c

[z] Values in lines followed by the same letter are not significantly different ($P = 0.005$) using one-way analysis of variance and Tukey's pairwise comparisons test with PAST (homogeneity of variance was tested with Levene's test); n.d. = not detected.

redoxin peroxidase (*THIO*), or two unknown proteins (*U1* and *U2*) were detected in spores (Fig. 2), whereas they were induced in appressoria and IRM. Twelve genes were upregulated in intraradical mycelium compared with spores. Expression of *26S*, *26SREG*, *PRECARB*, *U1*, and *U2* showed marked increases in intraradicular mycelium compared with appressoria (Fig. 2).

Effect of host plant genotype on fungal gene expression.

G. intraradices gene expression was analyzed by real-time RT-PCR in quiescent spores, in germinating spores elicited by root exudates, and at the appressorium stage in interactions with roots of wild-type J5 *M. truncatula* and the symbiosis-defective mutants *dmi1*, *dmi2/Mtsym2*, or *dmi3/Mtsym13*. Com-

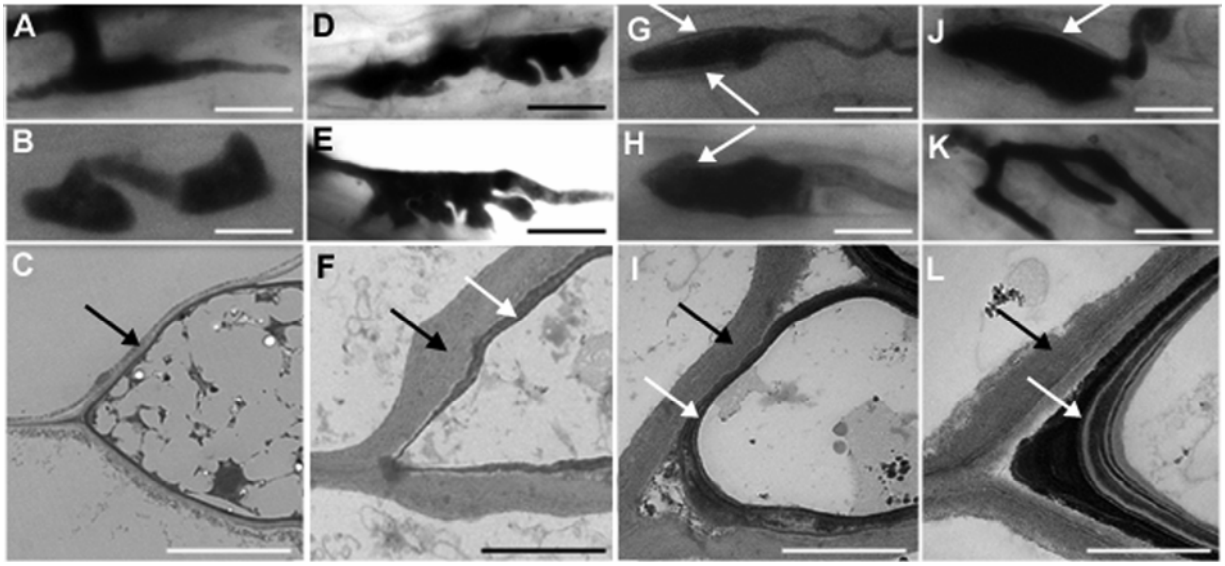

Fig. 1. Development of appressoria of *Glomus intraradices* on roots 7 days after inoculation of **A, B,** and **C,** wild-type J5; **D, E,** and **F,** *dmi1*; **G, H,** and **I,** *dmi2/Mtsym2*; and **J, K,** and **L,** *dmi3/Mtsym13* genotypes of *Medicago truncatula*. A, B, D, E, G, H, J, and K present appressoria stained for alkaline phosphatase activity; arrows indicate translucent material surrounding appressoria. Bar = 10 μm. C, F, I, and L are micrographs of sections through appressoria developing at cell junctions on the root surface; arrows indicate wall thickenings (black) and electron dense deposits (white). Bar = 1 μm.

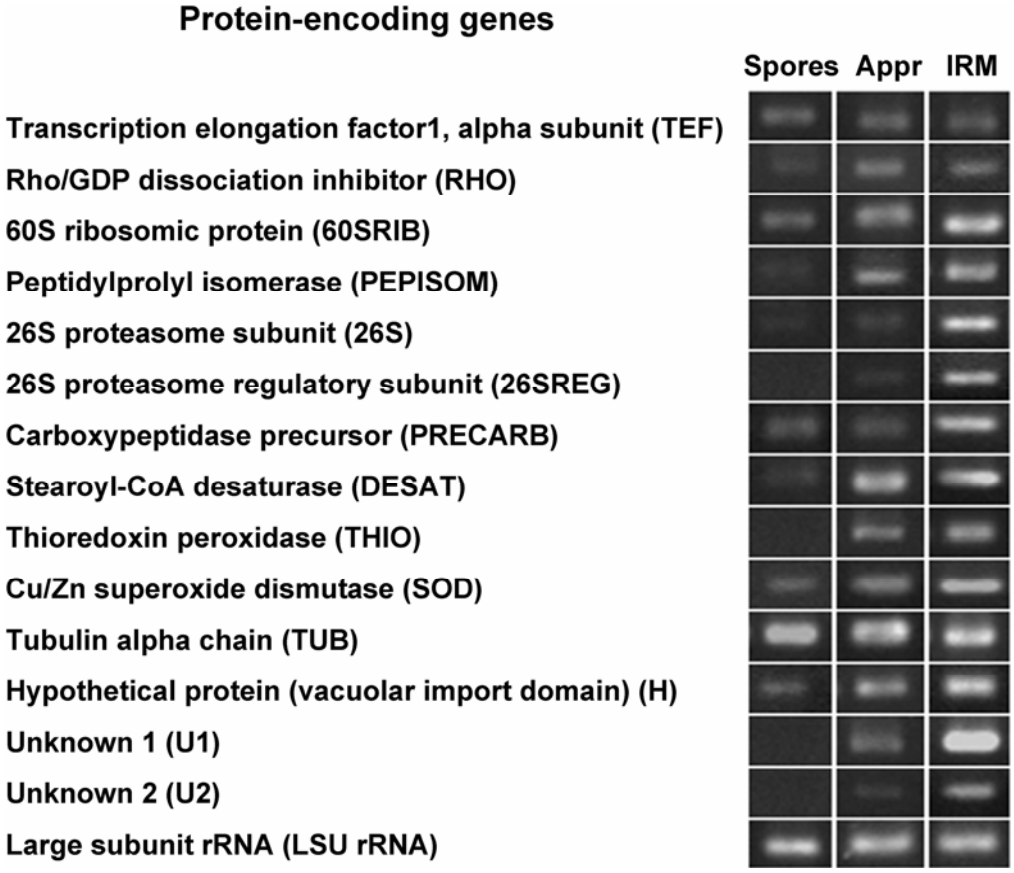

Fig. 2. Transcript accumulation of *Glomus intraradices* genes in spores, appressoria (Appr), and intraradical mycelium (IRM) when fungus developed in contact with J5 roots. Reverse-transcription polymerase chain reaction (RT-PCR) was performed on total RNA with specific primers for each gene and with 26 PCR cycles. PCR products separated by gel electrophoresis were stained with ethyl bromide.

parisons were made at 7 dai for the mutants and at 5 dai on roots of the genotype J5 after first appressoria formation and before root penetration (described above). The same amount of RNA and number of SMART cycles for cDNA synthesis were used for root extracts of the four inoculated plant genotypes and for extracts from germinated spores elicited by root exudates. Gene expression profiles observed by gel analysis of RT-PCR products were confirmed by real-time RT-PCR in quiescent spores and in appressoria developing at the root surface of wild-type J5 *M. truncatula* using the *TEF* gene as a constitutive reference gene, and all data for transcript levels of the *G. intraradices* candidate genes were normalized against values for the *TEF* gene.

Effect of root exudates on gene expression during spore germination.

Transcripts of most of the studied genes were detected in quiescent spores of *G. intraradices*, except those corresponding to *26SREG*, *THIO*, *U1*, and *U2* (Table 3). *26SREG* and *U1* were induced during germination of spores in water; *PEPISOM* and *SOD* were upregulated; *THIO* and *U2* remained inactive; *RHO*, *26S*, *PRECARB*, *DESAT*, and *H* were expressed at similar levels; and *60S* was downregulated compared with quiescent spores (Table 3). All fungal genes were expressed in spores germinating in root exudates of wild-type J5 *M. truncatula* but only the genes *RHO*, *60S*, *THIO*, *U1*, and *U2* were elicited compared with water controls (Table 3). When spores germinated in root exudates from the mycorrhiza-defective mutants, a number of fungal genes were downregulated or not expressed compared with wild-type J5 root exudates or water controls. Fungal genes were mostly affected by mutation of the SR plant gene *DMI2/MtSYM2* (eight) and, to a lesser extent, by inactivation of *DMI1* (six) or *DMI3/MtSYM13* (five) (Table 3). In the presence of *dmi1* mutant root exudates, the genes *RHO*, *60S*, *PEPISOM*, and *DESAT* were significantly downregulated, *U1* and *U2* were not expressed, and five genes (*26S*, *PRECARB*, *THIO*, *SOD*, and *H*) were expressed to a level similar to that in wild-type J5 root exudates. In contrast, five genes were not expressed in spores germinating in *dmi2/Mtsym2* root exudates (*26SREG*, *DESAT*, *THIO*, *U1*, and *U2*), three were significantly downregulated (*RHO*, *60S*, and *SOD*), and only four had transcript levels comparable with those germinating in J5 root exudates (*PEPISOM*, *26S*, *PRECARB*, and *H*). The genes *THIO*, *U1*, and *U2* were likewise not expressed in spores germinating in *dmi3/Mtsym13* root exudates, whereas no significant difference was observed for five other genes (*60S*, *26S*, *DESAT*, *SOD*, and *H*) compared with J5 root exudate-incubated spores, except for *PEPISOM* and *PRECARB*, which were significantly upregulated whereas *RHO* and *26SREG* were downregulated.

Gene expression associated with appressorium development.

G. intraradices transcript levels were similar for *26S* and *THIO* genes in appressoria developing on roots of all four genotypes of *M. truncatula* (Table 4). Fungal genes were mostly downregulated or not expressed in contact with roots of the mutants *dmi2/Mtsym2* (seven) or *dmi3/Mtsym13* (six) and, to a lesser extent, with *dmi1* (five) (Table 4). Mutation of the *DMI1* gene of *M. truncatula* decreased or inhibited expression of the *60S*, *PEPISOM*, *DESAT*, *U1*, and *U2* genes in appressoria in much the same way as corresponding root exudates. A more pronounced effect on *G. intraradices* gene expression was observed with appressorium formation on *dmi2/Mtsym2* roots: all the *G. intraradices* genes that were downregulated or not expressed in root exudates of the mutant, compared with wild-type J5 exudate, behaved similarly, except for *THIO*, which is activated and expressed at the same level as in appressoria formed on wild-type J5 such as *SOD*, and *PRECARB*, which is downregulated compared with wild-type J5 roots. When appressoria formed on *dmi3/Mtsym13* roots, the *U1* and *U2* genes were again not expressed; however, no effect on the 60S, PEPISOM, 26S, *26SREG*, *THIO*, and *SOD* genes was observed whereas *RHO*, *PRECARB*, *DESAT*, and *H* were down-

Table 4. Transcripts of *Glomus intraradices* genes (relative to translation elongation factor 1 [*TEF*]) quantified by real-time polymerase chain reaction during appressorium formation on roots of wild-type (J5) and mycorrhiza-defective (Myc⁻) mutant genotypes (*dmi1*, *dmi2/Mtsym2*, and *dmi3/Mtsym13*) of *Medicago truncatula*[z]

Gene	J5	*dmi1*	*dmi2/Mtsym2*	*dmi3/Mtsym13*
RHO	6.21 a	6.00 a	3.42 b	3.85 b
60S	7.66 a	6.14 b	6.00 b	8.06 a
PEPISOM	9.34 a	2.68 b	8.22 a	8.26 a
26S	5.91 a	5.69 a	4.99 a	6.11 a
26SREG	4.23 a	4.86 a	0 b	4.31 a
PRECARB	10.04 a	9.97 a	7.75 b	8.19 c
DESAT	9.54 a	0.50 b	0 b	3.00 c
THIO	1.42 a	2.06 a	1.95 a	1.12 a
SOD	3.60 ab	4.00 a	2.13 b	3.00 ab
H	3.62 a	3.36 a	4.43 a	1.96 b
U1	10.31 a	0 b	0 b	0 b
U2	4.86 a	0 b	0 b	0 b

[z] Values in lines followed by the same letter are not significantly different ($P = 0.005$) using one-way analysis of variance and Tukey's pairwise comparisons test with PAST (homogeneity of variance was tested with Levene's test).

Table 3. Transcripts of *Glomus intraradices* genes (relative to translation elongation factor 1 [*TEF*]) quantified by real-time polymerase chain reaction in quiescent spores and spores germinated in water or in root exudates from wild-type J5 and mycorrhiza-defective (Myc⁻) mutant genotypes (*dmi1*, *dmi2/Mtsym2*, and *dmi3/Mtsym13*) of *Medicago truncatula*[z]

Gene	Quiescent	Water	J5	*dmi1*	*dmi2/Mtsym2*	*dmi3/Mtsym13*
RHO (Rho/GDP dissociation inhibitor)	5.39 a	5.29 a	5.78 b	5.39 a	4.73 c	4.65 c
60S	8.95 a	5.79 b	8.81 a	7.25 c	6.69 bc	8.64 a
PEPISOM (peptidylprolyl isomerase)	1.83 a	5.64 b	6.60 b	2.89 a	5.53 b	9.57 c
26S (26S proteasome subunit)	2.66 a	2.12 a	2.43 a	2.41 a	2.53 a	3.19 a
26SREG (26S proteasome regulatory subunit)	0 a	2.12 b	2.51 b	3.71 c	0 a	0.32 a
PRECARB (carboxypeptidase precursor)	5.34 a	5.39 a	5.47 a	5.46 a	5.21 a	6.50 b
DESAT (stearoyl-CoA desaturase)	4.59 a	3.30 ac	3.40 ac	0.51 b	0 b	2.62 c
THIO (thioredoxin peroxidase)	0 a	0 a	1.61 b	2.21 b	0 a	0 a
SOD (Cu/Zn superoxide dismutase)	2.19 a	9.25 b	8.53 b	8.96 b	7.05 c	8.60 b
H (hypothetical protein)	1.29 a	1.26 a	1.26 a	1.32 a	1.34 a	1.36 a
U1 (Unknown 1)	0 a	1.07 b	2.84 c	0 a	0 a	0 a
U2 (Unknown 2)	0 a	0 a	2.38 b	0 a	0 a	0 a

[z] Values in lines followed by the same letter are not significantly different ($P = 0.005$) using one-way analysis of variance and Tukey's pairwise comparisons test with PAST (homogeneity of variance was tested with Levene's test).

regulated compared with appressoria formed on wild-type J5, with root contact.

DISCUSSION

Cell programs of AM fungi must undergo continual adaptation during the different developmental stages leading to the formation and functioning of the mycorrhizal symbiosis. Previous studies have mainly focused on modifications in fungal gene expression during colonization of host tissues (Ferrol et al. 2004), and very few have targeted early gene responses to root exudates (Tamasloukht et al. 2003) or gene activation in synchrony with appressorium formation on host roots (Breuninger and Requena 2004). Here, we provide evidence for a role of SR plant genes in the early activation of AM fungal genes putatively implicated in cellular signaling (*RHO*), protein turnover (*60SRIB*, *PEPISOM*, *26S*, *26SREG*, and *PRECARB*), lipid metabolism (*DESAT*), or antioxidative processes (*THIO* and *SOD*), or of unknown function (*H*, *U1*, and *U2*). Most of the modifications in gene responses of *G. intraradices* to *M. truncatula* roots required cell contact (appressorium stage) but root exudates were sufficient to modulate the molecular response of certain fungal genes (activation or inhibition). The response of AM fungi to host-exuded factors during precolonization stages of interactions is a well-described phenomenon (Buée et al. 2000; Gianinazzi and Gianinazzi-Pearson 1990; Giovannetti et al. 1996; Sbrana and Giovannetti 2005; Tamasloukht et al. 2003), although the chemical nature of host compounds acting as recognition and growth-enhancing signals for the fungal symbionts is still poorly defined. Both water-soluble and volatile compounds can be effectors (Buée et al. 2000; Gemma and Koske 1988; Nagahashi and Douds 1999), among which flavonoids and strigolactones have been proposed as candidates (Akiyama et al. 2005; Vierheilig and Piché 2002).

Root exudates of wild-type *M. truncatula* stimulated expression of five genes in germinating spores of *G. intraradices* compared with water. All the genes, except *RHO* and *SOD*, were upregulated when appressoria of *G. intraradices* differentiated in contact with root cells of wild-type *M. truncatula* and all were active in intraradical mycelium. In contrast, most of the *G. intraradices* genes were consistently downregulated or not activated by exudates from or contact with roots of one or other of the symbiosis-defective (mycorrhiza-defective [Myc$^-$]) *M. truncatula* mutants. Fungal gene expression was most affected by mutation of the SR *DMI2/MtSYM2* and *DMI3/MtSYM13* genes and, to a lesser extent, by inactivation of *DMI1*. This implies that the control of SR plant genes over the complex dialogue needed for AM establishment involves modulation of fungal activity in the early stages of interactions even prior to cell contact between the partners. On the plant side, recent work has shown that the mutation of only one plant SR gene can lead to the modulation of several hundred others at the appressorium stage of fungal development. *Medicago* GeneChip (Benedito et al. 2008) transcriptome profiling of *G. intraradices*-inoculated versus noninoculated *M. truncatula* wild-type and symbiosis-defective mutant roots at appressoria formation revealed that, although few encoding transcription factor are modulated in wild-type (7 factors) and *dmi2/Mtsym2* (5 factors) roots, more than 25 and 50 are downregulated in *dmi1* and *dmi3/Mtsym13* mutant roots, respectively (Seddas et al. 2009), Likewise, more genes that are implicated in cellular signalization are modulated in *dmi1* and *dmi3/Mtsym13* mutant roots than in wild-type and *dmi2/Mtsym2* roots. All together, these results underline the very complex molecular mechanisms that must be triggered in the mycorrhizal partners when an AM fungus comes into contact with roots. We can also hypothesize that the delay of 2 days between the formation of appressoria on wild-type roots or on roots of the three symbiosis-defective mutants could be due to a delay of synthesis of a signal molecule in the mutants or to the fact that *G. intraradices* has to activate some specific genes to overcome the inhibitory molecules produced by these mutants.

Some of the *G. intraradices* genes were similarly affected by the *M. truncatula* mutants during both spore germination and root contact. This was the case for the two genes *U1* and *U2* of unknown function which were consistently inactive or downregulated in the presence of all three *M. truncatula* mutants compared with their expression levels in interactions with the wild-type plant genotype. The *M. truncatula* mutants differentially affected the activity of other fungal genes during both spore germination and root contact: *dmi2/Mtsym2* and *dmi3/Mtsym13* downregulated *RHO* whereas *dmi1* and *dmi2/Mtsym2* downregulated *60S* and *DESAT*, *dmi1/Mtsym1* reduced *PEPISOM* expression, and *dmi2/Mtsym2* didn't activate *26SREG* expression. The strong downregulation of the stearoyl-CoA desaturase (*DESAT*) gene of *G. intraradices* suggests modifications in fungal lipid metabolism, and this may also be an element contributing to alterations in fungal development in the presence of the mutant roots. Known fungal fatty acid desaturases are all endoplasmic reticulum (ER) membrane-bound enzymes which have their active site on the ER's cytoplasmic face (Wongwathanarat et al. 1999). The transcription of such a gene, for example in yeast, is influenced by environmental factors such as temperature and exogenous fatty acids (McDonough et al. 1992) and modifications in these enzymes can alter the fatty acid composition of a fungus (Kawashima et al. 1997). PEPISOM, a peptidylprolyl isomerase, plays a role in cellular regulation as a chaperon protein that activates or inhibits regulatory proteins by catalyzing proline isomerization (Miele et al. 2003), while the *26SREG*-regulated proteasome is a protease complex that is responsible for selective degradation of abnormal proteins and naturally short-lived proteins related to metabolic regulation and cell-cycle progression (Murray 1995). The weaker expression of the *RHO* gene, encoding a putative Rho/GDP dissociation inhibitor, could reflect modifications in fungal cell signal events during appressorium development on mutant roots. GTP-binding proteins are active only in the GTP-bound state. GDP-association inhibitors affect the interconversion of GTP (active state) to GDP (inactive state) on Rho/GTPase proteins. Regulation of Rho/GTPase activity, which can be controlled by extracellular signals, is integral to many basic cellular functions such as cell cycle, movement and migration, metabolism, survival, proliferation, and differentiation (Groysman et al. 2002). Furthermore, inhibition of Rho/GTPase activity can result in blocking of calcium mobilization (Groysman et al. 2002) which may be relevant to altered signaling phenomena resulting from inactivation of the SR genes of *M. truncatula*. In contrast, the *PRECARB* gene of *G. intraradices* was only downregulated by root contact with *dmi2/Mtsym2* or *dmi3/Mtsym13*, and the *DESAT* and *H* genes by *dmi3/Mtsym13*.

Genes encoding the oxidative stress response-related proteins thioredoxin peroxidase (THIO) and Cu/Zn superoxide dismutase (SOD) have been previously reported to be active in AM fungi (Brechenmacher et al. 2004; Lanfranco et al. 2005). The *THIO* gene of *G. intraradices* was induced by root exudates of wild-type J5 and *dmi1 M. truncatula*, compared wit spore germinated in water, but this induction was generalized to all the plant genotypes after root contact. In contrast, *SOD* expression was strongly enhanced with spore germination in water and whatever the plant genotype, although transcript levels were lower after root contact, especially in interactions with *dmi2/Mtsym2* roots. These observations suggest that Myc$^-$ mutant roots of *M. truncatula* do not specifically induce a cel-

lular mechanism against oxidative stress in *G. intraradices*, which could eventually protect against incompatible responses preventing root colonization. The *SOD* gene was also found to be expressed at high levels in germinating spores of *Gigaspora margarita* (Lanfranco et al. 2000) and, as for *Glomus intraradices*, during root colonization (Lanfranco et al. 2005). Recently, Seddas and associates (2008) localized *SOD* expression in vesicles but not in arbuscules of *G. intraradices*-colonizing wild-type *M. truncatula* roots.

Whether inactivation of SR genes in *M. truncatula* modifies fungal responses through the lack of a plant signal or secretion of plant inhibitory molecules remains to be elucidated. In relation to the function of SR gene products in the signal transduction pathway after fungal perception, the fact that mutation of *DMI1*, *DMI2*/*MtSYM2*, or *DMI3*/*MtSYM13* results in nonactivation of some AM fungal genes should reflect a role of Ca^{2+} in such recognition events during early steps of symbiosis establishment. In this context, Navazio and associates (2007a and b) have recently shown that soybean cells perceive *G. intraradices* or *Gigaspora margarita* through a Ca^{2+}-mediated signaling response pathway which is not active in nonhost *Arabidopsis thaliana*. More recently, Kosuta and associates (2008) demonstrated that diffusible AM fungal factors activate a rapid calcium response in soybean cell cultures or *M. truncatula* root hair cells before direct fungal contact. Calcium oscillations, which are only induced by branched hyphae in root hair cells, are likely to prime host cells for fungal colonization. The nature of these inductive AM fungal signals (myc factors) is unknown but their perception is dependent on SR plant genes and altered in plant mutants where the fungus is unable to gain entry to epidermal cells (Kosuta et al. 2008; Weidmann et al. 2004). The mutation of SR plant genes could lead to the nonrecognition of the AM fungus through interference with signal exchange processes essential to symbiosis establishment and, subsequently, to the upregulation of plant defense as has been suggested for *Rhizobium* spp. (Niehaus et al. 1998).

Weak or transient plant defense responses during the early stages of AM interactions have been reported in different fungus-plant combinations (Garcia-Garrido and Ocampo 2002; Gianinazzi-Pearson et al. 1996). This phenomenon may result from the low capacity of a symbiotic fungus to trigger defense mechanisms or its ability to suppress or induce suppression of the plant defense system (Garcia-Garrido and Ocampo 2002; Gollotte et al. 1993). Appressoria of *Glomus intraradices* were metabolically active but their shape differed depending on the genotype of *M. truncatula* and they were surrounded by translucent material in the case of *dmi2/Mtsym2* and *dmi3/Mtsym13* mutants. This may correspond to the cell wall thickenings observed beneath appressoria in the symbiosis-defective mutant roots which recalls previous observations where appressoria of *G. mosseae* induced abnormal root cell wall reactions in the *dmi2/Mtsym2* mutant (Calantzis et al. 2001). Incompatible responses to *G. mosseae*, characterized by deposition of wall defense molecules and upregulation of defense-related genes, have also been described in Myc^- pea plants mutated for the *PsSYM9/psSYM30* gene ortholog of *DMI3/MtSYM13* (Gollotte et al. 1993, Ruiz-Lozano et al. 1999). Likewise, another SR plant gene, *LJSYM4*, is necessary in *Lotus japonicus* for correct host cytoskeleton reorganization in the presence of an AM fungus and avoidance of a hypersensitive-like reaction (Genre and Bonfante 2002). Suppression of plant defense responses has been proposed by Niehaus and associates (1993) for symbiotic *Rhizobium* spp.–legume interactions following observations that they can be induced in alfalfa by an asymbiotic *Sinorhizobium meliloti* mutant. Gollotte and associates (1993) have already hypothesized that, in analogy to plant–pathogen interactions, perception of an AM fungal elicitor by host roots could lead to activation of symbiosis genes, the products of which could interact or interfere with the expression of defense genes. Evidence that *M. truncatula* perceives AM fungal signals and that inactivation of SR genes interferes with this recognition process does exist (Genre et al. 2005; Weidmann et al. 2004). If SR gene activity is made redundant through mutation, then plant responses could be modified so that defense mechanisms are no longer suppressed. In this context, the lack of upregulation of antioxidative stress mechanisms involving *SOD* or *THIO* in *G. intraradices* when the SR plant genes are inactivated would contribute to the inability of the fungus to cope with defense responses in the plant mutants.

In conclusion, the cell program of an AM fungus must undergo reorganization in order for the symbiont to accomplish the developmental changes leading to mycorrhiza formation. Flavonoids and strigolactones have been proposed as plant signals that promote presymbiotic AM fungal development but those essential to mycorrhiza establishment still have to be identified, as well as the fungal receptors involved. Conversely, fungal signals (Myc factors) induce gene responses in host roots but the plant receptors are unknown. The present observations on *G. intraradices* gene expression during interactions with wild-type and Myc^- genotypes of *M. truncatula* provide a first indication that SR plant genes regulate AM fungal activity through stimulatory pathways or control of inhibitory factors. The inactivation of SR plant genes may modify fungal signaling events which could interfere with plant perception of the fungal symbiont and thereby impact on its morphological transition from appressorium differentiation to the biotrophic phase of root colonization. A future challenge for research will be to identify the secretome of AM fungi and determine how it is regulated by the SR constituents of the plant genome, because certain secreted fungal proteins could be effectors for processes essential to host–fungus interactions, as recently suggested for the obligate biotrophic pathogen *Uromyces fabae* (Kemen et al. 2005).

MATERIALS AND METHODS

Biological material.

Seed of *M. truncatula* Gaertn. cv. Jemalong, line J5, as well as corresponding *dmi2*/*Mtsym2* (TR25) and *dmi3/Mtsym13* (TRV25) mutants, were provided by G. Duc, URLEG, INRA-Dijon, France, and those of the mutant *dmi1* (Y6) by C. Gough, INRA-Toulouse, France. Seedlings of *M. truncatula* were inoculated or not with *G. intraradices* Smith & Schenck, isolate BEG 141, and grown as described by Weidmann and associates (2004). Briefly, seed were surface sterilized and germinated on 0.7% (wt/vol) Bactoagar (Difco Laboratories, Detroit) for 72 h at 25°C in the dark. Seedlings were used for root exudate production or transplanted individually into a 75-ml sterilized (autoclaved once at 120°C during 7 h) mix of Terragreen (OilDri-US special, Mettman, Germany) and a neutral γ-irradiated clay soil (2:1, vol/vol) for uninoculated plants, or into a 75-ml mix (2:1, vol/vol) of Terragreen and a soil-based inoculum of *G. intraradices* BEG 141, for inoculated plants. Plants were grown under constant conditions (420 $\mu E\ m^{-2}\ s^{-1}$; 24 and 19°C, 16 and 8 h, day and night, respectively; 70% humidity) and received 5 ml of Long Ashton solution without phosphate and a double quantity of nitrate twice a week (Hewitt 1966). Plants were harvested 5 to 11 and 28 dai for the J5 genotype and 5 to 11 dai for the three mutants; roots were washed and immediately stored in liquid nitrogen or stained to estimate the number of metabolically active appressoria on roots or to evaluate mycorrhiza colonization. Extraradical mycelium was manually eliminated under a binocular microscope from roots of J5 plants harvested 28 dai. Appressoria number and

shape were monitored between 5 to 11 dai by digesting root systems from three plants in cellulase and pectinase then staining for alkaline phosphatase activity as described by Tisserant and associates (1993). Mycorrhiza colonization was estimated using the MYCOCALC program after KOH digestion and trypan blue staining according to Weidman and associates (2004).

Root exudates were collected by placing five germinated seedlings of *M. truncatula* in 3 ml of sterile water in a six-well plate (Falcon Multiwell, BD Sciences, San Jose, CA, U.S.A.) under constant conditions (420 μE m^{-2} s^{-1}; 24 and 19°C, 16 and 8 h, day and night, respectively) for 7 days. After elimination of all plant residues, exudates were directly used with spores. Spores of *G. intraradices* BEG 141 were collected from a 6-month-old leek pot culture. Roots were washed under running tap water and lacerated in sterile water using a blender, three times during 1 min at maximum power. The resulting suspension was sieved (63 μm) and spores were collected; surface-disinfected during 10 min using 2% chloramine T, 0.02% streptomycine, 0.02% gentamycine, and 20 μl of Tween20; then rinsed twice with sterile water. After eliminating the seedlings, 2,000 disinfected spores were introduced into the root exudates in each well and incubated for 7 days at 25°C in 2% CO_2. Controls were performed by replacing exudates by 3 ml of sterile water. Germinated spores were collected by centrifugation and immediately used for RNA extraction.

Electron microscopy.

Pieces of roots samples (2 to 3 mm) 5 dai (wild-type) or 7 dai (three symbiosis-defective mutants) were fixed in 2% (vol/vol) glutaraldehyde diluted in 0.2 M cacodylate buffer, pH 7.2, and postfixed for 1 h at 4°C with 1% OsO_4. After gradient series of dehydration, samples were embedded in epoxy resin. Ultrathin (90-nm) sections were used for localizing 1-4, 1-6 polysaccharides with periodic acid and thiocarbohydrazide-silver proteinate PATAG reaction (Gollotte et al. 1993). Ultrathin sections were double contrast with uranyl acetate and lead citrate for normal ultrastructural observations. All ultrathin sections were observed using an Hitachi (Tokyo) electron transmission microscope 7500 at 80 Kv (INRA-CMSE, Centre de Microscopie, Dijon, France).

Expression analyses.

Protein-encoding genes from members of division Glomeromycota were selected from the GenBank public database. A Blastn comparison was performed against EST clusters from *M. truncatula* mycorrhizal roots (Journet et al. 2002) (MENS); 93 sequences with a score of more than 95% similarity over 100 bp were selected as potentially fungal genes, and we selected 14 among them for our study because of their potential function and because they were already active at different levels at the appressoria stage on wild-type roots.

Fungal identity of selected genes was confirmed by PCR on genomic DNA, cloning into the PCR-TOPO vector (Takara Bio, Shiga, Japan) as described by the manufacturer, and sequencing (MWG Biotech, Ebersberg, Germany). Genomic DNA was extracted from 1,000 spores of *G. intraradices* according to the modified protocol of Zézé and associates (1994) described by Gollotte and associates (2006).

DNA-free total RNA was extracted from 2,000 *G. intraradices* quiescent or germinating spores, or from 100 mg of *G. intraradices*-inoculated or noninoculated roots of wild-type J5 *M. truncatula* (5 dai) and symbiosis-defective mutants (7 dai), using the SV total RNA Isolation kit (Promega Corp., Madison, WI, U.S.A.), according to the manufacturer's instructions. RNA was quantified using the Qubit (Invitrogen, Carlsbad, CA, U.S.A.) system. Because of the low abundance of fungal transcripts in spores and inoculated roots, cDNA was prepared from 25 ng (quiescent spores) or 200 ng (germinating spores or plant roots) of total RNA using SMART technology (Takara Bio) in a final volume of 50 μl according to the manufacturer's instructions. long-distance PCR amplification (Takara Bio) was carried out using 10 μl of SMART-cDNA and 18 PCR amplification cycles to obtain DNA in the exponential phase of amplification (Endege et al. 1999; Vernon et al. 2000).

Total RNA was extracted from mycorrhizal (28 dai) and age-equivalent nonmycorrhizal roots of *M. truncatula* J5 according to the method of Franken and Gnädinger (1994), modified as described by Weidmann and associates (2004). RNA quantity and quality were estimated by absorbance at 260 and 280 nm and by electrophoresis in 1% (wt/vol) denaturing agarose gel. cDNA was prepared from 1 μg of total DNAseI-treated (Promega Corp.) RNA using 1.5 μg of oligodT_{15}, 300 U of MMLV reverse transcriptase (EC 2.7.7.49), and 80 U of RNAse inhibitor for 15 min at 25°C followed by 1 h at 42°C and 2 min at 72°C, as described by Weidmann and associates (2004).

Fungal transcript accumulation was monitored at different stages of *G. intraradices* development (quiescent spores, appressoria, and intraradicular mycelium) by RT-PCR. Fungal gene-specific fragments were amplified using primer pairs deduced from EST sequences (Table 1) or using LR1/8.24 (van Tuinen et al. 1998) for LSU rRNA. Amplification was performed in a Biometra thermocycler (Göttingen, Germany) at 94°C for 1 min, followed by 26 cycles at 94°C for 45 s, the appropriate primer annealing temperature for 45 s, 72°C for 45 s, and a final extension at 72°C for 1 min. Amplification products were analyzed by 2% (wt/vol) agarose gel electrophoresis in 0.1 Tris-acetate-EDTA (4 mM Tris, 0.1 mM EDTA, 2 mM acetic acid) (Fluka, St Gallen, Switzerland), stained with ethidium bromide for 10 min and observed using GelDoc EQ apparatus and the QuantityOne-4.5.1 computer program to determine the ratio of *TEF* to *LSU rRNA* transcripts (Bio-Rad Inc., Hercules, CA, U.S.A.).

Absolute quantitative real-time RT-PCR was performed for quiescent or germinating spores and at the appressorium stage of *G. intraradices* development on roots of wild-type J5 or symbiosis-defective *M. truncatula* mutants, according to Güimil and associates (2005). In preliminary experiments, the *LSU rRNA*, *TEF*, and *DESAT* genes were selected to compare expression in quiescent spores using either oligodT_{15} or SMART cDNA fragments. Because statistically comparable expression levels were obtained in both cases, SMART cDNA was used in quantitative real-time RT-PCR to overcome the low abundance of fungal transcripts detected at the appressorium stage. Fungal gene-specific cDNA fragments were amplified by PCR using QuantiTect SYBR GreenPCR mix (Qiagen, Hilden, Germany), the same sets of primers as for RT-PCR (Table 1), and fluorescence was quantified using an ABI PRISM 7900 apparatus (Applied BioSystems, Foster City, CA, U.S.A.). The expression of each gene was assayed in triplicate in a volume of 25 μl containing 1× SYBR green reagent and 1 μM each gene-specific primer pair. After 10 min of denaturation at 95°C, 40 PCR cycles were performed as recommended by the manufacturer (95°C for 15 s, the appropriate primer annealing temperature for 30 s, and 72°C for 30 s). To calculate the number of transcripts present in original samples, plasmid DNA containing each amplicon was prepared using the Macherey-Nagel kit (Macherey-Nagel, Düren, Germany), quantified by UV absorbance spectroscopy, and linearized by restriction enzyme digestion (EC 3.1.21.5) (*Eco*RI for MtBC plasmids [Journet et al. 2002] and *Not*1 for the two Topo plasmids [Promega Corp.]). Standard amplification curves were determined from duplicate samples of plasmid DNA at 10^2, 10^3, 10^4, 10^5, 10^6, and 10^7 copies for each assay. To verify amplifi-

cation of each specific target cDNA, a melting-curve analysis was included at the end of each PCR run according to the thermal profile suggested by the manufacturer (95°C for 15 s, the appropriate primer annealing temperature for 15 s, and 95°C for 15 s). The generated data were analyzed by SDS 2.2 software (Applied Biosystems). For all amplification plots, the baseline data were set with the automatic cycle threshold (C_T) function available with SDS 2.2, by calculating the optimal baseline range and threshold values by using the AutoC_T algorithm (SDS 2.2 User Manual). Candidate-gene expression data from real-time RT-PCR were plotted as $2^{(40\text{-}CT)}/10$, as described by Czechowski and associates (2004), and normalized against the constitutive reference gene determined in this study. According to the manufacturer's instructions, a C_T value of ≥39 corresponds to nonspecific amplification marking the limits of detection, which is equivalent to an expression threshold of 0.2. In order to compare effects of plant genotype on fungal gene expression, gene expression data from real-time RT-PCR obtained with the three mutated plants (*dmi1*, *dmi2/Mtsym2*, and *dmi3/Mtsym13*) were transformed in $\log_2$ for positive values, then plotted against $\log_2$ of fungal gene expression in wild-type J5 *M. truncatula*.

Statistical analysis.

Data from real-time RT-PCR analyses of each fungal gene were compared in replicate RNA batches (three biologically independent experiments) from *G. intraradices* quiescent or germinating spores, or *G. intraradices*-inoculated roots of wild-type J5 *M. truncatula*, or of the three symbiosis-defective mutants and were statistically compared using one-way analysis of variance and Tukey's pairwise comparisons test with PAST (Hammer et al. 2001). Homogeneity of variance was tested with Levene's test.

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LITERATURE CITED

Akiyama, K., Matsuzaki, K., and Hayashi, H. 2005. Plant sesquiterpenes induce hyphal branching in arbuscular mycorrhizal fungi. Nature 435:824-827.

Ané, J.-M., Kiss, G. B., Riely, B. K., Penmetsa, R. V., Oldroyd, G. E. D., Ayax, C., Lévy, J., Debellé, F., Baek, J.-M., Kalo, P., Rosenberg, C., Roe, B. A., Long, S. R., Dénarié, J., and Cook, D. R. 2004. *Medicago truncatula DMI1* required for bacterial and fungal symbioses in legumes. Science 303:1364-1367.

Balestrini, R., and Lanfranco, L. 2006. Fungal and plant gene expression in arbuscular mycorrhizal symbiosis. Mycorrhiza 16:509-524.

Benedetto, A., Magurno, F., Bonfante, P., and Lanfranco, L. 2005. Expression profiles of a phosphate transporter gene (*GmosPT*) from the endomycorrhizal fungus *Glomus mosseae*. Mycorrhiza 15:620-627.

Benedito, V., Torez-Jerez, I., Murray, J., Andriankaja, A., Allen, S., Kakar, K., Wandrey, M., Verdier, J., Zuber, H., Ott, T. Moreau, A., Niebel, A., Frickey, T., Weiller, G., He, J., Dai, X., Zhao, P. X., Tang Y., and Udvardi, M. K. 2008. A gene expression atlas of the model legume *Medicago truncatula.* Plant J. 55:504-513.

Borisov, A. Y., Voroshilova, V. A., Zhukov, V. A., Zhernakov, A. I., Danilova, T. N., Shtark, O. Y., Naumkina, T. S., Tsyganov, V. E., Madsen, L. H., Sanjuan, J., Olivares, J., Priefer, U. B., Ellis, N., Stougaard, J., and Tikhonovich, I. A. 2004. Pea (*Pisum sativum*) regulatory genes controlling development of nitrogen-fixing nodules and arbuscular mycorrhiza. Pages 502-505 in: Biology of Plant–Microbe Interactions, vol 4. I. Tikhonovich, B. Lugtenberg, and N. Provorov, eds. IS-MPMI, St. Paul, MN, U.S.A.

Brechenmacher, L., Weidmann, S., van Tuinen, D., Chatagnier, O., Gianinazzi, S., Franken, P., and Gianinazzi-Pearson, V. 2004. Expression profiling of up-regulated plant and fungal genes in early and late stages of *Medicago truncatula–Glomus mosseae* interactions. Mycorrhiza 14:253-262.

Breuninger, M., and Requena, N. 2004. Recognition events in AM symbiosis: Analysis of fungal gene expression at the early appressorium stage. Fungal Gen. Biol. 41:794-804.

Buée, M., Rossignol, M., Jauneau, A., Ranjeva, R., and Bécard, G. 2000. The pre-symbiotic growth of arbuscular mycorrhizal fungi is induced by a branching factor partially purified from plant root exudates. Mol. Plant-Microbe Interact. 13:693-698.

Calantzis, C., Morandi, D., Arnould, C., and Gianinazzi-Pearson, V. 2001. Cellular interactions between *G. mosseae* and a Myc$^-$ *dmi2* mutant in *Medicago truncatula*. Symbiosis 30:97-108.

Czechowski, T., Bari, R. P., Stitt, M., Scheible, W. R., and Udvardi, M. K. 2004. Real-time RT-PCR profiling of over 1400 *Arabidopsis* transcription factors: Unprecedented sensitivity reveals novel root- and shoot-specific genes. Plant J. 38:366-379.

David-Schwartz, R., Gadkar, V., Wininger, S., Bendov, R., Galili, G., Levy, A. A., and Kapulnik, Y. 2003. Isolation of a premycorrhizal infection (*pmi2*) mutant of tomato, resistant to arbuscular mycorrhizal fungal colonization. Mol. Plant-Microbe Interact. 16:382-388.

Duc, G., Trouvelot, A., Gianinazzi-Pearson, V., and Gianinazzi, S. 1989. First report of non-mycorrhizal plant mutants (Myc$^-$) obtained in pea (*Pisum sativum* L.) and faba bean (*Vicia faba* L.). Plant Sci. 60:215-222.

Endege, W., Steinmann, K., Boardman, L., Thibodeau, S., and Schlegel, R. 1999. Representative cDNA libraries and their utility in gene expression profiling. Biotechniques 26:542-547.

Endre, G., Kereszt, A., Kevei, Z., Mihacea, S., Kalo, P., and Kiss, G. B. 2002. A receptor kinase gene regulating symbiotic nodule development. Nature 417:962-966.

Feddermann, N., Boller, T., Salzer, P., Elfstrand, S., Wiemken, A., and Elfstrand, M. 2008. *Medicago truncatula* shows distinct patterns of mycorrhiza-related gene expression after inoculation with three different arbuscular mycorrhizal fungi. Planta 227:671-680.

Ferrol, N., Barea, J. M., and Azcon-Aguilar, C. 2000. The plasma membrane H^+-ATPase gene family in the arbuscular mycorrhizal fungus *Glomus mosseae*. Curr. Genet. 37:112-118.

Ferrol, N., Azcon-Aguilar, C., Bago, B., Franken, P., Gollotte, A., Gonzalez-Guerrero, M., Harrier, L. A., Lanfranco, L., van Tuinen, D., and Gianinazzi-Pearson, V. 2004. Genomics of arbuscular mycorrhizal fungi. Pages 379-403 in: Applied Mycology & Biotechnology, Vol. 4. Fungal Genomics, Elsevier Science B.V., St. Louis.

Franken, P., and Gnädinger, F. 1994. Analysis of parsley arbuscular endomycorrhiza: Infection development and mRNA Level of defense-related genes. Mol. Plant-Microbe Interact. 7:612-620.

Frenzel, A., Manthey, K., Perlick, A. M., Meyer, F., Puhler, A., Kuster, H., and Krajinski, F. 2005. Combined transcriptome profiling reveals a novel family of arbuscular mycorrhizal-specific *Medicago truncatula* lectin genes. Mol. Plant-Microbe Interact. 18:771-782.

Garcia-Garrido, J. M., and Ocampo, J. A. 2002. Regulation of the plant defence response in arbuscular mycorrhizal symbiosis. J. Exp. Bot. 53:1377-1386.

Gemma, J. N., and Koske, R. E. 1988. Pre-infection interactions between colonization of *Allium porrum* (leek) roots and the mycorrhizal fungus *Gigaspora gigantea*: Chemotropism of germ tubes and root growth response. Trans. Br. Mycol. Soc. 91:123-132.

Genre, A., and Bonfante, P. 2002. Epidermal cells of a symbiosis-defective mutant of *Lotus japonicus* show altered cytoskeleton organisation in the presence of a mycorrhizal fungus. Protoplasma 219:43-50.

Genre, A., Chabaud, M., Timmers, T., Bonfante, P., and Barker, D. G. 2005. Arbuscular mycorrhizal fungi elicit a novel intracellular apparatus in *Medicago truncatula* root epidermal cells before infection. Plant Cell 17:3489-3499.

Gianinazzi, S., and Gianinazzi-Pearson, V. 1990. Cellular interactions in vesicular-arbuscular endomycorrhizae: The host's point of view. Pages 127-131 in: Endocytobiology 4. P. Nardon, V. Gianinazzi-Pearson, A. M. Grenier, L. Margulis, and D. C. Smith, eds. INRA, Paris.

Gianinazzi-Pearson, V. 1996. Plant cell responses to arbuscular mycorrhizal fungi: Getting to the roots of the symbiosis. Plant Cell 8:1871-1883.

Gianinazzi-Pearson, V., Dumas-Gaudot, E., Gollotte, A., Tahiri-Alaoui, A., and Gianinazzi, S. 1996. Cellular and molecular defence-related root responses to invasion by arbuscular mycorrhizal fungi. New Phytol. 133:45-57.

Gianinazzi-Pearson, V., Brechenmacher, L., Weidmann, S., Sanchez, L., Küster, H., Gianinazzi, S., and van Tuinen, D. 2004. Molecular dialogue in arbuscular mycorrhiza: Exploring the symbiotic cell programme. Pages 453-459 in: Biology of Plant-Microbe Interactions, Vol. 4. I. Tikhonovich, B. Lugtenberg, and N. Provorov, eds. IS-MPMI, St. Paul, MN, U.S.A.

Gianinazzi-Pearson, V., Weidmann, S., Seddas, P., Massoumou, M., van Tuinen, D., and Gianinazzi, S., 2006. Signal-related gene responses in beneficial root interactions with non-rhizobial microorganisms. Pages 516-524 in: Biology of Plant-Microbe Interactions, vol. 5. F. Sanchez, C. Quinto, and O. Geiger. eds. IS-MPMI, St. Paul, MN, U.S.A.

Gianinazzi-Pearson, V., Séjalon-Delmas, N., Genre, A., Jeandroz, S., and Bonfante, P. 2007. Plants and arbuscular mycorrhizal fungi: Cues and communication in the early steps of symbiotic interactions. Adv. Bot. Res. 46:181-219.

Giovannetti, M., Sbrana, C., and Logi, C. 1994. Early processes involved in host recognition by arbuscular mycorrhizal fungi. New Phytol. 127:703-709.

Giovannetti, M., Sbrana, C., Citernesi, A. S., and Avio, L. 1996. Analysis of factors involved in fungal recognition responses to host-derived signals by arbuscular mycorrhizal fungi. New Phytol. 133:65-71.

Gollotte, A., Gianinazzi-Pearson, V., Giovannetti, M., Sbrana, C., Avio, L., and Gianinazzi, S. 1993. Cellular localization and cytochemical probing of resistance reactions to arbuscular mycorrhizal fungi in a 'locus A' myc⁻ mutant of *Pisum sativum* (L.). Planta 191:112-122.

Gollotte, A., L'Haridon, F., Chatagnier, O., Wettstein, G., Arnould, C., van Tuinen, D., and Gianinazzi-Pearson, V. 2006. Repetitive DNA sequences include retrotransposons in genomes of the Glomeromycota. Genetica 128:455-469.

Govindarajulu, M., Pfeffer, P. E., Jin, H., Abubaker, J., Douds, D. D., Allen, J. W., Bücking, H., Lammers, P. J., and Shachar-Hill, Y. 2005. Nitrogen transfer in the arbuscular mycorrhizal symbiosis. Nature 435:819-823.

Groysman, M., Hornstein, I., Alcover, A., and Katzav, S. 2002. Vav1 and Ly-GDI Two regulators of Rho GTPases, function cooperatively as signal transducers in T cell antigen receptor-induced pathways. J. Biol. Chem. 277:50121-50130.

Güimil, S., Chang, H.-S., Zhu, T., Ssesma, A., Osbourn, A., Roux, C., Loannidis, V., Oakeley, E. J., Docquier, M., Descombes, P., Briggs, S. P., and Paszkowski, U. 2005. Comparative transcriptomics of rice reveals an ancient pattern of response to microbial colonization. Proc. Nat. Acad. Sci. U.S.A. 102:8066-8070.

Hammer, Ø., Harper, D. A. T., and Ryan, P. D. 2001. PAST: Paleontological Statistics Software Package for Education and Data Analysis. Palaeontologia Electronica 4. Published online.

Harrison, M. J. 1998. Development of the arbuscular mycorrhizal symbiosis. Curr. Opin. Plant Biol. 1:360-365.

Harrison, M. J., and van Buuren, M. L. 1995. A phosphate transporter from mycorrhizal fungus *Glomus versiforme*. Nature 378:626-629.

Hause, B. and Fester, T. 2005. Molecular and cell biology of arbuscular mycorrhizal symbiosis. Planta 221:184-196.

Hewitt, E. J. 1966. Sand and Water Culture Methods used in Studies of Plant Nutrition. Commonwealth Agricultural Bureau, London.

Hohnjec, N., Vieweg, M. E., Puhler, A., Becker, A., and Kuster, H. 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.

Journet, E. P., van Tuinen, D., Gouzy, J., Crespeau, H., Carreau, V., Farmer, M. J., Niebel, A., Schiex, T., Jaillon, O., Chatagnier, O., Godiard, L., Micheli, F., Kahn, D., Gianinazzi-Pearson, V., and Gamas, P. 2002. Exploring root symbiotic programs in the model legume *Medicago truncatula* using EST analysis. Nucleic Acid Res. 30:5579-5592.

Kaldorf, M., Schmelzer, E., and Bothe, H. 1998. Expression of maize and fungal nitrate reductase genes in arbuscular mycorrhiza. Mol. Plant-Microbe Interact. 11:439-448.

Kawashima, H., Nishihara, M., Hirano, Y., Kamada, N., Akimoto, K., Konishi, K., and Shimizu, S. 1997. Production of 5,8,11-eicosatrienoic acid (Mead acid) by a (Delta) 6 desaturation activity-enhanced mutant derived from a (Delta) 12 desaturase-defective mutant of an arachidonic acid-producing fungus, *Mortierella alpina* 1S-4. Appl. Environ. Microbiol. 63:1820-1825.

Kemen, E., Kemen, A. C., Rafiqi, M., Hempel, U., Mengden, K., Hahn, M., and Voegele, R. T. 2005. Identification of a protein from rust fungi transferred from haustoria into infected plant cells. Mol. Plant-Microbe Interact. 11:1130-1139.

Kistner, C., Winzer, T., Pitzschke, A., Mulder, L., Sato, S., Kaneto, T., Tabata, S., Sandal, N., Stougaard, J., Webb, K. J., Szczyglowski, K., and Parniske, M. 2005. Seven *Lotus japonicus* genes required for transcriptional reprogramming of the root during fungal and bacterial symbiosis. Plant Cell 17:2217-2229.

Kosuta, S., Hazledine , S., Sun, J., Miwa, H., Morris, R. J., Downie, J. A. and Oldroyd, G. E. D. 2008. Differential and chaotic calcium signatures in the symbiosis signalling pathway of legumes. Proc. Natl. Acad. Sci. U.S.A. 105:9823-9828.

Krajinski, F., and Frenzel, A. 2007. Towards the elucidation of AM-specific transcription in *Medicago truncatula*. Phytochemistry 68:75-81.

Krings, M., Taylor, T. N., Hass, H., Kerp, H., Dozler, N., and Hermsen, E. J. 2007. Fungal endophytes in a 400-million-yr-old land plant: Infection pathways, spatial distribution, and host responses. New Phytol. 174:648-657.

Küster, H., H. N., Krajinski, F., El Yahyaoui, F., Manthey, K., Gouzy, J., Dondrup, M., Meyer, F., Kalinowski, J., Brechenmacher, L., van Tuinen, D., Gianinazzi-Pearson, V., Pühler, A., Gamas, P., and Becker, A. 2004. Construction and validation of c-DNA-based Mt6k-RIT macro- and microarrays to explore root endosymbioses in the model legume *Medicago truncatula*. J. Biotechnol. 108:95-113.

Küster, H., Vieweg, M. F., Manthey, K., Baier, M., Hohnjec, N., and Perlick, A. 2007. Identification and expression regulation of symbiotically activated legume genes. Phytochemistry 68:8-18.

Lanfranco, L., Vallino, M., and Bonfante, P. 1999. Expression of chitin synthase genes in the arbuscular mycorrhizal fungus *Gigaspora margarita*. New Phytol. 142:347-354.

Lanfranco, L., Gabella, S., and Bonfante, P. 2000. ESTs as a useful tool for studying gene expression in arbuscular mycorrhizal fungi. Pages 108-114 in: Abstract and Papers of the Third International Congress on Symbiosis. H. Weber, S. Imhof, and D. Zeuske, eds. Philipps University of Marburg, Germany.

Lanfranco, L., Novero, M., and Bonfante, P. 2005. The mycorrhizal fungus *Gigaspora margarita* possesses a Cu/Zn superoxide dismutase that is up-regulated during symbiosis with legume hosts. Plant Physiol. 137:1319-1330.

Lévy, J., Bres, C., Geurts, R., Chalhoub, B., Kulikova, O., Duc, G., Journet, E.-P., Ané, J.-M., Lauber, E., Bisseling, T., Dénarié, J., Rosenberg, C., and Debellé, F. 2004. A putative Ca^{2+} and calmodulin-dependent protein kinase required for bacterial and fungal symbioses. Science 303:1361-1364.

Liu, J., Blaylock, L. A., Endre, G., Cho, J., Town, C. D., VandenBosch, K. A., and Harrison, M. J. 2003. Transcript profiling coupled with spatial expression analyses reveals genes involved in distinct developmental stages of an arbuscular mycorrhizal symbiosis. Plant Cell 15:2106-2123.

Liu, J., Maldonado-Mendoza, I., Lopez-Meyer, M., Cheung, F., Town, C. D., and Harrison, M. J. 2007. Arbuscular mycorrhizal symbiosis is accompanied by local and systemic alterations in gene expression and an increase in disease resistance in the shoots. Plant J. 50:529–544.

Lum, M. R., Li, Y., LaRue, T. A., David-Schwartz, R., Kapulnik, Y., and Hirsch. A. M. 2002. Investigation of four classes of non-nodulating white sweet clover (*Melilotus alba* annua Desr.) mutants and their responses to arbuscular-mycorrhizal fungi. Integr. Comput. Biol. 42:295-303.

Maldonado-Mendoza, I. E., Dewbre, G. R., and Harrison, M. J. 2001. A phosphate transporter gene from the extra-radical mycelium of an arbuscular mycorrhizal fungus *Glomus intraradices* is regulated in response to phosphate in the environment. Mol. Plant-Microbe Interact. 14:1140-1148.

Maldonado-Mendoza, I. E., Dewbre, G. R., van Buuren, M. L., Versaw, W. K., and Harrison, M. J. 2002. Methods to estimate the proportion of plant and fungal RNA in an arbuscular mycorrhiza. Mycorrhiza 12:67-74.

Manthey, K., Krajinski, F., Hohnjec, N., Firnhaber, C., Puhler, A., Perlick, A. M., and Kuster, H. 2004. Transcriptome profiling in root nodules and arbuscular mycorrhiza identifies a collection of novel genes induced during *Medicago truncatula* root endosymbioses. Mol. Plant-Microbe Interact. 17:1063-1077.

Massoumou, M., van Tuinen, D., Chatagnier, O., Arnould, C., Brechenmacher, L., Sanchez, L., Selim, S., Gianinazzi, S., and Gianinazzi-Pearson, V., 2007. *Medicago truncatula* gene responses specific to arbuscular mycorrhiza interactions with different species and genera of Glomeromycota. Mycorrhiza 17:223-234.

McDonough, V. M., Stukey, J. E., and Martin, C. E. 1992. Specificity of unsaturated fatty acid regulated expression of *Saccharomyces cerevisiae OLE1* gene. J. Biol. Chem. 267:5931-5936.

Miele, R., Borro, M., Mangoni, M. L., Simmaco, M., and Barra, D. 2003. A peptidylprolyl cis/trans isomerase from *Xenopus laevis* skin: Cloning, biochemical characterization and putative role in the secretion. Peptides 24:1713-1721.

Mitra, R. M., Gleason, C. A., Edwards, A., Hadfield, J., Downie, J. A., Oldroyd, G. E. D., and Long, S. R. 2004. A Ca^{2+}/calmodulin-dependent protein kinase required for symbiotic nodule development: Gene identification by transcript-based cloning. Proc. Natl. Acad. Sci. U.S.A. 101:4701-4705.

Morandi, D., Prado, E., Sagan, M., and Duc, G. 2005. Characterisation of new symbiotic *Medicago truncatula* (Gaertn.) mutants, and phenotypic or genotypic complementary information on previously described mutants. Mycorrhiza 15:283-289.

Murray, A. 1995. Cyclin ubiquitination: The destructive end of mitosis. Cell 81:149-152.
Nagahashi, G., and Douds, D. D., Jr. 1997. Appressorium formation by AM fungi on isolated cell walls of carrot roots. New Phytol. 136:299-304.
Nagahashi, G., and Douds, D. D. Jr. 1999. Rapid and sensitive bioassay to study signals between root exudates and arbuscular mycorrhizal fungi. Biotechnol. Tech. 13:893-897.
Navazio, L., Moscatiello, R., Genre, A., Novero, M., Baldan, B., Bonfante, P., and Mariani, P. 2007a. The arbuscular mycorrhizal fungus *Glomus intraradices* induces intracellular calcium changes in soybean cells. Caryologia 60:137-140.
Navazio, L., Moscatiello, R., Genre, A., Novero, M., Baldan, B., Bonfante, P., and Mariani, P. 2007b. A diffusible signal from arbuscular mycorrhizal fungi elicits a transient cytosolic calcium elevation in host plant cells. Plant Physiol. 144:673-681.
Niehaus, K., Kapp, D., and Pühler, A. 1993. Plant defence and delayed infection of alfalfa pseudonodules induced by an exopolysaccharide (EPS1)-deficient *Rhizobium meliloti* mutant. Planta 19:415-425.
Niehaus, K., Lagares, A., and Pühler, A. 1998. A *Sinorhizobium meliloti* lipopolysaccharide mutant induces effective nodules on the host plant *Medicago sativa* (alfalfa) but fails to establish a symbiosis with *Medicago truncatula*. Mol. Plant-Microbe Interact. 11:906-914.
Oldroyd, G. E. D., and Downie, J. A. 2004. Calcium, kinases and nodulation signalling in legumes. Nat. Rev. 5:566-576.
Oldroyd, G. E. D., and Downie, J. A. 2006. Nuclear calcium changes at the core of symbiosis signalling. Curr. Opin. Plant Biol. 9:351-357.
Redecker, D., Kodner, R., and Graham, L. E. 2000. Glomalean fungi from the Ordovician. Science 289:1920-1921.
Requena, N., Mann, P., Hampp, R., and Franken, P. 2002. Early developmentally regulated genes in the arbuscular mycorrhizal fungus *Glomus mosseae* : Identification of *GmGIN1*, a novel gene with homology to the C-terminus of metazoan hedgehog proteins. Plant Soil 244:129-139.
Requena, N., Breuninger, M., Franken, P., and Ocon, A. 2003. Symbiotic status, phosphate, and sucrose regulate the expression of two plasma membrane H^+-ATPase genes from the mycorrhizal fungus *Glomus mosseae*. Plant Physiol. 132:1540-1549.
Requena, N., Serrano, E., Ocón, A., and Breuninger, M. 2007. Plant signals and fungal perception during arbuscular mycorrhiza establishment. Phytochemistry 68:33-40.
Riely, B. K., Lougnon, G., Ané, J. M., and Cook, D. R. 2007. The symbiotic ion channel homolog DMI1 is localized in the nuclear membrane of *Medicago truncatula*. Plant J. 49:208-216.
Ruiz-Lozano, J. M., Roussel, H., Gianinazzi, S., and Gianinazzi-Pearson, V. 1999. Defense genes are differentially induced by a mycorrhizal fungus and *Rhizobium* sp. in wild-type and symbiosis-defective pea genotypes. Mol. Plant-Microbe Interact. 12:976-984.
Sbrana, C., and Giovannetti, M. 2005. Chemotropism in the arbuscular mycorrhizal fungus *Glomus mosseae*. Mycorrhiza 15:539-545.
Schüßler, A., Schwarzott, D., and Walker, C. 2001. A new fungal phylum, the Glomeromycota: Phylogeny and evolution. Mycol. Res. 105:1413-1421.
Seddas, P. M. A., Arnould, C., Tollot, M., Arias, C. M., and Gianinazzi-Pearson, V. 2008. Spatial monitoring of gene activity in extraradical and intraradical developmental stages of arbuscular mycorrhizal fungi by direct fluorescent *in situ* RT-PCR. Fungal Genet. Biol. 45:1155-1165.
Seddas, P. M. A., Gianinazzi-Pearson, V., Schoefs, B., Küster, H., and Wipf, D. 2009. Communication and signaling in the plant-fungus symbiosis: The mycorrhiza. In: Plant–Environment Interactions from Behavioral Perspective. F. Baluska, ed. Springer Verlag, Berlin, Heidelberg, New York.
Séjalon-Delmas, N., Genre, A., Jeandroz, S., and Bonfante, P. 2007. Plants and arbuscular mycorrhizal fungi: Cues and communication in the early steps of symbiotic interactions. Adv. Bot. Res. 46:181-219.
Siciliano, V., Genre, A., Balestrini, R., Cappellazzo, G., deWit, P. J. G. M., and Bonfante, P. 2007. Transcriptome analysis of arbuscular mycorrhizal roots during development of the prepenetration apparatus. Plant Physiol. 144:1455-1466.
Smith, S. E., and Read, D. J. 1997. Mycorrhiza Symbiosis, 2nd ed. Academic Press, San Diego, CA, U.S.A.
Stracke, S., Kistner, C., Yoshida, S., Mulder, L., Sato, S., Kaneto, T., Tabata, S., Sandal, N., Stougaard, J., Szczyglowski, K., and Parniske, M. 2002. A plant receptor-like kinase required for both bacterial and fungal symbiosis. Nature 417:959-962.
Tamasloukht, M. B., Séjalon-Delmas, N., Kluever, A., Jauneau, A., Roux, C., Bécard, G., and Franken, P. 2003. Root factors induce mitochondrial-related gene expression and fungal respiration during the developmental switch from asymbiosis to presymbiosis in the arbuscular mycorrhizal fungus *Gigaspora rosea*. Plant Physiol. 131:1468-1478.
Tisserant, B., Gianinazzi-Pearson, V., Gianinazzi, S., and Gollotte, A., 1993. In planta histochemical staining of fungal alkaline phosphatase activity for analysis of efficient arbuscular mycorrhizal infection. Mycol. Res. 97:245-250.
van Tuinen, D., Jacquot, E., Zhao, B., Gollotte, A., and Gianinazzi-Pearson, V. 1998. Characterization of root colonization profiles by a microcosm community of arbuscular mycorrhizal fungi using 25S rDNA-targeted nested PCR. Mol. Ecol. 7:879-887.
Vernon, S., Unger, E., Rajeevan, M., Dimulescu, I., and Nisenbaum, R. 2000. Approaches for gene expression profiling with arrays. J. Mol. Diagn. 2:124-127.
Vierheilig, H., and Piché, Y. 2002. Signalling in arbuscular mycorrhiza: Facts and hypotheses. Pages 23-29 in: Flavonoids in Cell Function. B. Buslig and J. Manthey, eds. Kluwer Academi, Plenum Publishers, New York.
Weidmann, S., Sanchez, L., Descombin, J., Chatagnier, O., Gianinazzi, S., and Gianinazzi-Pearson, V. 2004. Fungal elicitation of signal transduction-related plant genes precedes mycorrhiza establishment and requires the *dmi*3 gene in *Medicago truncatula*. Mol. Plant-Microbe Interact. 17:1385-1393.
Wongwathanarat, P., Michaelson, L. V., Carter, A. T., Lazarus, C. M., Griffiths, G., Stobart, A. K., Archer, D. B., and MacKenzie, D. A. 1999. Two fatty acid Δ9-desaturase genes, *ole1* and *ole2*, from *Mortierella alpina* complement the yeast *ole1* mutation. Microbiology 145:2939-2946.
Zézé, A., Dulieu, H., and Gianinazzi-Pearson, V. 1994. DNA cloning and screening of a partial genomic library from an arbuscular mycorrhizal fungus *Scutellospora castanea*. Mycorrhiza 4:251-254.

AUTHOR-RECOMMENDED INTERNET RESOURCES

Institut National de la Recherche Agronomique (INRA) MYCOCALC program: www.dijon.inra.fr/mychintec/Mycocalc-prg/download.html
Medicago EST navigation system (MENS) website: medicago.toulouse.inra.fr/Mt/EST/