

# Biocontrol potential of grapevine endophytes against grapevine trunk pathogens

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## Abstract

Grapevine Trunk Diseases (GTDs) are a major challenge to the grape industry worldwide. GTDs are responsible for considerable loss of quality, production, and vineyard longevity. Seventy five percent of Chilean vineyards are estimated to be affected by GTDs. GTDs are complex diseases caused by several species of fungi, including *Neofusicoccum parvum*, *Diplodia seriata*, and *Phaeoconiella chlamydospora*. In this study, we report the isolation of 169 endophytic and 209 epiphytic fungi from grapevines grown under organic and conventional farming in Chile. Multiple isolates of *Clonostachys rosea*, *Trichoderma* sp., *Purpureocillium lilacium*, *Epicoccum nigrum*, *Cladosporium* sp., and *Chaetomium* sp. were evaluated for their potential of biocontrol activity against fungal trunk pathogens. Tests were carried out using two dual-culture-plate methods with multiple media types, including agar containing grapevine wood extract to simulate in planta nutrient conditions. Significant pathogen growth inhibition was observed by all isolates tested. *C. rosea* showed 98.2% inhibition of all pathogens in presence of grapevine wood extract. We observed 100% pathogen growth inhibition when autoclaved lignified grapevine shoots were pre-inoculated with either *C. rosea* strains or *Trichoderma* sp.. Overall these results show that *C. rosea* strains isolated from grapevines are promising biocontrol agents against GTDs.

## Introduction

Grapevine trunk diseases (GTDs) are a major challenge to viticulture worldwide, because they compromise the productivity and longevity of grapevines (*Vitis vinifera* L.) and increase production costs (Munkvold et al. 1994; Bertsch et al. 2013; Kaplan et al. 2016; Gramaje et al. 2018). GTDs are one of the main phytosanitary problems of the grape industry also in Chile (Auger et al. 2004; Díaz et al. 2011). Chile is the first and fourth largest grape and wine exporter in the world, respectively (Felzensztein, 2014; Pizarro, 2018; USDA Foreign Agricultural Center 2019). In 2013, about 22% of the commercial vineyards in Chile showed symptoms of GTDs (Díaz et al. 2013; Guzmán, 2018).

38

39 GTDs are caused by fungi that often infect established grapevines through wounds produced during  
40 winter pruning (Rolshausen et al. 2010). GTDs can also spread during plant propagation (Aroca et al.  
41 2010; Gramaje and Armengol, 2011), with infections found in dormant wood cuttings and young  
42 grafted plants (Gramaje and Armengol, 2011; Waite and Morton, 2007; Billones-Baaijens et al.  
43 2013). In Chile, as in other viticulture areas, the most common microorganisms isolated from arms  
44 and trunks of grapevines with symptoms of GTDs are ascomycetous fungi and include  
45 *Phaeomoniella* (Pa.) *chlamydospora*, *Diplodia seriata* De Not., and *Neofusicoccum parvum* (Auger  
46 et al. 2004; Díaz et al. 2011; Díaz et al. 2011; Díaz and Latorre, 2013; Besoain et al. 2013).

47 Currently there are no curative treatments against GTDs beside surgical removal of the infected  
48 organs (Surico et al. 2006; Wagschal et al. 2008; Gramaje et al. 2018; Mondello et al. 2018;  
49 Sosnowski and Mundy, 2018). GTDs are managed mostly by practices that aim to prevent infections  
50 (Gramaje et al. 2018; Mondello et al. 2018). Widely adopted preventive practices include late  
51 pruning (Petzoldt, 1981; Munkvold et al. 1994), double-pruning (Weberet et al. 2007), and the  
52 application of protectants on fresh pruning wounds (Díaz and Latorre, 2013). Pruning wounds can be  
53 protected by benomyl and tebuconazole (Bester et al. 2007), inorganic compounds as boric acid  
54 (Rolshausen and Gubler, 2005), or natural antifungal compounds as organic extracts (Mondello et al.  
55 2018). Manual applications of these formulations as paints are effective, but costly and time-  
56 consuming, while spray applications are difficult due to the small surface and orientation of pruning  
57 wounds (Bertsch et al. 2013; Rolshausen et al. 2010; Wightwick et al. 2010). In addition, no genetic  
58 resistance against GTDs has been found in the grapevine germplasm (Surico et al. 2006; Wagschal et  
59 al. 2008).

60 Biocontrol of GTDs using microorganisms is a promising alternative. For example, *Trichoderma* spp.  
61 are effective as a protectant of pruning wounds (Halleen et al. 2010; Mondello et al. 2018). The goal  
62 of our work was to identify microorganisms with biocontrol potential among the natural microbial  
63 inhabitants of grapevines. Endophytes are microorganisms that inhabit and colonize the internal plant  
64 tissue without causing visible damage or illness in the host (Petri, 1991; Schulz and Boyle, 2005;  
65 Zabalgoageazcoa, 2008). These microorganisms are known to mediate plant-environment as well as  
66 plant-pathogen interactions (Zabalgoageazcoa, 2008). The contribution of different epiphytes and  
67 endophyte species to plant defenses has been widely documented (Arnold et al. 2003; Azevedo et al.  
68 2000; Pieterse et al. 2014). Plant defense induction and antibiotic substance production that inhibits  
69 the growth of pathogens and pests (Mousa and Raizada, 2013), such as fungi (Zabalgoageazcoa,  
70 2008), bacteria (Hardoim et al. 2008), viruses (Lehtonen et al. 2006), and insects (Azevedo et al.  
71 2000) have been reported. The rationale behind focusing on endophytes in the search of effective  
72 biocontrol agents against GTDs was two-fold (Wicaksono et al. 2017). First, endophytes are adapted  
73 to survive inside grapevines, therefore once applied they should have better chances to establish  
74 permanent populations than biocontrol agents selected from other biological systems and therefore  
75 provide long-lasting protection (Hardoim et al. 2008; Hardoim et al. 2015; López-Fernández et al.  
76 2016; Zabalgoageazcoa, 2008). Second, endophytes share the same niche with plant pathogens, thus  
77 in addition to plant-defense induction and antibiosis, they could also compete for space and nutrients  
78 with GTD pathogens (Zabalgoageazcoa, 2008).

79 Here we report the isolation and identification of endophytic and epiphytic fungi from grapevines  
80 grown in commercial vineyards in Chile. From this collection, we selected antagonist candidates and  
81 evaluated them for growth inhibition activity against the main GTD fungal species found in Chile, in  
82 co-culture, and in planta assays. We provide compelling evidence that endophytic and epiphytic

83 strains of *C. rosea* are strong antagonists of the main GTD species, which makes this species a  
84 promising candidate as a biocontrol agent to control GTDs. results.

85

## 86 **Materials and Methods**

### 87 **1 Vineyard sampled and plant material**

88 Samples of grapevine (*Vitis vinifera* L.) cv. Cabernet Sauvignon and Chardonnay were collected  
89 from four commercial vineyards located in the central valleys in Chile under either organic or,  
90 conventional farming systems in May 2017 (**Table 1**). Samples of cv. País were collected in  
91 September 2017 from a vineyard where diseases are not managed located in the Codpa Valley, Chile  
92 (**Table 1**).

93 **TABLE 1:** Sample locations

Vineyard	Variety	Location	Disease control	Planting Year
Site 1	Chardonnay	-35°26'26.8764"S, -071°50'01.8600"W	conventional	
	Cabernet Sauvignon	-35°26'26.8764"S, -071°50'01.8600"W	conventional	
Site 2	Chardonnay	-34°42'53.3736"S, -071°02'20.5008"W	organic	2011
	Cabernet Sauvignon	-34°42'53.3736"S, -071°02'20.5008"W	organic	2009
Site 3	Cabernet Sauvignon	-33°44'592476"S, -070°56'18.6972"W	conventional	
Site 4		-33°44'592476"S, -070°56'18.6972"W	organic	2000
Site 5	País	-18°28'42.6"S, -070°05'16.2"W	none	1850

94

### 95 **2 Isolation of endophytic fungi**

96 The isolation of endophytic fungi was performed following the methodology described in (Pancher et  
97 al. 2012). Briefly, shoots (50 cm long) and roots were cut into 10-cm-long fragments. Fragments  
98 were surface disinfected by rounds of 2 min serial immersions in 90% ethanol, then 2% sodium  
99 hypochlorite solution, and, 70% ethanol, followed by double-rinsing in sterile distilled water under  
100 laminar airflow. Absence of microbial growth on surface-sterilized shoots was confirmed by plating  
101 the distilled water from the last wash step on potato dextrose agar (PDA; BD-Difco) in Petri dishes,  
102 that were then incubated for 2 weeks at 25°C. After disinfection, fragments were further cut into 2.5  
103 mm pieces. Each section was placed on Petri dishes (90-mm diameter), placing the vascular bundle  
104 towards the growing media, containing: i) PDA (39 g L<sup>-1</sup>; BD-Difco), ii) malt extract agar (MEA,  
105 33.6 g L<sup>-1</sup>; BD-Difco), and iii) plain agar (AA, 20 g L<sup>-1</sup>; Difco), each one with antibiotics  
106 (streptomycin, 0.05 g L<sup>-1</sup>, and chloramphenicol, 0.05 g L<sup>-1</sup>). All Petri dishes were incubated at 25°C  
107 for 7 to 10 days under 12 h of light and 12 of darkness. Different colonies were tentatively identified  
108 based in morphology (Barnett and Hunter, 1955). Pure cultures were obtained from hyphal tip  
109 transfer to PDA media and maintained at 5°C.

### 110 **3 Isolation of epiphytic fungi**

111 For each plant, 1.5 g of soil in direct contact with roots was carefully collected. In a laminar flow  
112 bench, 13.5 ml of sterile distilled water was added, before vigorous agitation for 20 min in a  
113 horizontal position. After 5 min of decantation, serial dilutions of the supernatant were made. 10<sup>-3</sup>

114 and  $10^{-4}$  dilutions were used to inoculate PDA, MEA, and AA. To all media streptomycin,  $0.05 \text{ g L}^{-1}$   
115 and chloramphenicol,  $0.05 \text{ g L}^{-1}$  were added. Plates were incubated for 7 to 14 days at  $25^{\circ}\text{C}$ .

#### 116 **4 Taxonomic characterization of the fungal isolates**

117 DNA extraction from cultivable isolated fungi ( $n=387$  isolates) was performed as described in  
118 Morales-Cruz et al. (2015), with the following modifications. Mycelia from 7 to 21 days old fungal  
119 cultures were frozen with 3 mm metal beads in tubes at  $-80^{\circ}\text{C}$ . Tubes were shaken vigorously with a  
120 vortex for 5 minutes at maximum speed. Disrupted mycelia were resuspended in  $200 \mu\text{L}$  of nuclease-  
121 free sterile-distilled water and then homogenized in a vortex for 15 s. Mycelia was incubated at  
122  $100^{\circ}\text{C}$  for 10 min, followed by a centrifugation step at 14500 rpm for 2 min. An aliquot of  $10 \mu\text{L}$  of  
123 the supernatant was used for the PCR runs. A 1:20 or 1:50 dilution was made in case of PCR  
124 inhibition occurred. ITS sequences were PCR amplified using ITS1  
125 (TCCGTAGGTGAACCTGCGG) and ITS4 (TCCTCCGCTTATTGATATGC) primers (White et al.  
126 1990). A  $25 \mu\text{L}$  PCR reaction was carried out using  $2.5 \text{ uL}$  1XThermopol reaction buffer,  $0.5 \text{ uL}$  of  
127  $10\text{mM}$  dNTPs,  $0.5 \text{ uL}$  of  $10\text{uM}$  ITS forward and reverse primers,  $0.125 \mu\text{L}$  ( $1.25\text{U}/50 \mu\text{L}$ ) Taq DNA  
128 polymerase (Promega, USA) and  $10 \mu\text{L}$  of sample supernatant as a template. PCR reaction was  
129 performed with an initial denaturing step at  $95^{\circ}\text{C}$  for 2 min, and 35 cycles of  $95^{\circ}\text{C}$  for 30 s,  $52^{\circ}\text{C}$  for  
130 30 s (White et al. 1990), and  $72^{\circ}\text{C}$  for 1 min, followed by a final extension phase at  $72^{\circ}\text{C}$  for 5 min.  
131 The PCR product was purified and sequenced at Macrogen Inc., South Korea. Amplicon sequencing  
132 analysis was carried out with Geneious (R11.1). Taxonomic identities were determined with  
133 BLASTN using the UNITE database 7.2 (Nilsson et al. 2019).

#### 134 **5 Pathogenic fungal strains and control antagonists**

135 Isolates of *Phaeomoniella chlamydospora* (#11 A), *Diplodia seriata* (N°117 Molina),  
136 *Neofussicoccum parvum* (N°156 Lolol) and the endophytic antagonist *Trichoderma* sp. (Altair 607  
137 QR6 PB 6.0) were obtained from the Phytopathology Lab of Universidad de Talca. These isolates  
138 were purified in 2017 from *V. vinifera* L. trunks as part of another project. Also, MAMULL  
139 (*Trichoderma gamsii* Volqui strain, *Bionectria ochroleuca* Mitique strain, *Hypocrea virens* Ñire  
140 strain, BioInsumos Nativa, Chile), TIFI (Giteniberica de Abonos, España), Tebuconazole 430 SC  
141 (SOLCHEM, concentrated suspension, Chile) were used as positive controls.

#### 142 **6. Test of fungal antagonism**

143 Initial assessment of antagonistic properties was conducted against *D. seriata* as pathogen. Further  
144 evaluations on selected antagonists were carried out using *D. seriata*, *N. parvum*, and *P.*  
145 *chlamydospora*. Agar discs from a 7-day old actively growing colony were used. Co-culture assays  
146 were performed placing a 5 mm agar disc on one side of the Petri dish with PDA ( $39 \text{ g L}^{-1}$ ; Difco) or  
147 PA ( $200 \text{ g L}^{-1}$  grapevine propagation material,  $20 \text{ g L}^{-1}$  agar) and on the opposite side a 5 mm agar  
148 disc containing the antagonist strain. Plates were incubated at  $25^{\circ}\text{C}$  for 7-28 days in darkness  
149 (Badalyan et al. 2002) using a randomized complete block design. Registered bioproducts MAMULL  
150 and TIFI were used as antagonistic controls. Pathogen growth area was evaluated at 7, 14, 21, and, 28  
151 days post-co-culture (Schindelin et al. 2012). Inhibition percentage was calculated using the pathogen  
152 growth area when was cultured alone (C) or in interaction with the antagonist (T) according to the  
153 formula  $I = ((C-T)/C) * 100$  (Thampi and Bhai, 2017).

154 An in planta assay was also performed. Annual shoots were used for the experimental set-up to verify  
155 the antagonistic potential shown in plate co-culture. Several preliminary evaluations were carried out  
156 in order to test variability caused by autoclave sterilization of pruning material, humid-chamber moist

157 maintenance, type of inoculum and time needed for the pathogen to grow through the wood piece.  
158 Even though tissue was death, the overall shoot matrix structure was conserved after autoclave  
159 sterilization (data not shown). Internode portions of dormant cuttings were cut in 4.5 cm length  
160 pieces and then used fresh or autoclaved for 25 min at 121 °C. Agar mycelium plugs were evaluated  
161 as inoculum. In 2 days, pruning material in contact with the pathogen and/or antagonist plugs were  
162 covered in the mycelium. As the inoculum was too high, a spore suspension solution was used to  
163 inoculate the wood pieces. Mycelium/spore mix suspension of the pathogens *D. seriata* and *N.*  
164 *parvum* were prepared by flooding 30 days old plant agar culture (PA; 200 g L<sup>-1</sup> grapevine dormant  
165 cutting, 20 g L<sup>-1</sup> agar) with sterile distilled water. In the case of the antagonists *Clonostachys rosea*  
166 (isolates CoS3/4.24, CoR2.15 and R31.6) a spore suspension adjusted to 1 x 10<sup>7</sup> conidia mL<sup>-1</sup> was  
167 used as recommended. Antagonist inoculation was carried out adding 40 uL of antagonist fresh spore  
168 suspension until it reached the woody stem cut end by capillarity. Tebuconazole (60 mL/100L fields  
169 recommended doses; SOLCHEM, Chile) or sterile distilled water was applied in the same manner as  
170 controls. This experiment was carried out 5 times. Woody stem cuts were incubated in individual  
171 humid chambers for 24 hours. Then, 10 uL of fresh pathogen mycelia/spore mix suspension was  
172 inoculated on the same side where the antagonist was inoculated previously and immediately placed  
173 in a horizontal position, preventing suspension diffusion. Incubation was carried out in humid  
174 chambers for 3-7 days. Afterward, the surface of the woody stem was disinfected by rubbing with  
175 70% ethanol. With a hot sterile scalp, the bark and 0.5 cm of the woody stem ends were removed.  
176 Small pieces located at 1 and 2.5 cm from the inoculation point were collected and cultured in  
177 individual PDA plates at 25°C for 7 days. To evaluate the pathogen mycelia and spore suspension  
178 viability, 10 uL of the solution was inoculated in one side of the wooden piece as described above  
179 and immediately processed to obtain 3 mm pieces at 1 and 2.5 cm from the pathogen inoculation  
180 point. Every piece was cultured in PDA at 25 °C for 7 days. The presence of the pathogen on PDA  
181 was evaluated under a light microscope.

## 182 **7 Test of antagonist mechanism**

183 To characterize the mechanism of antagonism, the same experimental setup of co-culture was carried  
184 out on water agar (AA, 20 g L<sup>-1</sup>; Difco) with a microscope sterile slide covered by a thin layer of the  
185 same agar in its surface. Using a light microscope (MOTIC BA410), the sample was screened for  
186 loops of the antagonist hyphae around *N. parvum* and *D. seriata*, indicating mycoparasitism. This  
187 experiment was carried out 3 times. To determine antibiosis as the type of antagonist mechanism  
188 used, isolated fungi *E. nigrum* R39.1, *C. rosea* CoS3/4.4, and *Cladosporium* sp. B38d.2 were  
189 cultured in PDA plates (39 g L<sup>-1</sup>; Difco) over cellophane paper for 7 days. Cellophane paper with the  
190 fungal colony was then removed from the plate and a mycelial plug of *D. seriata* or *N. parvum* was  
191 placed in the centre. Plates were incubated for 7 days at 25°C and pathogen growth was evaluated.  
192 This experiment was carried out three times.

## 193 **8 Statistical analysis**

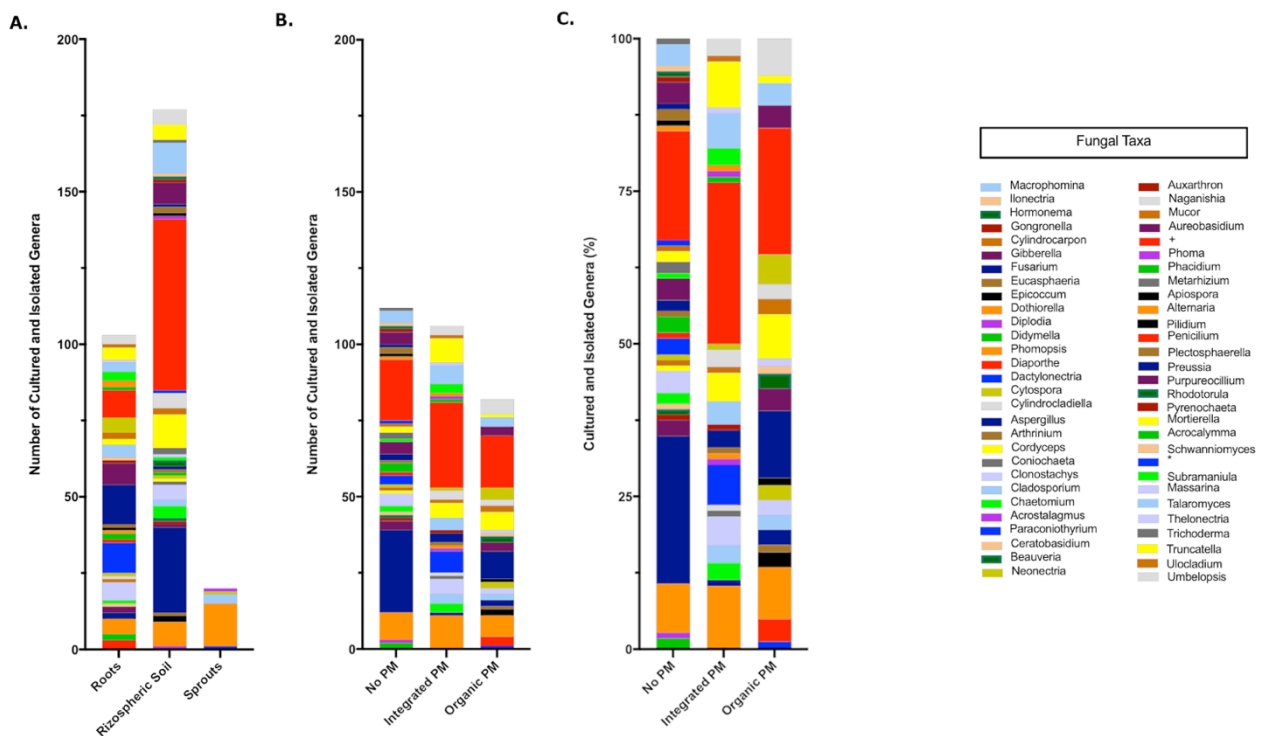
194 Statistical analysis was conducted with GraphPad PRISM 8 (8.1.1 version, 2019).

## 195 **Results**

### 196 **1. Isolation and identification of endophytic and epiphytic fungi**

197 A total of 102 vineyard samples were collected to isolate endophytic and epiphytic fungi associated  
198 with grapevines in Chile. Endophytic fungi were isolated from woody shoots, sprouts, and roots,  
199 while the epiphytic ones were obtained from the rhizosphere. Ninety samples were obtained from two

200 commercial vineyards in the central valleys of Chile and twelve from a vineyard in the Codpa Valley  
 201 that has not been managed for disease protection for over 150 years. A total of 222 and 166  
 202 morphologically distinct filamentous fungi and yeasts were isolated from the commercial vineyards  
 203 and the Codpa Valley, respectively. Fungi were isolated and characterized taxonomically using ITS1  
 204 and ITS4 sequences. All fungal sequences were at least 98% identical to the best BLASTn hit in the  
 205 UNITE database. We could assign taxonomy to a total of 300 isolates. The ITS sequence was  
 206 discriminant at the species level for 227 isolates. The remaining were assigned to the corresponding  
 207 genus or family. A total of 58 genera were represented, 37 and 38 among epiphytes and endophytes,  
 208 respectively. As expected, below ground samples (rhizosphere and roots) were more diverse (56  
 209 genera) than sprouts and woody stems (5 genera) (**Figure 1**).

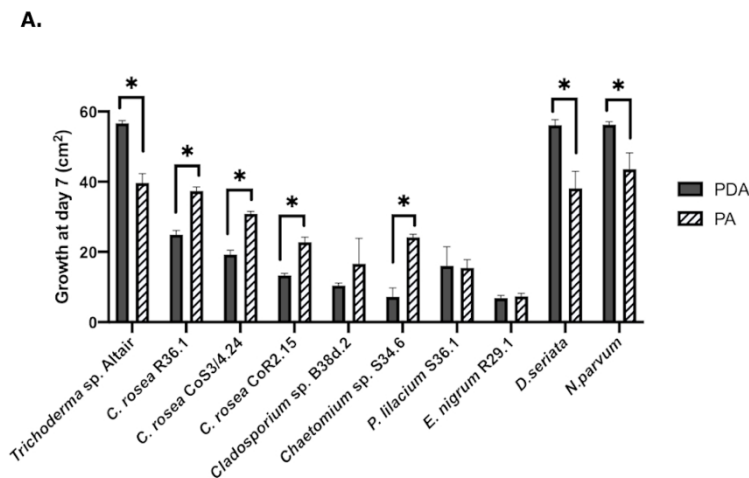


210  
 211 **FIGURE 1.** Taxonomic composition of the isolated fungi. Values are separated according to the source (A) and  
 212 phytosanitary regime (pest management program, PM) (B)(C). Cultured-isolates identified only to family level  
 213 Nectriaceae (+) and class level Dothideomycetes (\*) are also shown.

214  
 215 **2. Effect of fungal antagonists on the growth of GTD fungi in co-culture**

216 To identify potential biocontrol agents for further characterization, we screened all isolates for  
 217 antagonistic activity against *D. seriata* (**Supplementary Table S1**), a ubiquitous GTD pathogen.  
 218 Based on the results this initial screen, a total of ten isolates were selected for further  
 219 characterization: *Trichoderma* sp. Altair, *Epicoccum nigrum* R29.1, three isolates of *Clonostachys*  
 220 *rosea* (R 31.6, CoR2.15 and CoS3/4.24), *Cladosporium* sp. B38d.2, *Chaetomium* sp. S34.6 and  
 221 *Purpureocillium lilacium* S36.1. These ten isolates were chosen also because they were previously  
 222 described as antagonistic to other pathogens (Fávaro et al. 2012; Hung et al. 2015; Cota et al. 2009;  
 223 Solano Castillo et al. 2014; Costadone and Gubler, 2016).

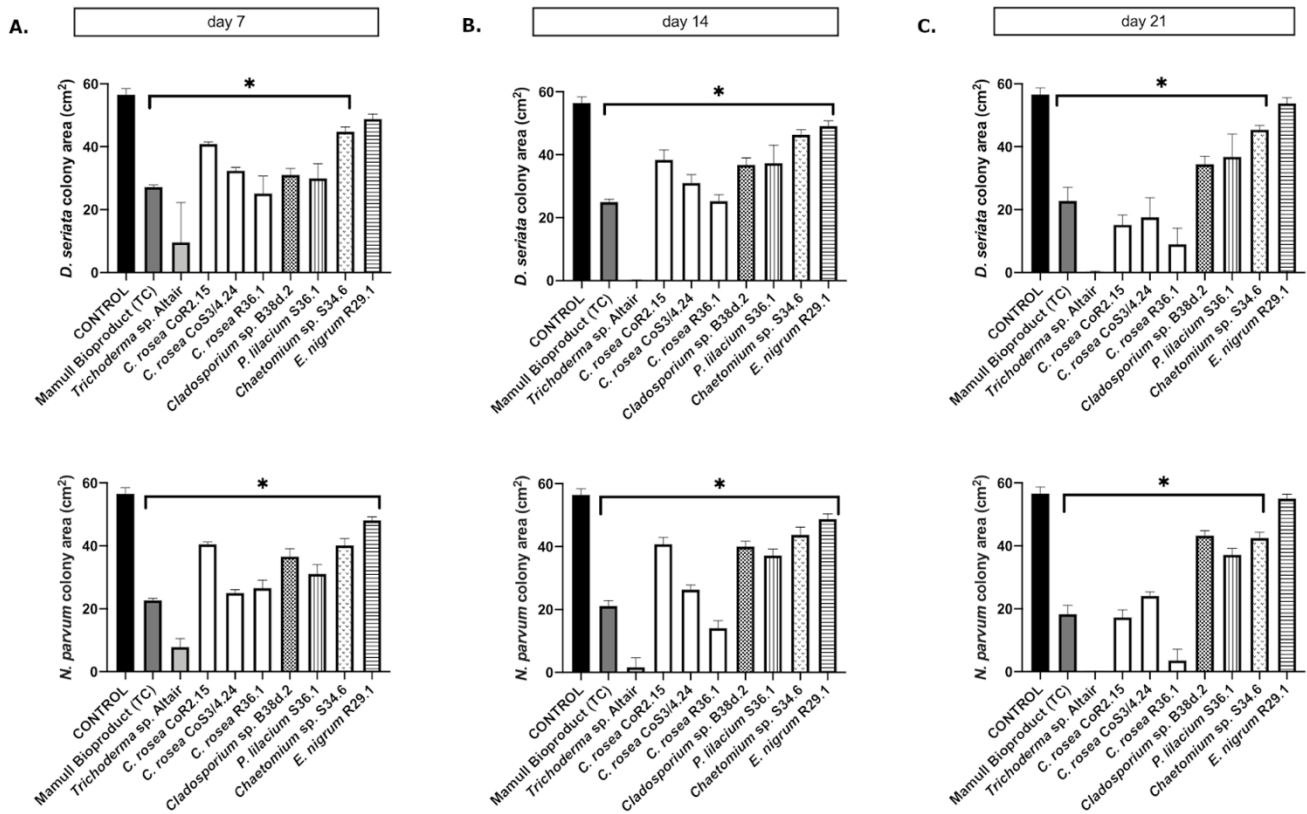
224 To assess the antagonistic ability of the ten selected isolates, we co-cultured each one of them with *D.*  
225 *seriata* and *N. parvum*, two of the main fungi causing GTDs in Chile. Co-cultures were carried out on  
226 two different types of growth media: the commonly used potato dextrose agar (PDA) and a substrate  
227 made of agar and ground woody grapevine tissue (aka, grapevine plant agar (PA)) that simulates in  
228 planta nutrient composition (Massonnet et al. 2017). Isolates displayed a wide range of growth rates,  
229 which often differed between PDA and PA (**Figure 2**). Interestingly, most endophytes, including all  
230 *C. rosea* isolates, grew faster on PA than PDA. Different growth rates reflected the patterns of  
231 inhibition of *D. seriata* and *N. parvum* (**Figures 3 and 4**). The *Trichoderma* Altair isolate grew faster  
232 than the rest on PDA and reached its maximum inhibitory effect on both pathogens as early as day 7  
233 in PDA. Growth inhibition only occurred upon physical contact between colonies of *Trichoderma* sp.  
234 and the pathogens. The faster growth on PA of the endophytes *Clonostachys*, *Chaetomium*,  
235 *Epicoccum*, and *Cladosporium* was associated with greater pathogen inhibition rates on this substrate  
236 compared to PDA, especially for the *Clonostachys* isolates. In PA, *C. rosea* overgrew the pathogen  
237 colony at least 7 days earlier than in PDA. All *C. rosea* strains inhibited over 98% pathogen growth  
238 in PA at day 21 (**Figure 4**). *Chaetomium* sp. S34.6 isolate inhibited pathogen growth by slowly  
239 growing in the plate until colony contact. By day 21 *Chaetomium* sp. S34.6 inhibited *D. seriata* and  
240 *N. parvum* growth by 59.1% and 86.75%, respectively, about two-fold the pathogen growth  
241 inhibition showed in PDA. Both species completely overgrew both pathogen colonies around 28  
242 days. The antagonistic effect of *C. rosea* R36.1 and CoS3/4.24 occurred upon direct contact between  
243 colonies, which overgrew the pathogen colony within 21 days of growth. Instead, pathogen growth  
244 inhibition of *C. rosea* CoR2.15, *Purpureocillium lilacium* S36.1, and *E. nigrum* R29.1 happened  
245 without evident physical contact between colonies. In PDA, *E. nigrum* produced a wide 0.8 to 1.2 cm  
246 orange-colored halo that was partially colonized only by *N. parvum* after 21 days of growth. The  
247 slow and limited growth of *Neofusicoccum parvum* was also visible in the halo produced by  
248 *Purpureocillium*. *Cladosporium* sp. B38d.2 showed an interesting difference in antagonist activity  
249 against *N. parvum* in PA, reaching its higher inhibition rate (**Figure 4**). When cultured with this  
250 pathogen, *Cladosporium* strongly sporulated, covering the entire plate, and stopped *N. parvum*  
251 early growth.



252

253 **FIGURE 2.** Comparison of the growth area of antagonists and pathogens in two media. Growth was measured after 7 days  
254 in PDA (potato dextrose agar) and PA (plant agar). Bars with asterisk are significantly different from the control (Paired T  
255 test,  $P < 0.001$ ). Error bars represent the standard error of the mean,  $n = 5$ .

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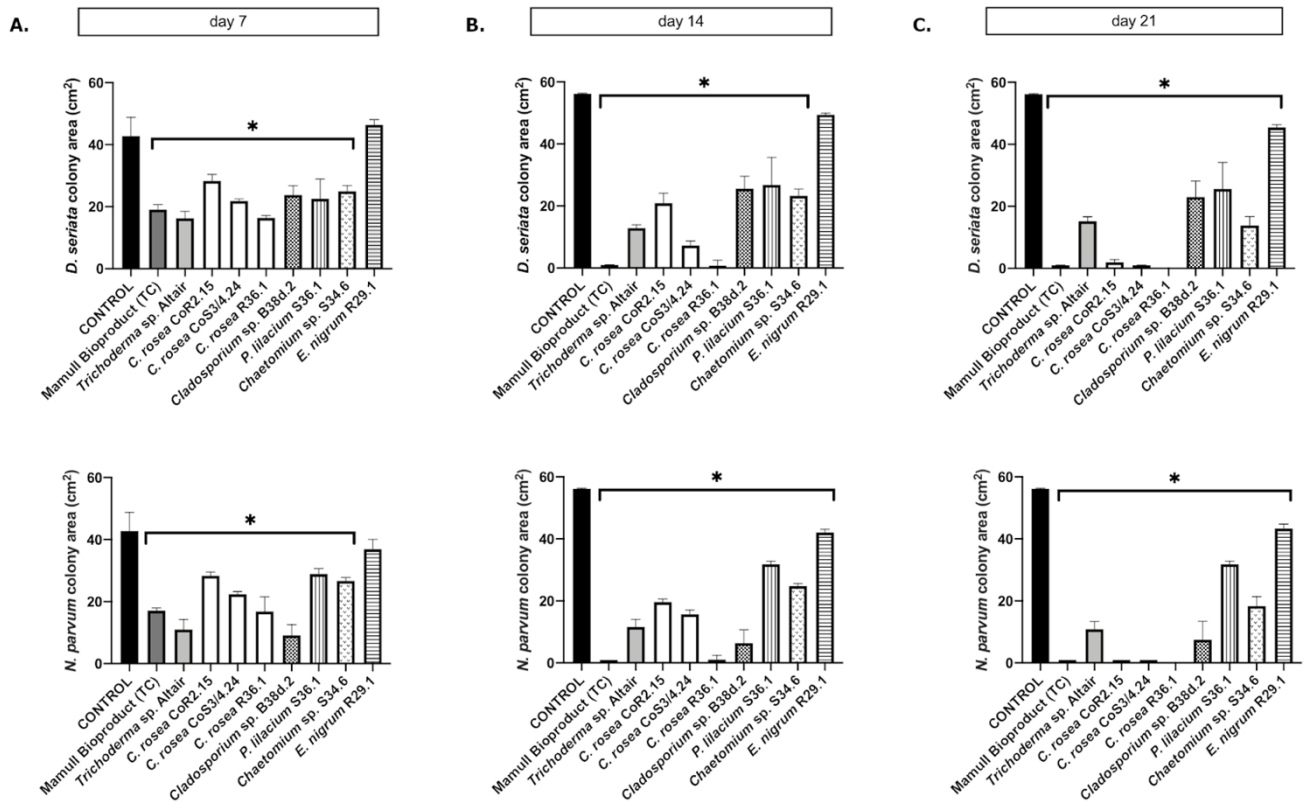


257

258 **FIGURE 3.** Colony area measured after (A) 7, (B) 14 and (C) 21 days of inoculation of *D. seriata* (upper graphics) and *N.*  
 259 *parvum* (bottom graphics), when growing alone (control) or in co-culture with the antagonists in PDA. Bars with asterisk  
 260 are significantly different to the control (Tukey's test,  $P < 0.001$ ). Error bars represent the standard error of the mean,  $n=5$ .

261



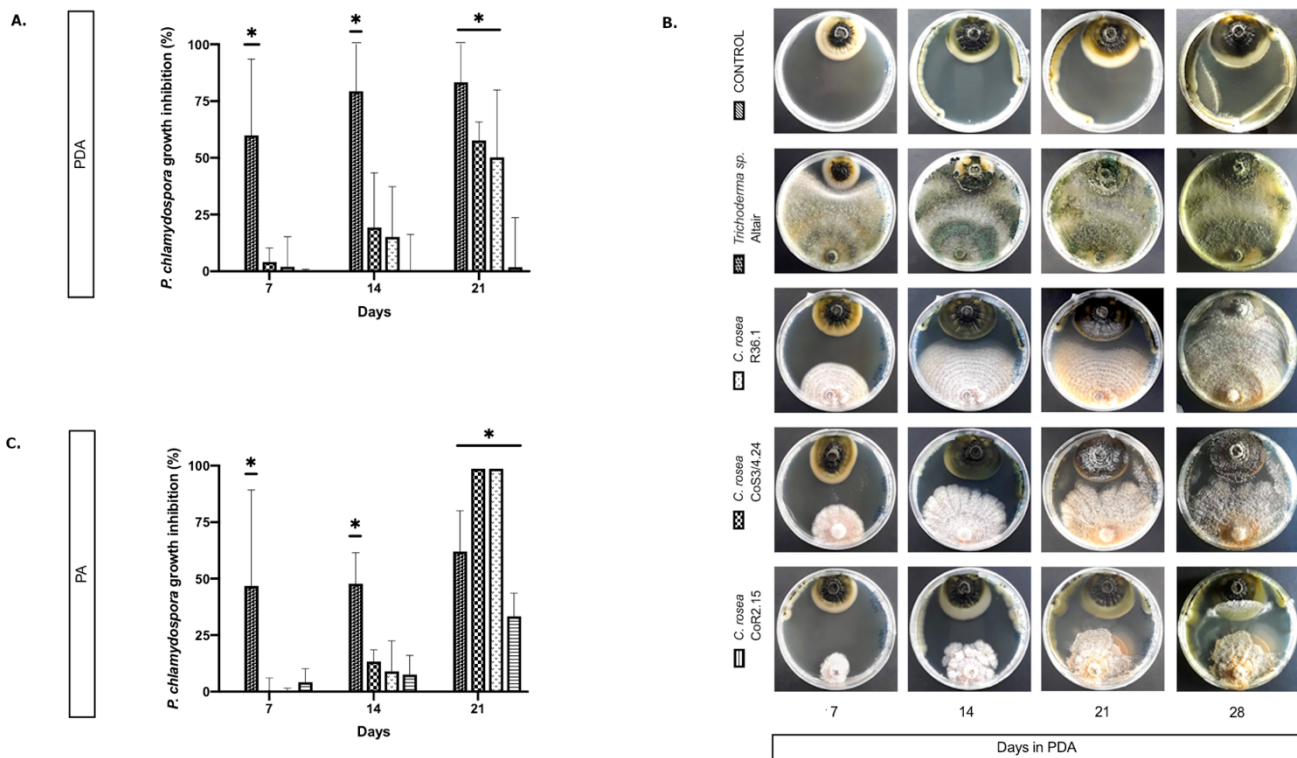


262

263 **FIGURE 4.** Colony area measured after (A) 7, (B) 14 and (C) 21 days of inoculation of *D. seriata* (top row) and *N. parvum*  
 264 (bottom row), when growing alone (control) or in co-culture with the antagonists in PA. Bars with asterisk are significantly  
 265 different to the control (Tukey's test, P<0.001). Error bars represent the standard error of the mean, n=5.

266

267 On PA, *C. rosea* inhibited *P. chlamydospora* almost completely (99.9%). Interestingly, *C. rosea*  
 268 growth first paused without evident contact between colonies (**Figure 5**) at day 7, but later, by 14  
 269 days, it overgrew completely the pathogen colony. Overgrowth was also observed with *Trichoderma*  
 270 sp. Altair in PDA.



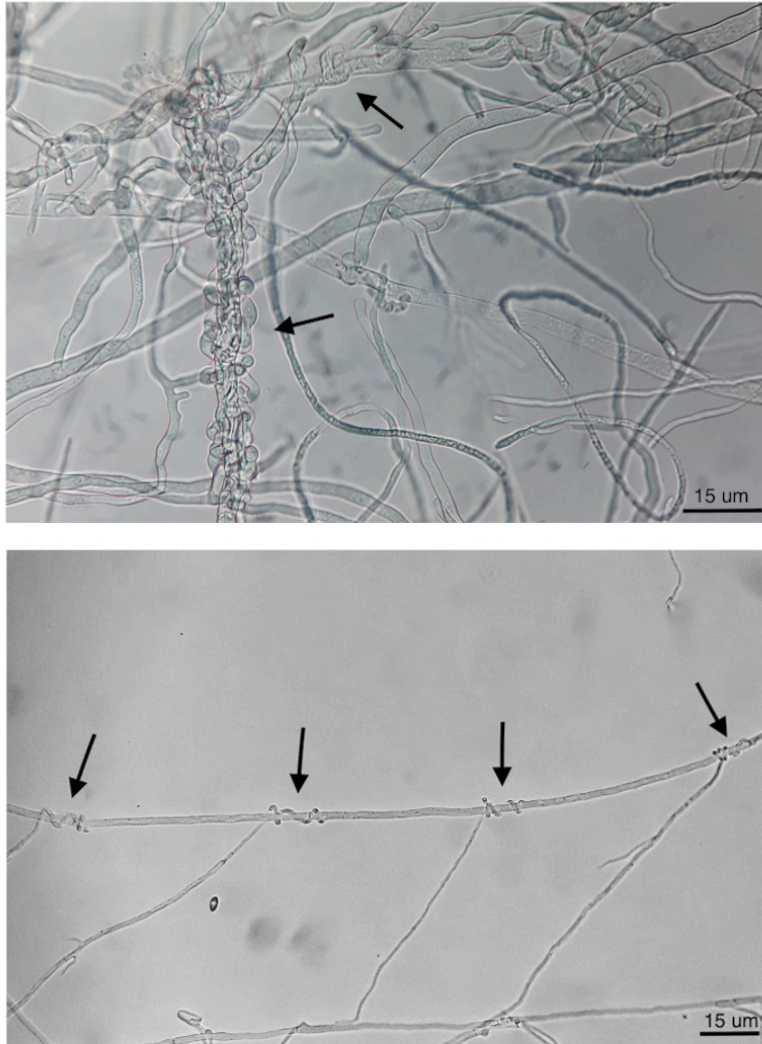
271

272 **FIGURE 5.** Colony area measured at day 7, 14 and 21 postinoculation of the pathogen *P. chlamydospora* when cultured  
 273 alone or with the antagonists: *C. rosea* CoR2.15, CoS3/4.24, R36.1 or *Trichoderma* sp. Altair. Growth area was evaluated  
 274 in potato dextrose agar, PDA, (A) and (B) and, in grapevine plant agar, PA, (C). Bars with asterisk are significantly different  
 275 to the control (Tukey's test,  $P < 0.001$ ). Error bars represent the standard error of the mean,  $n = 5$ .

276

### 277 3. Characterization of the mechanisms of antagonism

278 The antagonistic activity of endophytic biocontrol agents can depend on the competition for nutrients  
 279 and induced resistance in the plant, and/or direct interaction with the release of pathogen inhibitory  
 280 compounds or mycoparasitism (Köhl et al. 2019). During co-culture, isolates of *C. rosea* showed  
 281 pathogen inhibition both before and after direct contact between colonies, suggesting that both  
 282 mechanisms could underlie its antagonistic properties. To evaluate the mode of action of *C. rosea*  
 283 and *Trichoderma* sp. Altair, we studied under a light microscope the mycelia in the zone of  
 284 interspecific interaction. For *C. rosea* CoS3/4.24 and R36.1, hyphal coiling, a sign of  
 285 mycoparasitism, was consistently observed in all co-cultures with *N. parvum* and *D. seriata* (**Figure**  
 286 **6**). Hyphal coiling was only occasionally found in *Trichoderma* sp. Altair.



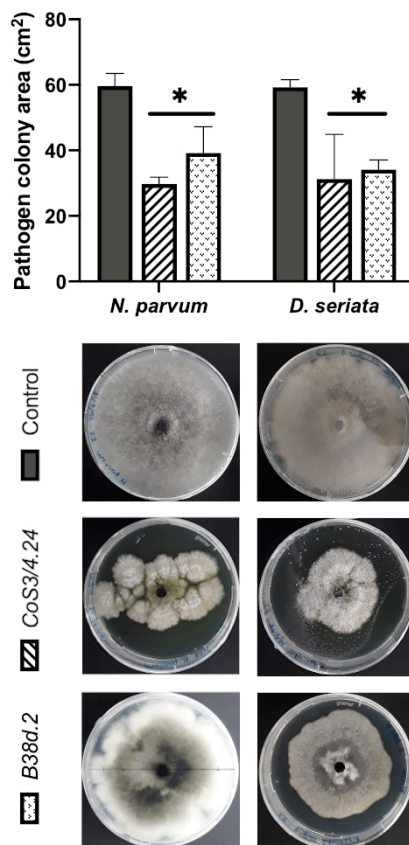
287

288 **FIGURE 6.** Hyphal coiling of (A) *Trichoderma* Altair against *D. seriata* and (B) *C. rosea* CoS3/4.24 around hyphae of *N.*  
289 *parvum* (magnification 400X).

290

291 When *C. rosea* epiphytic strain CoS3/4.24 was co-cultured with *D. seriata* or *N. parvum*, pathogen  
292 growth terminated before direct contact with *C. rosea* in correspondence of the halo surrounding the  
293 antagonist. In this case, the inhibitory activity of *C. rosea* may depend on a secreted antibiotic  
294 compound. This was also observed when *Cladosporium* sp. B38d.2 was used as antagonist. To test  
295 the inhibitory activity of the *C. rosea* secretome, we inoculated *C. rosea* on a sterilized cellophane  
296 membrane overlaid on PDA and incubated for seven days. The cellophane membrane was shown to  
297 be permeable to metabolites secreted by fungi (Dennis and Webster, 1971; Chambers, 1993;  
298 Sharmini et al. 2004; Rodriguez et al. 2011). After removing the cellophane membrane together with  
299 the *C. rosea* mycelia, we inoculated the plates with pathogens and measured their growth in  
300 comparison with normal PDA. Pathogen growth was significantly reduced on plates previously

301 incubated with *C. rosea*, likely due to the secreted metabolites that permeated through the cellophane  
302 membrane (**Figure 7**). The inhibition caused by the secreted metabolites of *C. rosea* CoS3/4.24 led to  
303 a 47.2% and 50.1% reduction in growth of *D. seriata* and *N. parvum*, respectively. In the case of  
304 *Cladosporium* sp., 34.26% and 42.46% inhibition was observed against *N. parvum* and *D. seriata*,  
305 respectively. Changes in the pathogen colony morphology were also observed, especially when in  
306 contact with *C. rosea* CoS3/4.24 isolate secondary metabolites. *N. parvum* colony turned into several  
307 flat independent colonies with undulate margins, while *D. seriata* grew as one colony with irregular  
308 shape.



309

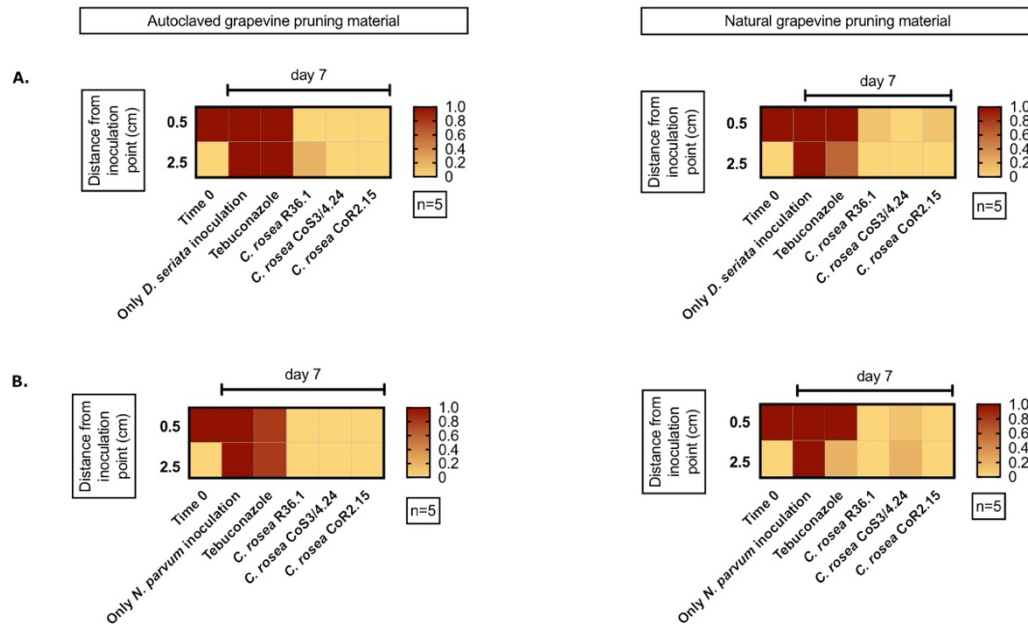
310 **FIGURE 7.** Pathogen growth over secondary metabolites produced by antagonists *C. rosea* CoS3/4.24, *Cladosporium* sp.  
311 B38d.2 in PDA. Bars with asterisk are significantly different to the control (Tukey's test,  $P < 0.001$ ). Error bars represent  
312 the standard error of the mean,  $n=5$ .

313

#### 314 **4. Effect of fungal antagonists on the growth of GTD fungi in one-year old grapevine woody** 315 **shoots**

316 As both growth and inhibition rates of GTD pathogens were significantly different in media  
317 containing grapevine annual shoot extract (plant agar, PA), we extended the testing of antagonism by

318 using one-year-old lignified shoots (aka canes) as a substrate for co-cultures. We tested both sterile  
319 (autoclaved) and non-sterile canes. After 7 days, *C. rosea*, *N. parvum*, and *D. seriata* colonized  
320 completely the internal tissue of 4.5 cm-long autoclaved canes. The antagonists *C. rosea* strains were  
321 recovered in all pathogen co-inoculated samples after 7 days (**Figure 8**). No pathogen growth was  
322 observed at 0.5 cm from the pathogen inoculation point when treated with the antagonists.  
323 Interestingly, under the same conditions, Tebuconazole, a commercial synthetic fungicide, did not  
324 reduce *D. seriata* nor *N. parvum* growth.



325

326 **FIGURE 8.** Presence of the pathogen *D. seriata* (A) and *N. parvum* (B) in autoclaved (left graphics) and natural (right  
327 graphics) grapevine pruning material pre-inoculated with the antagonist. In red is shown 100% recuperation of the pathogen.

328

329 We also performed the co-culture experiments on canes that were not subjected to autoclaving.  
330 Pathogens colonized the entire cane in 7 days in absence of any antagonist. In less than 0.1% and  
331 10% of the co-culture assays, *N. parvum* and *D. seriata* were recovered from plant tissue previously  
332 inoculated with *C. rosea* isolates, respectively. In the case of CoS3/4.24 isolate, *N. parvum* and *D.*  
333 *seriata* growth inhibition was observed in 80% and 100% of the assays, respectively. In summary,  
334 the antagonistic potential of the *C. rosea* isolates shown in agar plate was confirmed in grapevine  
335 propagation material.

## 336 Discussion

337 We isolated fungi from grapevines to find potential biocontrol agents against GTDs. As they share  
338 the same host with pathogens, these fungi may provide longer-lasting protection of grapevine tissues  
339 than biocontrol agents identified on other plant species (Zabalgogea, 2008; Latz et al. 2018).  
340 Three hundred eighty-seven different fungi and yeast were isolated and identified from multiple  
341 grapevine tissues and pest management systems. The observed diversity was limited to culturable

342 fungi, since no cultivation-independent identification tools were applied. Taxa were determined  
343 solely based on the ITS sequence. Further validation using other informative sites, such as nu-SU-  
344 0817-59 and nu-SU-1196-39 (Borneman and Hartin, 2000) or TEF-1a (Ichi-Ishi and Inoue, 2005),  
345 would provide additional resolution for some of the isolates we were not able to characterize at the  
346 species level. As expected, rhizospheric soil showed to hold more fungal diversity than roots, and  
347 sprouts showed less cultivable diversity than any other sample. This was in agreement with previous  
348 studies using amplicon sequencing (Tan et al. 2017).

349 As the focus of this work was to find microorganisms able to colonize the grapevine persistently, we  
350 conducted this search during late Winter, at the beginning of the cold and wet season, when  
351 potentially beneficial microorganisms may compete with pathogens for the colonization of the host  
352 through pruning wounds (Rolshausen et al. 2010; Travadon et al. 2016; Arnold et al. 2003). Even if  
353 we could collect more samples from commercial vineyards than from the 150 year-old vines in the  
354 Codpa valley, the number of fungal taxa isolated from Codpa was higher than in commercial  
355 vineyards. The greater diversity found in Codpa might be due to the older age of the vines as well as  
356 the lack of pathogen control practices throughout the life of the vineyard, even if other cultural  
357 management practices as fertilization with animal manure have been done over generations.

358 All fungi we isolated, characterized, and tested, with the exception of *Epicoccum nigrum* showed a  
359 significant growth inhibition of *N. parvum* and *D. seriata* in co-cultures on both PDA and PA. The  
360 *Trichoderma* Altair isolate and all *C. rosea* strains completely overgrew both pathogens by day 21.  
361 This was also observed against the pathogen *P. chlamydospora* in PA. However, variable biocontrol  
362 efficacy was observed between different isolates of the same species, as reported in (Inch and Gilbert,  
363 2007). For example, the epiphytic isolate *C. rosea* CoS3/4.24 grew faster on media and overgrew the  
364 pathogen earlier than the other *C. rosea* isolates. In contrast, the endophytic isolates of *C. rosea*  
365 showed better inhibition of *N. parvum* in grapevine woody shoots. The endophytic isolate of  
366 *Cladosporium* also displayed antagonism in co-culture, in particular against *N. parvum* on PA. Its  
367 inhibitory activity seemed to be due to the high sporulation rate and not to the rapid growth of the  
368 mycelium observed in others (Schöneberg et al. 2015). *Cladosporium* sp. produces a great amount of  
369 black, hydrophobic spores, and a small mycelium underneath the dense spore mass. On PA as well as  
370 PDA, *Chaetomium* sp. showed a significant reduction of growth of *N. parvum* and *D. seriata*,  
371 although weaker than that of *Trichoderma*. The antagonistic activity of *Chaetomium* may be due to a  
372 slow mycoparasitism. Hyphae of *Chaetomium* has been described to penetrate and coil around  
373 pathogen hyphae at day 30 of co-culture (Hung et al. 2015). Strains of *Chaetomium* have also shown  
374 antagonist activity against different pathogens as *Phytophthora nicotianae* (Hung et al. 2015),  
375 *Rhizoctonia solani* (Gao et al. 2005) and *Fusarium oxysporum* (Huu Phong, 2016) among others.  
376 Some strains presented antibiosis as an antagonist strategy, but mycoparasitism has been also  
377 described for this genus (Hung et al. 2015).

378 *C. rosea* showed limited antagonism at early stages of co-culture on artificial media and completely  
379 inhibited pathogen growth only after 21 days. Importantly, *C. rosea* was particularly effective against  
380 pathogen colonization of autoclaved woody shoots. Fungal growth dynamics and, therefore, the  
381 interaction between colonies are likely influenced by the type of media (Schöneberg et al. 2015b), in  
382 particular when nutrient-rich media are compared with substrates poor in nutrients, such as PA and  
383 woody tissue. It is worth noting that different isolates displayed different antagonistic activities  
384 depending on the substrate. For example, *C. rosea* isolates R36.1 and CoR2.15 showed higher  
385 pathogen inhibition than CoS3/4.24 on woody shoots that were not autoclaved. Interestingly, R36.1  
386 and CoR2.15 were endophytic, while CoS3/4.24 was isolated from the rhizosphere. Although we did  
387 not find the same pattern when autoclaved tissue was used, the different behavior of endophytic and

388 epiphytic isolates supports the overall strategy to search for potential biocontrol agents among the  
389 natural inhabitants of grapevines.

390 Generally recognized control mechanisms for fungal biocontrol agents are (1) competition for  
391 nutrients and space, (2) induced resistance in the plant, both consisting in an indirect interaction with  
392 the pathogen, (3) inhibition through antibiosis, and, (4) mycoparasitism (Latz et al. 2018; Köhl,  
393 2019). The formation of short loops of the antagonist's hyphae around hyphae from another fungal  
394 species also called hyphal coiling (Assante et al. 2004; Barnett and Lilly, 1962; Gao et al. 2005). The  
395 coiling establishes an intimate contact with the parasitized hypha, penetrating the hypha and  
396 delivering antibiotic compounds and cell-wall degrading enzymes (Barnett and Lilly, 1962). This  
397 type of mycoparasitism has been commonly found in the genus *Trichoderma* (Howell, 2003; Benítez  
398 et al. 2004) and reported in *C. rosea* (Barnett and Lilly, 1962; Morandi, 2001). The *Trichoderma* sp.  
399 Altair isolate produced hyphal coils and also the *C. rosea* strains we tested. In all cases, we found a  
400 strong correlation between coiling and antagonism suggesting that mycoparasitism plays an  
401 important role in the interaction with the pathogens. In the case of *C. rosea* CoS3/4.24, a yellowish  
402 halo around the antagonist colony was present. Antibiosis was previously described for this species  
403 (Iqbal et al. 2017), but not all strains of the species show antibiotic production (Moraga-Suazo,  
404 2016). Further studies should be performed with the *C. rosea* isolates as this might have important  
405 applications in agro-industrial areas (Karlsson et al. 2015). Direct interaction with the pathogen mode  
406 of action, as mycoparasitism and antibiosis, are highly desirable mechanisms for further production  
407 of commercial biocontrol agents, as they expose lower risks of human, plant and, environmental  
408 toxicity (Köhl, 2019).

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#### 413 **Conflict of Interest**

414 No conflict of interest declared.

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