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## Assessing host specialization of *Botrytis cinerea* on lettuce and tomato by genotypic and phenotypic characterization

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1 **Short title:** Host specialization of *B. cinerea*

2

3 **Informative title:** Assessing host specialization of *Botrytis cinerea* on lettuce and tomato by  
4 genotypic and phenotypic characterization.

5

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9

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11 *Lactuca sativa*

12

### 13 **Abstract**

14 This study tested the hypothesis that *B. cinerea* shows host specialization on tomato and lettuce,  
15 using phenotypic and genotypic tools. Strains were isolated from tomato and lettuce grown  
16 together in a same greenhouse. Forty-four lettuce strains and forty-two tomato strains were  
17 investigated for their genetic diversity and their aggressiveness. Both gene diversity and allelic  
18 richness were significantly higher in lettuce strains than in tomato strains (P=0.01). Cluster  
19 analysis revealed a clear structure of the strains under study in two clusters. However, this  
20 structure did not separate the strains according to their host of origin. Tomato strains were  
21 significantly more aggressive than lettuce strains when inoculated on tomatoes (P=0.001). But  
22 no significant differences in aggressiveness were observed when the strains were inoculated on  
23 lettuce (P=0.17) or on apple (P=0.87). Our results suggest an absence of clear host  
24 specialization of *B. cinerea* on tomato and lettuce.

25

## 26 **Introduction**

27 *Botrytis cinerea* is an Ascomycete (teleomorph *Botryotinia fuckeliana*) responsible for grey  
28 mould on cultivated and wild plants in temperate regions worldwide (Jarvis 1980). Some of the  
29 plant species susceptible to *B. cinerea* are of economic importance (lettuce, tomato, grapevine  
30 among others). When a crop is attacked by *B. cinerea* its yield may be reduced and products  
31 may become unmarketable. This fungus may produce several million spores in a few days on  
32 diseased plants when conditions are favourable (Nicot *et al.*, 1996). These spores are easily  
33 dispersed by air currents (Jarvis, 1962; Harrison & Lowe, 1987) and may cause rapid  
34 development of epidemics (Decognet *et al.*, 2009; Bardin *et al.*, 2014).

35 It has long been considered that *B. cinerea* lacks host specificity, as it was reported to attack  
36 more than 200 plant species (Jarvis, 1980) and it is also known to develop as a saprophyte on  
37 numerous types of substrates (Holtz *et al.*, 2004). However, several studies have revealed  
38 genetic differentiation among isolates collected from different host plants. In France, Diolez *et*  
39 *al.* (1995) showed that strains of *B. cinerea* containing the transposable element *Boty* were  
40 present on grapes and tomatoes but not on lentil. Giraud *et al.* (1999) reported that the frequency  
41 of transposable elements *Boty* and *Flipper* was significantly different in populations of *B.*  
42 *cinerea* collected on different host plants. In Chile, Muñoz *et al.* (2002) showed that strains  
43 collected from tomato and grapes were genetically differentiated on the basis of PCR-RFLP  
44 markers. Using microsatellite markers, Rajaguru & Shaw (2010) and Fournier & Giraud (2008)  
45 reported similar situations, respectively between strains sampled from raspberries and  
46 blackberries in England, and between strains sampled from grapevine and bramble in France.  
47 Genetic differentiation of fungal populations through host shift speciation has been  
48 hypothesized to result from several possible mechanisms, including the cessation of gene flow  
49 between two populations (Giraud *et al.*, 2010). Thus, former studies reporting genetic

50 differentiation on different hosts may challenge the initial assumptions and indicate that *B.*  
51 *cinerea* presents a certain degree of host specialization in certain situations.

52 Comparisons of aggressiveness have also revealed differences between *B. cinerea* isolates  
53 depending on their host of origin. For example, strains isolated from tomato were more  
54 aggressive on tomato leaves than strains isolated from grapevine (Cotoras & Silva, 2005) and  
55 strains collected on grapevine were more aggressive on this plant than strains from other host  
56 plants (Derckel *et al.*, 1999). Pie & Brouwer (1993) also reported that strains of *B. cinerea*  
57 collected on roses had higher aggressiveness on rose petals than strains collected on gerbera  
58 flowers or pea leaves. Such differences in aggressiveness may provide a limitation in gene flow  
59 among strains of the pathogen present on different hosts, as successive generations of inoculum  
60 (possibly numerous in one growing season, depending on the crop) result in the gradual  
61 selection of the most aggressive strains (Decognet *et al.*, 2009).

62 Knowledge of host specialization among strains of *B. cinerea* could be of great importance for  
63 disease control as crops considered to be susceptible are often grown simultaneously in close  
64 vicinity or successively in rotation schemes. This is often the case in vegetable production.  
65 Transfer of inoculum from one crop to the other is likely through dissemination of airborne  
66 spores (Jarvis, 1980). Then, in case of a lack of host specialization, airborne inoculum produced  
67 on a species, easily released and disseminated by air currents, may induce symptoms on another  
68 species located in a close vicinity. Thus, the management of greenhouse vents will have to take  
69 into account not only the climate inside the greenhouse but also possible entry of inoculum  
70 from the outside. Limiting the exposure of crop to airborne inoculum can be achieved by  
71 separating crops in time. But *B. cinerea* produces also survival structures such as sclerotia and  
72 mycelium in plant debris (Coley-Smith, 1980). Then, in case of a lack of host specialization,  
73 the inoculum left in the soil by one susceptible species may serve as primary inoculum in a  
74 following susceptible different species and thus provoke a grey mould outbreak. In such a case,

75 soil disinfestation would be useful. On the contrary, if *B. cinerea* shows clear host specialization  
76 on tomato and lettuce less attention will be required on a possible role as inoculum source for  
77 crops grown in close vicinity or in rotation.

78 The objective of our work was thus to assess host specialization of *B. cinerea* on two vegetable  
79 crops, lettuce and tomato, which are usually cultivated in close vicinity or in rotation in southern  
80 France and sustain particularly high risks of yield loss from grey mould. To this aim, we used  
81 genetic and phenotypic tools to characterize a collection of isolates sampled from diseased  
82 lettuce and tomato plants. The strains were also inoculated on a third host plant (apple) to assess  
83 if their level of aggressiveness was host-dependant or conversely, consistent across host  
84 species.

85

## 86 **Materials and methods**

### 87 *Isolate collection*

88 Lettuce (cv Zendria, Rijk Zwaan) and tomato (cv Brenda, Gautier Semences) plants were grown  
89 at the Alenya-Roussillon experimental domain of the French National Institute of Agricultural  
90 Research (INRA) in southern France (lat. 42.64N; long. 2.98E). In order to minimize  
91 geographical and temporal factors that may interfere with the detection of host specialization,  
92 both crops were grown in the same greenhouse (Fig. 1) with a two-month overlapping period.  
93 Following the development of grey mould on both crops in the greenhouse, isolates were  
94 collected on diseased lettuce and tomato plants. Sample collection consisted of rubbing sterile  
95 cotton buds on sporulating lesions. The cotton buds were then stored at -20°C until isolate  
96 purification. All isolates used in this study were purified and single spored in a classical way  
97 (Leyronas *et al.*, 2012) prior to their genotypic and phenotypic characterization. Hereafter,  
98 characterized single spore isolates will be referred to as ‘strains’. Those originating from tomato

99 will be referred to as “tomato strains” while those from lettuce will be referred to as ‘lettuce  
100 strains’.

101

### 102 *Isolate genotyping*

103 Genomic DNA was extracted from aliquots of 15 mg lyophilized fungal material (harvested  
104 from two-week old cultures on Potato Dextrose Agar) in 96-well plates, following the Dneasy  
105 Plant extraction Kit protocole (Qiagen). The nine microsatellite markers designed for *B. cinerea*  
106 by Fournier *et al.* (2002) were amplified with forward primers conjugated with the following  
107 fluorescent dyes: Fam for BC1, BC4, BC9 and BC10; Hex for BC2 and BC6; Tamra for BC3,  
108 BC5 and BC7 (MWG). Reverse primers did not carry any fluorescent dye. Primers were  
109 multiplexed for amplification of several microsatellites in a single PCR as follows. Four pairs  
110 of markers were amplified together at the following hybridization temperatures: BC1 and BC9  
111 at 50°C; BC2 and BC5 at 53°C; BC3 and BC6 at 50°C; BC4 and BC10 at 59°C. Marker BC7  
112 was amplified singly at 59°C. To determine the size of the microsatellites, the PCR products  
113 were diluted and multiplexed prior to scanning with the help of a Megabace sequencer  
114 (Amersham Pharmacia). The multiplexing consisted of mixing in a same well the PCR products  
115 of several markers (either BC1, BC2, BC5 and BC9 or BC3, BC6, BC4, BC7 and BC10). In  
116 each well, ET-400 labelled with Rox dye (Amersham Pharmacia) was used as a size marker.  
117 Genetic Profiler software (Amersham Biosciences) was then used for the microsatellite size  
118 analysis.

119 Complete microsatellite size profiles (referred to as "haplotypes" hereafter) were obtained for  
120 44 lettuce strains and 42 tomato strains.

121

### 122 *Genetic diversity of tomato and lettuce strains*

123 Unbiased gene diversity (Hnb) and allelic richness were computed separately for the tomato  
124 and for the lettuce strains with the Genetix software (Nei, 1978). The software FSTAT version  
125 2.9.3 (Goudet, 1995) was used to compute allelic richness per locus corrected for minimum  
126 sample size of 16 isolates. Several other diversity indices (all taking values between 0 and 1; 1  
127 indicating the maximum level of diversity) were also computed with GenClone 1.0 software  
128 (Arnaud-Haond & Belkhir, 2007) as follows. We used the Simpson diversity index ( $D^*$ ), which  
129 measures the probability that two randomly selected individuals in a population have different  
130 genotypes. We also used the evenness index, whose value tends to 1 when genotypes have a  
131 similar abundance (equitable distribution of clones) (Arnaud-Haond *et al.*, 2007). The number  
132 of different multilocus haplotype (MLH) was also computed with GenClone. Finally, we used  
133 the index of haplotypic diversity (based on the number of individuals and the number of distinct  
134 MLH), which estimates the proportion of haplotypes present in a population and takes a value  
135 of 1 when a population is composed exclusively of unique haplotypes (Arnaud-Haond *et al.*,  
136 2007).

137

### 138 *Linkage disequilibrium*

139 The existence of linkage disequilibrium among the lettuce strains and among the tomato strains  
140 was estimated by computing the  $r_d$  index with Multilocus software version 1.3 (Agapow & Burt,  
141 2001). The null hypothesis of complete panmixia ( $r_d = 0$ ; absence of clonality) was tested by  
142 permuting alleles (microsatellite sizes) among strains, independently for each microsatellite  
143 marker (1000 permutations).

144

### 145 *Genetic structure*

146 To test the hypothesis of host specialization in *B. cinerea*, we used the discriminant analysis of  
147 principal components (DAPC) implemented in the R package adegenet (Jombart, 2008). In this

148 analysis, we fixed the number of clusters to two, with one cluster including all strains from  
149 tomato and the other one including all strains sampled from lettuce. We used the optimisation  
150 procedure implemented in adegenet to select the optimal number of principal components to be  
151 retained in the analysis (Jombart *et al.*, 2010). In a second step, the DAPC was also performed  
152 without any *a priori* on the genetic structure. In this case, we first identified the optimal number  
153 of clusters in our data set, using the k mean clustering approach (function ‘find.clusters’ in  
154 adegenet). The best clustering solution was determined, using Bayesian Information Criterion  
155 (BIC). The distribution of tomato and lettuce strains among clusters and their probability of  
156 assignment were analysed. A strain was considered as accurately assigned to a cluster when its  
157 membership probability was greater than 0.8. The level of genetic differentiation between the  
158 identified clusters was assessed by computing Weir & Cockerham’s  $F_{ST}$  values with the  
159 software Arlequin version 3.5 (Excoffier *et al.*, 2005).

160 Finally, to better understand the relationships between the different strains, we computed a  
161 neighbor-joining (NJ) tree with the program POPULATIONS (version 1.2.32 provided by  
162 Olivier Langella, UMR de génétique végétale, Gif-sur-Yvette, France). The NJ-tree was based  
163 on the distances of Cavalli-Sforza & Edwards (1967), computed from our microsatellite loci.  
164 The tree was visualized and edited under the program TREEVIEW (Page, 1996). All analyses  
165 were conducted on data sets excluding clone replicates.

166

#### 167 *Evaluation of aggressiveness on tomato*

168 The aggressiveness of tomato strains and lettuce strains was compared on 8-week old tomato  
169 plants cv. Swanson (De Ruiter Seeds). Plants were grown in a greenhouse in individual pots  
170 containing a horticultural mix (De Baat) and watered daily with a nutrient solution as described  
171 by Decognet *et al.* (2009). Each strain was inoculated on three plants. On each plant, three  
172 leaves were removed, leaving 1cm petiole stubs on the stems and the wounds were inoculated



173 with 10  $\mu\text{L}$  aliquots of spore suspension. The spore suspensions were prepared from two-week  
174 old cultures on Potato Dextrose Agar (PDA) and were adjusted to  $10^6$  spores  $\text{mL}^{-1}$ . All plants  
175 were incubated in a growth chamber with a photoperiod of 14 h, with a light intensity of 162  
176  $\mu\text{mol. m}^{-2}. \text{s}^{-1}$ , maintained at  $21^\circ\text{C}$  with a relative humidity above 90%. The length of resulting  
177 stem lesions was monitored daily from the 3<sup>rd</sup> to the 7<sup>th</sup> day after inoculation and these data  
178 were used to compute the area under the disease progression curves (AUDPC). Based on prior  
179 work, strain BC1 was used as a reference for aggressiveness (Decognet *et al.*, 2009). For each  
180 strain, an index of aggressiveness (IA) was calculated, relative to that of strain BC1, as  $\text{IA} =$   
181  $100 * (\text{AUDPC}_{\text{strain}} / \text{AUDPC}_{\text{BC1}})$ . The test was conducted twice independently.

182

### 183 *Evaluation of aggressiveness on lettuce leaves*

184 The aggressiveness of the strains was also compared on detached lettuce leaves (cv Mantilia).  
185 Leaves were taken from 8-week old lettuce plants and placed in clear polystyrene boxes over  
186 water-saturated filter paper in order to keep high humidity. Each leaf was inoculated in its centre  
187 with a mycelial plug (diameter 5 mm) excised from a 3-day old colony on PDA. Care was taken  
188 to position the mycelium in direct contact with the plant tissue. The inoculated leaves were  
189 incubated in a growth chamber at  $21^\circ\text{C}$  with a light intensity of  $162 \mu\text{mol. m}^{-2}. \text{s}^{-1}$  and a  
190 photoperiod of 10h. The leaves were photographed at 48, 72 and 96 hours after inoculation and  
191 the surface of lesions was measured with image analysis software Assess 2.0 (APS Press). The  
192 AUDPC and IA were calculated as described above. The test was conducted twice  
193 independently and nine leaves were inoculated for each strain in a given test.

194

### 195 *Evaluation of aggressiveness on apple*

196 In order to test a third host, the aggressiveness of both tomato and lettuce strains was  
197 investigated on apples (cv Golden delicious) purchased from an organic farm. Apple was

198 selected because *B. cinerea* can induce economic losses in postharvest storage. Wounds (2 mm  
199 in diameter and 10 mm deep) were made with the help of a sterile pipet tip on the equator of  
200 the fruits. Each apple received two wounds on opposite sides. Each wound was inoculated with  
201 10  $\mu\text{L}$  of a spore suspension ( $10^6$  spores. $\text{mL}^{-1}$ ) prepared as described above. The fruit were then  
202 incubated at 21°C and lesion diameter was measured from the 3<sup>rd</sup> to the 7<sup>th</sup> day after inoculation.  
203 The AUDPC and IA were calculated as described above. The test was conducted twice  
204 independently and three apples (6 wounds) were inoculated for each strain in a given test.

205

#### 206 *Statistical analyses*

207 Statistical analyses were performed with StatView (version 5, SAS Institute). Non-parametric  
208 Mann-Whitney tests were used to determine significant differences between gene diversity,  
209 allelic richness, aggressiveness of tomato and lettuce strains. Correlation between  
210 aggressiveness on tomato and on lettuce was estimated using the non-parametric Spearman's  
211 rank correlation coefficient (Rho). Statistical inferences were made at the 5 % level of  
212 significance, unless indicated otherwise.

213

## 214 **Results**

### 215 *Genetic diversity*

216 Eighty-six isolates sampled from tomato and lettuce were genotyped through amplification of  
217 9 microsatellites. None of these carried the private allele at microsatellite locus BC6 associated  
218 with the cryptic species *B. pseudocinerea* (Walker *et al.*, 2011). Thus the 86 strains (44  
219 collected on lettuce and 42 collected on tomato) were considered to belong to *B. cinerea* and  
220 were kept for further genetic analyses.

221 The lettuce strains showed higher genetic diversity than tomato strains when considering the  
222 unbiased gene diversity and the allelic richness (Table 1). The number of alleles in each

223 microsatellite locus and the gene diversity per locus were significantly higher in lettuce strains  
224 than in tomato strains (respectively  $P_{\text{Mann-Whitney}}=0.0089$ ,  $P_{\text{Mann-Whitney}}=0.0149$ ) (Table 2). Some  
225 alleles were not shared between tomato and lettuce strains. Among a total of 89 alleles observed  
226 within the 9 microsatellites, 5 alleles were only present in tomato strains and 46 alleles were  
227 only present in lettuce strains.

228 Differences between tomato and lettuce strains were also observed when examining haplotypic  
229 diversity. Forty-three different multilocus haplotypes (MLH) were found among the 86 strains,  
230 of which four were shared by tomato and lettuce strains (Table 1). These MLHs appeared in 2,  
231 4, 12 and 14 copies among the 86 isolates. The haplotypic diversity of lettuce strains was much  
232 higher than that of tomato strains (Table 1). Haplotypic diversity was also assessed with  
233 Simpson's index (D). This index was overall high for the two groups, although slightly higher  
234 for lettuce strains than for tomato strains (Table 1). Evenness values (ED) reflected a more  
235 equitable distribution of haplotypes within tomato strains. Linkage disequilibrium was equally  
236 low and highly significant in both tomato and lettuce strains thus rejecting the null hypothesis  
237 of random mating in both groups of strains (Table 1).

238

### 239 *Genetic structure*

240 A first DAPC was performed by fixing the number of clusters ( $K=2$ ) to test the hypothesis that  
241 the genetic structure of *B. cinerea* strains corresponded to their host of origin. The scatter plot  
242 of the analysis showed large overlap between tomato and lettuce strains (Fig. 2a). Moreover, a  
243 low percentage of strains were clearly assigned to a given cluster (data not shown): only 51%  
244 of lettuce and 25% of tomato strains had a membership probability above 0.8. This result is  
245 supported by the distribution of the strains in the NJ tree (Fig. 3). Although lettuce strains were  
246 more abundant than tomato strains in certain branches, all strains were widely intermixed in the  
247 tree regardless to their host of origin.

248 A second DAPC was performed to investigate the genetic structure of lettuce and tomato strains  
249 without any *a priori* hypothesis about the factors shaping the structure. The BIC showed a rapid  
250 decrease and a sharp elbow at  $K=2$  (see supplementary material). The resulting structure  
251 visualized with the scatter plot showed almost no overlap between tomato and lettuce strains  
252 (Fig. 2b). Moreover 97% and 100% of the lettuce and tomato strains, respectively, were  
253 assigned to a cluster with a posterior probability greater than 0.8. The first cluster included 42%  
254 and 82% of the lettuce and tomato strains, respectively. The second cluster included 55% and  
255 18% of the lettuce and tomato strains, respectively (3% of lettuce strains were not clearly  
256 assigned to a cluster  $P<0.8$ ). These two clusters were significantly differentiated ( $P<0.001$ ) with  
257 an  $F_{ST}$  value of 0.252.

258

### 259 *Aggressiveness*

260 All 72 strains were able to infect and cause symptoms on the three plant species tested. For tests  
261 on apple, there was no significant difference ( $P=0.87$ ) between the average aggressiveness of  
262 the 33 lettuce ( $IA=89.9 \pm 22$ ) and the 39 tomato strains ( $IA=89.6 \pm 18$ ). When inoculated on  
263 lettuce, there was no significant difference ( $P=0.17$ ) between the average aggressiveness of the  
264 lettuce strains ( $IA=81.6 \pm 4.9$ ) and the tomato strains ( $IA=72.8 \pm 5.1$ ) (Fig. 4a). In contrast, when  
265 inoculated on tomato, tomato strains were significantly more aggressive ( $P = 0.0012$ ) than  
266 lettuce strains (Fig. 4b), with mean IA values of  $70.7 (\pm 3.5)$  and  $52.8 (\pm 3.8)$  respectively.

267 There was no significant correlation between aggressiveness on tomato and on lettuce  
268 ( $Rho_{\text{Spearman}} = 0.033$ ;  $P=0.78$ ). Strains with the highest level of aggressiveness on one species  
269 were not highly aggressive on the other. However, regardless of their host of origin, strains with  
270 low aggressiveness on one host tended to have also low aggressiveness on the other plants.  
271 Among the 16 strains least aggressive on tomato ( $IA<40$ ), seven (4 tomato strains and 3 lettuce  
272 strains) were also among the 13 least aggressive on lettuce ( $IA<50$ ). Furthermore, among the

273 14 strains with the lowest aggressiveness on apple, 10 were also among the least aggressive on  
274 tomato and/or on lettuce.

275

## 276 **Discussion**

277 This study is the first attempt to address a possible host specialization of *B. cinerea* on tomato  
278 and lettuce by genotypic and phenotypic characterization. In addition, it provides the first data  
279 on genetic diversity of *B. cinerea* strains collected on lettuce. Based on the examination of 44  
280 lettuce strains and 42 tomato strains, our results suggest an absence of clear host specialization  
281 of *B. cinerea* on tomato and lettuce.

282 The genetic diversity indices of lettuce strains were compared to those reported for populations  
283 collected from other crops grown under greenhouses (Table 3). The gene diversity (H<sub>nb</sub> and  
284 mean number of alleles per locus) of lettuce strains was higher than that of strains from all  
285 greenhouse crops (Karnachi-Balma *et al.*, 2008). In contrast, the haplotypic diversity of lettuce  
286 strains was higher than that of strains from tomato but lower than that of strains from strawberry  
287 and grapevine (Karnachi-Balma *et al.*, 2008). When comparing to strains from crops grown in  
288 open field, all genetic diversity indices for lettuce strains were in the mean range of values  
289 (Table 3). All diversity indices for tomato strains in our study (unbiased gene diversity, mean  
290 number of allele per locus, haplotypic diversity and Simpson's index of diversity) were  
291 systematically lower than those of lettuce strains. They were comparable to those reported for  
292 tomato strains in Tunisia by Karchani-Balma *et al.* (2008). As the tomato and lettuce strains of  
293 our study were collected from the same greenhouse, an explanation for the differences in  
294 diversity between the two groups could come from differences in the epidemiology of the  
295 disease on the two crops. On tomato plants, *B. cinerea* sporulates on leaves, stems or fruits and  
296 the spores are easily disseminated by air currents and by the frequent technical interventions  
297 necessitated by this crop. As this often coincides with favourable microclimatic conditions for

298 disease development, this allows for successive cycles of inoculum production to occur in the  
299 greenhouse (Dik & Wubben, 2004; Decognet *et al.*, 2009; Bardin *et al.*, 2014). Indeed, in our  
300 experimental greenhouse, sporulating lesions were observed on aerial parts of about 11% of  
301 tomato plants during the growing period. Considering that *B. cinerea* can produce spores within  
302 one week (Nicot *et al.*, 1996), during the two-month overlapping period with tomato and lettuce  
303 grown in the same tunnel, 8 cycles of spore production may have occurred on tomato. This in  
304 turn may have fostered a gradual selection of strains with the highest fitness on tomato.  
305 Decognet *et al.* (2009) showed that two strains of *B. cinerea* became rapidly predominant after  
306 their introduction in four experimental tomato greenhouses. On lettuce plants in contrast, the  
307 disease mostly develops on the underside of older leaves which are in contact with the soil, and  
308 cropping practices do not include frequent manipulation of the plants. As a consequence,  
309 sporulation occurs in a confined environment (between the soil and the oldest leaves covering  
310 it) and secondary inoculum is essentially released and disseminated when the lettuces are  
311 harvested. This could explain the lower haplotypic diversity of tomato strains compared to  
312 lettuce strains in our study, with 52% of tomato strains present in at least two copies compared  
313 to only 30% of lettuce strains.

314 This situation is also compatible with the results of the genetic structure analysis with clone-  
315 corrected data. We found a clear genetic structure in two clusters, but this structure did not  
316 separate the strains according to their host of origin. However, lettuce strains were distributed  
317 quite equitably among the two clusters (55% and 42% - together with 3% that were not  
318 assigned) whereas tomato strains were mainly assigned to one cluster (18% and 82%). It may  
319 reflect the occurrence of two types of primary inoculum in the greenhouse, from two different  
320 origins. Both lettuce and tomato plants are likely to have been exposed to airborne inoculum  
321 entering from the outside of the greenhouse. Exchange of air between the inside and the outside  
322 of a greenhouse can occur regularly through vents (Leyronas *et al.*, 2011) and Bardin *et al.*

323 (2014) have recently shown that the contribution of external inoculum was non-negligible. In  
324 addition to airborne inoculum, the plants may have been confronted to soilborne inoculum, with  
325 a greater impact on lettuce whose foliage quickly covers the soil. Further studies will be needed  
326 to assess the relative impact of soilborne and airborne primary inoculum in grey mould  
327 epidemics on tomato and lettuce crops.

328 Taken together, our results support the hypothesis of a lack of specialization for tomato or  
329 lettuce among the strains of *B. cinerea* examined in our study. Similar observations have been  
330 reported for strains collected from grape, kiwifruit, pea and squash in California (Ma &  
331 Michailides, 2005) and from strawberry and faba beans in Tunisia (Karnachi-Balma *et al.*,  
332 2008). The polytrophic behaviour of the lettuce and tomato strains of our study was also  
333 supported by their systematic ability to produce symptoms on the three plant species tested and  
334 by the absence of significant difference in the aggressiveness of the two groups on apple and  
335 lettuce. The significant difference observed when strains were inoculated on tomato could be  
336 attributed, as hypothesized above, to a progressive selection on tomato of the strains with the  
337 best fitness on that plant. This hypothesis could be tested in further experiments by combining  
338 genotypic and phenotypic characterization of sequentially sampled strains of *B. cinerea* during  
339 a growing season.

340 In conclusion, our results showed an ability of all examined *B. cinerea* strains to attack both  
341 tomato and lettuce and point to a lack of clear host specialization. This implies that the inoculum  
342 produced on one host species would be able to trigger a grey mould epidemic on the other  
343 species. In rotations implicating tomato and lettuce, caution should be used about possible  
344 carry-over of inoculum, as *B. cinerea* can survive on plant debris or in soil as sclerotia (Coley-  
345 Smith, 1980). Moreover, possible exchange of airborne inoculum between neighbouring plots  
346 (Jarvis, 1962; Harrison & Lowe, 1987), including in greenhouse systems (Leyronas *et al.*, 2011)  
347 need to be considered when planning the arrangement of crops on the farm.

348

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354 Experimental Unit of INRA Alenya-Roussillon and of the Plant Pathology Research Unit of  
355 INRA Avignon.

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Table 1: Genetic diversity of *B. cinerea* strains collected on lettuce and tomato.

	Sample size	Hnb <sup>a,f</sup>	Allelic richness	No. of distinct MLH <sup>b</sup>	Haplotypic diversity	D* <sup>c</sup>	Evenness	r <sub>d</sub> <sup>d,f</sup>
<b>Total</b>	<b>86</b>	<b>0.74 (0.11)</b>	<b>9.8</b>	<b>43</b>	<b>0.49</b>	<b>0.947</b>	<b>0.835</b>	<b>0.15 HS<sup>e</sup></b>
Lettuce	44	0.77 (0.12)	9.2	31	0.69	0.969	0.758	0.13 HS
Tomato	42	0.62 (0.12)	4.7	16	0.37	0.912	0.867	0.13 HS

a : unbiased gene diversity (standard deviation between brackets)

b : multilocus haplotype

c : Diversity Simpson's index

d : linkage disequilibrium

e : highly significant at the 5% level

f: computed with clone-corrected data (data set with only one example of each haplotype) to remove bias of overrepresentation of clones.

Table 2: Allelic richness based on minimum sample size (AR) and unbiased gene diversity (Hnb) per microsatellite locus in lettuce and tomato strains of *B. cinerea*

Host of origin	BC1		BC2		BC3		BC4		BC5		BC6		BC7		BC9		BC10	
	AR	Hnb	AR	Hnb	AR	Hnb	AR	Hnb	AR	Hnb	AR	Hnb	AR	Hnb	AR	Hnb	AR	Hnb
Lettuce	9.7	0.84	10.88	0.89	7.6	0.77	2.7	0.50	8.9	0.83	11.4	0.81	8.2	0.79	5.3	0.61	8.3	0.84
Tomato	6	0.71	6	0.74	4	0.65	2	0.51	4	0.42	5	0.51	4	0.69	5	0.51	6	0.75

Table 3: Genetic diversity reported for *B. cinerea* strains collected from crops grown under greenhouse and in open field. In all studies, strains were genotyped using the microsatellites described by Fournier *et al.* (2002)

Plant host	Growing system	Location	Gene diversity	Mean number of allele/locus	Haplotypic diversity <sup>a</sup>	Reference
<i>lettuce</i>	<i>greenhouse</i>	<i>France (South West)</i>	<i>0.77</i>	<i>9.20</i>	<i>0.69</i>	<i>present study</i>
<i>tomato</i>	<i>greenhouse</i>	<i>France (South West)</i>	<i>0.62</i>	<i>4.70</i>	<i>0.37</i>	<i>present study</i>
tomato	greenhouse	Tunisia (Cap Bon+North)	0.62	3.89	0.48	Karnachi-Balma <i>et al.</i> , 2008
strawberry	greenhouse	Tunisia (Cap Bon)	0.70	7.11	0.87	Karnachi-Balma <i>et al.</i> , 2008
grapevine	greenhouse	Tunisia (Grand Tunis)	0.70	5.89	0.90	Karnachi-Balma <i>et al.</i> , 2008
grapevine	open field	France (Bourgogne)	0.51	3.62	1	Fournier & Giraud, 2008
chickpea	open field	Bangladesh	0.54	na	0.47	Isenegger <i>et al.</i> , 2008
grapevine	open field	France (Anjou)	0.59	4.87	0.97	Fournier & Giraud, 2008
grapevine	open field	Tunisia (North)	0.60	3.78	0.75	Karnachi-Balma <i>et al.</i> , 2008
grapevine	open field	France (Champagne)	0.64	4.75	1	Fournier & Giraud, 2008
grapevine	open field	France (Alsace)	0.64	5	1	Fournier & Giraud, 2008
rooibos	open field	South Africa	0.67	5.6	0.48	Wessels <i>et al.</i> , 2013



grapevine	open field	France (Bordelais)	0.69	5.75	1	Fournier & Giraud, 2008
faba bean	open field	Tunisia	0.75	6.33	1	Karnachi-Balma <i>et al.</i> 2008
strawberry	open field	Tunisia (Cap Bon)	0.80	8.33	0.95	Karnachi-Balma <i>et al.</i> 2008
raspberry and strawberry	open field	Hungary	0.82	na	0.37	Asadollahi <i>et al.</i> , 2013
strawberry	open field	England	0.86	17.10	na	Rajaguru & Shaw, 2010
primrose	open field	England	0.87	9.9	na	Rajaguru & Shaw, 2010
blackberry	open field	England	0.88	20.80	na	Rajaguru & Shaw, 2010
dandelion	open field	England	0.88	13.8	na	Rajaguru & Shaw, 2010

a: haplotypic diversity index directly available or computed (on the basis of reported information) as the ratio of (number of distinct MLG - 1) over ( sample size - 1)

na : data not available

Figure 1: Experimental set up combining a lettuce crop (on each side of a greenhouse) grown together with a tomato crop (in the middle).



Figure 2: Scatter plots from Discriminant Analysis in Principal Components. A: K value *a priori* fixed to 2; B: no *a priori* on the value of K.

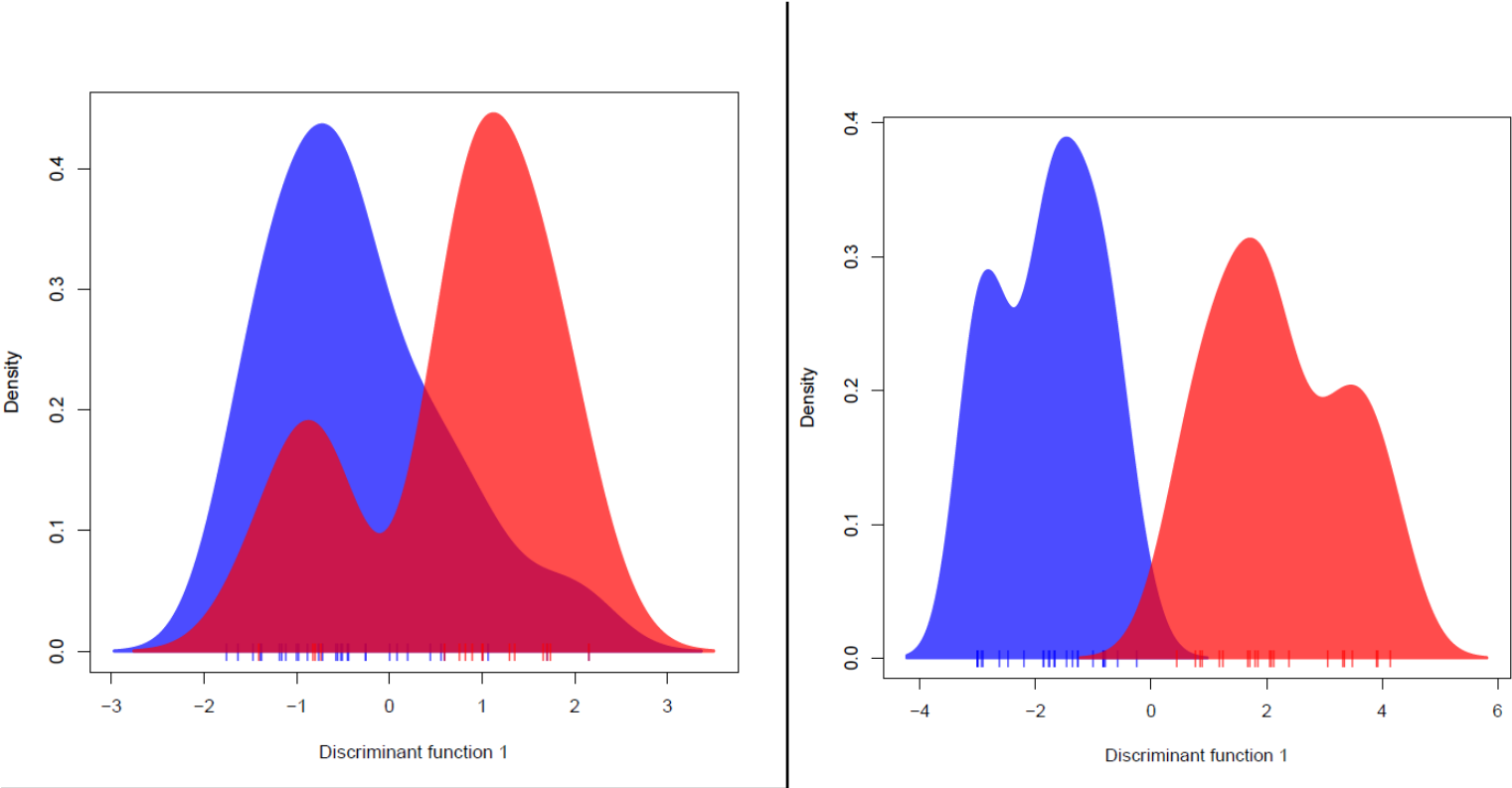


Figure 3: Neighbor-joining tree (based on the distance of Cavalli-Sforza & Edwards (1967)) showing the genetic relationships among 31 strains of *Botrytis cinerea* collected from lettuce and 16 strains collected from tomato. The analysis was done on the set of data corrected for clonality. Support for the nodes was assessed by bootstrapping loci 1500 times. Red boxes identify tomato strains. Circles identify haplotypes common to lettuce strains and tomato strains.

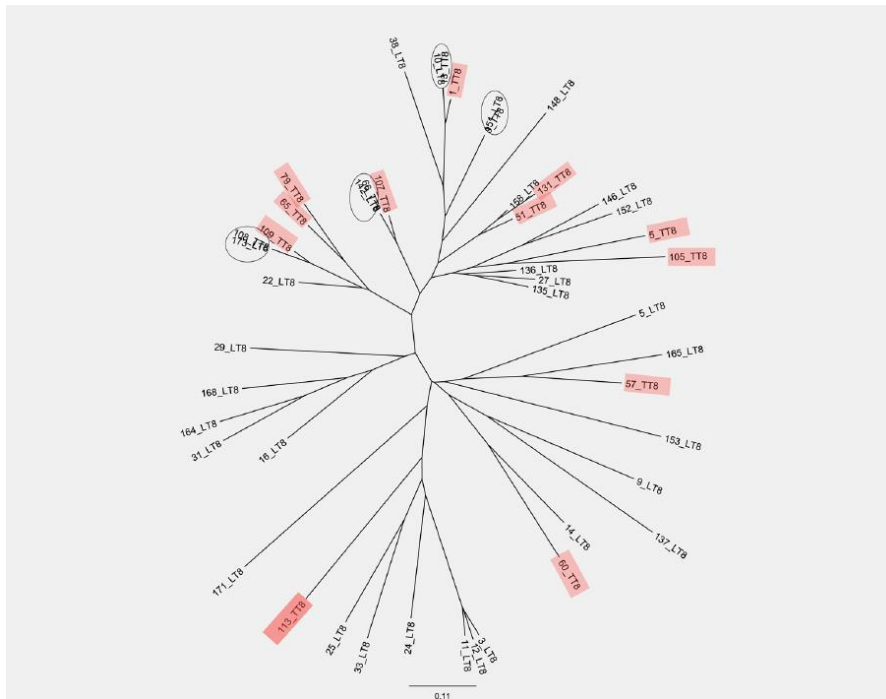


Figure 4: A: Aggressiveness on lettuce of lettuce strains (green bars) and tomato strains (red bars) of *B. cinerea*. B: Aggressiveness on tomato of lettuce strains and tomato strains of *B. cinerea*.

Error bars indicate the standard deviation of the mean.

