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1        **Balance between resilient fruit surface microbial community and**  
2        **population of *Monilinia* spp. after biopesticide field applications**

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22 **Abstract**

23 The microbial diversity on the host plant surface must be maintained because population  
24 diversity and quantity are essential to avoid disease development. It would be necessary  
25 examine the patterns and mechanisms associated with the massive and reiterative  
26 introduction of a microbial pest control agent. The effect of inundative releases of the  
27 biopesticide contained *Penicillium frequentans* for the control of *Monilinia* spp  
28 populations, and the effect on the fruit surface microbiota on 18 stone fruit orchards  
29 located in four European countries for more than two crop seasons against brown rot were  
30 studied. *P. frequentans* was monitoring after application in order to assess whether was  
31 persistent or not in the environment. Hydrolysis of fluorescein diacetate and denaturing  
32 gradient gel electrophoresis were used to studied *P. frequentans* effects on fungal and  
33 bacteria non-target on fruit surface. Effect of *P. frequentans* formulations on the  
34 populations of *Monilinia* spp. on fruit was also recovered in different orchards. *P.*  
35 *frequentans* population on stone fruit surfaces showed a large range between 100  
36 CFU/cm<sup>2</sup> to 10,000 CFU/cm<sup>2</sup>, where postharvest recovered populations were more than  
37 10-100-fold than preharvest. Population of *P. frequentans* varied between orchards and  
38 years, rather than by formulations. *P. frequentans* formulation reduced *Monilinia* spp.  
39 population and brown rot and latent infections caused by this pathogen at preharvest and  
40 harvest time, while stabilizing or increasing antagonist populations and avoiding non-  
41 target impacts. However, fungicides reduced significantly the microbial activity on peach  
42 surfaces.

43 **Keywords:** non target effect, risk assessment, biocontrol, microbiota, *Penicillium*  
44 *frequentans*.

45

## 46 1. Introduction

47 *Penicillium frequentans* Westling is an indigenous specie from Mediterranean area  
48 and is also found in different types of climates worldwide (Melgarejo et al., 1985;  
49 Ramirez, 1982). *P. frequentans* has been isolated from various substrates and habitats  
50 such as water, wood pulp, food products (cereals, seeds and dried fruits, fresh fruits and  
51 fruit juices, dairy products), and soils (Domsch et al., 1983). *P. frequentans* strain 909  
52 (Pf909) is common constituent of the resident microbiota of Spanish peaches, was  
53 isolated from of peach flowers and have previously demonstrated good efficacy to control  
54 brown rot caused by *Monilinia* spp. in stone fruit (Melgarejo et al., 1986). Species present  
55 naturally in the pathosystems should be good candidate for biocontrol agents (BCA)  
56 (Köhl et al., 2019). Pf909 can be used as an effective and safe biological control agent  
57 (BCA) against brown rot because it is able to adapt to different environmental conditions  
58 such as a broad range of pH, it was resistant to UV damage, low and high temperatures,  
59 and desiccation conditions (Guijarro et al., 2017a). Suspension concentrate of Pf909  
60 conidia are potential biocontrol products to reduce the occurrence of peach and nectarine  
61 brown rot caused by *Monilinia* spp. at pre- and postharvest by competitively excluding  
62 the pathogen from twigs and the fruit surface (Guijarro et al., 2017b). Natural background  
63 level of *P. frequentans* during stone fruit growth season ( $10-10^2$  CFU per flower or fruit)  
64 are insufficient for controlling brown rot (De Cal and Melgarejo 1992; Guijarro et al.,  
65 2008). Peach surface had to be extensively covered by Pf909, where it will only be  
66 effective when its concentration is high enough and substantially greater than that of  
67 *Monilinia* (Guijarro et al., 2008).

68 BCAs could disturb indigenous microbial populations if they were applied to plant in  
69 sufficient numbers (Brimner et al., 2003; Winding et al., 2004), such as had been observed  
70 after chemical treatments (De Cal and Melgarejo, 1992). One of the most important

71 concerns associated with the use of BCAs in plant protection is the possible disruption of  
72 microbial processes and the important ecological functions associated therewith. Many  
73 BCAs produce metabolites that inhibit or suppress other organisms as *Trichoderma*  
74 *atroviride* strain SC1 used against the fungus *Armillaria mellea* by the production of cell  
75 wall-degrading enzymes and antibiotics (Lu et al., 2004; Pertot, 2016). The host microbial  
76 communities play very important roles in the equilibrium of the ecosystem, especially in  
77 the maintained of non-disable microorganism population (Massart et al., 2015). To  
78 conserve or improve biodiversity is a general objective of sustainable cropping and  
79 enhancing abundance and efficacy of the natural enemies existing community as a priority  
80 for this production system (IFOAM Anonymous, 2014; Zehnder et al., 2007).

81 Non-target effects can be defined as effects of the introduced BCA on organisms other  
82 than the target organisms or on biogeochemical cycles (Winding et al., 2004). For  
83 environmental risk analysis, direct or indirect non-target effects mediated through a chain  
84 of events or interactions among organisms will cause concern. Non-target effects can be  
85 categorized in the same way as Domsch et al. (1983) categorized the side effects of  
86 agrochemicals on soil microorganisms, as negligible, tolerable, and critical, depending on  
87 the magnitude of the effect and the time needed for the system to recover. A prerequisite  
88 for introducing the BCA into the environment is generally that, in addition to effective  
89 disease suppression, the effects on non-target organisms should be at least tolerable, if  
90 not negligible (Winding et al., 2004). To this end, knowledge concerning the microbial  
91 ecology of the target habitats is necessary for reasonable risk assessment studies relating  
92 to the release of beneficial microorganisms (Anonymous, 2007, OECD).

93 Understanding the dynamic populations of the BCA and among the BCA and resident  
94 microbial communities in the environment is crucial not only for the efficacy of the BCA  
95 in the control of the target pathogens, but also for the environmental risk assessment.

96 Community-level physiological profiles of soil bacteria were evaluated using the  
97 Biolog® method, which tests the ability of a microbial community to utilize different C  
98 substrates contained in a microplate (Lupwayi et al., 2009). In the last decade, several  
99 techniques based on culture-independent molecular methods have also been developed  
100 for the study of microbial environmental communities (Massart et al., 2015). For the rapid  
101 estimation of the population composition with a highly reproducible profile in a large  
102 number of samples, fingerprinting techniques such as terminal restriction fragment length  
103 polymorphism (T-RFLP) or the denaturing gradient gel electrophoresis (DGGE) were  
104 probably one of the most suitable approaches (Hunter et al., 2006). Fingerprinting  
105 techniques provided information on the diversity and dynamics of, e.g., ribotypes in an  
106 environmental sample in response to environmental triggers (Dunbar et al., 2001, 2000;  
107 Gans et al., 2005). Fluorescein diacetate (FDA) has also been used since early 90s as a  
108 measure of microbial activity, and it is generally applied to estimate total microbial  
109 activity and has been proposed to be used as a biochemical/biological indicator of  
110 microbial activity in different ecological niches (Vivian et al., 2013). The current  
111 approach tools are based on next generation technologies (NGS) are revolutionizing  
112 research on environmental microbiology and in the future will shed light into relevant  
113 further questions in BCA environmental behavior.

114 Biocontrol research on Pf909 has long been focused on the study of strain biology  
115 and on its interaction with pathogens (Guijarro et al., 2017a; 2017b) and host plants  
116 (Guijarro et al., 2008). Further focus on plant-associated microbial communities is  
117 necessary for better understanding the integrate role of Pf909 as a BCA with the natural  
118 microbiota on brown rot control. Therefore, unwanted, unspecific actions of the  
119 introduced Pf909 beneficial microorganism against non-target organisms have to be  
120 assessed. The objectives of these studies were to determine the potential effect of

121 inundative releases of Pf909 for non-target species and to investigate whether their  
122 suitability differs from those of the target *Monilinia* spp. under different real field  
123 conditions, and their relationship to the success of the Pf909 in brown rot management.

## 124 **2. Material and methods**

### 125 *2.1 Field experimental design and treatments*

126 Eighteen field experiments were carried out along different European climatic zones  
127 in stone fruit commercial orchards located in Spain (Lleida) over three growing seasons  
128 from 2015 to 2017, and in France (Roquecourbe, Aude), Belgium (Velm and Metsteren)  
129 and Italy (Bagnacavallo) over two growing seasons from 2016 to 2017 (Table 1).  
130 Different cultivars of cherries (*Prunus avium* L.), peaches (*P. persica* (L.) Batch) and  
131 nectarines (*P. persica* var. *nucipersica* (L. ex Borkh.) C.K.Schneid.) were used (Table 1).  
132 Plots were distributed in a completely randomized block design with four replicates per  
133 treatment. Each replicate consisted in 3 trees. Buffer trees (non-treated trees) were used  
134 to separate treatments and replicates. Biological treatments consisted of Pf909 formulates  
135 (adjusted at  $10^6$  conidia/mL in 2015, 2016 and 2017 or  $10^7$  conidia/mL in 2017) Chemical  
136 positive control were applied based on fungicide treatments and doses (CH) according to  
137 good agriculture practice for each countries: DMI (demethylation inhibitors), SDHI  
138 (succinate dehydrogenase inhibitors), and AP (aniline-pyrimidine)-fungicides were  
139 applied every year in all orchards, except in Italy where DMIs were not applied, and in  
140 France where only DMIs were applied. QoI (quinone outside inhibitors), and PP  
141 (phenylpyrroles)-fungicides were also applied in Italy and Belgium in 2016 and 2017.  
142 One ketoreductase inhibitors (fenhexamid) and captan were also applied in Belgium  
143 orchards in 2016 and 2017. All treatments were preharvest applied four times following

144 application schedule for controlling brown rot: 30, 14, 7 and 3 days approximately before  
145 harvest. Negative control treatment based on non-treated trees (NT) was also included.

146 The area of the orchards where the trials were conducted received the standard cultural  
147 and plant protection practices for the crop and agronomical conditions until 45 days  
148 before harvest. The compatibility of Pf909 with all pesticides used was previously  
149 evaluated (Guijarro et al., 2019a).

## 150 2.2 *Pf909* isolation, production and formulation

### 151 2.2.1 Culture

152 A monosporic isolate of *P. frequentans* strain (Pf909) (ATCC 908-81), which was  
153 obtained from peach twig surfaces (Melgarejo and M-Sagasta, 1984), was used for all  
154 studies as a microbial pest control agent (MPCA). The isolate was stored at  $-80\text{ }^{\circ}\text{C}$  in  
155 20% glycerol (long-term storage) or at  $4\text{ }^{\circ}\text{C}$  on potato dextrose agar (PDA; Difco, Detroit,  
156 MI, USA) slants in the dark (short-term storage).

### 157 2.2.2 Formulation preparation

158 For trials using formulates of Pf909, the microbial plant active substance (MPCA) is  
159 a dried conidia powder of Pf909 with a concentration of  $1.8 \times 10^{11}$  conidia/g and a viability  
160 range of 94-98%. This MPCA was used with different liquid carriers to obtain different  
161 formulation products. The production process of pure dried conidia powder followed the  
162 description of Guijarro et al., (2006) and was made under pilot plant process conditions.  
163 A MPCA of 9.16 g was suspended in 90.84 g of carrier or formulation mixture to have a  
164 final concentration of MPCA of  $1 \times 10^{10}$  conidia/g for all formulated products. The mixture  
165 was homogenized by using an Ultra-Turrax at 3000 rpm for two min and the conidia  
166 concentration was determined by microscopic counting using a haemocytometer.

167 Three oil-based formulations were applied: Pf1= PSPF214-OD-A, based on plant oil;



168 and Pf2=PSPF214-OD-B and Pf3=PSPF214-OD-2 based on technical oil. Pf1 was  
169 applied in 2015, 2016 and 2017, while Pf2 and Pf3 were only applied in 2015 or 2016,  
170 respectively. Furthermore, Pf1 was also tested at two different application rates  $10^6$  and  
171 conidia/mL in 2015 to 2017 and  $10^7$  conidia/mL in 2017. All Pf909 formulates were  
172 developed and produced by Bayer CropScience Biologics GmbH.

### 173 2.3 *Pf909* population dynamic evaluation

174 Fruit from the different treatments, either biological (Pf1, Pf2 and Pf3), or chemicals  
175 (CH), and non-treated (NT) were sampled for *Pf909* population dynamic evaluation at 30  
176 days before harvest (after first treatment application) and at harvest, in the eighteen  
177 commercial orchards of stone fruit in Europe over the three growing seasons (2015 to  
178 2017). Four replicate with five (nectarines or peaches) or twenty (cherries) fruit per  
179 replicate were evaluated for each treatment. Fruit were immersed in 250 mL of sterile  
180 distilled water (SDW) in a plastic container, and shaken for 60 min at 90 rpm at room  
181 temperature (RT). Then, the liquid was treated according to Guijarro et al. (2008).

182 *P. frequentans* population was estimated as the number of colony forming units  
183 (CFU) of *P. frequentans* per  $\text{cm}^2$  of fruit surface for peaches and nectarines and CFU per  
184 fruit in cherries. CFU of *P. frequentans* per  $\text{cm}^2$  were estimated by calculating each fruit  
185 surface from the measurement of two of its diameters following the formula:

$$186 \quad \text{CFU}/\text{cm}^2 = [\text{CFU per fruit} / 4 \Pi (\text{fruit mean diameter}/2)^2]$$

187 Colonies were phenotypically evaluated as *P. frequentans*, and 10% of these colonies  
188 of each treatment were confirmed as Pf909 by specific strain molecular characterization  
189 (Guijarro et al., 2019b).

### 190 2.4 *Pf909* effect on target microorganism (*Monilinia* spp.) and brown rot disease

#### 191 2.4.1 *Monilinia* spp. population dynamic

192 Fruit were sampled and treated as described above in section 2.3., but, in this case,  
193 for assessing the *Monilinia* spp. populations. *Monilinia* spp. population was estimated as  
194 the number of colony forming units (CFU) of *Monilinia* per cm<sup>2</sup> of fruit surface for  
195 peaches and nectarines and CFU per fruit in cherries.

#### 196 2.4.2 Latent infections and brown rot incidence assessment

197 Latent infection incidence was estimated at 30 days before harvest fruit (on immature  
198 fruit before first treatment application) and brown rot incidence on asymptomatic fruit  
199 was estimated at harvest in the eighteen commercial orchards described above.  
200 Asymptomatic immature fruit were treated as described by Gell et al. (2008). After  
201 freezing, four replicates per treatment with five (nectarines or peaches) or twenty  
202 (cherries) fruit per replicate were placed in sealed packing trays at 22°C, 100% RH, each  
203 containing 20 nectarines or peaches or 40 cherries for 7 days. Brown rot incidence was  
204 estimated at harvest on asymptomatic mature fruit in sealed packing trays such as  
205 described above.

206 Latent infection and brown rot incidence were determined by the percentage of  
207 decayed and healthy fruit by visualization the presence of *Monilinia* conidia sporulating  
208 on fruit lesions after 5-7 days of incubation. At this point, cross-infections did not occur,  
209 because it takes seven days for conidia of *Monilinia* spp. to germinate, produce mycelia,  
210 and sporulate (Byrde and Willetts 1977).

#### 211 2.5 *Pf909* effects on non-target microbiota

212 Fruit were sampled from trees treated with the *Pf909* formulates (Pf1, Pf2 and Pf3),  
213 CH, and untreated (NT) at 7, 15, 30 days before harvest and at harvest in two commercial  
214 orchards of nectarines in Spain during 2015 and 2016 growing seasons (ES15.2 and  
215 ES16.2). Four replicates, with five nectarines per replicate were evaluated for each

216 treatment. Five nectarines were immersed in 250 mL of potassium phosphate buffer  
217 SPMS (pH 7.6; 60 mM sodium phosphate monobasic salt) (Sigma Chemical Co. St Louis,  
218 MO) in a plastic container, and shook for 60 min at 110 rpm at RT. The liquid was  
219 centrifuged for 10 min at 4 °C and 10,000 rpm and the pellet suspended in 20 mL buffer  
220 (SPMS). The pellets were lyophilized for 24 hours using a Cryodos-50 lyophilizer  
221 (Telstar, Barcelona, Spain). The fruit lyophilized pellets (FLP) were then made into a  
222 powder using a high-speed benchtop tissue homogenizer (FastPrep -24Instrument, MP  
223 Biomedicals, Solon, OH, USA) for 30 seconds for microbial density and microbial  
224 diversity analysis.

#### 225 2.5.1 Fruit microbiota density analysis by FDA.

226 Quantification of epiphytes microbial density on nectarine surface over the crop  
227 seasons was assessed by measuring FDA hydrolysis through adaptation of Adam and  
228 Duncan procedure (2001). Briefly, 1g of FLP sample was incubated in 50 mL conical  
229 flasks containing 10 mL of 60 mM sodium phosphate buffer (pH 7.6) and 2000 ng/ $\mu$ l  
230 FDA (Sigma Chemical Co. St. Louise) for 60 min at 30 °C and 90 rpm on an orbital  
231 shaker. Samples without FDA were used as controls. After incubation, reaction was  
232 quickly stopped by adding 10 mL of acetone to each flask and shaken briefly by hand.  
233 Samples were filtrated through No 1 Whatman filter paper and the filtrates measured at  
234 492 nm in a spectrophotometer (S-20 Spectrophotometer, BOECO, Germany).

#### 235 2.5.2 Fruit microbiota diversity analysis by PCR-DGGE.

236 Quality analysis effect of each treatment (Pf1, Pf2, Pf3, CH) was related with the  
237 structure of the fruit microbial community on each sample compared to NT. The structure  
238 of the fruit microbial community was assessed using PCR-DGGE.

239 DNA was extracted from each sample of FLP (0.5 g) byVWR Omega EZNA water

240 DNA Kit (MoBio Laboratories, Inc., USA) according to manufacturer's instructions.  
241 PCR amplification of the bacterial 16S or fungal 18S rRNA gene was performed. PCR  
242 was carried out using 25 to 50 ng of DNA template and 5 pmol of each primer in a final  
243 reaction volume of 50 µL GoTaq Green Master Mix (Promega).

244 Fungi DNA was amplified used a nested PCR approach that included two rounds of  
245 amplification. Primers were EF4F (TCCTCCGCTTATTGATATG) and ITS4  
246 (GGAAGGGRTGTATTTATTAG) for the first round (Smith et al., 1999; White et al.,  
247 1990), and ITS2 (GCTGCGTTCTTCATCGATGC) and ITS1  
248 (CTTGGTCATTTAGAGGAAGTAA) for the second (Gardes and Bruns, 1993; Smith et  
249 al., 1999). A GC-rich tail (5'-  
250 CGCCCGCCGCGCGCGGGCGGGGCGGGGGCACGGGGGG-3') was  
251 incorporate at the 5' end of the ITS1 primer. The PCR conditions were 94 °C for 5 min;  
252 35 cycles of 94 °C for 0.5 min, 55 °C for 0.5 min, 72 °C for 0.5 min and a final incubation  
253 at 72 °C for 5 min. A 999 bp DNA fragment of fungi was obtained and diluted up to  
254 1/1000 to proceed to the nested PCR. Next PCR was performed with same PCR cycle.  
255 Final PCR product had 300 bp.

256 Bacteria were amplified with primer forward 341-GC  
257 (CGCCCGCCGCGCCCCGCGCCCGTCCCGCCGCCCCCGCCCGCCTACGGGAGG  
258 CAGCAG) and reverse 907r (CCGTCAATTCCTTTGAGTTT) (Schmalenberger and  
259 Tebbe, 2003). The PCR amplification conditions were 94 °C for 5 min; 35 cycles of 95  
260 °C for 1 min, 53 °C for 1 min, 72 °C for 2 min and a final incubation at 72 °C for 10 min.  
261 A 550 bp DNA fragment of bacteria were amplified.

262 DGGE analysis was performed with a DCode DGGE system (Bio-Rad Laboratories,  
263 Hercules, CA, USA). PCR product (300 to 500 ng) was loaded into 6% (w/v)  
264 polyacrylamide gels (acrylamide/bisacrylamode 37.5/1) with denaturing gradients

265 ranging from 20–60% for fungi and from 20–80%. DGGE was performed in 0.5 TAE  
266 buffer (40 mM Tris, 20 mM acetic acid, 1 mM EDTA [pH 8.0]) for bacteria and 1.0 for  
267 fungi at 60 °C for 4 h at 200 V in the case of fungi and at 60 °C, during 5 h at 150 V for  
268 bacteria. The gel was then stained with GelRed (Biotium) visualized and photographed  
269 using a gel imaging system (Bio-Rad Lab., Hercules, CA, USA).

270 The bands observed in the DGGE analysis were identified. For this, selected bands  
271 were excised from gels with sterile scalpel blades and DNA was purified by Wizard SV  
272 Gel and PCR Clean Up System (Promega) according with manufacture instructions.  
273 Extracted DNA (10 µL) was used as template for PCR amplification was conducted as  
274 described previously, using a non-GC-clamped version of the forward primer. The  
275 sequences recovered were aligned with bacterial and fungal gene fragments available  
276 from the National Center for Biotechnology Information (NCBI) databases.

## 277 2.6 Data analysis

278 All data were analysed by one-way analysis of variance (ANOVA) using a statistical  
279 program (Statgraphics-Centurion XVI version 16.1.03). Statistical significance was set at  
280 5 %. Data of CFU per fruit cm<sup>2</sup> and latent infection or brown rot incidence for each  
281 treatment were log (x+1) or arcsine transformed, respectively, in order to improve  
282 homogeneity of variances before analysis. When the results of the F-test were significant  
283 ( $p \leq 0.05$ ), means were compared using the Student–Newman–Keuls multiple range test  
284 (Snedecor and Cochran, 1980).

285 Using the combined data from all surveys, correlation and regression analyses were  
286 performed using Statgraphics-Centurion XVI version 16.1.03 in order to analyze the  
287 relationships between brown rot latent infection and brown rot incidence at harvest to *P.*  
288 *frequentans* population at preharvest and harvest, respectively.

289 For microbial activity evaluation, the amount of fluorescein content that was  
290 hydrolyzed by enzymatic activity in the samples was calculated by reference to a standard  
291 curve prepared from the fluorescein standards.

292 DGGE banding patterns were compared with Sammon's nonlinear mapping using  
293 NTSYS 5.0 and with dendrograms based on distance matrices, using the unweight-pair  
294 group method using average linkages. Unweight pair pair group method with arithmetic  
295 averages (UPGMA) cluster analysis of dice distance matrix calculated from DGGE  
296 banding patterns (based on presence/ absence).

### 297 **3. Results**

#### 298 *3.1 Pf909 population dynamic evaluation*

299 The number of Pf909 CFU on fruit surfaces at pre and harvest were presented in  
300 Figures 1 to 4, where Pf909 formulations maintained a range of log CFU/cm<sup>2</sup> on fruit  
301 surface from 1.8 to 5.38.

302 Population of Pf909 after first application and just before harvest during three crop  
303 seasons at Spanish orchards were shown in Fig. 1. There were significant differences  
304 between Pf909 CFU/cm<sup>2</sup> at the first application and harvest in 2015, 2016, and 2017 (Fig.  
305 1), except on nectarines in 2015 in Albesa after Pf2 application (Fig. 1b). A significant  
306 10-fold increase on Pf909 population was observed between preharvest and at harvest  
307 application (P=0.05) in each orchard (Fig. 1). Population of Pf909 was variable among  
308 years in each orchard to the same Pf1 formulate (P=0.05) (Fig. 1). The highest Pf909  
309 population was recovered in 2015 when Pf1 was sprayed at 10<sup>6</sup> conidia/mL (between 3.35  
310 log CFU/cm<sup>2</sup> at preharvest in ES15.2 to 4.64 log CFU/cm<sup>2</sup> at harvest in ES15.1) (Figs.  
311 1a and 1b). Dynamic populations of Pf1 during 2016 (between 1.98 log CFU/cm<sup>2</sup> at  
312 preharvest in ES16.2 to 3.07 log CFU/cm<sup>2</sup> at harvest in ES16.2) (Figs. 1c and 1d) reached

313 similar adequate levels than in 2017 when Pf1 was sprayed at  $10^6$  conidia/mL (between  
314  $1.80 \log \text{ CFU/cm}^2$  at preharvest in ES17.1 to  $3.55 \log \text{ CFU/cm}^2$  at harvest in ES17.2)  
315 (Figs. 1e and 1f). However, similar Pf909 population resulted from different Pf909  
316 formulations on fruit surface (Figs. 1a-d) when they were applied at a dose of  $10^6$   
317 conidia/mL on Spanish orchards during 2015 or 2016 ( $P=0.05$ ). A significant increase of  
318 Pf909  $\text{CFU/cm}^2$  were recorded when Pf1 was applied at  $10^7$  conidia/mL, specially on  
319 nectarines (between  $4.23 \log \text{ CFU/cm}^2$  at preharvest to  $5.38 \log \text{ CFU/cm}^2$  at harvest in  
320 ES17.2) ( $P=0.05$ ) (Figs. 1f).

321 The same biological formulates (Pf1 and Pf3) applied in Spanish orchards in 2016  
322 and 2017, were used on peach and nectarine orchards in France (Fig. 2) and Italy (Fig. 3),  
323 and on cherries in Belgium (Fig. 4) during 2016 and 2017. Population of Pf909 was  
324 variable among years in each orchard without any formulate effects. Population of Pf909  
325 on fruit surface at harvest, after four application of each formulate along crop, was more  
326 than 10-fold higher than preharvest application at  $10^6$  conidia/mL ( $P=0.05$ ), except in  
327 French peach orchards (Figs. 2a and 2c), Italian peach orchard 2017 (Fig. 3c), and  
328 Belgium orchards cv. Lapin in 2017 (Figs. 4c). The 10-fold higher dose of Pf1 in 2017  
329 provided a better conidia surface cover during the application period with 2.31 to 4.81  
330  $\log \text{ CFU/cm}^2$  after first application and 3.31 to  $5.17 \log \text{ CFU/cm}^2$  at harvest ( $P=0.05$ )  
331 (Figs. 2c-d, 3c-d, 4c-d).

### 332 3.2 Pf909 effect on the target microorganism (*Monilinia spp.*) and brown rot disease

#### 333 3.2.1. *Monilinia* population dynamic

334 The effects of the three Pf909 formulates on the CFU of *Monilinia spp.* conidia  
335 on fruit surfaces were illustrated in Figs. 1 to 4, where the number of *Monilinia spp.*  
336 conidia on non-treated fruit surfaces was significantly higher at harvest than at preharvest

337 in all orchards ( $P=0.05$ ). Pf1, Pf2, Pf3, and the CH significantly reduced the pathogen  
338 population on fruit surfaces both at preharvest and harvest when it was compared with  
339 untreated fruit surfaces ( $P=0.05$ ), except on Spanish nectarines in 2016 (Fig. 1d), Italian  
340 peaches (Figs. 3a and 3c), and Lapins cherries in 2016 (Fig. 4a). No significant  
341 differences were observed between pathogen population reduction by biological and  
342 chemical treatments.

### 343 3.2.2. Latent infections and disease severity assessment

344 Brown rot and latent infection incidence caused by *Monilinia* spp. on untreated  
345 fruit were between 2.5 to 68.75%, and 5 to 91%, respectively in Spanish orchards (Fig.  
346 1), while between 52.63 to 66.6 % and 0 to 58.8%, respectively in French orchards (Fig.  
347 2), between 40.0 to 55% and 0 to 36.84%, respectively in Italian orchards (Fig. 3), or  
348 between 31.5 to 55% and 0 to 45%, respectively in Belgium orchards (Fig. 4).

349 Pf1, Pf2, and Pf3 treatments significantly reduced latent infections and/or brown  
350 rot severity incidence on fruit at preharvest and/or harvest, respectively when they were  
351 compared with untreated fruit ( $P=0.05$ ) (Figs. 1 to 4). No control was recovered on  
352 nectarines Red Jim in Spain in 2015 (Fig. 1b), where no latent infection and brown rot  
353 was observed in the untreated control, and on nectarines in Spain and France in 2017  
354 (Figs. 1d and 2d), and on peaches Corindom in Italy (Figs. 3a and 3c). Similar disease  
355 control was recovered on biological and chemical treated fruit ( $P=0.05$ ) (Figs. 1 to 4),  
356 except on nectarines in Spain, France, and Italy in 2017 (Fig. 1d, 2d, and 3d), and on  
357 peaches in Italy (Fig. 3c).

358 The percentage of brown rot incidence was significantly and negatively correlated  
359 with Pf909 population at harvest ( $r = -0.72$ ,  $P = 0.00001$ ). Furthermore, the percentage of  
360 latent infections was also significantly and negatively correlated ( $r = -0.54$ ,  $P = 0.0001$ )  
361 with Pf909 population at preharvest.



362 In addition, the brown rot incidence was a function of the number of *P. frequentans*  
363 CFU at harvest and could be fitted by the following equation:

$$364 \quad \% \text{ BR} = 52.22 - 7.36 \text{ LOG}_{10} (\text{CFU Pf909} + 1) \quad (R^2 = 52.54\%)$$

### 365 3.3 *Pf909* treatments on non-target microbiota

#### 366 3.3.1. Fruit microbiota density analysis

367 Microbial activity was shown as fluorescein per gram of dry skin fruit for non-  
368 treated and treated nectarine surface samples in two orchards in Spain, ES15-2 (Fig. 5a)  
369 and ES16-2 (Fig. 5b) with Pf1, Pf2 and Pf3 biological products. The application of Pf909  
370 at preharvest and harvest significantly ( $P = 0.05$ ) increased microbial activity. However,  
371 chemical applications significantly ( $P = 0.05$ ) reduced the microbial activity on peach  
372 surface compare to the untreated control in both orchards.

#### 373 3.3.2. Fruit microbiota diversity analysis

374 Analysis by DGGE of PCR-amplified eubacterial 16S rDNA fragments and with  
375 18S rRNA fungi fragment along treatments on peach surface with Pf909 formulates (Pf1,  
376 Pf2 and Pf3) during two consecutives growing seasons in Spain (2015 and 2016) revealed  
377 distinctly different profiles for the different fruit surface treated with the biologicals, the  
378 chemical or untreated (data not shown). Results were confirmed by cluster analysis (Figs.  
379 6 and 7).

380 Fungi and bacterial microbial epiphytic populations from 2015 and 2016 Spanish  
381 orchards evaluated were distributed into two main clusters (Figs. 6 and 7). There were no  
382 differences among Pf909 formulates in microbial population distribution. The  
383 reproducibility of the profiles from different DNA extractions belonging to the same  
384 sample was unaffected. The profiles of the fungal populations were more variable than  
385 bacterial populations and the dendrogram reflected the difficulty in grouping the

386 application dates together (Figs. 6 and 7).

387 The CH (cyproconazole, tebuconazole and fenbuconazole) were grouped, and the  
388 biological applications (Pf1, Pf2 and Pf3) did not present divergence from untreated  
389 fungal samples in both years (Fig. 6a and 6b). The biological samples from fruit treated  
390 by Pf1, Pf2, and Pf3 as well as the untreated controls presented a distribution grouped by  
391 dates, except in the case of 2015 samples at seven and fifteen days before harvest, where  
392 no effect of samples date were observed (Fig. 6a).

393 In the case of effect of Pf909 applications on bacteria community diversity, chemical  
394 fungicides are grouping together with no effect on application dates, since biological  
395 treatments are grouping by dates (Fig. 7a and 7b).

#### 396 **4. Discussion**

397 Biological brown rot control by Pf909 reduced disease incidence and *Monilinia*  
398 population growth rate, while stabilizing or increasing antagonist populations and  
399 avoiding non-target impacts. However, chemical fungicides reduced significantly the  
400 microbial activity on peach surfaces compare to the untreated control. Pesticide  
401 applications had a large effect on peach non-target epiphytic fungi, reducing populations  
402 in the field in some case by up to 50% (De Cal and Melgarejo, 1992).

403 To conserve or improve biodiversity is a general objective of sustainable cropping  
404 and enhancing abundance and efficacy of the natural antagonist existing community is a  
405 priority for this production system (IFOAM Anonymous, 2014). Before beginning any  
406 biocontrol program, it is also important to determine the lethal and sublethal impact of  
407 BCAs on non-target organisms (Lefebvre et al., 2011; Preetha et al., 2010), because the  
408 microbial communities play very important roles in the ecosystem. Therefore, the  
409 potential impact of any fungicide application on natural antagonist populations must be

410 previously investigated (López et al., 2018). The influence of a single microorganism on  
411 the microbial community has already been studied for plant pathogens and/or BCAs  
412 (Kröber et al., 2014; Schreiter et al., 2014). Fungal and bacterial populations on nectarines  
413 treated with Pf1, Pf2 and Pf3 did not present divergence from both populations in  
414 untreated samples, and they showed an increasing FDA activity in the treated fruit was  
415 observed. It could suggest a general trend for disease control with increasing FDA activity  
416 in biological applications, and related to the highest levels of Pf909 populations on fruit.

417 FDA and DGGE helped us to demonstrate that there was no need to worry about non-  
418 target effects of Pf909 on peach epiphytic micro-organisms. The use of molecular tools  
419 enabled the presence of genes encoding for important functions to be traced, and showed  
420 that release of a relatively small quantity of a BCA did not modify the epiphytic  
421 functioning (Sessitsch et al., 2002). Another family of methods enables a global  
422 assessment of the impact of BCA introduction on the structure of the microbial  
423 communities showed that even when an impact was detected shortly after BCA  
424 introduction, the structure of the microbial communities tended to revert rapidly to their  
425 initial stage (Alabouvette et al., 2011). After a few weeks, there was no difference in the  
426 structures of the microbial communities between the infested soil and the non-infested  
427 control. Moreover, similar studies have shown that traditional agricultural practices have  
428 much more impact on microbiota than the release of a BCA. This is especially the case  
429 with chemical treatments (Vivian et al., 2013).

430 Pf1, Pf2, and Pf3 treatments significantly reduced pathogen population on fruit  
431 surfaces, latent infection and brown rot incidence, both at harvest and preharvest, when  
432 they were compared with untreated fruit. No significant differences were observed  
433 between brown rot control by biological and chemical treatments on cherries and up to  
434 55% of peach and nectarine orchards. Successful brown rot biological control depends on

435 establishing large populations of Pf909 on stone fruit surface (De Cal et al., 1990;  
436 Guijarro et al., 2018). A significant correlation was recorded between brown rot control  
437 and Pf909 population. A Pf909 population greater than 500,000 CFU/cm<sup>2</sup> would be  
438 necessary to reduce the brown rot incidence to below 10%. Various agro-ecological  
439 factors play an important role for the success of a BCA in the augmented site. These  
440 include fitness of the BCA (Borzoui et al., 2016), its capacity to disperse in augmented  
441 sites (Zappala et al., 2012), tolerance to abiotic factors (Hasan and Ansari 2015),  
442 availability and suitability of host (Alam Shah et al., 2016), interaction with other natural  
443 enemies (Vanaclocha et al., 2013), target specificity (Jalali et al., 2009) and tolerance to  
444 pesticides and its residual effects (Hasan and Ansari 2017; 2016; Pozzebon et al., 2010).  
445 Pf909 can be used as an effective and safe BCA because it is able to adapt to different  
446 environmental conditions (Guijarro et al., 2017a). Pf909 was also compatible with 76%  
447 of the fungicides and 90% of the insecticides commonly used against stone fruit pests  
448 (Guijarro et al., 2019a). The stability of Pf909 field populations under fungicide regimes  
449 may be also due to their highly competitive nature and their ability to exploit any  
450 ecological niche left vacant than to any tolerance to fungicides (De Cal and Melgarejo  
451 1992).

452 Population of Pf909 on stone fruit surfaces showed a large range between 100  
453 CFU/cm<sup>2</sup> to 100,000 CFU/cm<sup>2</sup>, where all formulations at harvest were more than 10-100-  
454 fold than preharvest application in 2016 and 2017. Population of *P. frequentans* varied  
455 between orchards and years, rather than by the type of the applied formulate or fruit  
456 surface. A consistent population of *P. frequentans* Pf909, ranging from 1,000 to 10,000  
457 CFU of *P. frequentans* per flower or fruit had already been reported by other Pf909  
458 formulates (Guijarro et al., 2008). Colonization of peach surfaces by *P. frequentans*  
459 followed a general pattern with a higher colonization of fruit at preharvest than on the

460 flowers at bloom (Guijarro et al., 2008). A significant increase of *P. frequentans* CFU/cm<sup>2</sup>  
461 were recorded when Pf1 was applied at 10<sup>7</sup> conidia/mL. Pf909 was dispersed well in  
462 treated trees, persisting in the ecosystem up to 2 weeks and staying genetically stable after  
463 36 months of storage (Guijarro et al., 2019b).

464 Pf909 reduced brown rot and pathogen population, while avoiding non-target  
465 impacts. The formulations of Pf909 allowed to maintain a population on the fruit of the  
466 biocontrol agent above natural background, will suppose an effective tool in the  
467 sustainable control of brown rot on stone fruit.

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641

642 **Table 1** Orchard datas used in Spain, France, Italy and Belgium between 2015 and 2017  
 643 seasons for field experiments.



Country	Growing season	Orchard	Location	coordinates	cultivar
Spain	2015	ES15.1	Albesa	41.779151N-0.629172E	Peach, var. Roig d'Albesa
		ES15.2	Sudanell	41.552120N-0.573463E	Nectarine, var. Red Jim
	2016	ES16.1	Alamús	41.615024N-0.740212E	Peach, var. Tardibelle
		ES16.2	Sudanell	41.552120N-0.573463E	Nectarine, var. Red Jim
	2017	ES17.1	Alfarras	41.8363652N-0.531158E	Peach, var. Groc d'Ivars
		ES17.2	Sudanell	41.552120N-0.573463E	Nectarine var. Red Jim
France	2016	FR16.1	Roquecourbe Minervoies	43.220277N-2.653888E	Peach, var. Fidelia
		FR16.2	Roquecourbe Minervoies	43.2208333N-2.651666666E	Nectarine, var. Tourmaline
	2017	FR17.1	Roquecourbe Minervoies	43.220277N-2.653888E	Peach, var. Fidelia
		FR17.2	Roquecourbe Minervoies	43.2208333N-2.651666666E	Nectarine, var. Tourmaline
Italy	2016	IT16.1	Bagnacavallo	44.4401694N-11.96811944E	Peach, var. Corindom
		IT16.2	Bagnacavallo	44.4274305N-11.9474888E	Nectarine, var. Morsiani 90
	2017	IT17.1	Bagnacavallo	44.4401694N-11.96811944E	Peach, var. Corindom
		IT17.2	Bagnacavallo	44.4274305N-11.9474888E	Nectarine, var. Morsiani 90
Belgium	2016	BE16.1	Velm	50.77931N-5.13162W	Cherry, var. Lapins
		BE16.2	Metsteren	50.503887N-4.469936W	Cherry, var. Sweetheart
	2017	BE17.1	Velm	50.77931N-5.13162W	Cherry, var. Lapins
		BE17.2	Metsteren	50.503887N-4.469936W	Cherry, var. Sweetheart

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
648 **Fig. 1** Population of *Penicillium frequentans* Pf909 (  ) and *Monilinia* spp (  ) as  
649 (log<sub>10</sub> CFU/cm<sup>2</sup>) on fruit surface in three Spanish orchard during 2015 (a, b), 2006 (c, d),  
650 and 2017 (e, f): (a) ES15.1, (b) ES15.2, (c) ES16.1, (d) ES16.2, (e) ES17.1, and (f)  
651 ES17.2, after first treatment application and at harvest. Percentage of latent infection  
652 caused by *Monilinia* spp at 30 days before harvest was represented by (▲) and percentage  
653 of brown rot disease incidence at harvest by (●) on peaches (a, c, e) and on nectarines (b,  
654 d, f). The treatments were: NT (control, without treatment); CH (chemical); and Pf909  
655 formulations: Pf1, Pf2, and Pf3 at 10<sup>6</sup> conidia/mL, and Pf1 at 10<sup>7</sup> conidia/mL in 2017  
656 (Pf1x10). Value are the average of four determinations. Within the same pattern, different  
657 letters indicate significant differences (P < 0.05) according to the Student Newman Keuls  
658 test. A-D uppercases and dark grey bars refer to Pf909 population; a-d lower cases and  
659 light grey bars to *Monilinia* spp population. X-Z uppercases refer to latent infection and  
660 disease incidence (%)

661



662 **Fig. 2** Population of *Penicillium frequentans* Pf909 (  ) and *Monilinia* spp (  ) as  
663 (log<sub>10</sub> CFU/cm<sup>2</sup>) on fruit surface in two French orchard during 2016 (a, b) and 2017 (c,  
664 d): (a) FR16.1, (b) FR16.2, (c) FR17.1, and (d) FR17.2, after first treatment application  
665 and at harvest. Percentage of latent infection caused by *Monilinia* spp at 30 days before  
666 harvest was represented by (▲) and percentage of brown rot disease incidence at harvest  
667 by (●) on peaches (a, c) and on nectarines (b, d).The treatments were: NT (control,  
668 without treatment); CH (chemical); and Pf909 formulations: Pf1 and Pf3 at 10<sup>6</sup>  
669 conidia/mL, and Pf1 at 10<sup>7</sup> conidia/mL in 2017 (Pf1x10). Value are the average of four  
670 determinations. Within the same pattern, different letters indicate significant differences  
671 (P < 0.05) according to the Student Newman Keuls test. A-D uppercases and dark grey

672 bars refer to *Penicillium frequentans* Pf909 population; a-d lower cases and light grey bars to *Monilinia* spp  
673 population. x-z lower cases refer to latent infection and disease incidence (%)

674

675 **Fig. 3** Population of *Penicillium frequentans* Pf909 (  ) and *Monilinia* spp (  ) as  
676 ( $\log_{10}$  CFU/cm<sup>2</sup>) on fruit surface in two Italian orchard during 2016 (a, b) and 2017 (c,  
677 d): (a) IT16.1, (b) IT16.2, (c) IT17.1, and (d) IT17.2, after first treatment application and  
678 at harvest. Percentage of latent infection caused by *Monilinia* spp at 30 days before  
679 harvest was represented by (▲) and percentage of brown rot disease incidence at harvest  
680 by (●) on peaches (a, c) and on nectarines (b, d). The treatments were: NT (control,  
681 without treatment); CH (chemical); and Pf909 formulations: Pf1 and Pf3 at 10<sup>6</sup>  
682 conidia/mL, and Pf1 at 10<sup>7</sup> conidia/mL in 2017 (Pf1x10). Value are the average of four  
683 determinations. Within the same pattern, different letters indicate significant differences  
684 ( $P < 0.05$ ) according to the Student Newman Keuls test. A-D uppercases and dark grey  
685 bars refer to Pf909 population; a-d lower cases and light grey bars to *Monilinia* spp  
686 population. x-z lower cases refer to latent infection and disease incidence (%)

687

688 **Fig. 4** Population of *Penicillium frequentans* Pf909 (  ) and *Monilinia* spp (  ) as  
689 ( $\log_{10}$  CFU/cm<sup>2</sup>) on CHERRY fruit surface in two Belgium orchard during 2016 (a, b)  
690 and 2017 (c, d): a) BE16.1, (b) BE16.2, (c) BE17.1, and (d) BE17.2, after first treatment  
691 application and at harvest. Percentage of latent infection caused by *Monilinia* spp at 30  
692 days before harvest was represented by (▲) and percentage of brown rot disease  
693 incidence at harvest by (●) on cv. Lapin (a, c) and on cv. Sweetheart (b, d). The treatments  
694 were: NT (control, without treatment); CH (chemical); and Pf909 formulations: Pf1 and  
695 Pf3 at 10<sup>6</sup> conidia/mL, and Pf1 at 10<sup>7</sup> conidia/mL in 2017. Value are the average of four  
696 determinations. Within the same pattern, different letters indicate significant differences

697 (P < 0.05) according to the Student Newman Keuls test. A-D uppercases and dark grey  
698 bars refer to Pf909 population; a-d lower cases and light grey bars to *Monilinia* spp  
699 population. x-z lower cases refer to latent infection and disease incidence (%)

700

701 **Fig. 5** Effect of *Penicillium frequentans* (Pf909) applications on microbial biomass  
702 activity measure as fluorescein diacetate FDA-staining on fruit skin in two Spanish  
703 nectarine orchards: (a) ES15.2 in 2015 and (b) ES16.2 in 2016. Data are means of three  
704 replicates each of 5 fruit samples from each treatment. Different letters indicate  
705 significant differences (P < 0.05) according to the Student-Newman-Keuls test. The  
706 treatments were: NT (control without treatment); Pf909 formulations: Pf1, Pf2 and Pf3,  
707 at 10<sup>6</sup> conidia/mL and CH (chemical treatment)

708

709 **Fig. 6** Cluster analysis of fungal community structures on the nectarines phyllosphere  
710 community after the introduction of *Penicillium frequentans* (Pf909) from two orchards  
711 in Spain (a) ES15.2 and (b) ES16.2, as generated from the pooled applications profiles.  
712 The UPGMA (Unweighted Pair-Group Method with Arithmetic Means) on the DNA  
713 average peak height for each base length were used to build the dendrograms of the fungal  
714 communities. Samples were obtained after application of different treatments in each  
715 orchard. The treatments were: NT (control without treatment); Pf1, Pf2 and Pf3 (Pf909  
716 conidia formulated) and CH (chemical treatment). For every treatment sampling were  
717 made: after first application or 30 days before harvest (-30dbh); after second application  
718 or 15 day before harvest (-15dbh); after last application or seven days before harvest (-  
719 7dbh), and at harvest (-h). UPGMA cluster analysis of dice distance matrix calculated  
720 from DGGE banding patterns (based on presence/ absence)

721



722 **Fig. 7** Cluster analysis of bacterial community structures on the nectarines phyllosphere  
723 community after the introduction of *Penicillium frequentans* (Pf909) from two orchards  
724 in Spain (a) ES15.2 and (b) ES16.2, as generated from the pooled applications profiles.  
725 The UPGMA (Unweighted Pair-Group Method with Arithmetic Means) on the DNA  
726 average peak height for each base length were used to build the dendrograms of bacterial  
727 communities. Samples were obtained after application of different treatments in each  
728 orchard. The treatments were: NT (control without treatment); Pf1, Pf2 and Pf3 (Pf909  
729 conidia formulated) and CH (chemical treatment). For every treatment sampling were  
730 made: after first application or 30 days before harvest (-30dbh); after second application  
731 or 15 day before harvest (-15dbh); after last application or seven days before harvest (-  
732 7dbh), and at harvest (-h). UPGMA cluster analysis of dice distance matrix calculated  
733 from DGGE banding patterns (based on presence/ absence)