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#### Effect of elevated atmospheric CO2 and temperature on the disease severity of rocket plants caused by Fusarium wilt under phytotron condition.

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1	Effect of elevated atmospheric CO <sub>2</sub> and temperature on
2	the disease severity of rocket plants caused by Fusarium
3	wilt under phytotron conditions
4	
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23	pathogen interaction, soilborne pathogen, fungal microbiota

## 24 Abstract

25 The severity of F. oxysporum f.sp. conglutinans on rocket plants grown under 26 simulated climate change conditions has been studied. The rocket plants were cultivated on an infested substrate (4 log CFU g<sup>-1</sup>) and a non-infested substrate over three cycles. Pots were 27 placed in six phytotrons in order to simulate different environmental conditions: 1) 400-450 28 29 ppm CO<sub>2</sub>, 18–22 °C; 2) 800-850 ppm CO<sub>2</sub>, 18–22 °C; 3) 400-450 ppm CO<sub>2</sub>, 22–26 °C, 4) 800-850 ppm CO<sub>2</sub>, 22-26 °C, 5) 400-450 ppm CO<sub>2</sub>, 26-30 °C; 6) 800-850 ppm CO<sub>2</sub>, 26-30 °C. 30 31 Substrates from the infested and control samples were collected from each phytotron at 0, 60 32 and 120 days after transplanting. The disease index, microbial abundance, leaf physiological 33 performances, root exudates and variability in the fungal profiles were monitored. The 34 disease index was found to be significantly influenced by higher levels of temperature and CO<sub>2</sub>. Plate counts showed that fungal and bacterial development was not affected by the 35 different CO<sub>2</sub> and temperature levels, but a significant decreasing trend was observed from 0 36 37 up to 120 days. Conversely, the F. oxysporum f.sp. conglutinans plate counts did not show 38 any significantly decrease from 0 up to 120 days. The fungal profiles, evaluated by means 39 of polymerase chain reaction denaturing gradient gel electrophoresis (PCR-DGGE), showed a 40 relationship to temperature and CO<sub>2</sub> on fungal diversity profiles. Different exudation patterns 41 were observed when the controls and infested plants were compared, and it was found that 42 both CO<sub>2</sub> and temperature can influence the release of compounds from the roots of rocket 43 plants. In short, the results show that global climate changes could influence disease 44 incidence, probably through plant-mediated effects, caused by soilborne pathogens. 45 46

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- 48

## 49 Introduction

50 Nowadays, how climate changes will influence plant-pathogen interactions and their 51 impact on production is largely debated and represents a challenge for future programmes 52 focused on disease management under global change conditions [1]. An increasing numbers 53 of multidisciplinary approaches have reported the effects of rising temperature and CO<sub>2</sub> 54 levels on crop productions and physiological changes [2]. On the other hand, researchers 55 have only recently focused on plant disease prediction and management under climate 56 changes [3]. Plant pathogens represents an important constraint for the security of our future 57 food as a consequence of population increases, urbanization, globalization and changes in 58 climate [4]. Moreover, several pathogens produce toxins and other compounds that are 59 dangerous to human and animal health which could affect market and world trade. On these 60 grounds, a multidisciplinary approach is needed to implement predictive models and include 61 higher levels of ecological interactions [5]. As recently reported by an Intergovernmental 62 Panel on Climate Changes [6], anthropogenic emissions of greenhouse gases have caused 63 negative impacts on human and natural systems over the last three decades. In other words, 64 changes in the atmospheric composition and temperature as well as humidity alterations can 65 have an impact on host plant physiology and influence a plant's resistance against pathogens 66 [7-9]. On one hand, rises in CO<sub>2</sub> and temperature can affect the sense and responses of a 67 plant by increasing the photosynthesis rates, water and light-use efficiency, leaf surface 68 properties, changes in anatomy, morphology, phenology and root exudates, thus profoundly 69 modifying native plants and soil microbial communities [1,3,8,10,11]. On the other hand, 70 elevated CO<sub>2</sub> influences the pathogenicity, host-pathogen interaction and epidemiology of 71 fungal diseases [3,12-15,16]. An enlarged canopy coupled with a favourable microclimate 72 offers more sites for infection and increases fungal pathogen fecundity, which has been 73 shown to lead to twice the number of lesions for high  $CO_2$  concentrations [17,18].

Furthermore, the mutation and selection of plant pathogens and the consequent developmentof new strains have also been predicted [3,19].

76 Phytotron-based studies are optimized to study the interactions that occur between plants, soil 77 and soil microbiota and they combine environmental parameters such as light intensity, CO<sub>2</sub> 78 concentrations, temperature, and relative humidity [20]. Phytotron chambers have in fact 79 been largely used to study the effects of global changes on several pathosystems [11, 14– 16,21]. Plants directly or indirectly affect the development of soil microbiota in the 80 81 rhizosphere and in bulk soil by means of root exudates [22]. However, most studies 82 conducted so far report contrasting results; such as a decrease [23], an increase [24] or no 83 changes [25] in microbial diversity and activities. The development of soil microbial 84 populations needs a multiphasic approach that can couple traditional microbial analysis with 85 molecular tools such as polymerase chain reaction denaturing gradient gel electrophoresis 86 (PCR-DGGE). This technique has been optimized to monitor soil microflora changes under 87 climate change conditions [16,26,27]. Fusarium oxysporum and the related formae specialis 88 cause greater economic damage to several crops than other plant pathogens [28]. Rocket 89 (Eruca sativa) is a high-value horticultural crop, mainly cultivated in the Mediterranean area, 90 up to 3-5 times in the same soil which is affected by emerging soilborne pathogens [20,29] 91 and Fusarium oxysporum f.sp. conglutinans has recently been detected in Italy on cultivated 92 (Eruca sativa) and wild rocket (Diplotaxis tenuifolia) [30].

The aim of this work was to study the effect of *F. oxysporum* f.sp. *conglutinans*,
artificially infested in a growing substrate, on rocket plants grown under simulated climate
change conditions with rising CO<sub>2</sub> concentrations and temperatures in phytotron chambers.
Six temperature/CO<sub>2</sub> combinations were studied. Disease incidence, the physiological
performances of leaves, microbial and fungal cultivable abundance and the main root exudate
components were monitored to evaluate the effects of climatic changes on disease

development over time. Furthermore, shifts in fungal communities were assessed using theDGGE technique on DNA directly extracted from an infested growing substrate.

101

## 102 Materials and methods

## 103 Inoculum preparation

104 F. oxysporum f.sp. conglutinans (ATCC16600RB, Agroinnova, Grugliasco, Italy), 105 which is resistant to benomyl [31], was used and cultured in 1000-mL Erlenmeyer flasks 106 containing 250 mL of hydrolized casein. The flasks were incubated on a platform shaker at 107 20-25 °C for 12 days. Chlamydospores were recovered by means of centrifugation for 20 min 108 at 8000g at 20 °C, following the removal of mycelia fragments by sieving through 109 cheesecloth. The chlamydospore suspension was dried and mixed with sterile talc powder 110 (1:2 w/w), as described by Locke & Colhoun [32], and stored at room temperature for further 111 use. The number of chlamydospores per gram of talc was assessed by serial plating on a Komada medium [33] containing 10 mg L<sup>-1</sup> of benomyl (Benlate, 50% a.i.; DuPont de 112 113 Nemours, Milan, Italy). The talc formulation was incorporated into the soil to achieve the desired inoculum of 4 Log colony forming units (CFU)  $g^{-1}$ . 114

115

## 116 Plant material and experimental set-up

117 Two experimental trials were carried out at Agroinnova (Grugliasco, Itay). Plastic

tanks containing 100L of a mixture (1:1 v/v) of peat-perlite substrate (Tecno2, Turco

119 Silvestro sphagnum peat moss, Albenga, SV, Italy) and sandy loam soil (pH, 7.3; organic

- 120 matter content, 2.2 %; cation exchange capacity, 2.6 meq/100 g soil) were prepared. The final
- 121 substrate was made up of: sand, 76 %; silt, 14 %; clay, 10%; pH, 7.51; organic matter
- 122 content, 2,59 % and had a cation exchange capacity of 5.99 meq/100 g soil and subjected to

steam sterilization before use. The substrate was artificially inoculated with *F. oxysporum* f.
sp. *conglutinans* (ATCC16600RB) to reach a final concentration of 4 Log CFU ml<sup>-1</sup>. A noninoculated tank was used as the control.

126 Eruca sativa Mill seeds (cultivated rocket) were disinfected in a solution of 1% 127 sodium hypocloride plus 0.01% of Tween-20, and then rinsed twice in water for 1 min. The 128 seeds were air-dried at RT and stored at 4 °C until use. The seeds were sown in a greenhouse 129 in plug trays (20-26 °C, 70% RH and natural light condition). After 15-20 days, the first 130 seedling-leaves were developed. The rocket plants were left to grow under Phytotron 131 conditions for 7 days. Subsequently, 48 pots (2L each) were prepared from the inoculated 132 tank and another 48 pots were prepared from the non-inoculated tank and used as controls. 133 The rocket plants were then transplanted (4 plants/pot), and 8 inoculated and 8 non-134 inoculated pots were placed in 6 different phytotrons (PGC 9.2, TECNO.EL, Italy). One 135 replicate consisted of two pots. The rocket plants were kept in the phytotrons under six 136 different temperature and CO<sub>2</sub> combinations according to the following ranges: 1) 400-450 137 ppm CO<sub>2</sub>, 18-22 °C; 2) 800-850 ppm CO<sub>2</sub>, 18-22 °C; 3) 400-450 ppm CO<sub>2</sub>, 22-26 °C, 4) 800-138 850 ppm CO<sub>2</sub>, 22-26 °C, 5) 400-450 ppm CO<sub>2</sub>, 26-30 °C; 6) 800-850 ppm CO<sub>2</sub>, 26-30 °C. 139 The temperatures, light and humidity were changed gradually during the day in order to 140 simulate natural conditions. Three subsequent cultivation cycles were carried out in the same 141 pot. Each crop cycle lasted 35-37 days after transplanting. The plants were irrigated daily in 142 order to maintain the soil moisture at field capacity.

Substrate samples were taken at time 0 (immediately before plant transplanting) and after 60 and 120 days for microbial enumeration and molecular analyses (PCR-DGGE), while the physiological measurements of the plant leaves were conducted at the end of each rocket cycle.

### 148 **Disease incidence evaluation**

149 The effectiveness of the different simulated climate change conditions on the severity 150 of F. oxysporum f.sp. conglutinans on rocket was checked weekly by evaluating the pathogen 151 development using a previously reported disease index [34]. Wilted plants were counted and 152 removed and the final disease rating was made at the end of the experiment (35-37 days after 153 transplanting). At the end of each cycle, re-isolation from infected plants on a Komada medium supplemented with 10 mg L<sup>-1</sup> of benomyl was performed to confirm the presence of 154 155 F. oxysporum as the causal agent of the observed symptoms. During the latter survey, the 156 total fresh plant biomass was also rated using a technical balance (Orma SNC, Milano, Italy) 157 to evaluate the effect of the treatments on plant growth.

158

## 159 **Physiological measurements of the leaves**

160 In order to observe the effects of the climate change conditions on the leaf 161 physiological activity of the infected and control rocket plants, the photosynthetic efficiency 162 and chlorophyll content were monitored. Measurements were performed following the 163 experimental protocol reported by Pugliese et al. [35], with only minor modifications. 164 The chlorophyll content index (CCI) was measured with the SPAD 502 chlorophyll meter 165 (CCM-200, Opti-Sciences, Inc., Hudson, NH, USA), which determined the relative amount 166 of chlorophyll in the leaf by measuring the absorbance in the red and near-infrared regions 167 (650 and 940 nm, respectively). Chlorophyll meter readings were taken from each rocket 168 plant in the second or third leaves (fully developed) from the top on ten randomly selected 169 plants (one leaf/plant) at the end of each cultivation cycle. 170 The photosynthetic efficiency measurements were performed on five randomly selected

171 leaves using a portable continuous-excitation type fluorimeter (Handy-PEA, Hansatech

172	Instruments Ltd, Norfolk, UK), according to the manufacturer's instructions, at the end of
173	each cultivation cycle of rocket plants grown in infested and control substrates.

174

### 175 Root exudate analyses

176 In order to investigate the relationship between climate changes and the turnover of 177 low molecular weight organic compounds in the rhizosphere, water-soluble root exudates 178 were collected and analyzed. A sterilized CaSO<sub>4</sub> 0.01M solution (collection media) was used 179 to collect the root exudates [36]. For each condition tested, three randomly selected rocket 180 plants were taken from infested and not infested pots and the soil was carefully removed 181 using deionized water, without damaging the roots. The plants were then placed in a 50 mL 182 centrifuge tube with 15 mL of collection media for 2 hours in each phytotron. The collection 183 media was then filtered through a 0.45 µm membrane filter. pH was measured and the 184 samples were freeze dried and dissolved in 3 mL of ddH<sub>2</sub>O. Three main groups of organic 185 substances were analyzed: total organic carbon (TOC), total organic acids and amino acid 186 compounds.

187 TOC was determined by means of the colorimetric method. An aliquot of 1 mL was mixed

188 with 2 mL of  $K_2Cr_2O_7$  (2 N) and 1 mL of  $H_2SO_4$  concentrate and kept at 150 °C for 10 min.

189 The samples were cooled to room temperature and then analyzed by using a Spectroquant

190 Pharo 300 spectrophotometer (Merck, Darmstadt, Germany) at  $\lambda$ =585 nm. Glucose was used

as the reference C substance. For the amino acids analysis, 1 mL of sample was mixed with 1

192 mL of borate buffer (0.4 M pH=9.5) and 1 mL of dansyl chloride solution (Sigma-Aldrich,

193 St. Louis, MO, USA) at 10 mg/mL. The samples were incubated at 65 °C for 30 min [37].

- 194 The analysis was performed using an Agilent 1100 HPLC system (Agilent Technologies,
- 195 Palo Alto, CA). Zorbax Eclipse Plus C18 (4.6x100 mm, 3.5 µm, Agilent Technologies) was
- used for the chromatographic separation of the amino acids with a linear gradient from 10 to

197 100% of acetonitrile (Merck) in 15 min. The derivatized amino acids were detected by means 198 of a fluorescent detector with excitation at 335 nm and emission at 524 nm. A mixture of 20 199 standard amino acids (Sigma-Aldrich) was used as the reference. The organic acids were 200 separated with a Synergi Hydro-RP column (4.6x250 mm, 4  $\mu$ m, Phenomenex, Torrance, CA, 201 USA) in an isocratic condition, using buffer phosphate (50 mM) as the mobile phase. The 202 detector was set at  $\lambda$ =214 nm. A mixture of standard organic acids (Sigma-Aldrich) was used 203 as the reference.

204

## 205 Microbial count

206 Substrate samples (25 grams) were collected from 8 pots for both infested and control 207 treatments, at a depth of 2-5 cm, and were placed in sterilized polyethylene bags using a 208 sterilized spatula. The samples were passed through a sieve to remove any vegetation, and 209 mixed at room temperature for 30 min with 225 mL of quarter strength Ringer's solution 210 (Merck) in sterilized flasks on a rotary shaker (100 rpm). Decimal dilutions were prepared in 211 quarter strength Ringer's solution and aliquots of 1 ml of the appropriate dilutions were 212 poured, in triplicate, onto the following media: plate count agar (PCA, Oxoid, Milan) 213 incubated at 28°C for 48h for the total bacterial counts; potato dextrose agar (PDA, Merck) 214 supplemented with streptomycin (0,5 g/L) and a Komada medium supplemented with 10 mg L<sup>-1</sup> of benomyl (Benlate, 50% w.g., DuPont, USA), kept at 25°C for 7 days for the total 215 216 fungal and F. oxysporum f.sp. conglutinans enumerations, respectively. The results were 217 calculated as the mean of the Log counts of three independent determinations.

218

## 219 Substrate DNA extraction and DGGE analysis

Infested substrate samples (250 mg) were taken from 4 pots/phytotron at 0, 60 and
120 days after transplanting for DNA extraction. DNA exctract according to the protocol

described by the NucleoSpin® Soil manufacturer (Macherey-Nagel, Germany) and was
quantified using the NanoDrop 1000 spectrophotometer (Thermo Scientific) and standardized
at 10 ng µl<sup>-1</sup>. Fungal DNA was amplified using fungal ITS primers according to Gao *et al*.
[38]. PCR products for the ITS region were analyzed by denaturing gradient gel
electrophoresis (DGGE) at 25-35% using a Bio-Rad Dcode, as previously described [16].

227

## 228 Statistical analysis

229 The data obtained from the plate counts, root exudates and leaf physiological 230 measurements were analyzed using one-way analysis of variance (ANOVA), with treatments 231 being the main factor. ANOVA analyses were performed with the SPSS 22.0 statistical 232 software package (SPSS Inc., Cary, NC, USA). The Duncan HSD test was applied when 233 ANOVA revealed significant differences (P < 0.05). A database of fingerprints was created 234 using the PyElph software. A combined data matrix that included all the fingerprints for the 235 ITS region was obtained, and dendrograms of similarity were retrieved using the Dice 236 coefficient and the Unweighted Pair Group Method with the Arithmetic Average (UPGMA) 237 clustering algorithm [39] utilizing PyElph software [40]. The similarity distance matrix 238 generated through PyElph was used to build a Projection on Latent Structures - Discriminant 239 Analysis (PLS-DA) utilizing "mixOmics" in the R environment (www.r-project.org). The 240 obtained binary band-matching tables were considered to calculate the Shannon-Wiener 241 diversity index (H') [41] using PAST (PAleontological STatistics) software [42].

242

## 243 **Results**

## 244 Disease index assessment and fresh biomass production

245	The disease index (DI, 0-100) was found to be significantly influenced by the
246	temperature and $CO_2$ levels (Table 1). No symptoms were observed for the control plants in
247	any of the cycles or phytotron conditions that were considered. Generally, higher levels of
248	CO <sub>2</sub> and temperature were factors that significantly influenced the DI in the infected plants in
249	the simulated conditions. At 18-22 °C, the DI was significantly lower for both $CO_2$ ranges (P
250	< 0.05) than the other conditions. Conversely, the DI significantly increased at 22-26 °C,
251	particularly for higher CO <sub>2</sub> levels (P < 0.05) where a DI of 54 was reached. At 26-30 °C, a
252	slightly decreasing trend was recorded for both $CO_2$ levels, although a higher DI (43,4) was
253	observed at 800-850 ppm CO <sub>2</sub> , with a significantly different value than that of the 18-22 $^{\circ}$ C
254	conditions (P < 0.05). The fresh weight (FW) data pertaining to the infected plants showed
255	significant differences (P < 0.05) as a consequence of temperature, $CO_2$ and disease
256	development (Table 1). Lower FW values were obtained at 18-22 °C for both CO <sub>2</sub> conditions
257	and in phytotrons 4 and 6 (800-850 ppm CO <sub>2</sub> , 22-26 $^\circ C$ and 800-850 ppm CO <sub>2</sub> , 26-30 $^\circ C$ ,
258	respectively) where disease development was higher (Table 1). The control plants showed a
259	higher FW than the diseased rocket plants, with the exception of 18-22 °C (phytotrons 1
260	and 2: 400-450 ppm CO <sub>2</sub> , 18–22 $^{\circ}$ C and 800-850 ppm CO <sub>2</sub> , 18–22 $^{\circ}$ C) in which FW was
261	significantly lower (P < 0.05) than the other tested.

262

## **Effect on the physiological performances of the leaves**

The photosynthetic efficiency index (PI) for the infected plants showed a particularly pronounced and statistically significant (P < 0.05) decreasing trend for all the conditions tested at the end of the cycles (Fig. 1). In other words, PI appeared to be particularly affected by disease development (Table 1) coupled with the environmental conditions. Lower PI values (P < 0.05) were recorded for the infected plants from phytotrons 1, 2 and 4 (400-450 ppm CO<sub>2</sub>, 18–22 °C; 800-850 ppm CO<sub>2</sub>, 18–22 °C and 800-850 ppm CO<sub>2</sub>, 22-26 °C,

270 respectively). Moreover, the highest temperature provided the best evidence of impaired PI at
271 high CO<sub>2</sub> in the infected plants.

272 In general, the non-inoculated plants showed higher photosynthetic efficiency than the

infected ones, with the exception of those from phytotron 4 (800-850 ppm CO<sub>2</sub>, 22-26 °C)

274 where PI was lower than for the other conditions.

275 Similar trends were also observed for the CCI measurements in the infected samples

276 (Fig. 2) where no significant differences were observed between the phytotrons (P < 0.05).

277 The non-infected plants showed higher levels of chlorophyll content than the infected rocket

278 plants. Furthermore, significantly lower values were measured in the non-infected plants in

279 phytotrons 3 and 5 (400-450 ppm CO<sub>2</sub>, 22–26 °C and 400-450 ppm CO<sub>2</sub>, 26-30 °C,

respectively) (P < 0.05). Overall, the physiological measurements have confirmed that the

disease development led to a remarkable decrease in the physiological performances of theleaves.

283

### 284 Effect on root exudates

285 The results pertaining to the root exudates (Table 2) showed a similar trend for TOC 286 and amino acids (AA), when the exudates from the infected roots and the control plants were 287 compared. In both cases, when the temperature was lower (18-22 °C), an increased 288 concentration was registered in the samples from the infected plants. At 22-26 °C and 26-30 289 °C, the TOC and AA concentrations significantly increased for higher CO<sub>2</sub> levels (P < 0.05). 290 No significant differences were observed between the infected and non-infected plants for 291 lower CO<sub>2</sub> concentrations. The root exudates from the infected samples did not show any 292 significant differences in TOC concentration at 400-450 ppm of CO<sub>2</sub>; conversely, an 293 increasing trend of TOC concentration was registered when the temperature and CO<sub>2</sub> level 294 were increased (P < 0.05).

The amino acid levels from the infected plants were not different at lower  $CO_2$  levels; conversely, higher  $CO_2$  levels only induced a significant increase in amino acids at high temperatures (P < 0.05).

The organic acids, in general, showed a different trend. When  $CO_2$  and temperature were kept low, no significant differences were registered between the treatments or in the phytotrons. However, increasing the concentration of  $CO_2$  led to an increased production of organic acids, but only in the control samples. Furthermore, at 22-26 °C, for both levels of  $CO_2$ , the organic acid concentration increased for all the samples. In general, the organic acid concentrations of all the samples were always significantly higher for higher  $CO_2$  levels (P < 0.05).

305

### 306 Microbial analysis of substrate samples

307 The results of the bacterial and fungal plate counts on specific media are shown in 308 Tables 3, 4 and 5. The plate counts of mesophilic bacteria (TBC) (Table 3) from infested 309 substrate samples were not affected by the different CO<sub>2</sub> and temperature levels. A significant 310 decreasing trend was observed from time 0 up to 120 days for all the conditions considered (P 311 < 0.05). Furthermore, the samples at 120 days were not significantly different between the 312 phytotrons. The control substrate samples showed a similar trend to that observed in the 313 infested samples. However, the samples taken after 120 days in phytotrons 2 and 4 (800-850 314 ppm CO<sub>2</sub>, 18–22 °C and 800-850 ppm CO<sub>2</sub>, 22-26 °C) were significantly higher (P < 0.05), that is, 7.17 and 6.87 Log CFU  $g^{-1}$ , respectively. 315

The total fungal community plate counts (TFC, Table 4) from the infested samples mirrored the bacterial counts; a significant decreasing trend (P < 0.05) was observed over time from time 0, without any significant differences between the phytotrons at 120 days. The control substrate sample counts were similar to the infested ones, with the exception of those from 320 phytotron 2 (18-22 °C and 850 ppm CO<sub>2</sub>) at 120 days, when the statistical values were higher (4.89 Log CFU g<sup>-1</sup>) than in the other conditions. However, (among fungal community) 321 322 Fusarium oxysporum f.sp. conglutinans development was observed over time on the Komada 323 medium supplemented with benomyl in the infested substrate samples. In general, most of the 324 fungal community was represented by the pathogen, which developed over time and almost 325 completely covered the total fungal community values up to the last survey (120 days). In 326 particular, a general increasing trend was observed for all the conditions from time 0 in the 327 phytotrons compared to time 120. Although no significant differences between phytotrons 328 were observed at 120 days. A significant increasing trend from time 0 was observed for 329 phytotrons 2 and 4 for high CO<sub>2</sub> conditions in the last survey (from 3.80 to 4.38 and from 3.73 to 4.32 Log CFU g<sup>-1</sup>, respectively) (P < 0.05). With the exception of 26-30 °C, high 330 331 concentrations of CO<sub>2</sub> were shown to positively affect the growth of *Fusarium oxysporum* 332 f.sp. conglutinans. No pathogen was detected in the control substrate samples.

333

## 334 DGGE analysis of the fungal microbiota

The PCR-DGGE fingerprints of the fungal community obtained from the DNA extracted directly from the infested samples in all the adopted conditions are presented in Figure 3. Repeated DNA extraction and PCR-DGGE analysis confirmed the results of the fingerprinting.

The ITS based DGGE analysis showed an average result of 11.7 bands per sample (min 3,

340 max 17), (S1Fig.). The similarity matrix generated through the PyElph software was used to

341 build a PLS-DA, as a function of the CO<sub>2</sub> concentration, and the results showed a clear

342 separation between samples at 850 and samples at 450 ppm CO<sub>2</sub> (Fig. 3A). Regardless of the

343 temperature, the PLS models showed a clear separation of the samples (Fig. 3B). When the

344 samples were grouped on the basis of the sampling time, the samples at time 0 were clearly

345	separated from the other samples (Fig. 3C). The PLS-DA analysis, as a function of the
346	phytotrons (Fig. 3D), resulted in a certain degree of separation. The separation was
347	particularly important for the samples from phytotron 4, which appear to group together and
348	to be separated from the other phytotrons.
349	Furthermore, a binary band-matching table was analyzed in order to calculate the
350	index of diversity (Shannon-Wiener diversity index $H'$ ). The results, using only the data from
351	the ITS region, revealed, on the basis of their phytotron origin, that there was a biological
352	diversity in the samples. In particular, the $H'$ index and richness of the fungal community
353	changed according to the environmental conditions that were set, and ranged from 1.61 to
354	2.83 and 5 to 17, respectively. At the end of the experiment, the $H'$ index (1.79) and richness
355	(10) were lower for phytotrons 4 and 6 (22-26 and 26-30 $^{\circ}$ C at 850 ppm CO <sub>2</sub> ), and the H'
356	index (2.83) and richness (17) were higher for Phytotron 1 (18-22 °C and 450 ppm CO <sub>2</sub> ).
357	Higher CO <sub>2</sub> and temperature were shown to be selective and to reduce fungal community

358 diversity.

359

045

1.0

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.1

**(--·** 

DICD

C .1

## 360 **Discussion**

361 Plants that grow under elevated temperature and CO<sub>2</sub> concentrations often exhibit 362 positive responses by increasing photosynthesis and/or water and nutrient use efficiency [43]. 363 However, how increases in CO<sub>2</sub> might affect plant-pathogen interaction has not been 364 addressed or debated to any great extent. The aim of this work was to evaluate the effect of 365 simulated climate changes, by increasing CO<sub>2</sub> concentrations and temperature levels, on the 366 severity of Fusarium oxysporum f.sp. conglutinans on rocket plants. Phytotron chambers 367 have already been used in several studies, since they provide total control of the 368 environmental conditions and reproducible data in diverse pathosystems [20, 14-16]. Climate 369 change is an on-going phenomenon, which affects whole ecosystems and causes multitrophic

370 interactions that are difficult to understand [1]. The possibility of reproducing different 371 climatic conditions by coupling carbon dioxide and temperature levels can/has been 372 considered be very useful to obtain a better understanding of plant-pathogen interactions, as 373 has been done in the present work which deals with a soilborne pathogen. Focusing on plant-374 soil systems, it is well known that plants directly or indirectly control and influence the 375 multitrophic interactions of the soil through root exudates [22]. The results reported in this 376 study refer to disease incidence, cultivable abundance, leaf physiological performances, root 377 exudate analyses, and variability in substrate fungal profiles by PCR-DGGE. Several studies 378 have reported that rising CO<sub>2</sub> concentrations can cause plants to modify their root 379 architecture and exudation compounds in the rhizosphere [44,45]. In addition, it has been 380 predicted that global warming will directly influence multitrophic interactions if the soil 381 temperature exceeds its buffering capacity and this could be followed by changes in the 382 quality, quantity and diversity of plant and soil microbial communities and therefore plant pathogen development [1]. In the present study, a good disease level was reached under 383 384 artificial inoculation of F. oxysporum f.sp. conglutinans, thus making it possible to evaluate 385 the effect of the different climate change simulations. The temperatures and CO<sub>2</sub> 386 combinations in the six environmental conditions had a significant influence on the incidence 387 of Fusarium wilt. Higher CO<sub>2</sub> concentrations and temperatures caused a significant increase 388 in DI, in particular in the 22-26 °C range (Phytotron 4, Table 1). The effect of increased CO<sub>2</sub> 389 concentrations was still observed at 26-30°C on disease severity development, although 390 lower values were observed than in the 22-26 °C range, probably due to the suboptimal range 391 of temperature that limits pathogen development. Although elevated CO<sub>2</sub> had a significant 392 effect on Fusarium wilt incidence, the increase in temperature also had a significant effect on 393 disease development, particularly at 22-26 °C, which is a favourable range of temperatures 394 for disease development [30]. As previously reported, higher temperature or CO<sub>2</sub> levels

395 generally correspond to a greater severity of *Fusarium* wilt in other crops such as lettuce 396 [16,46] or wheat [47]. As reviewed by Ainsworth and Rogers [8], rising CO<sub>2</sub> concentrations 397 and temperatures could influence leaf physiology, morphology and indirectly crop production 398 by increasing or blocking their metabolic performances and photosynthetic efficiency. 399 However, no relevant effects linked to disease development or environment conditions have 400 been observed on PI and CCI data for infested and control plants, respectively. In fact, in 401 infected rocket plants, large reductions of both indices have been recorded compared to 402 controls, thus suggesting the high susceptibility of the photosynthetic machinery already at 403 lower disease severity values. Furthermore, photosynthetic efficiency and leaf chlorophyll 404 content are indicators of photosynthetic activity and chlorophyll stability. Fluorimeters and 405 SPAD chlorophyll meters are frequently used for the measurement of foliar damage provoked 406 by different biotic and abiotic stresses [35,48], although they were not considered useful for 407 the present investigation.

408 Recent research in plant biology has pointed out the importance and the role of root 409 exudates in mediating biological interactions in the rhizosphere. The chemical components of 410 root exudates could deter or attract an organism with different effects on the plants. This 411 would be particularly important during the pathogenesis of root-infecting fungal pathogens. 412 However, the signalling and composition of root exudates in plant-pathogen interactions have 413 not yet been elucidated [49-51]. To the best of the authors' knowledge, this is the first report 414 to have been made on the analysis of root exudates on wilted rocket plants under simulated 415 climate change conditions. The results have shown a different exudation pattern between the 416 controls and infected plants. Interestingly, higher levels of pH, organic acid and TOC (mainly 417 composed of sugars) were observed in the infected samples in phytotron 4 where the disease 418 index was higher. In addition, high values of organic acid, TOC and amino acids were also 419 recorded in phytotron 6, where a consistent level of DI was observed. These results suggest

420 the combined temperature and high CO<sub>2</sub> effect on root component release. In particular, the 421 TOC compounds underwent a significant increase, since they represent a carbon source for 422 microbial metabolism and energy that in turn could influence the attraction and severity of 423 the soilborne pathogen. Similarly, Kerks et al. [52] reported the activation of root exudate 424 chemotaxis and pathogenicity genes of S. enterica serovar Typhimurium in lettuce, which are 425 involved in root attachment and subsequent colonization. Although a great deal of 426 information is available concerning the relationships between symbionts and plants, limited 427 knowledge exists about the communication between plants and root pathogens mediated by 428 rhizodeposits and/or by pathogen metabolite production (e.g. volatile organic compounds, 429 VOCs) [53]. Further studies are needed to increase analytical skills and to analyse the 430 chemistry of root exudates, and thus to resolve the dialogue that takes place between 431 pathogens and plant roots. In addition, root exudates represent the main source of soil organic 432 carbon, defined as soluble low-molecular weight components that are mainly composed of 433 sugars, amino acids, organic acids and other secondary metabolites which vary from plant to 434 plant and which are able to shape the rhizosphere microbiome [22]. Conversely, no relevant 435 effects of CO<sub>2</sub> or temperature levels have been observed in the control plants to explain the 436 variation in the root exudate components in phytotron conditions, in line with what has been 437 reported by Uselman et al. [54] in Robinia pseudoacacia.

It is well known that DGGE fingerprints can be used to describe microbial composition and diversity, but they do not provide any information on the abundance and concentration of separate microbial species [55]. For this reason, this limitation has partially been addressed here by conducting plate counts on several media. In the present experimental conditions, the total bacteria and fungi plate counts in both the infested and control substrate samples showed a decreasing trend over time up to the end of the experiment, without climate simulation effects being observed. These results suggested that the forecast increase in CO<sub>2</sub>

445 and temperature levels due to climate changes would have a limited effect on fungal and 446 bacterial development. Recent reports [16,26,56] have shown similar results, while other 447 studies have reported results that depend to a great extent upon the host, microorganisms and 448 environment [57]. Conversely, the F. oxysporum f.sp. conglutinans plate counts at the end of 449 the present experiment have shown a slight increase or no significant variation for time 0, 450 except for phytotron 4 at higher  $CO_2$  concentrations, where the development and disease 451 incidence were significantly higher. In phytotron 6, where disease incidence was high, no 452 significant development of pathogen over time was detected. This behaviour supports the 453 hypothesis of a plant-mediated effect increasing disease incidence. The variability in the 454 fungal profiles was assessed by means of the PCR-DGGE approach, which has frequently 455 been used, with good results, in other simulated global change studies [16,26]. The samples 456 were clearly separated in relation to the temperature or CO<sub>2</sub>. In addition, this result was 457 further confirmed from an examination of the Shannon-Wiener indices. Interestingly, 458 phytotrons 4 and 6 showed the least diversity and the highest DI. Thus, a low diversity might 459 have a higher impact on disease development efficiency than the species visualized from the 460 DGGE examination. The loss in diversity caused by higher temperature and CO<sub>2</sub> levels could 461 be due to a plant-mediated effect that causes the selection of a few dominant species and 462 which may exclude others species through a competition strategy.

463

### 464 **Conclusions**

The disease incidence of pathogenic *Fusarium* species could increase due to the effects of the global changes that have been predicted for the future. The present experimental conditions have shown a coupled temperature and CO<sub>2</sub> effect on disease severity, which is probably plant-mediated, as reported for other pathosystems. Although no specific predictions can be made on field conditions, the data obtained from phytotron growth

470 chambers could help to unravel the complexity of plant-soilborne pathogen interactions that

471 take place under climate change conditions, in order to implement model prediction and

472 prevention strategies.

473

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- 632 **Fig 1. Photosynthetic efficiency measurements.** Effect of different  $CO_2$  and temperature 633 combinations on the photosynthetic efficiency of the leaves (PI) of rocket plants grown in a 634 substrate artificially infested with *F. oxysporum* f.sp. *conglutinans* and the control. Tukey's 635 HSD test (P < 0.05). 636
- **Fig 2. Assessment of chlorophyll content.** Effect of different CO<sub>2</sub> and temperature
- 638 combinations on the chlorophyll content of the leaves (CCI, °SPAD) of rocket plants grown 639 in a substrate artificially infested with *F. oxysporum* f.sp. *conglutinans* and the control. 640 Tukey's HSD test (P < 0.05).
- 641

642 Fig 3. PLS-DA models based on DGGE similarity distance matrix. Plot A, PLS-DA

- 643 models based on the DGGE similarity matrix as a function of CO<sub>2</sub>: 400-450 ppm (blue),
- 644 800-850 ppm (yellow); Plot B, PLS-DA models based on the DGGE similarity matrix as a
- function of the temperature: 26°C (blue), 22°C (yellow) ,and 30°C (red): Plot C, PLS-DA
- 646 models based on the DGGE similarity matrix as a function of the time: time 0 (red), time 60
- 647 (yellow) and time120 (blue); Plot D; PLS-DA models based on the DGGE similarity matrix
- as a function of the phytotrons: 1 (red), 2 (yellow), 3 (blue), 4 (black), 5 (green), 6 (pink).
- 649

### 651

	Parameters	Phytotron <sup>a</sup>								
		1 (400-450ppm CO <sub>2</sub> 18-22°C)	2 (800-850ppm CO <sub>2</sub> 18-22°C)	3 (400-450ppm CO <sub>2</sub> 22-26°C)	4 (800-850ppm CO <sub>2</sub> 22-26°C)	5 (400-450ppm CO <sub>2</sub> 26-30°C)	6 (800-850ppm CO <sub>2</sub> 26-30°C)			
Infected plants	Disease Index (0-100)	$17.2 \pm 9.4$ a	$18.80 \pm 11.40$ a	$25.00\pm12.5~ab$	$54.00\pm12.20\ \text{c}$	$22.90\pm3.60~ab$	$43.40\pm11.90~\text{bc}$			
	Fresh Weight (g plants <sup>-1</sup> )	$3.43 \pm 0.21 \ a$	$2.73 \pm 0.29$ a	$12.33\pm0.21~\text{c}$	$3.87 \pm 0.06 \ a$	$14.45 \pm 0.13 \ d$	$9.70\pm0.18~\text{b}$			
Control plants	Disease Index (0-100)	0.00 a								
	Fresh Weight (g plants <sup>-1</sup> )	$3.80\pm0.44\ a$	$3.88\pm0.21\;a$	$13.33\pm0.41\ b$	$14.50\pm0.63~\text{b}$	$16.27\pm0.86\ c$	$13.03\pm0.46\ b$			

<sup>a</sup>The disease index (0-100) and total plant fresh weight were expressed on the basis of three replicates. Values with different superscripts in the same row differ significantly according to Tukey's HSD test (P<0.05)

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### **Table 2.** Main root exudate components analyzed on rocket plants cultivated in infested and control substrates collected at the end of the cycle.

### 

	Parameters	Phytotron <sup>a</sup>	Phytotron <sup>a</sup>							
		1	2	3	4	5	6			
		(400-450ppm CO <sub>2</sub> 18-22°C)	(800-850ppm CO <sub>2</sub> 18-22°C)	(400-450ppm CO <sub>2</sub> 22-26°C)	(800-850ppm CO <sub>2</sub> 22-26°C)	(400-450ppm CO <sub>2</sub> 26-30°C)	(800-850ppm CO <sub>2</sub> 26-30°C)			
	pH	$7.23\pm0.15~ab$	$7.38\pm0.32 \text{ ab}$	$7.10\pm0.09~ab$	$7.65\pm0.55\ b$	$7.36\pm0.19 \text{ ab}$	$7.35 \pm 0.23$ ab			
Infested	Amino acids (mM g <sup>-1</sup> )	1.57 ±0.04 ab	$1.92\pm0.18$ a-c	$1.92\pm0.28~\text{a-c}$	$2.78\pm0.18$ a-c	$2.00\pm0.17$ a-c	4.97 ±0.66 e			
samples	Organic acids (mM g <sup>-1</sup> )	$1.90 \pm 0.14$ a	$2.35\pm0.12\text{ a-c}$	$5.86 \pm 0.14 \text{ e}$	$7.39\pm0.42\ f$	$1.54 \pm 0.18$ a	$3.01\pm0.33~\text{cd}$			
	TOC (mg $g^{-1}$ )	$57.2\pm1.09~\text{a-c}$	$50.6\pm2.97~a$	$67.1 \pm 3.17$ de	$77.8\pm5.80~ef$	$57.2\pm1.09 \text{ ab}$	$98.7\pm3.06\;g$			
	pН	6.83 ± 0.10 a	$7.08 \pm 0.13$ ab	$7.01 \pm 0.12$ ab	$7.29 \pm 0.07 \ ab$	$7.26 \pm 0.11$ ab	$7.22 \pm 0.14$ ab			
Controls	Amino acids (mM g <sup>-1</sup> )	$2.27 \pm 0.24$ a-c	$3.20 \pm 3.14$ a-d	$2.19\pm0.26~a\text{-c}$	$1.54 \pm 0.03$ a	$2.08\pm0.35~\text{a-c}$	$2.43 \pm 0.46 \text{ b-d}$			
	Organic acids (mM g <sup>-1</sup> )	$1.99 \pm 0.07 \text{ ab}$	$5.72 \pm 0.27 \ e$	$8.07\pm0.68~f$	$2.90\pm0.22~b\text{-d}$	$3.57 \pm 0.41 \ d$	$2.37\pm0.38~\text{a-c}$			
	TOC (mg $g^{-1}$ )	$74.0 \pm 3.89 \text{ de}$	$89.3 \pm 5.58 \text{ fg}$	$58.0\pm2.69~\text{a-c}$	$46.0 \pm 3.70 \text{ a}$	$56.1 \pm 3.82$ a-c	$65.1 \pm 6.22$ b-d			

<sup>a</sup> The root exudate parameters were expressed as the mean values of three plants for three cultivation cycles. Values with different superscripts in the same row differ significantly according to Tukey's HSD test (P<0.05)

**Table 3.** Total bacterial counts (TBC) of mesophilic bacteria from the infested and control substrate samples following incubation in phytotrons

659 for 120 days.

	Sampling day	Phytotron (Log CFU $g^{-1} \pm SD^a$ )							
		1	2	3	4	5	6		
		(400-450ppm CO <sub>2</sub> 18-22°C)	(800-850ppm CO <sub>2</sub> 18-22°C)	(400-450ppm CO <sub>2</sub> 22-26°C)	(800-850ppm CO <sub>2</sub> 22-26°C)	(400-450ppm CO <sub>2</sub> 26-30°C)	(800-850ppm CO <sub>2</sub> 26-30°C)		
Infested samples	0	$7.38\pm0.07~\text{e}$	$7.08\pm0.11~\text{c-e}$	$7.19\pm0.02~de$	$6.86\pm0.03~b\text{-e}$	$7.05\pm0.02~\text{c-e}$	$7.09\pm0.02~\text{c-e}$		
	60	$6.36\pm0.10~ab$	$7.01\pm0.05~\text{c-e}$	$6.80\pm0.17$ a-d	$6.77\pm0.07$ a-d	$6.56\pm0.17$ a-c	$6.32\pm0.28~ab$		
	120	$6.45\pm0.35 \text{ ab}$	$6.43 \pm 0.13$ ab	$6.54\pm0.09~\text{a-c}$	$6.30 \pm 0.52$ a	$6.34\pm0.09~ab$	$6.26 \pm 0.10$ a		
Controls	0	$7.15\pm0.08\text{ c-e}$	$7.39 \pm 0.09$ de	$7.60 \pm 0.02$ e	$7.19 \pm 0.11$ c-e	$7.46 \pm 0.02 \text{ de}$	$7.22\pm0.04\text{ c-e}$		
	60	$6.40 \pm 0.35$ a	$7.19\pm0.18~\text{c-e}$	$6.62\pm0.28$ ab	$7.13 \pm 0.09 \text{ cd}$	$6.91\pm0.28$ bc	$7.57 \pm 0.23$ de		
	120	$6.26 \pm 0.15$ a	$7.17\pm0.07\text{ c-e}$	$6.42\pm0.07\;a$	$6.87\pm0.10\ c$	$6.57\pm0.07\ ab$	$6.17 \pm 0.06 \text{ a}$		

<sup>a</sup>The plate counts were calculated as the mean Log counts of the three replicates. Values with different superscripts differ significantly according to Tukey's HSD test

662 (P<0.05)

### **Table 4.** Total fungi community counts (TFC) from the infested and control substrate samples following incubation in phytotrons for 120 days.

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	Sampling day	Phytotron (Log CFU $g^{-1} \pm SD^a$ )							
		1	2	3	4	5	6		
		(400-450ppm CO <sub>2</sub> 18-22°C)	(800-850ppm CO <sub>2</sub> 18-22°C)	(400-450ppm CO <sub>2</sub> 22-26°C)	(800-850ppm CO <sub>2</sub> 22-26°C)	(400-450ppm CO <sub>2</sub> 26-30°C)	(800-850ppm CO <sub>2</sub> 26-30°C)		
Infested samples	0	$6.59\pm0.36\text{ g-i}$	$6.19\pm0.23~f\text{-}h$	$7.13\pm0.06\ i$	$6.43 \pm 0.11$ g-i	$5.92 \pm 0.11 \text{ e-g}$	$6.88 \pm 0.08$ hi		
	60	$5.12\pm0.20~a\text{-}d$	$5.30\pm0.24\text{ b-e}$	$5.47\pm0.05\text{ c-e}$	$5.56\pm0.14~d\text{-}f$	$5.06\pm0.72~\text{a-d}$	$5.35\pm0.15\text{ b-e}$		
	120	$4.65\pm0.07~ab$	$4.77\pm0.10\text{ a-c}$	$4.81\pm0.04~a\text{-c}$	$4.42 \pm 0.16$ a	$4.84 \pm 0.13$ a-c	$4.80\pm0.06~\text{a-c}$		
Controls	0	$6.52\pm0.09~f$	$6.69\pm0.40~f$	$6.30\pm0.13~f$	$6.23 \pm 0.24$ ef	$6.30\pm0.00\ f$	$6.55\pm0.30~f$		
	60	$5.12\pm0.18\ bc$	$5.75\pm0.07~de$	$5.08\pm0.16\ ab$	$5.45\pm0.04\ cd$	$5.08\pm0.07~bc$	$5.08\pm0.11~bc$		
	120	$4.53 \pm 0.07 \ a$	$4.89\pm0.16\text{ c-e}$	$4.75\pm0.13\ ab$	$4.93\pm0.21~\text{a-c}$	$5.00\pm0.08~\text{a-c}$	$4.74\pm0.14\ ab$		

<sup>a</sup>The plate counts were calculated as the mean Log counts of the three replicates. Values with different superscripts differ significantly according to Tukey's HSD test

668 (P<0.05)

671 **Table 5.** Plate counts of *Fusarium oxysporum* f.sp. *conglutinans* from the infested substrate samples following incubation in phytotrons for 120

672 days.

673

	Sampling day	Phytotron (Log CFU $g^{-1} \pm SD^a$ )						
		1	2	3	4	5	6	
		(400-450ppm CO <sub>2</sub> 18-22°C)	(800-850ppm CO <sub>2</sub> 18-22°C)	(400-450ppm CO <sub>2</sub> 22-26°C)	(800-850ppm CO <sub>2</sub> 22-26°C)	(400-450ppm CO <sub>2</sub> 26-30°C)	(800-850ppm CO <sub>2</sub> 26-30°C)	
Infested samples	0	$3.77\pm0.04\ ab$	$3.80\pm0.05\ ab$	$4.24\pm0.00~a\text{-}d$	$3.73 \pm 0.12 \ a$	$3.78\pm0.08\ ab$	$4.00\pm0.18~\text{a-c}$	
	60	$4.00\pm0.10~\text{a-c}$	$4.89\pm0.02~\text{e}$	$4.46\pm0.04~de$	$4.91\pm0.15\;e$	$4.06\pm0.04~\text{a-c}$	$4.81\pm0.10\;de$	
	120	$4.11\pm0.04~\text{a-c}$	$4.38\pm0.19\text{ b-e}$	$4.34\pm0.74~a\text{-e}$	$4.32\pm0.10\ bc$	$4.18\pm0.19~a\text{-c}$	$3.87\pm0.11~\text{a-c}$	

<sup>a</sup>The plate counts were calculated as the mean Log counts of the three replicates. Values with different superscripts differ significantly according to Tukey's HSD test

675 (P<0.05)

# 677 Supporting Information

- 679 S1 Fig. Similarity dendrogram generated from the digitized PCR-DGGE fingerprints of DNA
- 680 directly extracted from the substrate infested with *F. oxysporum* f.sp. *conglutinans*.
- 681