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# Mycorrhiza

## The arbuscular mycorrhizal symbiosis attenuates symptom severity and reduces virus concentration in tomato infected by Tomato yellow leaf curl Sardinia virus (TYLCSV) --Manuscript Draft--

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| <b>Abstract:</b>                                     | <p>The mutualistic association established between arbuscular mycorrhizal (AM) fungi and the majority of land plants has been extensively studied and is considered a natural instrument to improve plant health and productivity, since mycorrhizal plants often show higher tolerance to abiotic and biotic stresses. However, the impact of the AM symbiosis on the infection by viral pathogens is still largely uncertain and little explored. In our study tomato plants were grown under controlled conditions and inoculated with the AM fungus <i>Funneliformis mosseae</i>. Once the colonization had developed, plants were inoculated with Tomato yellow leaf curl Sardinia virus (TYLCSV), a geminivirus causing one of the most serious viral diseases of tomatoes in Mediterranean areas. Four biological conditions were set up: control plants (C), TYLCSV-infected plants (V), mycorrhizal plants (M) and TYLCSV-infected mycorrhizal plants (MV). At the time of analysis, the mycorrhization level, as well as the expression profiles of mycorrhiza-responsive selected genes, were not significantly modified by virus infection, thus indicating that the AM colonization was unaffected by the presence and spread of the virus. On the contrary, in MV plants viral symptoms were milder than in V plants and the concentration of viral DNA was lower in both shoots and roots. Overall <i>F. mosseae</i> colonization appears to exert a beneficial effect on tomato plants attenuating the disease caused by TYLCSV.</p> |

1       **The arbuscular mycorrhizal symbiosis attenuates symptom severity and reduces virus**  
2       **concentration in tomato infected by *Tomato yellow leaf curl Sardinia virus* (TYLCSV)**

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28

29   **Abstract**

30   The mutualistic association established between arbuscular mycorrhizal (AM) fungi and the majority of land plants has  
31   been extensively studied and is considered a natural instrument to improve plant health and productivity, since  
32   mycorrhizal plants often show higher tolerance to abiotic and biotic stresses. However, the impact of the AM symbiosis  
33   on the infection by viral pathogens is still largely uncertain and little explored. In our study tomato plants were grown  
34   under controlled conditions and inoculated with the AM fungus *Funneliformis mosseae*. Once the colonization had  
35   developed, plants were inoculated with *Tomato yellow leaf curl Sardinia virus* (TYLCSV), a geminivirus causing one of  
36   the most serious viral diseases of tomatoes in Mediterranean areas. Four biological conditions were set up: control  
37   plants (C), TYLCSV-infected plants (V), mycorrhizal plants (M) and TYLCSV-infected mycorrhizal plants (MV). At  
38   the time of analysis, the mycorrhization level, as well as the expression profiles of mycorrhiza-responsive selected  
39   genes, were not significantly modified by virus infection, thus indicating that the AM colonization was unaffected by  
40   the presence and spread of the virus. On the contrary, in MV plants viral symptoms were milder than in V plants and the

41 concentration of viral DNA was lower in both shoots and roots. Overall *F. mosseae* colonization appears to exert a  
42 beneficial effect on tomato plants attenuating the disease caused by TYLCSV.

43 **Keywords**

44 AM symbiosis; *Funneliformis mosseae*; viral infection; tomato; Tomato yellow leaf curl Sardinia virus; geminivirus

45

46

47 **INTRODUCTION**

48 The arbuscular mycorrhizal symbiosis (AM), one of the most widespread mutualistic symbiosis, is formed between  
 49 fungi belonging to the Glomeromycota phylum and the roots of the majority of land plants, including crops and  
 50 horticultural species (Bonfante and Genre 2010). AM fungi colonize the root cortex where they form intracellular highly  
 51 branched structures called arbuscules. The arbusculated cells are considered key structures of the symbiosis and the  
 52 main site for reciprocal nutrient exchanges: the fungus provides mineral nutrients (phosphorus, nitrogen, sulphur) to the  
 53 plant and receives carbon compounds derived from photosynthesis (Bonfante and Genre 2010; Lanfranco and Young  
 54 2012). Beside an improved mineral nutrition, mycorrhizal plants often show a higher tolerance to biotic and abiotic  
 55 stresses leading, in the end, to an improved plant fitness (Gernns et al. 2001; Van der Heijden and Sanders 2002;  
 56 Hildebrandt et al. 2007; Pozo and Azcón-Aguilar 2007; Aroca et al. 2008; Pozo et al. 2010). This symbiotic association  
 57 is therefore considered a natural instrument that improves the health and productivity of host plants.

58 The AM symbiosis can influence the outcome of plant-pathogen interactions (Pozo and Azcón-Aguilar 2007; Pozo et al.  
 59 2010). A well established symbiosis prior the challenge with the attacker seems a requirement for mycorrhizal  
 60 protection against pathogens (Rosendahl 1985; Cordier et al. 1998; Slezack et al. 2000; Khaosaad et al. 2007). Although  
 61 the effect may also depend by the specific plant-fungus combination and by environmental factors, mainly beneficial  
 62 effects have been observed in the case of soil-borne pathogens: alleviation of damage was shown for diseases caused by  
 63 fungi such as *Rhizoctonia*, *Fusarium* and *Verticillium* spp., by oomycetes including *Phytophthora*, *Pythium* and  
 64 *Alphanomices* spp. (Pozo et al. 2010; Whipps 2004) and parasitic nematodes such as *Pratylenchus* and *Meloidogyne*  
 65 spp. (de la Pena et al. 2006, Li et al. 2006; Vos et al. 2013). The bioprotective role may rely on different mechanisms but  
 66 is surely not exclusively dependent on an improved mineral nutrition. To control root pathogens competition for  
 67 colonization sites or photosynthates, changes in the root apparatus and/or in the microbial rhizosphere communities and  
 68 also activation of plant defence have been proposed (Whipps 2004; Pozo et al. 2002; Pozo et al. 2010; Ismail and Hijri  
 69 2012; Vos et al. 2013).

70 Information on the effects of the AM symbiosis on pathogens attacking the epigeal parts of plants, i.e. the parts that  
 71 grow above the ground surface (hereafter called shoot pathogens) are scarce and more controversial. The effects on  
 72 shoot-targeting organisms seem to greatly depend on the attacker life style (Pozo and Azcón-Aguilar 2007). Enhanced  
 73 susceptibility to biotrophic pathogens such as powdery mildew and rust fungi was observed (Whipps et al. 2004;  
 74 Gernns et al. 2009). However, colonization by AM fungi has been reported to reduce symptoms caused by phytoplasma  
 75 (Lingua et al. 2002; Garcia-Chapa et al. 2004; D'Amelio et al. 2007) the necrotrophs *Alternaria solani* (Fritz et al. 2006)  
 76 and *Botrytis cinerea* (Pozo et al. 2010; Fiorilli et al. 2011), as well as the bacterial pathogen *Xanthomonas campestris*  
 77 (Liu et al. 2007).

78 Very little information is available about the interaction with viral infections. Mycorrhizal colonization was shown to  
 79 increase the multiplication of some viruses (Daft and Okusanya 1973; Dehne 1982; Miozzi et al. 2011). Shaul et al.  
 80 (1999) focused on disease symptoms and demonstrated that mycorrhizal tobacco plants infected by *Tobacco mosaic*  
 81 *virus* (TMV) showed an enhanced disease severity compared to non-mycorrhizal plants. More recently, Miozzi et al.  
 82 (2011) analysed the interactions between *Funneliformis mosseae* and *Tomato spotted wilt virus* (TSWV) in tomato and  
 83 observed that regulation of plant genes responding to virus infection was attenuated by mycorrhization, causing, in the  
 84 long term, a higher virus titer in mycorrhizal than non mycorrhizal plants.

85 With the aim to extend our knowledge on the impact of the AM colonization on viral infection we focused our attention  
 86 on a virus family, the *Geminiviridae*, not yet explored, with characteristics different from those examined so far. They  
 87 are important pathogens on many crops in tropical and sub-tropical regions, and their economic relevance is constantly  
 88 growing (Varma and Malathi 2003; Mansoor et al. 2006; Jeske 2009). Several of them infect tomato (*Solanum*  
 89 *lycopersicum*), one of the most important vegetable crops worldwide and currently used as a model plant for basic  
 90 research with an increasing number of genomics and functional genomics tools available (The Tomato Genome  
 91 Consortium 2012).

92 Among the members of the genus *Begomovirus*, *Tomato yellow leaf curl Sardinia virus* (TYLCSV) and *Tomato yellow*  
 93 *leaf curl virus* (TYLCV) are the cause of one of the most serious diseases of tomato cultivation (Accotto et al. 2000).  
 94 Like all geminiviruses, they have a single-stranded DNA genome and replicate in the cell nucleus. They colonize the  
 95 phloem vessels (Morilla et al. 2004) and the typical disease symptoms they induce consist in leaf curling and yellowing  
 96 of leaf edges, plant growth reduction, flower abortion and drastic loss of fruit production (Czosnek 2007).

97 In this work we have examined the impact of colonization by the AM fungus *Funneliformis mosseae* on infection by  
 98 TYLCSV in tomato plants and showed that the AM symbiosis exerts a positive systemic effect leading to an attenuation  
 99 of the disease.

100

## 101 MATERIALS AND METHODS

### 102 Biological material

103 *Solanum lycopersicum* cv. Moneymaker seeds were surface-sterilized by washing in 70% ethanol with a few drops of  
 104 Tween 20 for 3 min and in sodium hypochlorite 5% for 13 min, and rinsed three times in distilled water for 10 min each  
 105 time. The seeds were placed in Petri dishes containing H<sub>2</sub>O:agar (0.6%), incubated for one week in the dark (25 °C) and  
 106 then exposed to light for another week with a photoperiod of 14/10 light/dark. Seedlings were then transferred to pots  
 107 containing sterile quartz sand. Altogether, the experiment aiming to study the impact of colonization by the AM fungus  
 108 *F. mosseae* on infection by TYLCSV in tomato consisted in four groups of plants: control plants (C), TYLCSV-infected  
 109 plants (V), mycorrhizal plants (M), TYLCSV-infected mycorrhizal plants (MV). Inoculation of *Funneliformis mosseae*  
 110 (Syn. *Glomus mosseae*; Krüger et al. 2012) Gerd. & Trappe BEG12 (Mycagrolab, France) was performed by mixing the  
 111 inoculum with sterile quartz sand (30% v/v). The plants were maintained in a growth chamber under 14 h light (2,500  
 112 lux) / 10 h dark at 23°C and watered twice a week: once with a modified Long-Ashton nutrient solution (Hewitt, 1966)  
 113 containing 320 µM phosphate and once with water. Phosphate content in the nutrient solution was optimized so that non  
 114 mycorrhizal plants were not suffering from phosphate starvation and did not show growth defects compared to  
 115 mycorrhizal ones. To guarantee the establishment of a good mycorrhization level, virus inoculation was performed 4  
 116 weeks after AM fungus inoculation. Two groups of plants (V and MV) were inoculated with TYLCSV using the  
 117 agroinoculation method with 20 µL of a suspension of *Agrobacterium tumefaciens* strain LBA4404 cells carrying  
 118 infectious viral clone (Kheyr-Pour et al. 1991). The remaining plants (C and M) were mock-inoculated with 20 µL of a  
 119 suspension of *A. tumefaciens* cells strain LBA4404 cells containing the binary plasmid without viral insert.

120 To detect the virus presence a tissue print was performed 21 days post-infection (dpi). The petiole of a young leaf from  
 121 each plant was printed on positively charged nylon membrane (Roche, Mannheim, Germany). Membranes were then

122 hybridized with a digoxigenin-labeled TYLCSV-specific probe (Accotto et al. 2000). Infected plants were retained for  
123 further analysis (data not shown).

124 Plants were harvested 28 dpi for analysis. First, shoot (the aboveground portion) and root (the underground portion)  
125 components were separately weighted for biomass evaluation. Roots from mycorrhizal plants were checked for the  
126 presence of extraradical mycelium under a stereomicroscope. A portion of the root system was then used to assess the  
127 mycorrhization level while the remaining portion of the roots, the apex and the second youngest leaf (leaf -2) of each  
128 plant were frozen in liquid nitrogen and stored at -80 C. Following the preliminary screening for virus infection and *F.*  
129 *mosseae* colonization, 15 plants per condition were considered for further analyses.

130

### 131 **Mycorrhizal evaluation**

132 Mycorrhizal roots were stained with 0.1 % (w/v) cotton blue overnight and then washed with lactic acid. Randomly  
133 selected roots segments were cut in 1 cm pieces and observed under a light microscope. According to Trouvelot et al.  
134 (1986), four parameters were considered: frequency of mycorrhization (F%): percentage of fragments showing  
135 intraradical mycelium; intensity of mycorrhization (M%): mean volume of individual root segments colonized by  
136 mycelium; percentage of arbuscules within infected areas (a%): arbuscules in the colonized portions of the root system;  
137 percentage of arbuscules in the root system (A%): presence of arbuscules in the whole roots system.

138

### 139 **Estimation of viral infection and quantification of viral genomes**

140 At 28 dpi the symptom severity was estimated by visual inspection using a Disease Severity Index (DSI) ranging from 1  
141 (very mild symptoms) to 4 (severe symptoms), according to Lapidot and Friedman (2002).

142 To estimate the amount of viral genomes in infected plants qPCR assays were performed on shoot and root total DNA.  
143 About 100 mg of tissue were ground in liquid nitrogen, 800 µl of TLES (5% SDS, 150 mM LiCl, 50 mM Tris-HCl pH  
144 9.0, 5 mM EDTA) were added, followed by 0.5 vol of phenol and 0.5 vol of chloroform. Following mixing and  
145 centrifugation, the aqueous phase was recovered and the DNA was precipitated with 2.5 vol of cold ethanol and 1/20  
146 vol of 4 M Na-acetate. The DNA was finally resuspended in 200 µl of TE solution. TYLCSV DNA was amplified with  
147 primers TY2222(+) (5'- TTTTACTTGTATATTCGAAGTGTGCCA-3') and TY2371(-) (5'-  
148 ACAACTGCAAAATTAGAATCTAGTTGGTA-3'). PCR reactions were run in parallel with primers QTOMAPX-  
149 2818(+) (5'- TTTTACTTGTATATTCGAAGTGTGCCA-3') and QTOMAPX-2910(-) (5'-  
150 ACAACTGCAAAATTAGAATCTAGTTGGTA -3') for the reference plant gene APX encoding an ascorbate  
151 peroxidase. Quantitative PCR assay were carried out using EvaGreen Mix (Bio-Rad) in a StepOnePlus™ apparatus  
152 (Applied Biosystems). The reactions were conducted in a total volume of 10 µl, containing 40 ng DNA, 5 µl Eva Green,  
153 1 µl of each primer 3µM, 0.3 µl of ROX. The PCR cycling program was: 95 °C for 5 min, and 40 cycles each consisting  
154 of 95 °C for 15 s and 60 °C for 1 min. A melting curve was recorded at the end of each run to assess amplification  
155 production specificity. All reactions were performed with three technical replicates and three biological replicates. PCR  
156 efficiency was determined from standard curves constructed with serial dilutions of genomic DNA from TYLCSV-  
157 infected tomato. For each sample we calculated the relative viral amount using the  $\Delta C_t$  method where  $\Delta C_t$  is  $|C_{t_{virus}} -$   
158  $C_{t_{apx}}|$ . The fold change in viral amount between non mycorrhizal (V) and mycorrhizal (MV) samples was calculated as  
159  $2^{-\Delta\Delta C_t}$  where  $\Delta\Delta C_t = \Delta C_{t_{MVplants}} - \Delta C_{t_{Vplants}}$ .



160

161 **RNA extraction and RT-qPCR assays**

162 About 100 mg of shoot and root samples were ground in liquid nitrogen and used for total RNA extraction. RNA  
 163 extractions were performed using the SIGMA RNA plant kit. DNA contaminations were removed using the Turbo DNA  
 164 free kit (Bio-Rad) following manufacturer's instructions. RNA quantification was carried out using a Picodrop 1000  
 165 spectrophotometer. The quality of RNAs was checked using the Experion automated electrophoresis station (BioRad)  
 166 following the manufacturer's instructions. Total RNA (500 ng) from each pool was transcribed into cDNA with the  
 167 High-Capacity cDNA reverse Transcription Kit (Applied Biosystems). All RT-qPCR assays were carried out using  
 168 EvaGreen Mix (Bio-Rad) in a StepOnePlus™ apparatus (Applied Biosystems) as described above. The comparative  
 169 threshold cycle method (Rasmussen 2001) was used to calculate relative expression level using the tomato UBC  
 170 (ubiquitin conjugating enzyme, SGN-U582847) as reference gene. The list of analyzed genes and corresponding  
 171 primers are shown in Table 1. For each condition three biological replicates, each consisting of RNA extractions from  
 172 four plants, were analysed.

173

174 **RESULTS**

175 To study the impact of colonization by the AM fungus *Funneliformis mosseae* on TYLCSV infected tomatoes, four  
 176 biological conditions were considered: control plants (C), TYLCSV-infected plants (V), mycorrhizal plants (M),  
 177 TYLCSV-infected mycorrhizal plants (MV). At the time of sampling (28 dpi), shoot and root fresh weight was  
 178 measured.

179 No difference was observed in shoot and root biomass between C and M plants, confirming that the phosphate content  
 180 in the nutrient solution was optimized to avoid phosphate starvation in C plants. The only statistically significant  
 181 difference was a slight reduction of shoot and root biomass in MV plants (Fig. 1).

182 AM colonization level was also evaluated: of the four parameters considered, only the mycorrhization frequency was  
 183 moderately but significantly increased in TYLCSV-infected mycorrhizal plants compared to mycorrhizal plants (Fig.  
 184 2). In their whole these data indicate that the viral infection has no major impact on the intraradical growth of the AM  
 185 fungus.

186 Viral symptoms on leaves were estimated according to the DSI (Fig. 3). Overall, the infected mycorrhizal plants (MV)  
 187 showed less severe symptoms than the infected non mycorrhizal plants (V): the majority (53%) of TYLCSV-infected  
 188 plants presented the most severe symptoms (DSI=4) while most (53%) of TYLCSV-infected mycorrhizal plants  
 189 presented the mildest symptoms (DSI=1). To gain a more accurate description of viral infection, the relative amount of  
 190 viral genomes in shoot and root tissues was estimated by qPCR assays with primers specific for a viral DNA sequence.  
 191 Investigations were performed on genomic DNA from both shoots and roots. Viral DNA was detected also in roots  
 192 confirming that the virus causes a systemic infection. The amount of viral DNA was higher in V plants compared to MV  
 193 plants, both in shoots (2.6 times) and in roots (1.9 times) (Fig. 4). Such differences were statistically significant ( $p < 0.05$ ,  
 194 ANOVA). Interestingly, this result is in agreement with the observed symptoms, that were more severe in V plants. In  
 195 addition, the amount of viral DNA was higher ( $p < 0.05$ , ANOVA) in shoots than in roots, irrespectively from the  
 196 presence of the AM fungus. In both V and MV plants, the difference in viral concentration between shoots and roots  
 197 remained similar, indicating that mycorrhization does not influence virus movement towards the roots.

198

199 **Expression profiles of genes considered markers of a functional AM symbiosis**

200 A molecular analysis was performed to analyse whether a functional AM symbiosis was active in mycorrhizal plants  
 201 infected by the virus. We first considered *LePT4*, a phosphate transporter encoding gene specifically induced in  
 202 arbusculated cells (Balestrini et al. 2007) and recognized as a molecular marker of a key function of the AM symbiosis.  
 203 The transcript was highly induced in mycorrhizal plants and, remarkably, *LePT4* induction was not affected by the  
 204 presence of the virus (Fig. 5). In addition, the expression profiles of a selection of genes (a kinesin-like protein, a  $\beta$ -  
 205 xylosidase  $\beta$ -l-arabinosidase, a cytochrome P450 CYP707A3 and a UDP-glucuronosyl transferase), previously  
 206 identified as up-regulated in tomato roots colonized by the AM fungus *F. mosseae* (Fiorilli et al. 2009), were also  
 207 investigated. All the genes showed an up-regulation in mycorrhizal roots compared to control roots. A similar level of  
 208 gene expression was found in TYLCSV-infected mycorrhizal plants.

209

210 **DISCUSSION**

211 Tomato plants are subjected to a number of viral diseases (Hanssen 2010). Since viruses cannot be eradicated by  
 212 chemical treatments alternative protection strategies need to be developed. Among beneficial microorganisms such as  
 213 PGPR (plant growth promoting rhizobacteria), tomato plants interact with AM fungi (Conrath et al. 2006; Beckers and  
 214 Conrath 2007) which, with their multifunctional roles, have also been proposed as sustainable alternative to chemicals  
 215 in pest management. The degree of protection seems highly dependent on the AM fungus involved (Kobra et al. 2009)  
 216 with *F. mosseae* in natural and agricultural systems, showing a stronger bioprotective role compared to other AM fungi  
 217 (Pozo et al. 2002; Utkhede 2006; Ozgonen and Erkilic 2007; Veresoglou and Rillig 2012).

218 In this work we have analysed in tomato plants the impact of *F. mosseae* colonization on infection by TYLCSV, a  
 219 devastating viral pathogen responsible of the tomato yellow leaf curl disease in the Mediterranean region. Since a well  
 220 established symbiosis prior the challenge with the pathogen is considered a requirement for bioprotection (Rosendahl  
 221 1985; Cordier et al. 1998; Slezack et al. 2000; Khaosaad et al. 2007), plants were first inoculated with the AM fungus,  
 222 then 28 days later with TYLCSV. Four weeks were then allowed before sampling and analyzing plants, to let systemic  
 223 viral infection with the typical symptoms. Considering plant biomass, a month of viral infection was probably not  
 224 sufficient to affect plant growth, a typical systemic symptom of TYLCSV, although a slight reduction of shoot and root  
 225 biomass was observed in MV plants (Fig. 1), probably due to the simultaneous presence of the two microorganisms.

226 Morphological observation of roots (for fungal colonization) and young leaves (for yellow leaf curling) showed that the  
 227 colonization by *F. mosseae* attenuates TYLCSV symptoms. In line with this, the amount of viral DNA in both shoots  
 228 and roots was reduced in TYLCSV-infected mycorrhizal (MV) vs TYLCSV-infected non-mycorrhizal (V) plants. These  
 229 results indicate that, at least under our experimental conditions, the AM symbiosis appears to confer some protection  
 230 against TYLCSV in tomato.

231 Interestingly, the viral infection does not affect mycorrhization: analysis of AM colonization levels showed no major  
 232 difference between M and MV plants, indicating that the onset and spread of TYLCSV in the whole plant (including the  
 233 roots colonized by *F. mosseae*) does not interfere with the fungal intraradical development. Beside these morphological  
 234 observations, we detected the up-regulation of a selected group of genes previously described as mycorrhiza-responsive  
 235 and found as preferentially expressed in arbuscule-containing cells of tomato-*F. mosseae* mycorrhizal roots (Fiorilli et

236 al. 2009). With the exception of the well known AM-marker *LePT4* (Nagy et al. 2005; Balestrini et al. 2007; Xu et al.  
 237 2007; Gomez-Ariza et al. 2009), these genes have not been characterized yet. Based on sequence similarity their  
 238 functions might be related to reorganization of cell components (kinesin-like protein and  $\beta$ -xylosidase  $\beta$ -l-  
 239 arabinosidase), abscisic acid catabolism (cytochrome P450 CYP707A3) and control of carbon flux (UDP-glucuronosyl  
 240 transferase protein). Remarkably, their expression profiles in mycorrhizal plants were not modified by TYLCSV  
 241 infection (compare M vs MV in Fig. 5). These genes can be proposed for the role of novel markers of functional AM  
 242 symbiosis in tomato.

243 Although the mycorrhization develops only in roots, it clearly has long-distance effects on the non colonized  
 244 aboveground parts of the plants. Molecular evidences of this systemic effect have been shown in gene expression  
 245 studies, where up- or down-regulation of several genes has been detected not only in leaves (Taylor and Harrier 2003;  
 246 Liu et al. 2007; Fiorilli et al. 2009) but also in fruits (Salvioli et al. 2012). Transcript profiles of the shoots of  
 247 mycorrhizal plants indicated the systemic induction of many genes predicted to be involved in stress or defense  
 248 responses in *Medicago truncatula* (Liu et al. 2007) colonized by *G. intraradices* or *G. versiforme*, while down-  
 249 regulation of many defence-related genes was detected in shoots of tomato colonized by *F. mosseae* (Fiorilli et al.  
 250 2009). In spite of these apparently contradictory reports, it is clear that a systemic effect exists, and probably different  
 251 plants and/or different AM fungi-plant combinations may lead to distinctive reactions. Specific efforts will be necessary  
 252 to better elucidate the phenomenon and understand the mechanisms and signals involved.

253 The reduction in virus amount and disease symptomatology in mycorrhizal plants is a novel and interesting result. In the  
 254 limited literature, where the influence of mycorrhization on virus infection was studied, the AM fungal colonization in  
 255 roots did not reduce virus infection, but rather increased it (Daft and Okusanya 1973; Dehne 1982; Shaul et al. 1999).  
 256 This increase in virus amount was observed with several mycorrhizal plant/virus combinations, including tomato  
 257 infected by TMV and Potato virus X. In our previous work (Miozzi et al. 2011) with the same tomato cultivar, AM  
 258 fungus, growth condition (with the exception of Pi nutritional levels), we found that a different RNA virus, TSWV,  
 259 multiplied better in mycorrhizal plants. All these data suggest that the reason of the different reaction that we observed  
 260 with TYLCSV is likely due to the particular nature of this virus. In fact, this and other geminiviruses are phloem-limited  
 261 and colonize the nucleus of cells (Morilla et al. 2004), and encode proteins capable to interact with plant hormone  
 262 pathways.

263

264 Jasmonic acid (JA) and its methyl ester, methyl jasmonate (MeJA), are plant signaling molecules involved, among  
 265 others, in plant defense (Penninckx et al. 1998; Schenk et al. 2000; Heil and Ton 2008). JA is involved in the process of  
 266 mycorrhiza formation, as demonstrated in several host-fungus interactions (Hause et al. 2007; López-Ráez et al. 2010)  
 267 as well as specifically in tomato (Herrera-Medina et al. 2007), and it has been implicated in priming plant defenses  
 268 (Jung et al. 2012). In a previous work we demonstrated that mycorrhization induces in tomato roots a significant  
 269 increase of the JA level (Miozzi et al. 2011). Therefore, it is possible that a higher JA level renders the mycorrhizal  
 270 plants a less favourable environment for TYLCSV, limiting its replication and reducing the severity of symptoms. In  
 271 favour of this hypothesis there are some lines of evidence. First, in the case of another geminivirus, *Beet curly top virus*,  
 272 it was recently demonstrated in *Arabidopsis* that application of exogenous MeJA results in milder symptoms and lower  
 273 viral DNA accumulation, indicating a disruption of the geminivirus infection by this compound (Lozano-Duran et al.  
 274 2011). Second, using another geminivirus, *Cabbage leaf curl virus*, repression of jasmonate responsive genes was

275 reported (Ascencio-Ibañez et al. 2008). Third, geminiviruses have evolved proteins able to interfere with JA metabolism  
276 and response, repressing the JA pathway (Ascencio-Ibañez et al. 2008; Yang et al. 2008).

277 We are aware that the mycorrhizosphere is a complex environment where other microbes associates to mycorrhizal  
278 fungi and roots and may influence plant growth and health (Bonfante and Anca, 2009). However, to our knowledge, this  
279 is the first time that an amelioration of a viral disease severity in plants colonized by an AM fungus has been observed,  
280 at least under experimental conditions. If this will be confirmed in other plant/virus/fungus combinations, and in field  
281 conditions, the use of mycorrhizal inocula might help to limit the damage caused by *Geminiviridae*, a family of viruses  
282 which counts hundreds of species causing severe crop losses worldwide.

283

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288

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501

502 Table 1: Primers designed on selected genes used in RT-qPCR

| <b>Gene name<br/>and annotation</b>                           | <b>Primer sequence</b>               | <b>Amplicon size (bp)</b> |
|---|--------------------------------------|---------------------------|
| SGN-U223227<br>Cytochrome p450                                | C450F: GGAATCAACTTAGCCAAACTGG        | 241                       |
|   | C450R: ACAGCACCATGGTTATTTTTCC        |                           |
| SGN-U222911<br>Putative kinesin-like protein                  | 911F: CAAGAAATCAGAAGGGGACAAC         | 187                       |
|   | 911R: GAACCATCTCTTTCCGCTCTTA         |                           |
| SGN-U214669<br>UDP-gluconorosyl transferase family<br>protein | UDPF: GTTCAATGTTGTTGTTACGCCTTCA      | 228                       |
|   | UDPR: TAGCTAATCCCCAAGCAGTCTC         |                           |
| SGN-U236747<br>Beta-xylosidase $\alpha$ -l-arabinosidase      | $\beta$ xylF: GATGGTAATCCAAAAGCCGTA  | 152                       |
|   | $\beta$ xylR: ATGGCAGTCGGAGTTAAAGGTA |                           |
| LePT4<br>phosphate transporter                                | LePT4F: GAAGGGGAGCCATTTAATGTGG       | 182                       |
|   | LePT4R: ATCGCGGCTTGTTTAGCATTTCC      |                           |

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## FIGURE LEGENDS

508 **Fig. 1**

509 Biomass of the aboveground (a, shoot) and underground (b, root) portion of plants in the four conditions tested (C, M, V  
510 and MV), measured 28 days after virus inoculation. Vertical lines on each bar represent standard error. Different letters  
511 indicate statistically significant differences ( $p < 0.05$ , Kruskal-Wallis test).

512 **Fig. 2**

513 Mycorrhization levels of mycorrhizal (M) and TYLCSV-infected mycorrhizal (MV) plants. F%, frequency of  
514 mycorrhization; M%, intensity of mycorrhization; a%, percentage of arbuscules within infected areas; A%, percentage  
515 of arbuscules in the root system. Vertical lines on each bar represent standard error. Different letters indicate statistically  
516 significant differences ( $p < 0.05$ , Kruskal-Wallis test).

517 **Fig. 3**

518 Evaluation of symptoms caused by TYLCSV in mycorrhizal (MV) and non-mycorrhizal (V) tomato plants. Disease  
519 severity index (DSI) ranging between 1 (mild symptoms) and 4 (severe symptoms). a) graphic representation  
520 (percentage of plants scored 1 to 4 DSI in the two sets of plants; b) example of a plant with DSI=2 on the left and one  
521 with DSI=4 on the right.

522 **Fig. 4**

523 Virus concentration in shoots and roots.  $\Delta C_t$  values on the vertical axis represent the difference between  $C_t$  (threshold  
524 cycle) of TYLCSV and  $C_t$  of reference gene, and measure viral concentration in the four conditions. Vertical lines on  
525 each bar represent standard error. Different letters indicate statistically significant differences within the same organ  
526 ( $p > 0.05$ , ANOVA).

527 **Fig. 5**

528 Expression of selected AM symbiosis-responsive genes (Kin: kinesin-like protein,  $\beta$ -xyl:  $\beta$ -xylosidase  $\beta$ -l-  
529 arabinosidase; Cyt P450: cytochrome P450 CYP707A3; UDP-gluc: UDP-glucuronosyl UDP-glucosyl transferase; PT4:  
530 phosphate transporter. Expression values (bars  $\pm$  standard error) for each gene are given as  $\log_2$  of fold change (FC)  
531 relative to C. Different letters indicate statistically significant differences ( $p < 0.05$ , ANOVA).

532

533

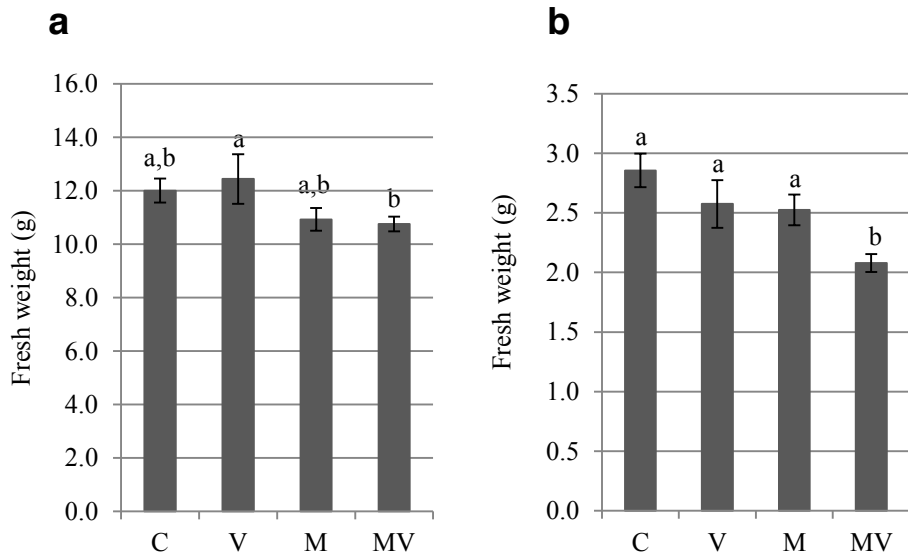


Figure 2

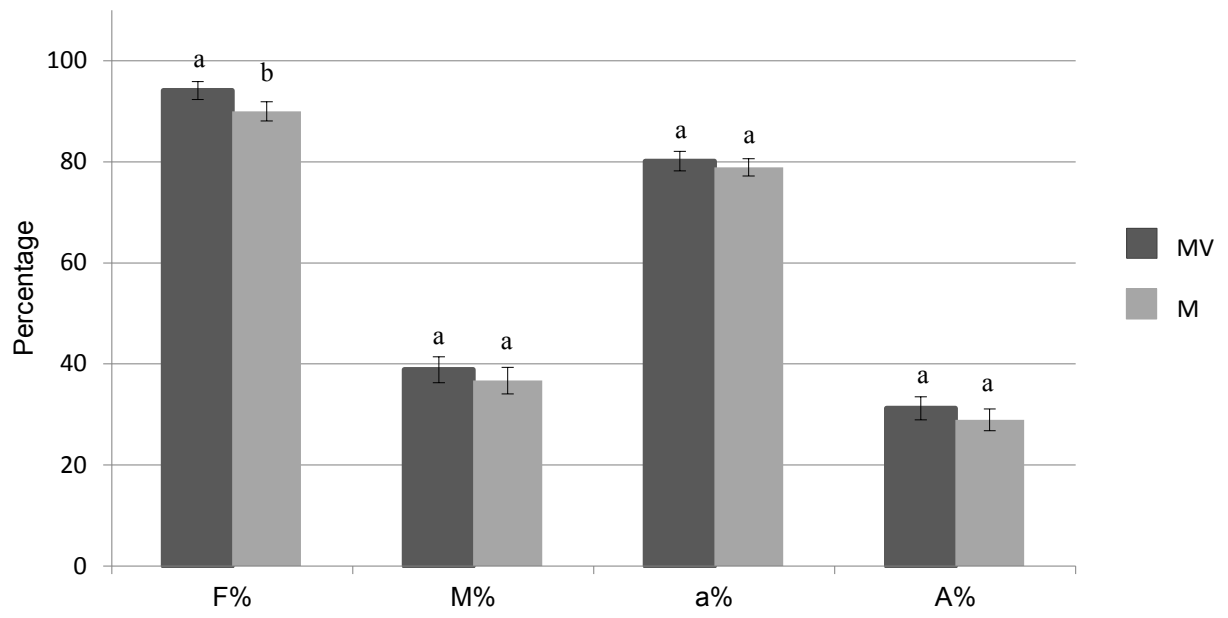


FIG 2

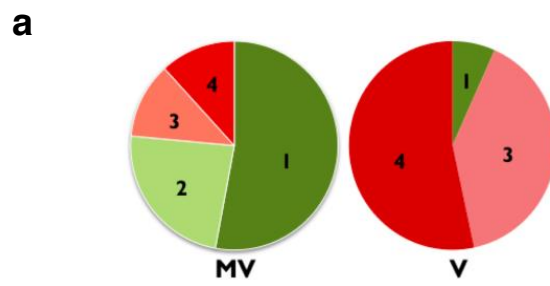


Figure 4

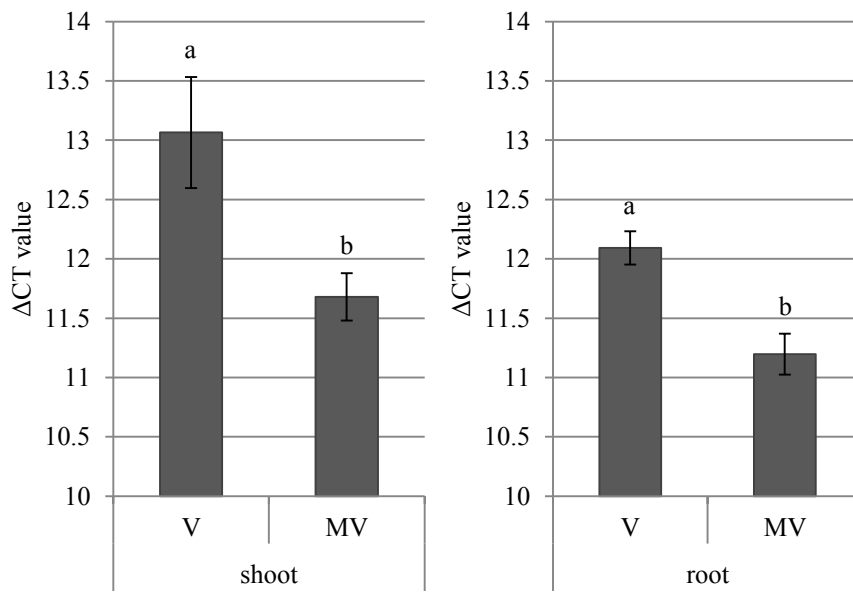


FIG.4

Figure 5

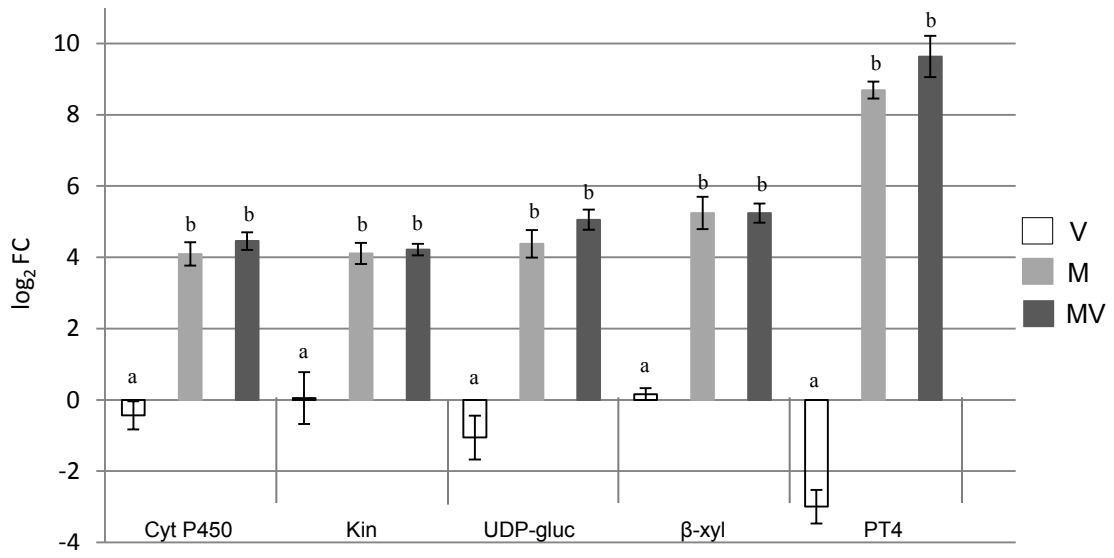


FIG. 5