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# The *Medicago truncatula* MtRbohE gene is activated in arbusculated cells and is involved in root cortex colonization

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► **To cite this version:**

Simone Belmondo, Cristina Calcagno, Andrea Genre, Alain Puppo, Nicolas Pauly, et al.. The *Medicago truncatula* MtRbohE gene is activated in arbusculated cells and is involved in root cortex colonization. *Planta*, 2016, 243 (1), pp.251-262. 10.1007/s00425-015-2407-0 . hal-02632926

**HAL Id: hal-02632926**

**<https://hal.inrae.fr/hal-02632926v1>**

Submitted on 9 Sep 2024

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**The *Medicago truncatula* MtRbohE gene is activated in arbusculated cells and is involved in root cortex colonization**

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*Original Citation:*

*Availability:*

This version is available <http://hdl.handle.net/2318/1535191> since 2016-08-05T11:13:42Z

*Published version:*

DOI:10.1007/s00425-015-2407-0

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(Article begins on next page)

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5 **Title:** The *Medicago truncatula* *MtRbohE* gene is activated in arbusculated cells and is involved in  
6 root cortex colonization

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23

24 **Main Conclusion**

25 Our study demonstrated that the NADPH oxidase gene *MtRbohE* is expressed in arbusculated cells and  
26 plays a role in arbuscule development.

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29

30 **Abstract**

31 Plant NADPH oxidases, known as respiratory burst oxidase homologs (Rboh), belong to a multigenic  
32 family that plays an important role in the regulation of plant development and responses to biotic and  
33 abiotic stresses. In this study we monitored the expression profiles of five *Rboh* genes (*MtRbohA*,  
34 *MtRbohB*, *MtRbohE*, *MtRbohG*, *MtRbohF*) in the roots of the model species *Medicago truncatula* upon  
35 colonization by arbuscular mycorrhizal fungi. A complementary cellular and molecular approach was  
36 used to monitor changes in mRNA abundance and localize transcripts in different cell types from  
37 mycorrhizal roots. *Rboh* transcript levels did not drastically change in total RNA extractions from  
38 whole mycorrhizal and non mycorrhizal roots. Nevertheless, the analysis of laser microdissected cells  
39 and transgenic roots expressing a GUS transcriptional fusion construct highlighted the *MtRbohE*  
40 expression in arbuscule-containing cells. Furthermore, the down regulation of *MtRbohE* by an RNAi  
41 approach generated an altered colonization pattern in the root cortex, when compared to control roots,  
42 with fewer arbuscules and multiple penetration attempts. Altogether our data indicate a transient up-  
43 regulation of *MtRbohE* expression in cortical cells colonized by arbuscules and suggest a role for  
44 *MtRbohE* in arbuscule accommodation within cortical cells.

45

46 **Keywords:** Arbuscular mycorrhizal symbiosis, NADPH oxidase, *Medicago truncatula*, gene  
47 expression, reactive oxygen species, respiratory burst oxidase homolog

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52 **Introduction**

53 Plants generate reactive oxygen species (ROS) as signaling molecules to control various cellular  
54 mechanisms (Neill et al. 2002; Apel and Hirt 2004). Pharmacological, molecular, and genetic studies  
55 strongly support that the primary source of ROS is a superoxide-generating membrane-bound NADPH  
56 oxidase (Torres and Dangl 2005) that catalyzes the production of superoxide by transferring electrons  
57 from NADPH to molecular oxygen, with secondary generation of H<sub>2</sub>O<sub>2</sub>. Seven mammalian NADPH  
58 oxidase enzymes have been identified and characterized: the best studied member of this family is the  
59 mammalian gp91phox (NOX2), which is responsible for high-level production of superoxide in  
60 phagocytic cells in response to microbial invasion (Aguirre and Lambeth 2010).

61 The NADPH oxidase homologs in plants, designated Rboh (respiratory burst oxidase homolog), are a  
62 family of enzymes, structurally more similar to mammalian calcium-regulated NADPH oxidase NOX5,  
63 which has an N-terminal calcium binding EF-hand motif (Oda et al. 2010; Suzuki et al. 2011; Marino  
64 et al. 2012). *Arabidopsis thaliana* possesses 10 Rboh homologues which differ in their expression  
65 profile and involvement in diverse processes of plant growth and metabolism (Sagi and Fluhr 2006;  
66 Suzuki et al. 2011). Only a few of these genes have been characterized: AtRbohD and AtRbohF are  
67 involved in ROS-dependent abscisic acid signalling in guard cells (Kwak et al. 2003), while AtRbohC  
68 plays a key role in root hair development (Foreman et al. 2003) and AtRbohB in seed germination  
69 (Müller et al. 2009). More recently, ROS production by AtRbohH and AtRbohJ has been clearly shown  
70 to be essential for proper pollen tube tip growth (Kaya et al. 2014).

71 Rboh-dependent superoxide generation by plants in response to microbial pathogen colonization is a  
72 well-known plant defense mechanism. ROS generation is associated to the oxidative burst linked to the  
73 perception of microbe/pathogen-associated molecular patterns and to the hypersensitive response  
74 coupled to the recognition of specific pathogens avirulence factors (Torres et al. 2006; Torres 2010).  
75 The activation of particular Rboh isoforms is responsible for ROS accumulation in several plant-  
76 microbe interactions (Simon-Plas et al. 2002; Torres et al. 2002; Torres and Dangl 2005; Yoshioka et  
77 al. 2003; for review see Torres 2010).

78 The involvement of ROS and Rboh enzymes in the legume-rhizobium symbiotic interaction has also  
79 been proved (for review Puppo et al. 2013). ROS accumulation has been detected in the wall of  
80 infected cells and infection threads, in both early steps of the interaction (Santos et al. 2001; Ramu et  
81 al. 2002; Rubio et al. 2004; Lohar et al. 2006; Peleg-Grossman et al. 2007, 2012) and in mature nodules

82 (Santos et al. 2001; Rubio et al. 2004). Delayed nodulation has also been observed in *Medicago*  
83 *truncatula* inoculated with a catalase-overexpressing *S. meliloti* strain, which acts as a H<sub>2</sub>O<sub>2</sub> scavenger  
84 (Jamet et al. 2007). Recently, *Rboh* genes were shown to regulate the early steps of rhizobial infection  
85 in *Phaseolus vulgaris* (common bean; Montiel et al. 2012) and affect nodule function in *M. truncatula*  
86 (Marino et al. 2011). ROS therefore appear to be produced in response to rhizobial infection, in  
87 association with nodule development, and are essential for optimal symbiosis establishment (Puppo et  
88 al. 2013).

89 Even if the arbuscular mycorrhizal (AM) symbiosis is known to share several cellular and molecular  
90 features with legume nitrogen-fixing symbiosis (Guthjar and Parniske 2013; Venkateshwaran et al.  
91 2013), little is known about ROS and Rboh-related processes in AM associations. Salzer et al. (1999)  
92 provided the first evidence for the accumulation of H<sub>2</sub>O<sub>2</sub> in *M. truncatula*-*Rhizophagus irregularis*  
93 (formerly *Glomus intraradices*) mycorrhizal interaction, in particular in arbuscule-containing cortical  
94 cells, and hypothesized the involvement of a plant plasma membrane NADPH oxidase. H<sub>2</sub>O<sub>2</sub>  
95 production was also observed in roots of *M. truncatula* and *Lotus japonicus* colonized by another AM  
96 fungus, *Gigaspora margarita*. In this case H<sub>2</sub>O<sub>2</sub> accumulation was mainly associated with the fungal  
97 structures and this was mirrored by the up-regulation of a gene encoding a superoxide dismutase in  
98 intraradical fungal structures (Lanfranco et al. 2005). In this frame, Fester and Hause (2005), using  
99 three independent staining techniques, suggested that both AM-colonized root cortical cells and fungal  
100 structures were involved in the H<sub>2</sub>O<sub>2</sub> production.

101 Direct evidence of a specific role for an *Rboh* gene in the AM symbiosis has recently been provided by  
102 Arthikala et al. (2013), who demonstrated, through an RNA interference (RNAi) approach, that  
103 *PvRbohB* negatively regulates AM colonization in *Phaseolus vulgaris*. In line with this, the silencing of  
104 *MtROP9*, a small GTPase considered to be a positive regulator of Rboh enzymes, was shown to  
105 stimulate early mycorrhizal colonization in *M. truncatula* (Kiirika et al. 2012). Nevertheless, many  
106 questions remain open as to the involvement of other Rboh-encoding genes in the AM symbiosis.

107 We here investigated the expression profiles of five *Rboh* genes (*MtRbohA*, *MtRbohB*, *MtRbohE*,  
108 *MtRbohG*, *MtRbohF*) in mycorrhizal roots of the model species *M. truncatula*: we used a  
109 complementary cellular and molecular approach to monitor changes in mRNA abundance and localize  
110 transcripts within different root cell types. Our results show that *MtRbohE* is transiently expressed in  
111 arbusculated cells and has a role in root cortex colonization and arbuscule accommodation.

112 **Materials and Methods**

113

114 Biological materials, growth conditions and inoculation methods

115 *Rhizophagus irregularis* (Syn. *Glomus intraradices*, DAOM 197198) inoculum for seedlings and ROC  
116 (root organ cultures) mycorrhization, was produced through *in vitro* monoxenic cultures. These were  
117 established in bi-compartmental Petri dishes with a watertight plastic wall separating the root  
118 compartment (RC) from the hyphal compartment (HC) (Fortin et al. 2002). The RC was filled with 25  
119 ml of M minimal medium and an explant of transgenic chicory (*Cichorium intybus*) roots colonized  
120 with the AM fungus was added. The HC was filled with 25 ml of solid M Minimal medium lacking  
121 sugar. Once the mycelium of *R. irregularis* had grown over the plastic wall and completely filled the  
122 HC compartment, the medium was dissolved with sterile citrate buffer 10 mM, pH 6.0 (mix 0.018 ml  
123 of citric acid 0.1 M and 0.082 ml of sodium citrate 0.1 M and reach the final volume of 50 ml with  
124 sterile distilled water). Spores were then collected and used for plant colonization.

125 Spores of *Gigaspora margarita* (BEG34) were collected from *Trifolium repens* L. pot cultures.  
126 Aliquots of 100 spores were surface sterilized twice for 10 minutes with 3% chloramine-T and 0.03%  
127 streptomycine sulfate, then rinsed several times with sterile distilled water.

128 To obtain seedlings colonized by *R. irregularis* or *G. margarita* the Millipore sandwich method  
129 (Giovannetti et al. 1993) was used. Seeds of *Medicago truncatula* Gaertn cv Jemalong were first  
130 scarified using sandpaper P180-200, sterilized with 5% commercial bleach for 3 minutes and rinsed  
131 three times for 10 minutes with sterile distilled water. Germination was induced under sterile  
132 conditions in 0.6% agar/water, incubated for 5 days in the dark (25°C) and then exposed at the light for  
133 4 days. Plants were watered with Long-Ashton solution containing a low phosphorus concentration (3.2  
134  $\mu\text{M Na}_2\text{HPO}_4 \cdot 12\text{H}_2\text{O}$ ) (Hewitt 1966) and they were grown in a growth chamber under 14 h light  
135 (24°C)/10 h dark (20°C) regime. Plants were harvested 60 days post-inoculation (dpi). For mycorrhizal  
136 plants, only portions of the root system showing extraradical fungal structures were collected under a  
137 stereomicroscope. The colonization level was assessed according to Trouvelot et al. (1986). For the  
138 molecular analyses, roots were immediately frozen in liquid nitrogen and stored at -80°C.

139 *Agrobacterium rhizogenes*-transformed lines of *M. truncatula* expressing GUS-GFP reporter genes

140 under the promoter of 5 different *Rboh* genes (*MtRbohA*, *MtRbohB*, *MtRbohE*, *MtRbohF* and  
141 *MtRbohG*; Marino et al. 2011) were inoculated with AM fungi. Spores of *R. irregularis* were collected  
142 and placed in Petri dishes containing the transgenic roots and cultured for 2 months at 26°C in the dark.  
143 For *G. margarita* the targeted AM inoculation technique developed by Chabaud et al. (2002) was  
144 chosen since it allows the direct observation of colonization events and easy collection of samples.  
145 Spores were placed in M medium and incubated at 30°C to induce germination. About ten germinated  
146 spores were then transferred to Petri dishes containing three growing *M. truncatula* hairy root explants  
147 and positioned below the growing lateral roots, to facilitate reciprocal contacts. Root cultures were  
148 incubated at 26°C in the dark and vertically oriented. Root and hyphal growth was followed daily under  
149 a stereomicroscope. After inoculation, *G. margarita* germ tubes grew upwards and branched,  
150 contacting root epidermis. Hyphopodia were generally observed after 5 days and first arbuscules were  
151 observed after 10 days. Root fragments surrounded by extraradical mycelium and displaying  
152 hyphopodia were selected under a stereomicroscope, excised and stored at -80°C.

153

154 Nucleic acid extraction and RT-qPCR assays

155 Total genomic DNA was extracted from *R. irregularis* extraradical structures, *G. margarita* spores and  
156 *M. truncatula* leaves using the DNeasy Plant Mini Kit (Qiagen), according to the manufacturer's  
157 instructions. Conventional PCR assay were set up to exclude cross-hybridization of *MtRboh* specific  
158 primers described by Marino et al. (2011) on fungal DNA.

159 Total RNA was isolated from about 20 mg root fragments for hairy roots and about 100 mg for  
160 seedling roots using the RNeasy Plant Mini Kit (Qiagen). Samples were treated with TURBO™ DNase  
161 (Ambion) according to the manufacturer's instructions. The RNA samples were routinely checked for  
162 DNA contamination by RT-PCR analysis, using primers MtTef-f  
163 5'AAGCTAGGAGGTATTGACAAG 3' and MtTef-r 5' ACTGTGCAGTAGTACTTGGTG 3' for  
164 *MtTef* (Vieweg et al. 2005) and the One-Step RT-PCR kit (Qiagen). The *MtPT4* phosphate transporter  
165 gene was amplified using MtPT4F (5'TCGCGCGCCATGTTTGTGT3') and MtPT4R



166 (5'CGCAAGAAGAATGTTAGCCC3') primers. For single-strand cDNA synthesis about 500 ng of  
167 total RNA were denatured at 65°C for 5 min and then reverse-transcribed at 25°C for 10 min, 42°C for  
168 50 min and 70° for 15 min in a final volume of 20 µl containing 10 µ M random primers, 0.5 mM  
169 dNTPs, 4 µl 5X buffer, 2 µl 0.1 M DTT, and 1 µl Super-ScriptII (Invitrogen).

170 qRT-PCR experiments were carried out in a final volume of 20 µl containing 10 µl of Power Sybr  
171 Green PCR master mix (Applied Biosystems), 1 µl of 3 µM *MtRboh* specific primers, and 1 µl of  
172 cDNA. Samples were run in the StepOne Real-Time PCR system (Applied Biosystems) using the  
173 following program: 10 min pre-incubation at 95°C, followed by 40 cycles of 15 s at 95°C, and 1 min at  
174 60°C. Each amplification was followed by melting curve analysis (60°C to 94°C) with a heating rate of  
175 0.3°C every 15 s. All reactions were performed with three technical replicates and only Ct values with  
176 a standard deviation that did not exceed 0.3 were considered. The comparative threshold cycle method  
177 (Rasmussen 2001) was used to calculate relative expression level using the *MtTef* as reference gene.  
178 The analyses were performed on at least three independent biological replicates. Statistical tests were  
179 carried out through one-way analysis of variance (one-way ANOVA) and Tukey's post hoc test, using a  
180 probability level of  $p < 0.05$ .

181

182 Semi-quantitative RT-PCR on laser microdissected cells

183 Roots colonized by *R. irregularis* and uninoculated roots obtained with the millipore sandwich system,  
184 as described above, were dissected into 5-10 mm pieces and treated with ethanol and glacial acetic acid  
185 (3:1) under vacuum for 30 min, then placed at 4°C overnight. Roots were subsequently dehydrated in a  
186 graded series of ethanol (50%-70%-90% in sterilized water and 100% twice) followed by Neoclear  
187 (twice) with each step on ice for 30 min. Neoclear was gradually replaced with paraffin (Paraplast Plus;  
188 Sigma-Aldrich, St. Louis) according to PPlus; Pérez-Tienda et al. (2011). A Leica AS LMD system  
189 (Leica Microsystem, Inc.) was used to collect cortical cells from paraffin root sections as described by  
190 Balestrini et al. (2007).

191 RNA was extracted using the PicoPure kit protocol (Arcturus Engineering) and treated with RNase-free  
192 DNase (Promega Corp., Madison, WI, USA) following the manufacturer's instructions. RNAs were  
193 precipitated using Na-acetate-ethanol, and resuspended in 21  $\mu$ l of sterile water.

194 All RT-PCR assays were carried out using the One Step RT-PCR kit (Qiagen). DNA contaminations  
195 were assessed using the *MiTef* primers described above. RNAs extracted from the three different cell  
196 populations were then calibrated using *MiTef* as housekeeping gene. In detail, reactions were carried  
197 out in a final volume of 25  $\mu$ l containing 5  $\mu$ l of 5X buffer, 1.2  $\mu$ l of 10 mM dNTPs, 0.6  $\mu$ l of each  
198 primer 10 mM, 0.5  $\mu$ l of One Step RT-PCR enzyme mix and 1  $\mu$ l of RNA. Samples were incubated for  
199 30 min at 50°C, followed by 15 min incubation at 95°C. Amplification reactions were run for 40 cycles  
200 of 94°C for 30 sec, 60°C for 30 sec, and 72°C for 40 sec. An aliquot of the PCR reaction was taken  
201 after the 36, 38 and 40 cycles.

202 Reactions with *MiRboh* specific primers (Marino et al. 2011) were carried out in a final volume of 10  
203  $\mu$ l containing 2  $\mu$ l of 5X buffer, 0.4  $\mu$ l of 10 mM dNTPs, 1  $\mu$ l of each primer 10 mM, 0.2  $\mu$ l of One  
204 Step RT-PCR enzyme mix, and 1  $\mu$ l of a total RNA diluted 1:1. The samples were incubated for 30  
205 min at 50°C, followed by 15 min incubation at 95°C. Amplification reactions were run for 40 cycles of  
206 94°C for 30 sec, 60°C for 30 sec, and 72°C for 40 sec. RT-PCR experiments were conducted on two  
207 different biological replicates of 1500-2000 microdissected cells each.

208

209 GUS histochemical assay

210 Root fragments from *Agrobacterium rhizogenes*-transformed lines showing extraradical fungal  
211 structures and hyphopodia were selected under a stereomicroscope, excised and placed in a single wells  
212 of a Multiwell plate and covered with freshly prepared GUS-buffer (0.1 M sodium phosphate buffer pH  
213 7.0, 5 mM  $K_4Fe(CN)_6$ , 5 mM  $K_3Fe(CN)_6$ , 0.3% Triton X, 0.3% x-Gluc). The samples were incubated at  
214 37°C for 16 hours in the dark, destained with distilled water and observed under an optical microscope  
215 (Nikon eclipse E300). Two independent lines were analysed for each construct; GUS assays were

216 conducted on about 20 root fragments for each condition collected from 5 distinct Petri dishes in two  
217 independent colonization experiments.

218

219 RNAi lines

220 A 344-bp cDNA fragment of 3'-UTR of *MtRbohE* (Mt4.0, Medtr8g095520.1) was amplified by PCR  
221 using the following primers: forward 5'-TGAGATAACAGTGAAGG-3' and reverse primer 5'-  
222 TCTCCTGGGACGACTATAA-3' and cloned into the pDNOR207 vector using the BP Gateway  
223 technology (Invitrogen). The resulting vector was recombined with the pK7GWIWG2D(II) vector  
224 (Karimi et al. 2002) using the LR Gateway technology (Invitrogen), according to the manufacturer's  
225 recommendations. The construct was checked by DNA sequencing introduced by electroporation into  
226 *Agrobacterium rhizogenes* strain ARqua1, and used for *M. truncatula* root transformation as previously  
227 described (Medicago handbook). The pK7GWIWG2D(II) empty vector has been used as control. After  
228 2 weeks, transgenic roots were selected under fluorescent microscope (Leica), and transferred on  
229 SHb10 medium (Medicago handbook) supplemented with 200 mg L<sup>-1</sup> augmentin  
230 (amoxicillin:clavulanic acid [5:1]) and 20 mg L<sup>-1</sup> kanamycin (Sigma-Aldrich). Root cultures were  
231 kept at 20°C in the dark and subcultured each 3 weeks on new medium. After 3 subculturing,  
232 augmentin was removed and the level of *MtRbohE* was evaluated by qRT-PCR (Fig. S2).

233

234 Confocal microscopy

235 Mycorrhizal roots were counterstained with 0.01% (w/v) acid fuchsin in lactoglycerol (lactic acid-  
236 glycerol-water, 14:1:1; Kormanik and McGraw 1982) and screened under an optical microscope  
237 (Nikon eclipse E300). Confocal microscopy observations were done using a Leica TCS-SP2  
238 microscope equipped with a 40x long-distance objective. Acid fuchsin fluorescence was excited at  
239 488nm and detected using a 560-680 nm emission window.

240 Alternatively, colonized root segments were excised under a stereomicroscope, rapidly embedded in  
241 8% agarose Type III (Sigma-Aldrich) and cut into 100 µm-thick longitudinal sections using a  
242 Vibratome 1000 microtome. Sections were stained with FITC-labelled wheat germ agglutinin to mark  
243 the fungal cell wall and imaged in confocal microscopy. FITC fluorescence was excited at 488 nm and  
244 recorded at 500-550 nm. Transmitted light images were acquired concomitantly and overlaid to the  
245 fluorescence images through the Leica Confocal Software.

246

## 247 **Results**

248

### 249 *MtRbohE* is upregulated in arbuscule-containing cells

250 To analyse *Rboh* gene expression profiles in *Medicago truncatula* arbuscular mycorrhizas we focused  
251 our attention on five genes, *MtRbohA*, *MtRbohB*, *MtRbohE*, *MtRbohF* and *MtRbohG*, since they were  
252 shown to be expressed in the *M. truncatula* root system by Marino et al. (2011). To this purpose qRT-  
253 PCR assays were first set up on fresh biological material obtained from whole roots of seedlings  
254 inoculated in the semi-sterile sandwich system with *Rhizophagus irregularis* (DAOM 197198) over a  
255 time course of 7, 14, 28 and 60 days post-inoculation (dpi). Morphological analyses of roots revealed  
256 almost no fungal structures at 7 or 14 dpi, while mycorrhization frequency increased from 28 to 60 dpi.  
257 Arbuscules were detected starting from 28 dpi while decreased at 60 dpi (Table 1). These data were  
258 confirmed by molecular analyses showing the parallel accumulation of *MtPT4* mRNA, the *M.*  
259 *truncatula* phosphate transporter which is considered a molecular marker for functional arbuscules  
260 (Harrison et al. 2002; Fig. 1a).

261 Specific primers designed for *MtRboh* genes (Marino et al. 2011) were first tested on *M. truncatula*  
262 DNA as a positive control and also on *R. irregularis* genomic DNAs to exclude any cross-  
263 hybridization. All the primers amplified a DNA fragment of the expected size from *M. truncatula*  
264 genomic DNA while no signal was detected from fungal DNA (data not shown). The *M. truncatula*  
265 *MtTef* was used as a housekeeping gene for the normalization of the *Rboh* expression levels. Among  
266 the 5 genes *MtRbohG* showed the highest expression levels in all the samples and slight fluctuations  
267 between control and mycorrhizal roots along the 4 time points. Almost no significant variation in  
268 transcripts abundance for the other genes (*MtRbohA*, *MtRbohB*, *MtRbohE*, and *MtRbohF*) was observed  
269 in most of the time points (Fig. 1b).

270 Since the AM colonization is an asynchronous process, whole roots analyses may hinder expression  
271 patterns limited to specific tissues or cell sub-populations (Balestrini et al. 2007). We therefore chose  
272 to monitor gene expression in different cell types, by using laser microdissection (LMD) coupled to  
273 semi-quantitative RT-PCR. Three different cell populations were collected from *M. truncatula* roots:  
274 cortical cells from control non-inoculated roots (C), non-colonized cells (NeMyc) and arbusculated  
275 cells (Arb) from roots colonized by *R. irregularis*. The quality of LMD samples was verified by

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276 monitoring *MtPT4* expression. The corresponding PCR product was only detected in the arbuscule-  
277 containing cells while no signal was obtained from the other two samples (Fig. 2b). In order to calibrate  
278 the amount of RNAs in the three different samples, RT-PCR assays using *MtTef* primers were  
279 performed (Fig. 2a).

280 *MtRbohB* and *MtRbohF* mRNAs were not detected in any cell type, while a weak *MtRbohA* signal was  
281 detected in cortical cells from control roots (Fig. 2b). By contrast, *MtRbohE* and *MtRbohG* transcripts  
282 were detected in all three cell types. *MtRbohE* displayed a slightly stronger signal in arbusculated cells  
283 compared to the other two cell types (Fig. 2b). These results were confirmed in a second independent  
284 experiment (data not shown).

285 To better localize gene expression in the root, histochemical staining was performed using a promoter  
286 transcriptional fusion approach based on *Agrobacterium rhizogenes*-transformed root of *M. truncatula*  
287 expressing the GUS reporter gene under *Rboh* promoters (Marino et al. 2011). Hairy roots expressing  
288 *pRboh:GUS* constructs were colonized by the AM fungus *G. margarita* using the targeted inoculation  
289 technique and then subjected to the GUS histochemical reaction. GUS staining was observed in root  
290 tips and central cylinders for all transgenic lines, in both control and mycorrhizal roots (Fig. 3). These  
291 results are largely in line with the observations by Marino et al. (2011) in composite plant roots.  
292 Altogether, these experiments highlight the role of *Rboh* genes during root growth, where they could  
293 have a role in cell wall extension (Monshausen et al. 2007; Macpherson et al. 2008).

294 When mycorrhizal roots were analyzed, the pattern of GUS activity largely overlapped to that observed  
295 in non mycorrhizal roots. Nevertheless, an additional GUS-positive district was found in the *MtRbohE*  
296 transgenic line, corresponding to some of the inner cortical cells (Fig. 3q,r). The same pattern was  
297 confirmed in a second set of experiments, where all five transgenic lines were inoculated with *R.*  
298 *irregularis*; a detail for the *MtRbohE* line is shown in Fig. 4. Since inner cortical cells are the site of  
299 arbuscule development, we verified the presence of fungal structures in GUS-positive cortical cells. To  
300 this aim, roots were counterstained with acid fuchsin. Since the blue GUS staining dominated the acid  
301 fuchsin pink color, a more detailed visualization of arbuscules was obtained with confocal microscope  
302 observations, taking advantage of acid fuchsin fluorescence. The results clearly showed that the cortical  
303 cells where GUS activity was detected also contained arbuscules (Fig. 5).

304 In short, different approaches consistently suggest that *MtRbohE* is upregulated in arbuscule-containing  
305 cells.

306

307 ***MtRbohE silencing affects arbuscule development***

308 To better understand the role of *MtRbohE* in the AM symbiosis, hairy roots expressing an RNA  
309 interference (RNAi) construct for the *MtRbohE* gene or the empty vector (EV) were obtained by *A.*  
310 *rhizogenes* transformation. Different independent transgenic lines displayed an average of 50%  
311 *MtRbohE* silencing (Fig. S1). To study their mycorrhizal phenotype, these roots were inoculated with  
312 *G. margarita* by the targeted inoculation method (Chabaud et al. 2002). EV roots showed the typical  
313 AM colonization pattern with abundant, fully developed arbuscules in the root cortex (Fig. 6). By  
314 contrast, *MtRbohE* RNAi lines displayed abundant intercellular hyphae, but rare arbuscules. In more  
315 detail, short - and occasionally multiple - hyphal protrusions were observed along the cell wall of  
316 cortical cells (Fig. 6; Fig. S2). We interpret these structures as cell penetration attempts from the  
317 intercellular hyphae that did not result in arbuscule formation. These observations strongly suggest that  
318 *MtRbohE* plays a role in arbuscule accommodation in the root cortex.

319 Interestingly, inoculation of *MtRbohE* RNAi roots of composite plants with *S. meliloti* showed no  
320 significant effect on nodule number (Fig. S3). Altogether, these results suggest that *MtRbohE* is  
321 involved in mycorrhizal but not in the rhizobial symbiosis.

322

323 **Discussion**

324 Many processes in the AM symbiosis have been hypothesized to be mediated by ROS: from the control  
325 of host compatibility and fungal morphogenesis (Lanfranco et al. 2005; Fester and Hause 2005) to the  
326 regulation of plant responses to biotic (Pozo and Azcon-Aguilar, 2007) and abiotic stress conditions  
327 (Dumas-Gaudot et al. 2000; Linderman 2000), but the precise underlying mechanisms are far from  
328 being completely elucidated.

329 Since the literature reports evidence of H<sub>2</sub>O<sub>2</sub> accumulation in arbuscular mycorrhizas (Salzer et al.  
330 1999; Fester and Hause 2005; Lanfranco et al. 2005) in this work we monitored the expression profiles  
331 of five *M. truncatula Rboh* genes during the AM interaction.

332 Investigations on RNA from whole roots revealed that *Rboh* transcript levels did not drastically change  
333 in *M. truncatula* roots upon colonization by *R. irregularis*. Similar results were obtained in mycorrhizal  
334 roots of *Phaseolus vulgaris* (Arthikala et al. 2013) although a weak up-regulation of putative orthologs  
335 of *MtRbohB*, *MtRbohA*, *MtRbohE* and *MtRbohF* (*PvRbohB*, *PvRbohD*, *PvRbohA* and *PvRbohH*

336 respectively; Montiel et al. 2012) was reported.

337 Since a mycorrhizal root is a heterogeneous environment where different cell types, either colonized or  
338 not by the AM fungus, coexist, we took advantage of the laser microdissection technique to investigate  
339 whether a fine tuning of gene expression was associated to specific cells. In recent years this method  
340 has been successfully applied to identify transcripts specifically or preferentially associated to the key  
341 structures of the AM symbiosis, that is arbusculated cells (Fiorilli et al. 2009; Gomez et al. 2009;  
342 Guether et al. 2009; Hoge-kamp et al. 2011; Gaude et al. 2012). Cortical parenchyma, the exclusive  
343 niche of arbuscule differentiation, was therefore the target of our analysis. Semi-quantitative RT-PCR  
344 showed that *MtRbohE* and *MtRbohG* were expressed in cortical cells from both mycorrhizal and  
345 control roots, but a slightly stronger intensity was detected for *MtRbohE* in arbusculated cells compared  
346 to adjacent, non-colonized, cortical cells or cortical cells from non mycorrhizal roots. This result is in  
347 agreement with data obtained from transcriptional fusion lines: upon colonization by AM fungi the  
348 *MtRbohE* line showed GUS activity in certain cells of the inner cortical parenchyma where arbuscules  
349 were present. This promoter activity appears a common response to colonization by AM fungi since it  
350 was observed with both *G. margarita* or *R. irregularis* inoculation.

351 In their whole the data suggest that *MtRbohE* gene is activated in cortical cells possibly in relation to  
352 specific events of formation, differentiation and/or senescence of arbuscules. We propose a transient  
353 activation of *MtRbohE* since the up-regulation was not evident in the qRT-PCR from whole roots. The  
354 molecular mechanisms underlying the formation and the turnover of arbuscules are largely unknown  
355 and remain a very enigmatic aspect of the AM symbiosis (Guthjar and Parniske 2013). It can be  
356 hypothesized that the spatio-temporal localized production of ROS mediated by *MtRbohE* may  
357 contribute to control the formation or the life span of these ephemeral intracellular structures. This  
358 hypothesis is also supported by the mycorrhizal phenotype of *MtRbohE* silenced lines; although the  
359 down regulation was only partial (about 50%) *MtRbohE* RNAi roots displayed abundant intercellular  
360 hyphae with many cell penetration attempts, but rare arbuscules.

361 As far as concerns the five genes under analysis, the situation is clearly different from that described in  
362 the nitrogen fixing symbiosis (Marino et al. 2011; 2012) and adds some points of divergence between  
363 the two root symbioses. Based on our expression data *MtRbohA* does not seem to have a role in the AM  
364 symbiosis. This is not surprising since *MtRbohA* was shown to control nodule nitrogen fixation activity  
365 also through the modulation of genes encoding the microsymbiont nitrogenase, a process which is

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366 indeed specific to the rhizobial symbiosis. However, we can not exclude regulations occurring at post-  
367 translational level (Marino et al. 2012). On the other hand, it has been recently demonstrated that the  
368 *PvRbohB* gene from *Phaseolus vulgaris* (homolog of *MtRbohG*), is required for root infection by  
369 rhizobia but acts as a negative regulator of the AM symbiosis (Arthikala et al. 2013). Also our data,  
370 showing that *MtRbohE* silencing did not impact the nodulation process, further hint at a divergent role  
371 for Rboh/ROS-related processes in the two root symbioses.

372 Two recent works on the model legume *M. truncatula* have provided indirect evidence for a role of  
373 *Rboh* genes in the AM symbiosis. The silencing of *MtROP9*, a small GTPase considered a positive  
374 regulator of Rboh enzymes, led to a stimulation of early mycorrhizal colonization (Kiirika et al. 2012).  
375 However, the specific Rboh isoform involved remain to be identified.

376 In a second publication, *M. truncatula* transcriptomic responses to a combined phosphate and nitrogen  
377 limited condition were supposed to be mediated by the action of a *Rboh* gene which would lead to  
378 alteration of plant defence and, in the end, to a better AM root colonization. Interestingly, the same  
379 authors, based on *in silico* analyses of expression profiles, identified *MtRbohE* as a candidate gene that  
380 deserves further investigation (Bonneau et al. 2013): our current results are in line.

381 Based on genomic analyses, *M. truncatula* possesses 10 *Rboh* genes some of which were proposed to  
382 have arisen by a recent whole genome duplication event (Shoemaker et al. 2006). It will be interesting  
383 to extend this investigation to other members of the *MtRboh* family to highlight potential specific roles  
384 of ROS in controlling root symbioses. Furthermore, given the emerging role of fungal NADPH  
385 oxidases in controlling many aspects of fungal development and interactions with plants (Tudzynski et  
386 al. 2012), NADPH oxidases in AM fungi will also deserve careful investigation.

387

#### 388 **Author Contribution Statement**

389 LL, NP and AP conceived and designed research. SB and CC conducted experiments and contributed  
390 to data elaboration. AG contributed to the confocal microscopy analyses. LL wrote the manuscript. All  
391 authors read and approved the manuscript.

392

#### 393 **Acknowledgments**

394 The Authors express their thanks to Raffaella Balestrini for her precious help in the microdissection  
395 experiments, Valentina Fiorilli for the help in the time course experiment and Mara Novero and Marion



396 Dunoyer de Segonzac for the technical assistance. Research was funded by the BIOBIT-Converging  
397 Technology project (WP2) to LL, the University grant (60%) to LL and AG, the BLAN07-2\_182872  
398 ANR research program to AP.

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553

554

555

#### 556 **Figure legends**

557

558 **Fig. 1** Relative expression values of *MtPT4* (a) and *MtRbohA*, *B*, *E*, *F* and *G* genes (b) in roots of *M.*  
559 *truncatula* colonized with *R. irregularis* at 7, 14, 28 and 60 days post-inoculation (dpi). Expression  
560 values (bars = standard deviations) are normalized to the *MtTef* housekeeping gene. In panel b, Y axis  
561 has a log<sub>10</sub> scale. Letters or asterisks indicate statistically significant difference ( $p < 0.05$ , ANOVA).

562

563 **Fig. 2** Gel electrophoresis of RT-PCR products obtained from laser microdissected samples from roots  
564 colonized by *R. irregularis* (Arb: arbusculated cortical cells; NcMyc: non colonized cortical cells from  
565 mycorrhizal roots; C: cortical cells from non mycorrhizal roots) using primers specific for the  
566 housekeeping gene *MtTef* (a) and for the different *MtRboh* genes or for *MtPT4*, used as marker of  
567 arbuscule-containing cells (b).

568

569 **Fig. 3** GUS histochemical staining of *M. truncatula* hairy roots expressing *pRboh:GUS* transcriptional  
570 fusion colonized (Myc) or not (Non myc) with the AM fungus *G. margarita*. In non mycorrhizal roots  
571 (figures from a to l) the GUS staining is localized in the root apex (arrows) and in the vascular system  
572 (asterisks). In roots colonized by the AM fungus *G. margarita* (figures from m to v) the GUS staining  
573 is localized in all the transgenic lines (as in the non mycorrhizal roots) in the root tips (arrows) and in  
574 the vascular system (asterisks). Only in *MtRbohE* transgenic roots the GUS staining is also localized in  
575 some cells of the inner cortex (arrowheads) where usually arbuscules are formed.

576

577 **Fig. 4** GUS histochemical staining of *M. truncatula* *MtRbohE* transgenic hairy roots expressing  
578 *pRboh:GUS* transcriptional fusion colonized (Myc) or not (Non myc) with the AM fungus *R.*  
579 *irregularis*. In non mycorrhizal roots (figures **a** and **b**) the GUS staining is localized in the root apex  
580 (arrowhead) and in the vascular system (asterisks). In roots colonized by the AM fungus *R. irregularis*  
581 (figures **c** and **d**) the GUS staining is localized in the vascular system (asterisks) and in some cells of  
582 the inner cortex (arrows) where usually arbuscules are formed.

583

584 **Fig. 5** GUS histochemical staining of *M. truncatula* *MtRbohE* transgenic hairy roots expressing  
585 *pRboh:GUS* transcriptional fusion colonized with the AM fungus *G. margarita* and counterstained with  
586 acid fuchsin to localize the intraradical hyphae. Under a confocal microscope (figures **a**, **b** and **c**) the  
587 acid fuchsin autofluorescence allows to localize the arbuscules (A) in some cortical cells. The  
588 observation of the same cortical cells under a light microscope (figures **d**, **e** and **f**) allow to appreciate  
589 the overlap of the GUS staining (blue) and the acid fuchsin staining (pink), clearly indicating the co-  
590 localization of the GUS staining and the arbuscules. Bars: 20  $\mu$ m.

591

592 **Fig. 6** Confocal microscopy images representative of hyphal and arbuscule development in WT (**a-c**)  
593 and *MtRbohE* RNAi-silenced lines (**d-f**). Both hyphae (h) and arbuscules (ar) are abundant in WT roots  
594 (**a**). Higher magnifications (**b** and **c**) show details of arbuscule morphology, with the fine branches  
595 occupying most of the cell volume and the large trunk (t) branching from the intercellular hypha  
596 (arrowhead). By contrast, arbuscules are much more sparse in *MtRbohE* RNAi-silenced lines (**d**),  
597 where extensive areas are mostly colonized by intercellular hyphae (h). When present, arbuscules have a  
598 WT-like morphology (**e**, **f**), while intercellular hyphae often show short protrusions that we interpret as  
599 recursive, aborted cell penetration attempts (arrowheads). Bars = 80 $\mu$ m in **a**, **d**, **e**; 40 $\mu$ m in **b**, **f**; 20 $\mu$ m  
600 in **c**.

601

602 **Table 1** Mycorrhization level in *M. truncatula* roots at different days post inoculation (dpi). Different  
603 letters indicate statistically significant differences ( $p > 0.05$ , ANOVA).

604

605 **Fig. S1** Relative expression of *MtRbohE* in transgenic root cultures. *MtRbohE* expression was  
606 evaluated by qRT-PCR on established transgenic root cultures expressing either an empty (EV) or a  
607 *MtRbohE* RNAi construct (RNAi). Values were normalized against the 40S2 ribosomal protein (Andrio  
608 et al. 2013). Data are reported as mean  $\pm$  standard error. Asterisk indicates a statistically significant  
609 difference between control (EV) and RNAi lines using t-test ( $p < 0.05$ ).

610

611 **Fig. S2** Details of intraradical fungal structures in the cortex of EV (**a**) or *MtRbohE* RNAi-silenced  
612 lines (**b**). A young arbuscule is displayed in **a**, filling up most of the host cell lumen with its trunk (t)  
613 and branches (b). A root segment only containing intercellular hyphae is shown in **b**: several short  
614 branches are evident, protruding from an intercellular hypha, corresponding to aborted cell penetration  
615 events. Bars = 20 $\mu$ m in **a**; 80 $\mu$ m in **b**.

616 **Fig. S3** Nodulation of composite plants expressing either an empty (EV) or a *MtRbohE* RNAi  
617 construct. Nodule number was evaluated 4 and 10 days after inoculation with *Sinorhizobium meliloti*.  
618 Data are reported as mean  $\pm$  standard error. Values are representative of two independent biological  
619 replicates ( $n > 30$ ). Differences are not statistically significant (t-test).