



# Exploring the role of cultivar, year and plot age in the incidence of esca and Eutypa dieback: Insights from 20 years of regional surveys in France

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1      **Exploring the role of cultivar, year and plot age in the incidence of esca and**  
2      **Eutypa dieback: insights from 20 years of regional surveys in France**

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12

13     keywords: esca; Eutypa dieback; epidemiology; INLA; surveillance; *Vitis vinifera*

14

## 15 Abstract

16 Grapevine trunk diseases cause yield losses and vine mortality in vineyards worldwide. However,  
17 there have been few quantitative studies evaluating grapevine dieback on a large spatial and  
18 temporal scale. Here, we consolidated and standardized databases from the 13 main wine regions  
19 of France, compiling records of leaf symptoms associated with esca and Eutypa dieback from 2082  
20 plots and 36 cultivars over a 20-year period. This large dataset was used (a) for quantitative  
21 analysis of the prevalence (number of plots with at least one symptomatic plant) and incidence  
22 (percentage of symptomatic plants) of esca and Eutypa dieback; and (b) to decipher the effects of  
23 cultivar, year and plot age on both the prevalence and incidence of esca leaf symptoms by temporal  
24 Bayesian modelling. Esca was present on a mean of  $74 \pm 2\%$  plots annually, with an incidence of  
25  $3.1 \pm 0.1\%$ . Eutypa dieback occurred in  $41 \pm 3\%$  of the plots, with an incidence of  $1.4 \pm 0.1\%$ . Our  
26 modelling approach revealed that the cultivar had a significant impact on the prevalence of esca,  
27 but not on its incidence when prevalence is greater than zero. Esca prevalence remained stable,  
28 whereas esca incidence was higher than the mean value in six of the years after 2012. We also  
29 found a significant non-linear effect of plot age, with 10- to 30-year-old plots significantly more  
30 susceptible, depending on the cultivar. This study clearly illustrates the importance of considering  
31 extensive and continuous monitoring to improve our understanding of the impact and evolution of  
32 crop diseases.

### 33 I) Introduction

34 Perennial plant dieback is characterised by the premature and progressive death of shoots, loss of  
35 plant vigor, and, ultimately, plant death. Abiotic factors, such as drought, have been shown to be  
36 a major cause of dieback in perennial plants (Allen et al., 2010; Cailleret et al., 2019; Hammond  
37 et al., 2022), as well as pathogens (Ciesla and Donaubauer, 1994) and their interactions (Jurskis,  
38 2005). Dieback is a well-known phenomenon in forest ecology, observed in various regions of the  
39 world (Allen, 2009; Hammond et al., 2022; Hartmann et al., 2018). However, there have been no  
40 large-scale quantitative studies assessing dieback in perennial crops.

41 Dieback of grapevine (*Vitis vinifera* L.) is caused by various abiotic and biotic factors, including  
42 diseases affecting grapevine wood. Trunk diseases, such as esca, Eutypa dieback, and  
43 Botryosphaeriaceae dieback, are the most widespread globally (Guerin-Dubrana et al., 2019;  
44 Mugnai et al., 1999). These diseases cause vine destruction leading to yield losses (Bertsch et al.,  
45 2009; Gramaje et al., 2018; Mondello et al., 2018), although these can be overestimated in some  
46 regions (Dewasme et al., 2022). The current epidemic spread of trunk diseases in Europe can be  
47 traced back to the early 1990s (Mugnai et al., 1999; Reisenzein et al., 2000; Surico et al., 2000).  
48 In the first few years of the 21st century, until at least 2008, the incidence of grapevine trunk  
49 diseases, including esca in particular, appears to have increased (Bruez et al., 2013). This increase  
50 is a matter of great concern to vine growers, particularly in the wake of the sodium arsenite ban  
51 introduced in France in 2001, as this was the only effective treatment for esca (Mugnai et al.,  
52 1999). Several factors may be associated with variation in the incidence of trunk diseases. These  
53 factors include cultivar (Gastou et al., 2024), year (Dewasme et al., 2022) and plot age (Fussler et  
54 al., 2008). Cultivar is a major factor underlying differences in the incidence of esca disease  
55 between vineyards and vine-growing regions. Indeed, there was a considerable variability of the  
56 proportion of symptomatic plants per cultivar in France during the monitoring of 46 cultivars  
57 planted in a common garden vineyard over a period of seven years (Gastou et al., 2024), in Italy

58 during the monitoring of 67 cultivars for one year (Murolo and Romanazzi, 2014) and in Spain,  
59 during the monitoring of 47 cultivars for three years (Chacón-Vozmediano et al., 2021). Certain  
60 cultivars, such as Merlot, only rarely display esca leaf symptoms whereas others, such as  
61 Sauvignon Blanc, are frequently affected. Moreover, strong interannual variability has been  
62 observed within vineyards (Calzarano et al., 2018; Dewasme et al., 2022). The age of the vines  
63 significantly influences their response to biotic and abiotic stresses, determining their tolerance or  
64 susceptibility. As a result, the incidence and expression of symptoms of stress increase linearly  
65 with plant age (Pandey et al., 2015). The effect of vineyard age on esca incidence is unclear. A  
66 few studies have reported an absence of correlation between plot age and esca incidence (Bruez et  
67 al., 2013; Péros et al., 2008), but others have reported a significant age effect for plots aged from  
68 10 to 21 years (Kovács et al., 2017). By contrast, other studies have suggested that the relationship  
69 between plot age and symptom expression is quadratic rather than linear, with disease incidence  
70 highest at intermediate ages (Fulchin et al., 2019; Fussler et al., 2008). Incidence appears to be  
71 higher in vineyards of between 15 and 25 years of age than in vineyards of other ages, as shown  
72 in a study of 22 cultivars (Fussler et al., 2008) and, more recently, in a study of five cultivars  
73 (Fulchin et al., 2019). However, in these studies, age was considered as a categorical ordered  
74 variable (e.g. ‘young’ if the plot was less than 7 years old and ‘old’ if more than 11 years old,  
75 Romanazzi et al., 2009, or 0-15, 15-25, 25-40, and over 40 years old, Fussler et al., 2008). No  
76 study has ever addressed age as a fully continuous quantitative variable, probably due to a lack of  
77 long-term, large-scale monitoring.

78

79 Distinguishing between the effects of year and plot age requires large-scale and long-term  
80 monitoring, to ensure that the variables are not correlated, or at least no more than weakly  
81 correlated. Large-scale monitoring is essential to improve pest surveillance for plants, particularly  
82 over large spatial scales, and to facilitate the implementation of effective measures for preventing

83 the spread of pathogens and insect pests and for controlling epidemics (Carvajal-Yepes et al., 2019;  
84 Mariette et al., 2023; Parnell et al., 2017). General surveillance encompasses the collection and  
85 analysis of information on plant disease and plays a crucial role in the detection and effective  
86 management of pathogens (Aguayo et al., 2021; ISPM 6 (FAO) 1997; Parnell et al., 2017). The  
87 extensive monitoring of significant pathogens, including native ones, is also crucial for obtaining  
88 spatial indicators of vineyard health, and for tracking temporal trends. This information enables  
89 managers and policymakers to implement sustainable management practices in vineyards. In  
90 France, a National Grapevine Trunk Diseases Survey was performed between 2003 and 2008, to  
91 monitor grapevine trunk disease incidence and mortality and to assess its significance for  
92 viticulture in seven vine-growing regions. This survey included 12 cultivars and 329 vineyard plots  
93 (Bruez et al., 2013; Fussler et al., 2008). However, the collection of more recent information over  
94 a longer period would be required to assess progression of grapevine trunk disease levels over the  
95 last few years.

96 In this study, we collected and curated different databases from the 13 main wine regions of  
97 France, to generate a unified database for leaf symptoms of two major trunk diseases, esca and  
98 Eutypa dieback, covering a period of 20 years (2003 to 2022). This unified national database  
99 covers 2082 plots and 36 cultivars and was used to describe the prevalence (percentage of plots  
100 with at least one symptomatic plant) and incidence (percentage of symptomatic plants per plot), as  
101 defined by Nutter et al. (2006), of esca and Eutypa dieback over the different years, cultivars,  
102 regions, and vineyard ages. Furthermore, the time-series data collected at plot scale were subjected  
103 to modelling by the integrated nested Laplace approximation (INLA) method (Rue et al., 2009,  
104 2017) to explore the effects of cultivar, year and plot age on both the prevalence and incidence of  
105 esca whilst accounting for temporal dependencies.

106

107 **II) Materials and methods**

108        **1) French database of grapevine trunk disease observations**

109        The database contains 12,587 observations of leaf symptoms of esca and Eutypa dieback, in the  
110        main wine-producing regions in France. This database is stored in the information system of the  
111        French Epidemiological Plant Health Surveillance Platform (ESV Platform). The observations  
112        were obtained from two sources: (i) regional surveys conducted from 2003 to 2022, and (ii) the  
113        historical “National Grapevine Trunk Diseases Survey”, which tracked the progression of  
114        grapevine trunk diseases throughout France from 2003 to 2008 (Fussler et al., 2008; Grosman and  
115        Doublet, 2012; Bruez et al., 2013). The historical and regional surveys were conducted by experts  
116        from diverse public or private agronomic institutes or associations in each of the regions.

117        Observations of esca leaf symptoms were obtained in 884 different municipalities ( $2.4 \pm 2.5$  plots  
118        per municipality, mean  $\pm$  standard deviation, SD), in 49 provinces, 13 vine-growing regions, and  
119        10 administrative regions (see Figure 1 and Table S1 for the number of plots per region and  
120        monitoring years). They took place at the end of August, which corresponds to the period of  
121        maximum cumulative incidence in French vineyards (see the intra-seasonal dynamics presented in  
122        Lecomte et al. 2024). Plants were scored symptomatic when typical leaf stripe symptoms were  
123        observed as presented in Lecomte et al. (2024). Thirty-six different cultivars were monitored, with  
124        a mean of  $58 \pm 69$  plots per cultivar, as described in Table S2. Three cultivars (Italia, Alphonse  
125        Lavallée and Sauvignon Gris) were monitored on only one plot each and were therefore excluded  
126        from the analysis. Moreover, only two plots were monitored in the Vendée wine region (Chenin  
127        cultivar), and these plots were also, therefore, excluded from the analysis. Finally, mean plot age  
128        was  $27 \pm 13$  years, and plot age ranged from 1 to 101 years (Figure 2). However, the date of  
129        plantation was not recorded for 25% of the plots. Each region was represented by a different set  
130        of cultivars (Figure S1).

131        For 63% of the plots monitored for esca, annotation was also available for Eutypa dieback  
132        symptoms. Eutypa dieback was monitored between April and May (Table S1) to score plants

133 presenting stunted shoots with necrotic leaves as shown in Mondello et al. (2018). In total 7,073  
134 observations were available for this disease, spread over 1,310 plots located in 592 municipalities  
135 ( $2.2 \pm 2.4$  (mean  $\pm$  SD) plots per municipality), 39 provinces, 10 wine regions, and 7 administrative  
136 regions. All cultivars other than Meunier, Sciaccarellu, Vermentinu, and Niellucciu were  
137 monitored for Eutypa dieback, with data available only for esca leaf symptoms for these  
138 exceptions.

139 Mortality was recorded, but the methods used to score dead plants were not homogeneous across  
140 regions. We, therefore, discarded these data from the analysis. Similarly, information on rootstock,  
141 pruning technique, young replanted vines, and apoplexy (total dehydration of the canopy) was  
142 scarce and inconsistently reported, and such data were not, therefore, considered in this analysis.

143 The number of vines with esca or Eutypa dieback symptoms on leaves was recorded on a defined  
144 number of vines in the plots described above. A mean of  $420 \pm 530$  vines was observed per plot  
145 (see supplementary materials, Table S2). One plot of Cabernet Sauvignon was monitored in its  
146 entirety as part of an experiment, accounting for the large mean number of vines observed for this  
147 cultivar (Table S2). The definitions of disease prevalence and incidence proposed by Nutter et al.  
148 (2006) were used.

149

150 **2) Estimations of the prevalence and incidence of leaf symptoms of esca and Eutypa  
151 dieback**

152 Disease prevalence was calculated, for a given year, as the percentage of plots on which esca, or  
153 Eutypa dieback (depending on the disease considered for the analysis) was observed on at least  
154 one plant. Disease incidence was calculated for each plot in a given year by dividing the number  
155 of plants presenting esca leaf symptoms (as described by Lecomte et al. 2012) or Eutypa dieback

156 leaf symptoms (as described by Sosnowski et al. 2007) by the number of plants monitored in the  
157 plot concerned (included dead or missing vines).

158

159 **3) Deciphering the effects of cultivar, year, and plot age on the prevalence and incidence**  
160 **of esca leaf symptoms**

161 In addition to the descriptive analysis of the whole database, a statistical model was developed to  
162 estimate the effect of cultivar, year and plot age on both prevalence and incidence of esca leaf  
163 symptoms at plot scale. In this modelling approach, only esca was used, as Eutypa dieback is  
164 affecting almost exclusively the Ugni Blanc cultivar and presents a decreasing incidence over time,  
165 in contrast to esca (Figure 3). To optimise model identifiability, we applied some criteria to select  
166 the data used in this approach. We selected observations (one plot in a given year) from plots under  
167 50 years old (older plots excluded), for which at least five years of observation were available (not  
168 necessarily consecutive), and cultivars for which at least 300 observations were available.

169 The application of these criteria resulted in a database of 5161 observations (from the 12587  
170 observations initially identified) spread over 12 cultivars (Table 1). On average, a plot was  
171 monitored for  $9 \pm 4$  [5, 20] years. Mean plot age ranged from 18 to 32 years (Table 1). Mean plot  
172 age tended to increase from 2003 to 2013, remaining stable thereafter (Figure 4).

173

174 The model consisted of two hierarchical structured components: one describing the prevalence of  
175 esca at plot scale (presence of esca, denoted 1, or absence, denoted 0), and the other the incidence  
176 of esca conditional on its occurrence (i.e. given that the plot prevalence is 1). A Bernoulli  
177 distribution with a logit link was used for the prevalence component. For the incidence component,  
178 the response variable was the number of vines with esca leaf symptoms divided by the total number  
179 of vines observed. For this component, we aimed to establish a binomial model conditional on  
180 there being at least one vine with esca symptoms in the plot. Thus, a zero-inflated binomial

181 distribution parameterised to exclude zero with a logit link was used for the incidence. Both the  
182 prevalence and incidence components included cultivar and plot identity as independent random  
183 effects and the year as an autoregressive process of order 1 (AR1). These effects account for  
184 interannual dependence arising from underlying meteorological or environmental factors and  
185 agricultural practices affecting esca symptoms. Finally, the incidence component included plot age  
186 as an AR1 process specific to each cultivar. We describe below the “full” model including all  
187 explanatory variables. Intermediate models with fewer explanatory variables were also estimated  
188 and compared to the full model on the basis of two information criteria: the deviance information  
189 criterion and the widely applicable information criterion (DIC and WAIC) (Table 2).

190

191 More specifically, the variables in the model are as follows: let  $y_i$  denote the esca prevalence of  
192 observation  $i$  ( $i = 1, \dots, 5161$ ), where the disease is either observed (value  $y_i = 1$ ) or not observed  
193 (value  $y_i = 0$ ). Let  $n_i$  denote the number of plants with esca symptoms among the  $n_i^{tot}$  monitored  
194 for this same observation  $i$ . We will consider the following explanatory variables associated with  
195 observation  $i$ . First, the variable  $plot(i)$  denotes the identity of the plot (554 levels for prevalence  
196 and 546 levels for incidence) on which observation  $i$  was performed;  $cultivar(i)$  denotes the  
197 cultivar (12 levels, see Table 1) on the plot corresponding to observation  $i$ . The variable  $year(i)$   
198 for prevalence denotes the year of monitoring (indexed by  $t = 2003, \dots, 2022$ ). Finally,  $age(i)$   
199 denotes plot age, a variable considered only for the incidence component (indexed by  $z = 1, \dots,$   
200 49) being specific to each cultivar.

201

202 The first component (prevalence) of the model can be written as follows:

203

204 
$$y_i \sim Bernoulli(\pi_i), i = 1, \dots, 5161$$

205 
$$\text{logit}(\pi_i) = \beta_0 + \mu_0(n_i^{tot}) + \alpha_0[plot(i)] + \gamma_0[cultivar(i)] + \delta_0[year(i)]$$

206 
$$\alpha_0[plot(i)] \sim Normal(0, \sigma_{plot0}^2)$$

207  $\gamma_0[cultivar(i)] \sim Normal(0, \sigma_{cultivar0}^2);$   
208  $\delta_0[2003] \sim Normal(0, \sigma_{year0}^2(1 - \rho_{year0}^2)^{-1})$   
209  $\delta_0[t] = \rho_{year0}[\delta_0[t - 1]] + \varepsilon_0[t], t = 2004, \dots, 2022$   
210  $\varepsilon_0[t] \sim Normal(0, \sigma_{year0}^2)$

211

212 ZIB<sup>+</sup> is a modified version of the zero-inflated binomial distribution supported from 1 to  $n_i^{tot}$   
213 (exclusion of the 0 value),  $S$  being the subset of index  $i$  associated when esca prevalence = 1 (4476  
214 observations).

215 The second component (incidence) of the model can therefore be written as follows:

216  $n_i|y_i = 1 \sim ZIB^+(n_i^{tot}, \omega_i), i \in S$   
217  $logit(\omega_i) = \beta_1 + \alpha_1[plot(i)] + \gamma_1[cultivar(i)] + \delta_1[year(i)] + \tau_{cultivar(i)}[age(i)]$   
218  $\alpha_1[plot(i)] \sim Normal(0, \sigma_{plot1}^2)$   
219  $\gamma_1[cultivar(i)] \sim Normal(0, \sigma_{cultivar1}^2)$   
220  $\delta_1[2003] \sim Normal(0, \sigma_{year1}^2(1 - \rho_{year1}^2)^{-1})$   
221  $\delta_1[t] = \rho_{year1}[\delta_1[t - 1]] + \varepsilon_1[t], t = 2004, \dots, 2022$   
222  $\varepsilon_1[t] \sim Normal(0, \sigma_{year1}^2)$   
223  $\tau_{cultivar1}[1] \sim Normal(0, \sigma_{age1,cultivar}^2(1 - \rho_{age1,cultivar}^2)^{-1}), cultivar = 1, \dots, 12$   
224  $\tau_{cultivar1}[z] = \rho_{age1,cultivar}[\tau_{cultivar1}[z - 1]] + \varepsilon_{age1,cultivar}[z], z = 2, \dots, 49$   
225  $\varepsilon_{age1,cultivar}[z] \sim Normal(0, \sigma_{age1,cultivar}^2)$

226

227 In the model,  $\beta_0$  and  $\beta_1$  are the intercepts of prevalence and incidence, respectively. The parameter  
228  $\mu_0$  takes into account the different numbers of plants monitored per plot (note that  $n_i^{tot}$  was  
229 standardised to ensure robust estimation). The autoregressive parameters  $\rho_{year0}$ ,  $\rho_{year1}$ ,  $\rho_{age1,cultivar}$   
230 (all of which have absolute values < 1) correspond to the correlation coefficients for the prevalence  
231 ( $\rho_{year0}$  for year) or incidence ( $\rho_{year1}$  for year and  $\rho_{age1,cultivar}$  for plot age for a given cultivar) of esca

232 between two consecutive time points. They indicate the extent to which the temporal trend in a  
233 given time step  $t$  depends on the trend from the previous time step  $t-1$ . Typically, estimates close  
234 to 0 indicate the absence of a significant temporal trend. By contrast, the closer the estimates are  
235 to 1, the more similar the temporal trends between two consecutive time steps (Zuur et al., 2017).  
236 The parameters  $\sigma^2_{year0}$ ,  $\sigma^2_{year1}$ ,  $\sigma^2_{age1,cultivar}$  define the precision of the AR1 process, with lower  
237 values corresponding to smoother temporal trends. The model was fitted in a Bayesian framework  
238 by the integrated nested Laplace approximation (INLA) method (Rue et al., 2009, 2017) with R  
239 (version 4.2.1). Bayesian inference requires the specification of prior distributions for the model  
240 parameters and hyperparameters, and we used the default internal vague priors recommended in  
241 R-INLA. Specifically, the different  $\sigma^2_{plot0}$ ,  $\sigma^2_{cultivar0}$ ,  $\sigma^2_{plot1}$ ,  $\sigma^2_{cultivar1}$  values for the independent  
242 random effects and the  $\sigma^2_{year0}$ ,  $\sigma^2_{year1}$ ,  $\sigma^2_{age1,cultivar}$  values of the AR1 process are assigned a log-  
243 gamma distribution with parameters 1 and 0.00005. For the cultivar and year effects, we then  
244 calculated the probability of direction ( $pd$ ), which varies between 0.5 and 1 and indicates the  
245 probability that a parameter, as defined by its posterior distribution, is either strictly positive or  
246 negative. This  $pd$  is the proportion of the posterior distribution that has the same sign as the median  
247 of the posterior distribution (Makowski et al., 2019) and can be used to identify trends in the  
248 distribution of the parameter. Finally, we compared fitted and observed values to evaluate model  
249 fit. For the probability of presence (prevalence), we used ROC curve analyses (Hoo et al., 2017,  
250 PRROC R package, Grau et al., 2015). For disease incidence, we calculated Pearson's R  
251 coefficient for the correlation between the mean of the fitted values and observed incidence  
252 (function *cor.test* package *stats*).  
253

### 254 **III) Results**

#### 255 **1) Prevalence and incidence of esca and Eutypa dieback leaf symptoms in France 256 between 2003 and 2022, by cultivar and wine region**

257 **1.1) Variability of the prevalence and incidence of esca leaf symptoms**

258 Only 10% of the 2,075 plots monitored over the 2003-2022 period contained no symptomatic vines  
259 (1,861 of 2,075 plots contained at least one vine presenting symptoms). The annual prevalence of  
260 esca ranged from 54% in 2010 to 84% in 2017, with a mean of  $74 \pm 2\%$  (mean  $\pm$  SEM, standard  
261 error of the mean) plots containing at least one symptomatic plant (Figure 3a). During the  
262 monitoring period, for all years considered together, the prevalence of esca in the regions ranged  
263 from 100% of the plots containing at least one vine with esca (Corse and Jura & Savoie) to 78%  
264 (Champagne) (data not shown).

265 Including plots without esca (prevalence = 0), the mean annual incidence of esca over the 2003-  
266 2022 period was  $3.1 \pm 0.1\%$  (mean  $\pm$  SEM). The lowest mean annual incidence of esca was  
267 observed in 2003 whereas the highest incidence was observed in 2012, 2014, and 2017 (Figure  
268 3a). The annual incidence of esca increased between 2003 and 2008 and then fluctuated until 2022.  
269 If we excluded plots with no vines presenting esca symptoms in a given year (prevalence = 0), the  
270 mean annual incidence increased to  $4.2 \pm 0.1\%$  (mean  $\pm$  SEM, Figure S2).

271 We observed considerable variability in the incidence of esca leaf symptoms between cultivars.  
272 The mean incidence by cultivar ranged from 0.6% to 10.6% (Figure 5a). The Trousseau cultivar  
273 had the highest incidence, followed by Savagnin and Ugni Blanc. Incidence was lowest for  
274 Meunier, followed by Pinot Noir and Syrah.

275 The incidence of esca also varied between wine regions, the highest incidence being recorded in  
276 Jura & Savoie and the lowest in Champagne (Figure 5a(i)). The incidence of esca by year, region  
277 and cultivar was not correlated with the number of plots monitored (Pearson's  $r, p > 0.13$ )

278

279 **1.2) Variability of the prevalence and incidence of Eutypa dieback**

280 In total, 1,296 plots were monitored for Eutypa dieback over the 2003-2022 period, and 31% were  
281 Eutypa-free (895 of the 1,296 plots contained vines displaying Eutypa dieback). The annual  
282 percentage of plots with Eutypa dieback (i.e, the prevalence) ranged from 20% in 2016 to 61% in  
283 2005, with a mean value of  $41 \pm 3\%$  (mean  $\pm$  SEM) (Figure 3b). During the monitoring period,  
284 the regional prevalence of Eutypa dieback ranged from 96% in Charentes to 40% in the Sud Ouest  
285 region.

286 If plots without Eutypa dieback (prevalence = 0) were included in the calculation, then the mean  
287 observed incidence of Eutypa dieback was  $1.4 \pm 0.1\%$  (mean  $\pm$  SEM) (Figure 3b). The incidence  
288 of Eutypa dieback tended to decrease from 2003 to 2022 (Figure 3b). Specifically, we observed a  
289 decrease from 2003 to 2008 and then a steady decrease since 2013 (except for 2020). The incidence  
290 of Eutypa dieback was highest in 2003. In addition, 2017 and 2021 were the years in which the  
291 incidence of Eutypa dieback was lowest. Finally, if plots in which none of the vines were affected  
292 by Eutypa dieback (prevalence = 0) in a given year were excluded, the mean incidence increased  
293 to  $3.3 \pm 0.1\%$  (mean  $\pm$  SEM, Figure S2).

294 The variability of Eutypa dieback incidence between cultivars was high, with values ranging from  
295 0% to 9.5% (Figure 5b). The region with the highest Eutypa dieback incidence was Charentes and  
296 with the lowest, Jura & Savoie and Alsace Lorraine (Figure 5b(ii)). The incidence of Eutypa  
297 dieback by year, region and cultivar was not correlated with the number of plots monitored  
298 (Pearson's  $r, p > 0.30$ ). Finally, there was a weak but significant correlation between the incidences  
299 of esca and Eutypa dieback assessed by plot/year observation (Pearson's  $r = 0.08, p < 0.001$ ).

300

301 **2) Deciphering the effects of cultivar, year, and plot age on the prevalence and incidence of**  
302 **esca leaf symptoms**

303 The two model selection criteria considered (DIC and WAIC) supported the full model (Table 2),  
304 suggesting that all the explanatory variables considered had a significant impact on esca dynamics.  
305 We therefore consider only the full model hereafter. The model fit was satisfactory for both the  
306 prevalence and incidence components. Specifically, the area under the ROC curve (AUC) for esca  
307 prevalence was 0.93. Pearson's r for the correlation between adjusted and observed values of esca  
308 incidence was 0.83 ( $p < 0.001$ ).

309

310 The model included the number of vines monitored as a covariate to account for the sampling  
311 effort in each plot used to determine incidence. As expected, the mean effect was positive (0.33),  
312 confirming that increasing the number of plants inspected in a plot increases the likelihood of at  
313 least one plant being symptomatic. The associated probability of direction was 0.95 ( $\mu_0$ , Table 3).  
314 The identity of the plot had a significant impact on both the prevalence and incidence of esca  
315 symptoms. For prevalence, 13% of the individual plot effects were negative (i.e. associated with a  
316  $q-97.5\% < 0$ ), < 1% were positive ( $q-2.5\% > 0$ ) and the remaining 87% were associated with  
317 individual effects including zero (the mean value) in their 95% credible intervals. For incidence,  
318 25% of the plots were negative, 30% were positive and the remaining 45% were associated with  
319 individual effects including zero in the 95% credible interval. These values correspond to the  
320 percentage of plots characterised by an esca prevalence or incidence lower than, higher than or not  
321 significantly different from the overall mean, respectively.

322

323 Cultivar had a significant impact on the prevalence of esca symptoms but a much weaker effect  
324 on esca incidence. Indeed, cultivar was significant if WAIC was used (64436 without the cultivar  
325 effect vs. 64418 for the full model) but not with the DIC (37835 without the cultivar effect vs.  
326 37842 for the full model, Table 2). The individual effects of each of the 12 cultivars considered  
327 are shown in Figure 6. Chardonnay, Merlot and Pinot Noir all had a prevalence of esca below the  
328 overall mean (mean = 0,  $q-97.5\% < 0$ ) whereas Gewurztraminer and Cabernet Sauvignon had a

329 prevalence above the overall mean ( $q-2.5\% > 0$ ) (Figure 6a). No such differences were observed  
330 for the incidence of esca. The 12 estimated 95% credible intervals included zero, meaning that  
331 esca incidence did not differ between cultivars, provided that esca was observed (prevalence  $> 0$ ;  
332 Figure 6b). However, the probability of direction ( $pd$ ) showed that cultivars such as  
333 Gewurztraminer, Riesling and Melon had a strong tendency to have a high incidence whereas  
334 Merlot and Chardonnay had a low incidence ( $pd > 0.90$ , Figure 6a, b).

335

336 Unlike the effect of cultivar, the effect of year did not affect the prevalence of esca symptoms, but  
337 did affect their incidence. However, the 95% credible interval [0.25, 0.89] of the hyperparameters  
338  $\rho_{year0}$  of the AR1 process modelling the effect of year on esca prevalence suggests that esca  
339 prevalence is strongly correlated across successive years. No such significant correlation was  
340 detected for esca incidence (the 95% CI of  $\rho_{year1}$  was [-0.20, 0.71]) (Table 3; Figure 6c, d). An  
341 analysis by year showed that the prevalence or incidence (if esca was recorded in the plot) of esca  
342 was significantly lower than the mean value ( $=0$ ) in the first year (2003) and that esca incidence  
343 was lower in 2022. The prevalence and incidence of esca tended to be below the mean value in  
344 2004, as was the incidence in 2005 (probability of direction,  $pd > 0.95$ ). In 2017, the prevalence  
345 and incidence of esca were significantly higher than the mean. Moreover, esca incidence has  
346 remained above the mean value since 2012, including the years 2013, 2014, 2016, 2017, and 2021.  
347 However,  $pd$  values showed that between 2010 and 2012, prevalence tended to be high ( $pd > 0.92$ ,  
348 as shown in Figure 6c, d).

349

350 The hyperparameters  $\rho_{age1,cultivar}$  of the AR1 process, modelling the effect of plot age on esca  
351 incidence for each cultivar, were strictly positive, suggesting a positive correlation between plot  
352 age and incidence (Table 3). A pattern of the effect of age on esca incidence common to all  
353 cultivars is emerging. Indeed, in most cultivars, esca symptoms peak at an intermediate age. With

354 the exception of Merlot, all cultivars had an incidence of esca above the mean value for plots aged  
355 between 10 and 40 years (in red, Figure 7). Conversely, the youngest plots (under 10 years old)  
356 sown with these cultivars had an esca incidence below the mean value (in blue, Figure 7). Finally,  
357 Cabernet Franc, Cabernet Sauvignon, Gewurztraminer, Merlot and Pinot Noir had incidences  
358 significantly below the mean value after the age of 30 years. Overall, when age had a significant  
359 positive effect on esca incidence (when esca prevalence  $> 0$ ), esca occurred at ages between nine  
360 and 45 years, with a peak of susceptibility between nine and 24 years, depending on the cultivar  
361 (Figure 8). Even though the cultivars with the lowest incidence had a narrower age range for peak  
362 incidence (Cabernet Franc, Cabernet Sauvignon, Chardonnay, Pinot Noir), a pattern remained in  
363 the relationship between cultivar susceptibility (from left to right, according to modelling, Figures  
364 6 and 8) and the age ranges for susceptibility to esca and peak incidence.

365

#### 366 **IV) Discussion**

367 We compiled and homogenised regional and historical databases to obtain a national quantification  
368 of the prevalence and incidence of leaf symptoms of esca and Eutypa dieback in France between  
369 2003 and 2022. Despite considerable variability between years and cultivars, the incidence and  
370 prevalence of esca leaf symptoms appear to be stable when looking at the raw data, whereas the  
371 incidence of Eutypa dieback tended to decrease over the 2003-2022 period. We used a hierarchical  
372 Bayesian model to decipher the responses of two components — the prevalence (percentage of  
373 symptomatic plots, i.e. plots with at least one symptomatic plant) and the incidence (percentage of  
374 symptomatic plants per plot, when prevalence  $> 0$ ) of esca disease — to the effects of year, cultivar,  
375 and plot age. This framework is compatible with the objectives of surveillance programmes in  
376 applied plant pathology, which often aim to estimate disease occurrence at national, regional, and  
377 local scales. The framework developed here takes into account disease occurrence at two nested  
378 spatial scales (a set of plots within each agricultural region and a set of plants within each plot). In

379 our case study, focusing on the prevalence of esca leaf symptoms is particularly relevant when  
380 comparing a wide range of cultivars with different levels of susceptibility, including some for  
381 which no leaf symptoms were reported on a large number of plots. Once the presence of leaf  
382 symptoms is confirmed in a plot, analyses of the variation of incidence are then required to identify  
383 the factors driving leaf symptom expression, as esca is characterised by fluctuating expression  
384 between years and plots. This approach showed that since the incidence of esca leaf symptoms  
385 was significantly higher than the mean value in six of the years since 2003, all occurring after  
386 2012.

387 This study highlights the strong annual variability of esca incidence. Analysis of the whole  
388 database showed an increase in the annual mean incidence of esca from 2003 (1.6%) to 2008  
389 (3.9%). This trend was already reported by Bruez et al., (2013). However, our longer-term  
390 monitoring revealed that this trend ceased after 2008. More specifically, the upward trend seems  
391 to have continued after 2008 for certain cultivars, such as Ugni Blanc and Riesling in particular,  
392 and their associated regions (Figure S3 and S4), whereas the opposite was observed for  
393 Chardonnay and Meunier (Figure S4). Statistically, when esca is observed in a plot, leaf symptoms  
394 may be expressed over a number of years. The differences between years may reflect climatic  
395 variations. Indeed, the lowest esca incidence was recorded in 2003, a year characterised by a very  
396 intense drought and heatwave (Chuine et al., 2004). Other years of low esca incidences seem to  
397 coincide with hot summers (e.g., 2015, 2019, 2022, <https://climate.copernicus.eu/europe-continued-swelter-july>, site visited on February 22<sup>nd</sup>, 2024). In the literature, it has been suggested  
398 that higher maximum temperatures between June and July (leading to drier environments) are  
399 associated with a lower incidence of esca leaf symptoms and similarly the incidence of esca leaf  
400 symptoms seems to be positively correlated with precipitation levels, as high rainfall levels during  
401 July tend to intensify leaf symptom development (Calzarano et al., 2018; Serra et al., 2018).  
402 Indeed, water availability has been shown to affect esca leaf symptom development as, under

404 controlled conditions, intense drought inhibits esca leaf symptom onset, suggesting an antagonistic  
405 interaction between drought and esca pathogenesis and a key role for plant water status and  
406 climatic conditions (Bortolami et al., 2021). Vascular diseases with similar characteristics to esca  
407 are rare. One example is provided by a trunk disease of kiwifruits in which there is a significant  
408 relationship between temperature and leaf symptoms (Di Marco and Osti, 2008).

409 An analysis of the whole database suggested that, unlike esca, Eutypa dieback decreased steadily  
410 in incidence during the 2003-2022 period. These patterns were observed across the most observed  
411 cultivars, years, and wine regions (Figure S5 and S6). The difference between the development of  
412 esca and Eutypa dieback symptoms over time may partly reflect the nature of these diseases. Esca  
413 is generally caused by a complex community of fungi, whereas foliar symptoms of Eutypa dieback  
414 is likely caused by a single fungus, *Eutypa lata*. Climate can affect the expression of Eutypa  
415 dieback (Sosnowski et al., 2007), but its gradual decrease in frequency over the years suggests that  
416 climate has a relatively limited impact. The observed gradual decrease in Eutypa dieback  
417 frequency may be due to the use of effective control methods, such as appropriate pruning, wound  
418 protection and the removal of infected wood from vines (Lecomte et al., 2006), or to a decrease in  
419 pathogen aggressiveness (Molyneux et al., 2002). In any case, Eutypa dieback has been relegated  
420 to the status of a secondary disease, attracting less attention from field technicians, as indicated by  
421 the decrease in the number of plots monitored for this disease over the years (Figure S5 and S6;  
422 except for Ugni Blanc).

423 Our findings revealed considerably variability in the incidence of esca between the 36 cultivars  
424 monitored in the whole database. Cultivar differences in esca incidence have already been  
425 documented in France (Bruez et al., 2013; Gastou et al., 2024), Italy (Murolo and Romanazzi,  
426 2014) and Spain (Chacón-Vozmediano et al., 2021). In these studies, Cabernet Sauvignon and  
427 Sauvignon Blanc were generally identified as much more susceptible than Merlot and Chardonnay  
428 (Murolo and Romanazzi, 2014; Chacón-Vozmediano et al., 2021; Gastou et al., 2024). However,

429 our statistical analysis revealed a lack of significant difference between the cultivars if esca  
430 incidence was calculated only for plots with at least one symptomatic plant. Interestingly, the  
431 prevalence of esca was significantly higher than the mean for two cultivars and lower than the  
432 mean for three cultivars. Moreover, the cultivars with the highest prevalence of esca also had the  
433 highest estimated incidence values (Figure 6). Only Cabernet Sauvignon displayed contrasting  
434 levels of esca prevalence and incidence, as most of the plots had at least one symptomatic plant  
435 but an intermediate incidence. Several confounding factors could potentially cause the cultivar  
436 effect highlighted in our analysis. Typically, some viticulture practices (e.g. the use of certain  
437 rootstocks or types of pruning) may be specific to a particular cultivar and wine region. Such  
438 factors are known to affect susceptibility to esca (Lecomte et al., 2018). It was not possible to  
439 investigate these confounding factors here, but the observed differences in esca incidence between  
440 the cultivars studied here were correlated with the range of susceptibility of the same cultivars  
441 quantified over several years in a common garden vineyard (Gastou et al., 2024).

442 Our results revealed a major impact of plot age on esca incidence, which was lower in younger  
443 vineyards (less than 10 years old) than in older ones. This age effect has also been observed in  
444 several field monitoring programmes (Fulchin et al., 2019; Fussler et al., 2008; Pollastro et al.,  
445 2000). The underlying mechanisms remain to be explored. We could hypothesize that certain traits  
446 known to differ with plant age, such as plant metabolism, wood properties, and pathogen or  
447 endophyte communities, are involved. As suggested by Fischer and Peighami-Ashnaei (2019),  
448 older plants might be more susceptible to disease due to cumulated wounds over time, as cultivated  
449 vines are pruned annually. Older plants may therefore have undergone more infection cycles than  
450 younger plants. In addition, older plants tend to accumulate more endophytes in their tissues than  
451 younger plants (Dissanayake et al., 2018). They also have different fungal communities (Bruez et  
452 al., 2016) and may undergo microbiome modifications during the course of their lifetime

453 (Bettenfeld et al., 2020; Fournier et al., 2022). Indeed, many endophytic fungi are pathogens and  
454 can induce plant dieback (e.g., Úrbez-Torres et al., 2009).

455 Interestingly, the effect of age on the incidence of esca differed between cultivars. There was a  
456 trend towards a relationship between cultivar susceptibility (i.e. esca incidence) and the age range  
457 during which the cultivar was most susceptible (i.e. highest incidence), the least susceptible  
458 cultivars had a narrower age range for susceptibility. In four of the 12 cultivars studied, esca  
459 incidence decreased significantly once a certain age was reached, this age depending on the  
460 cultivar but generally being greater than 30 years. This pattern may reflect a higher rate of plant  
461 mortality in older plots, with the most tolerant plants remaining, the others generally being  
462 replaced by new replanted vines. Indeed, in our database, we observed a slight gradual ageing of  
463 the plots from 2003 to 2014 and an increase in the diversity of plot ages (monitoring of new  
464 younger plots to replace the older ones) starting in 2015 (Figure 3). If we wish to study the effect  
465 of vine age on the incidence of esca more precisely, we need to be able to collect the age of the  
466 vines rather than the age of the plot (based on the year of first plantation). Alternatively, ontogenetic  
467 resistance (Ficke et al., 2002) could be involved, leading to a lower susceptibility to the  
468 development of esca leaf symptoms in the oldest vines, but little is known about this process in  
469 wood diseases. Secondary metabolism may change qualitatively or quantitatively with plant  
470 ageing (Haffner et al., 1991), potentially accounting for the persistence of long-lived perennial  
471 plants (Cui et al., 2024). With regard to other diseases, a higher incidence of Botryosphaeriaceae  
472 (Carlucci et al., 2013; Gubler et al., 2005) and *Phaeoacremonium* sp. (Carlucci et al., 2013, 2015)  
473 has been observed in older grapevines and olive trees. Similarly, an increase in branch canker and  
474 dieback incidence with the age of the tree has been observed in avocado orchards (Valencia et al.,  
475 2022). By contrast, for kiwifruit (Di Marco and Osti, 2008), no correlation was found between plot  
476 age (based on the year of first plantation) and the percentage of symptomatic plants, although the  
477 age range considered was rather small. However, there have been no studies of a possible non-

478 linear effect of age on wood diseases in perennial crops other than vines. Clearly, exploring the  
479 underlying mechanisms of wood disease resistance or tolerance according to plant age is a  
480 promising research avenue that could improve our understanding of the pathogenesis of such  
481 diseases.

482 By constituting and unifying large spatial and temporal surveillance databases, as in this study, it  
483 is possible to visualise and statistically quantify the long-term progression of wood diseases.  
484 However, some biases associated with the selection of the plots monitored must be taken into  
485 account. In particular, in some wine regions, plots planted with particular cultivars were selected  
486 on the basis of their susceptibility to disease rather than as a representative sample of the cultivars  
487 in the region. The use of different regional strategies may have decreased the representativeness  
488 of the data. This bias would result in a low or high estimated incidence in the region, distorted by  
489 the selection of the cultivars monitored. Thus, in such surveillance databases, incidence at regional  
490 levels should be interpreted with caution, with particular attention paid to the regional sampling  
491 strategy. These potential biases do not call into question the relevance and urgent need for the  
492 combination and unification of different regional datasets to develop a national epidemiological  
493 surveillance programme for complex diseases, such as esca, in order to help performing additional  
494 statistical analyses in both space and time. Pursuing efforts to develop surveillance initiatives and  
495 improve both quantity and quality of data is a crucial challenge in the context of global changes.  
496 Moreover, climate projections may have far-reaching long-term effects that can only be  
497 understood in the light of such long-term surveys.

498

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520 **Competing interests**

521 The authors declare that they have no competing interests.

522 **Data availability statement**

523 Part of the research data is available by contacting the corresponding author and a public data  
524 visualisation application is available: <https://observatoire.plan-deperissement-vigne.fr/adws/app/158a1259-b9ea-11ee-ac62-2997ecd1d68c/>

526

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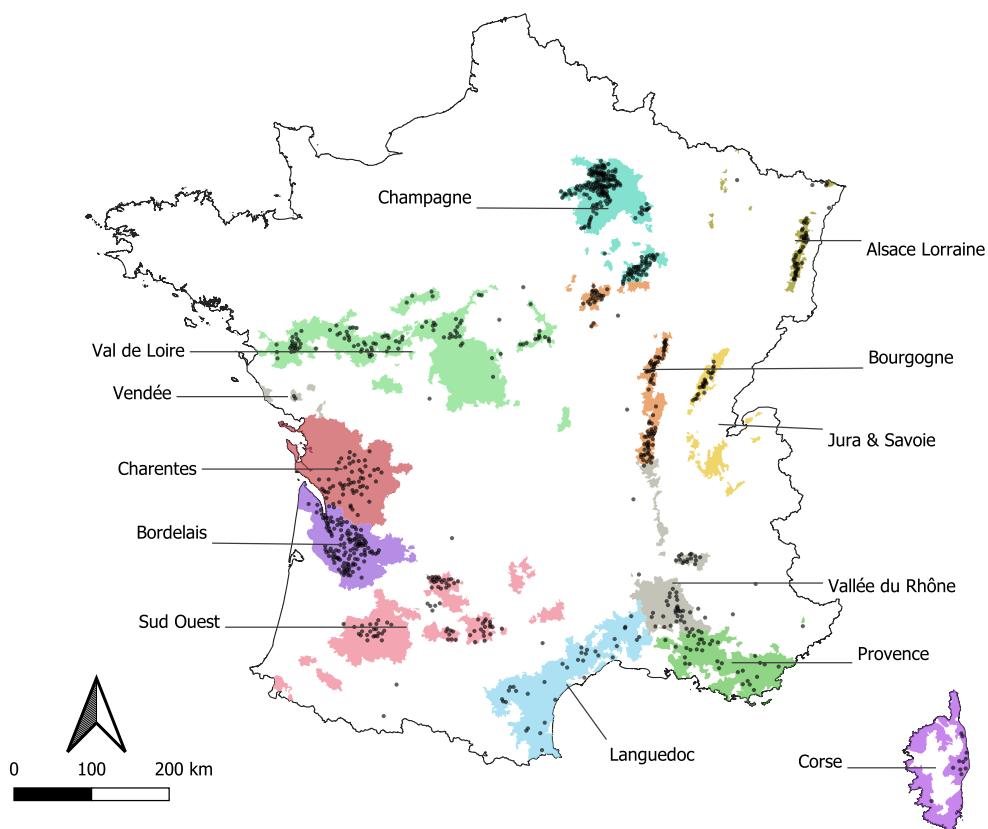
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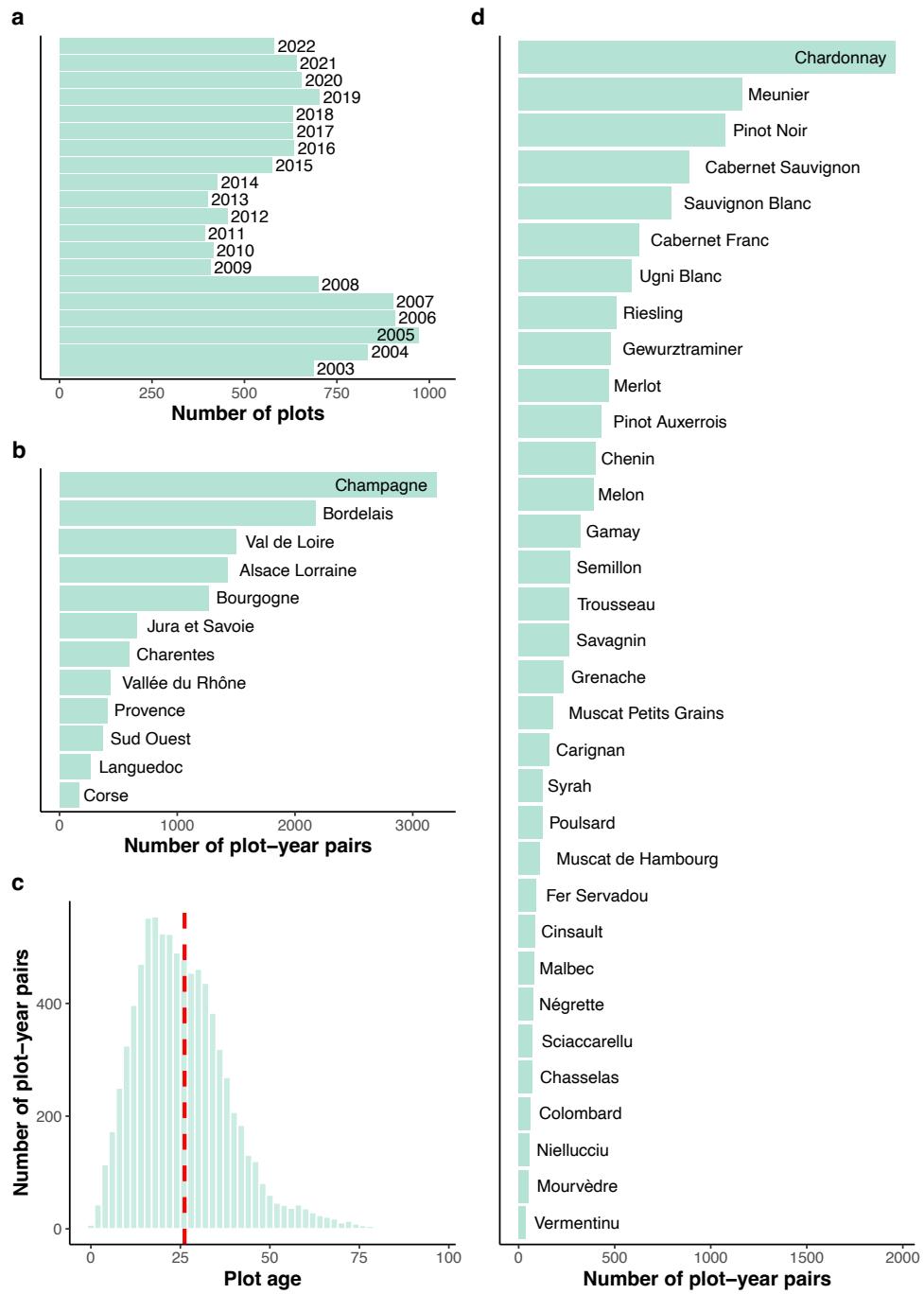
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721 **Figures**



722

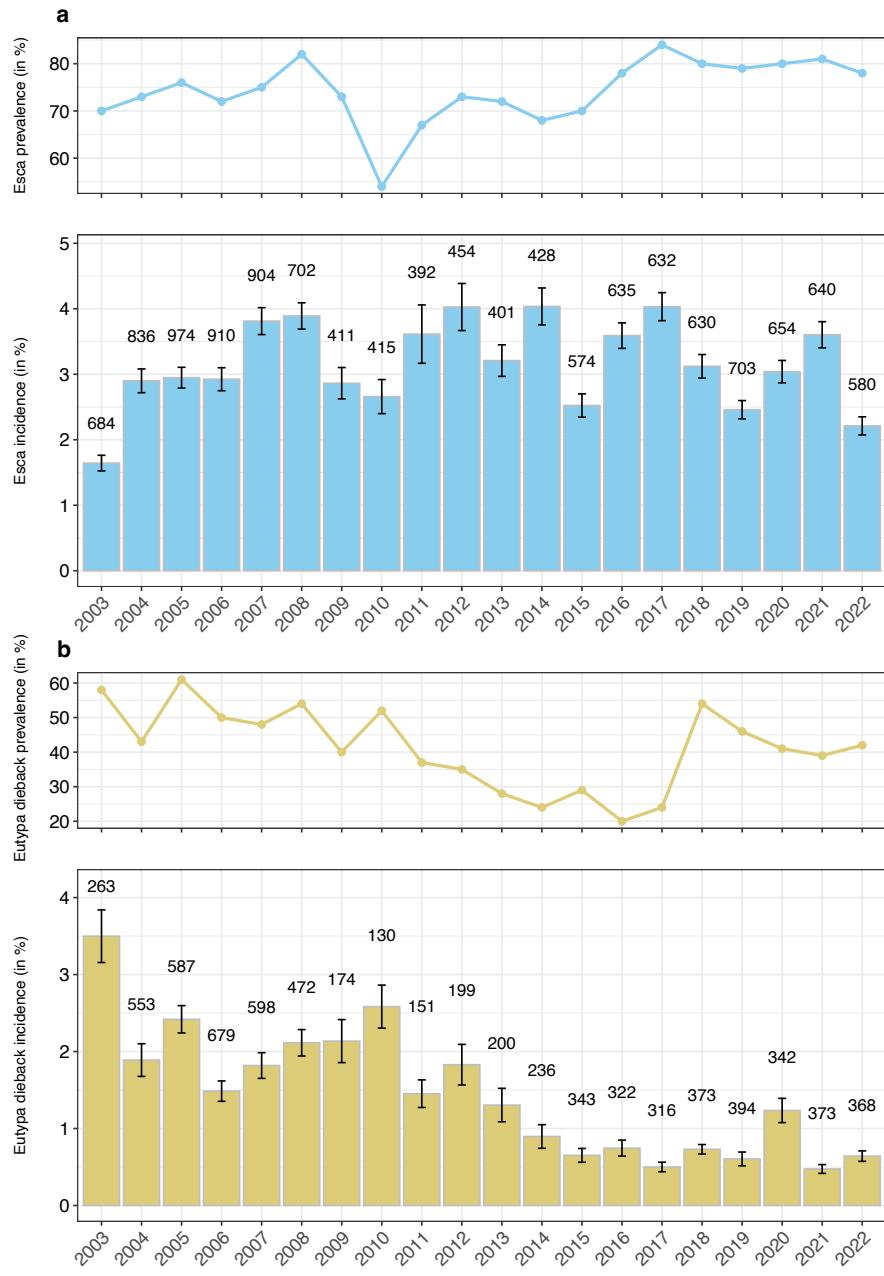
723 Figure 1: Map of the French wine-growing regions showing the locations of the 884 municipalities  
724 in which plots were monitored for esca leaf symptoms (black dots). These municipalities are  
725 located in 49 provinces, 13 vine-growing regions, and 10 administrative regions. Eutypa dieback  
726 was also monitored in 592 of these municipalities in 39 provinces, 10 wine regions, and 7  
727 administrative regions.



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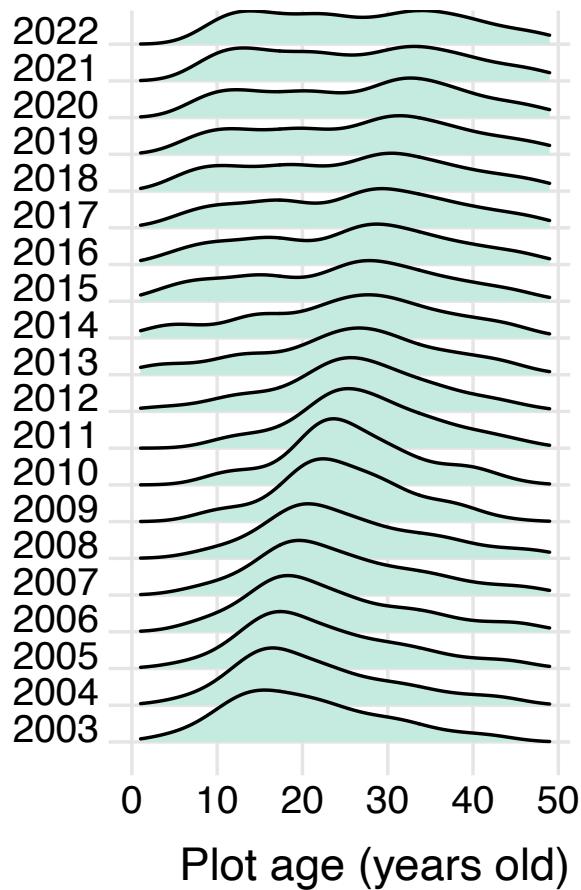
729 Figure 2: Number of plots or observations (plot-year pairs) monitored in France for esca between  
730 2003 and 2022 and recorded in the database, by year (a), wine region (b), plot age (c), and *Vitis*  
731 *vinifera* cultivar (d). An observation corresponds to one plot monitored in a given year. The red  
732 dotted line in (c) represents the mean age.

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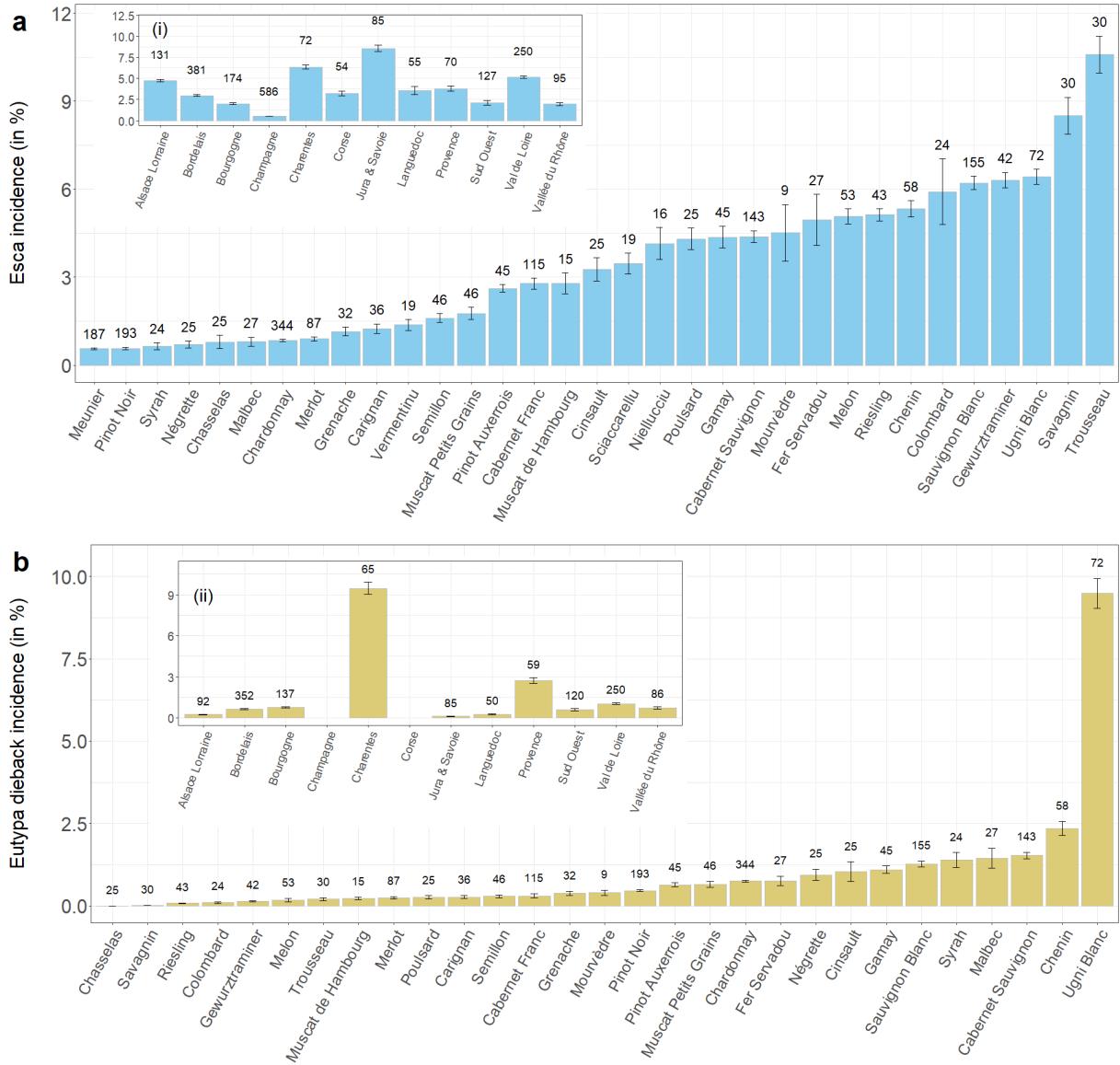
734

735 Figure 3: The mean prevalence and incidence of esca and Eutypa dieback leaf symptoms per year  
736 in France over the 2003-2022 period. The prevalence (shown as curves in the top panel) was  
737 determined as the number of plots with at least one symptomatic vine recorded per year. The  
738 incidence (represented by bar charts in the bottom panel) was determined as the percentage of  
739 symptomatic vines observed per plot each year. The numbers displayed correspond to the number  
740 of plots monitored for the incidence of (a) esca (blue dots, lines and bars) and (b) Eutypa dieback  
741 (mustard dots, lines and bars). The error bars indicate the standard error of the mean.



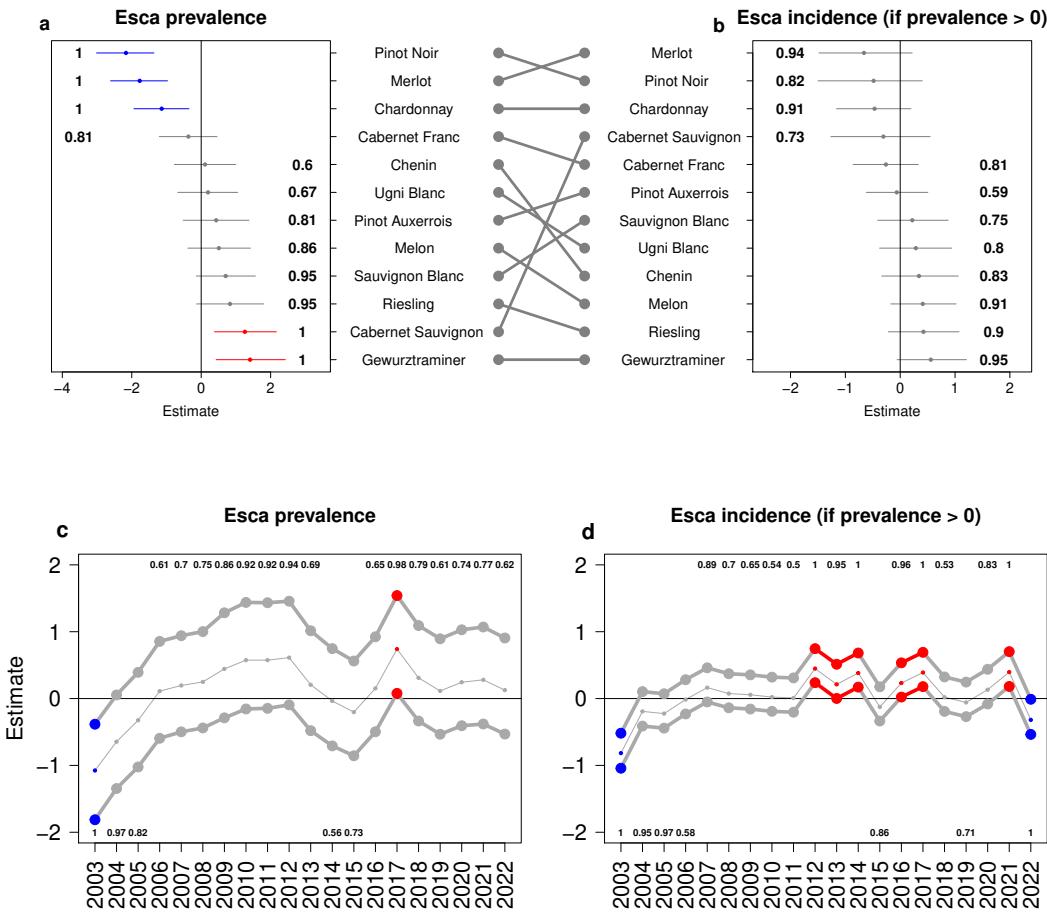
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743 Figure 4: Distribution of plot age (range: 1 to 49 years) for each year for the 12 *Vitis vinifera*  
744 cultivars used in the modelling approach.



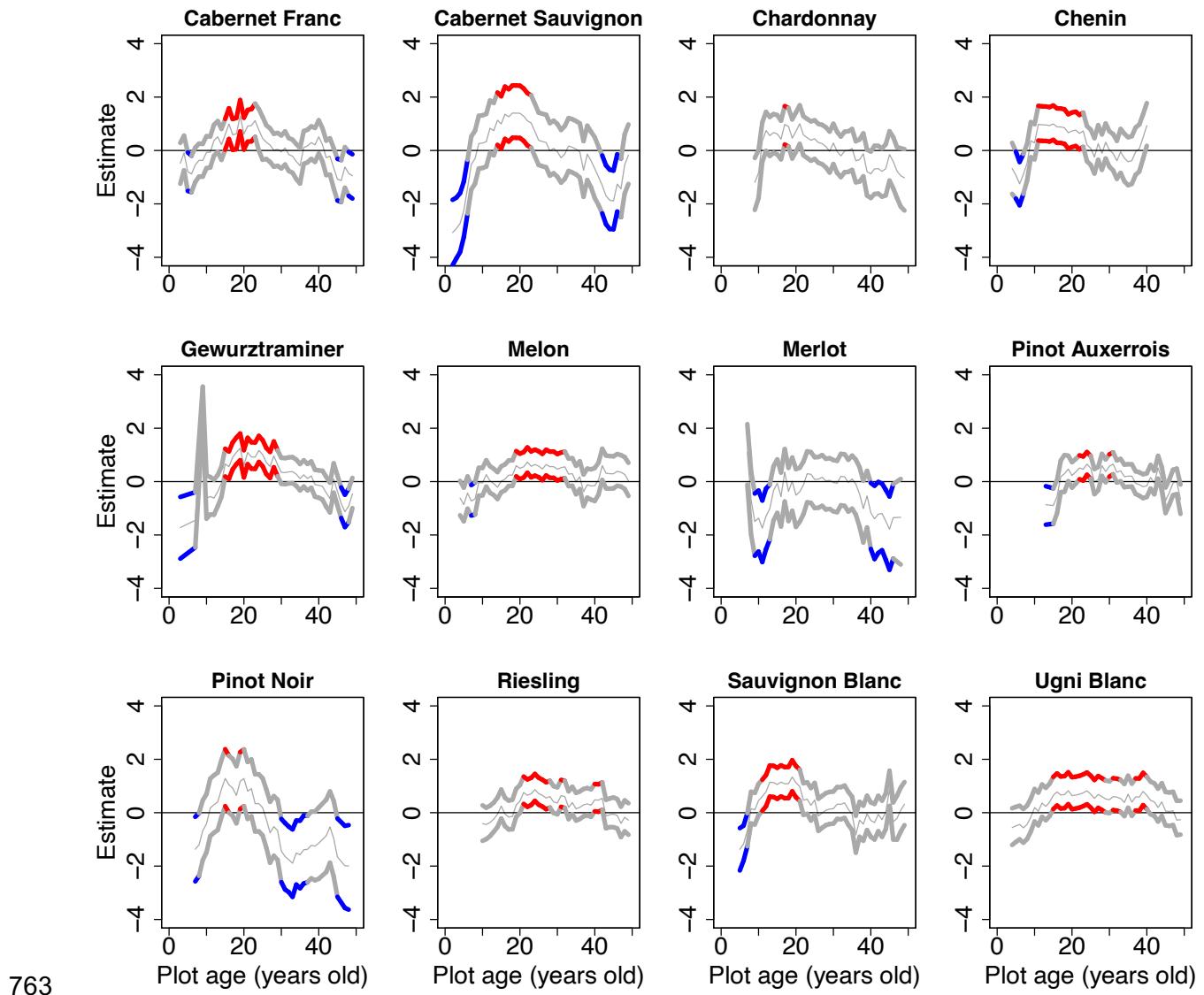
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746 Figure 5: The mean incidence of esca and Eutypa dieback leaf symptoms by cultivar and wine  
 747 region (inset, i : esca; ii : Eutypa dieback) in France over the 2003-2022 period. Numbers represent  
 748 the number of plots monitored for the incidence of (a) esca (blue bars) and (b) Eutypa dieback  
 749 (mustard bars). The error bars represent the standard error of the mean.



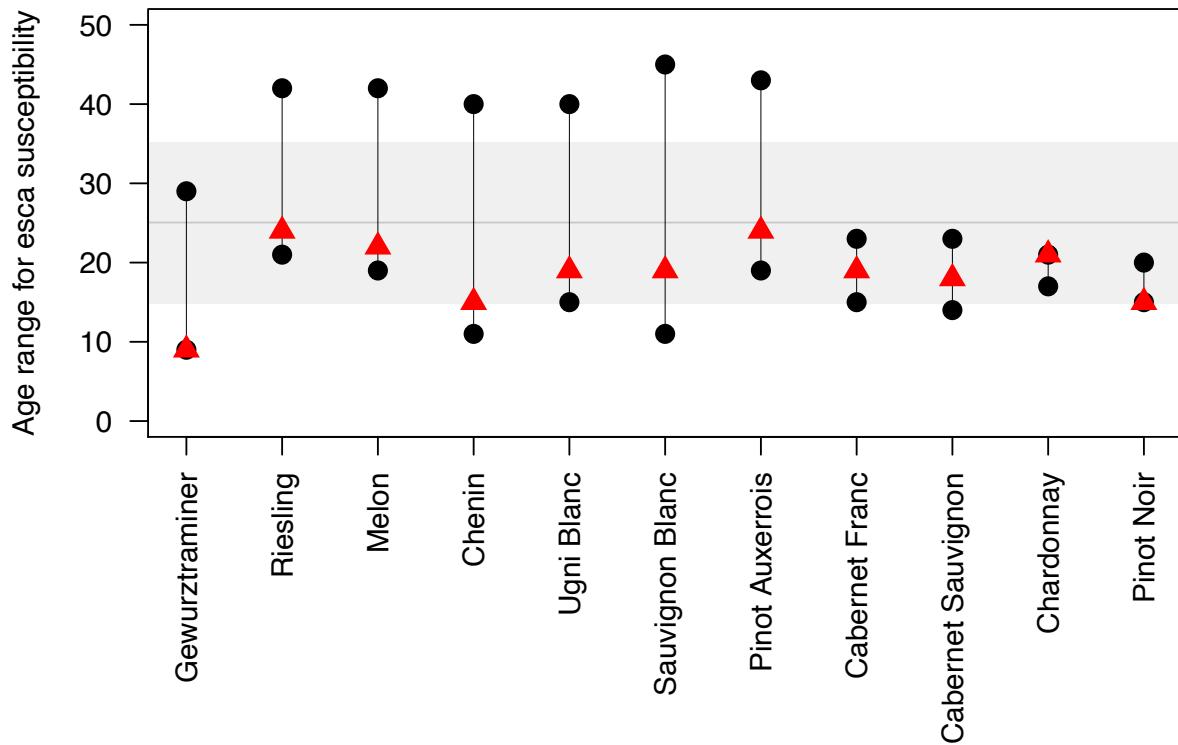
750

751 Figure 6: Effects of cultivar (upper panels, means in descending order) and year (lower panels) on  
 752 esca prevalence (left panels) or esca incidence if esca was observed in the plot (right panels). In  
 753 the upper panels, black points represent the posterior median (50th percentiles, middle) and  
 754 horizontal lines the lower (2.5th percentiles) and upper (97.5th percentiles) limits of the credible  
 755 interval for the independent random effects associated with each cultivar. The segments between  
 756 the upper panels (a and b) show the relationship between the estimated prevalence and incidence  
 757 of the different cultivars. The lower panels display the year effects for esca prevalence and  
 758 incidence, as fitted with an autoregressive model of order 1. Estimates in blue correspond to years  
 759 associated with significantly negative effects (97.5th percentile < 0) relative to the mean (0),  
 760 whereas those in red correspond to years with significantly positive effects (2.5th percentile > 0).  
 761 The values shown correspond to the probability of direction for each cultivar (see the materials  
 762 and methods section).



763

764 Figure 7: Impact of plot age (in years), by cultivar, on standardised estimates of the esca incidence  
765 for the plots in which esca was observed. The posterior median (50th percentile, middle), lower  
766 (2.5th percentiles) and upper (97.5th percentiles) limits of the credible interval are shown.  
767 Estimates in blue correspond to ages associated with significantly negative effects (97.5th  
768 percentile < 0) relative to the mean (0) whereas those in red correspond to ages associated with  
769 significantly positive effects (2.5th percentile > 0). Estimates are shown in colour if the findings  
770 for at least two consecutive years are significant.



771

772 Figure 8: Range of ages during which vines are susceptible to esca (black points) and peak (red  
773 triangle) susceptibility for cultivars with significant and positive results between the first and the  
774 last plot age. The cultivars are ordered by estimated mean incidence and only cultivars with an age  
775 significantly and positively above the mean of 0 are shown (Figure 6b, Merlot is therefore not  
776 represented). The wide horizontal grey band represents the standard deviation from the mean,  
777 which is represented by the horizontal dark grey bar, for all cultivars combined.

778

779 Table 1: Summary statistics for plot age and number of plots (total and per year) monitored for the  
780 12 *Vitis vinifera* cultivars retained for statistical modelling. Maximum plot age was fixed at 49  
781 years.

Cultivar	Plot age (mean $\pm$ SD [min, max] years)	Total plots	number of plots per year	Mean ( $\pm$ SD) number of plots per year
Cabernet Sauvignon	23 $\pm$ 9 [2, 49]	85		14 $\pm$ 13
Sauvignon Blanc	20 $\pm$ 10 [3, 49]	62		8 $\pm$ 10
Chardonnay	30 $\pm$ 9 [7, 49]	61		6 $\pm$ 10
Cabernet Franc	23 $\pm$ 13 [2, 49]	53		9 $\pm$ 12
Merlot	24 $\pm$ 10 [7, 49]	52		13 $\pm$ 11
Pinot Noir	29 $\pm$ 9 [7, 49]	47		6 $\pm$ 8
Ugni Blanc	26 $\pm$ 12 [4, 49]	41		20 $\pm$ 28
Melon	21 $\pm$ 10 [2, 49]	39		6 $\pm$ 4
Chenin	18 $\pm$ 8 [1, 40]	38		5 $\pm$ 5
Gewurztraminer	28 $\pm$ 9 [2, 49]	28		9 $\pm$ 10
Pinot Auxerrois	32 $\pm$ 8 [11, 49]	24		8 $\pm$ 8
Riesling	28 $\pm$ 9 [10, 49]	24		8 $\pm$ 10

782

783

784 Table 2: Deviance information criterion (DIC) and widely applicable information criterion  
785 (WAIC) for the eight model structures considered. Number of vines monitored per plot:  $n_{vines}$ .

Model ID	Prevalence model	Incidence model	DIC	WAIC
M8 “Full”	plot + cultivar + year + $n_{vines}$	plot + cultivar + year + age x cultivar	37842	64418
M7	plot + cultivar + year + $n_{vines}$	plot + cultivar + year + age	40272	80397
M6	plot + cultivar + year + $n_{vines}$	plot + cultivar + year	39771	111086
M5	plot + cultivar + year + $n_{vines}$	plot + cultivar	44832	142323
M4	plot + cultivar + year + $n_{vines}$	plot	44871	142351
M3	plot + cultivar + year + $n_{vines}$	1	132737	121358
M2	plot + cultivar + year	1	132736	121357
M1	plot + cultivar	1	132813	121436
M0	plot	1	132913	121497

786

787

788 Table 3: Summary statistics for the parameters of the full model of the prevalence and incidence  
 789 of esca leaf symptoms. For both model components (prevalence and incidence for plots with a  
 790 prevalence of 1), the table summarises the posterior mean, standard deviation (SD), 0.025, 0.5,  
 791 0.975 quantiles (quant.) and mode for intercepts ( $\beta_0$ : intercept for esca prevalence;  $\beta_1$ : intercept for  
 792 esca incidence), the number of vines monitored ( $\mu_0$ ), the variance of the independent random  
 793 effects associated with cultivars and plots ( $\sigma^2_{cultivar0}$ ,  $\sigma^2_{cultivar1}$ ,  $\sigma^2_{plot0}$  and  $\sigma^2_{plot1}$ ), the correlation  
 794 coefficients and variance of the AR1 process associated with year ( $\rho_{year0}$  and  $\rho_{year1}$ ) and the  
 795 correlation coefficients and variance of the AR1 process associated with age for each cultivar  
 796 ( $\rho_{age1,cultivar}$  and  $\sigma^2_{age1,cultivar}$  to be detailed).

	Mean	SD	0.025quant.	0.5quant.	0.975quant.	Mode
<b>Esca prevalence</b>						
$\beta_0$	2.75	0.47	1.83	2.75	3.69	2.74
$\mu_0$	0.33	0.20	-0.05	0.33	0.73	0.33
$\sigma^2_{cultivar0}$	0.90	0.40	0.35	0.83	1.88	0.70
$\sigma^2_{plot0}$	0.36	0.04	0.29	0.36	0.44	0.36
$\rho_{year0}$	0.64	0.16	0.25	0.67	0.89	0.72
$\sigma^2_{year0}$	5.11	2.40	1.84	4.65	11.08	3.82
<b>Esca incidence (when prevalence &gt; 0)</b>						
$\beta_1$	-3.91	0.20	-4.41	-3.90	-3.46	-3.88
$\sigma^2_{cultivar1}$	3.53	2.42	0.94	2.89	9.95	2.01
$\sigma^2_{plot1}$	1.25	0.09	1.09	1.25	1.43	1.25
$\rho_{year1}$	0.30	0.24	-0.20	0.32	0.71	0.36
$\sigma^2_{year1}$	12.58	4.35	5.87	11.98	22.79	10.84
$\rho_{age1,Cabernet Franc}$	0.80	0.09	0.59	0.82	0.93	0.85
$\sigma^2_{age1,Cabernet Franc}$	2.81	1.32	1.03	2.54	6.12	2.09
$\rho_{age1,Cabernet Sauvignon}$	0.95	0.03	0.87	0.95	0.98	0.96
$\sigma^2_{age1,Cabernet Sauvignon}$	0.72	0.38	0.24	0.64	1.68	0.50
$\rho_{age1,Chardonnay}$	0.80	0.10	0.55	0.82	0.93	0.85
$\sigma^2_{age1,Chardonnay}$	2.62	1.36	0.89	2.32	6.09	1.83

$\rho_{age1,Chenin}$	0.82	0.09	0.60	0.83	0.94	0.87
$\sigma^2_{age1,Chenin}$	2.59	1.27	0.87	2.35	5.77	1.89
$\rho_{age1,Gewurztraminer}$	0.43	0.16	0.09	0.44	0.71	0.46
$\sigma^2_{age1,Gewurztraminer}$	1.33	0.39	0.72	1.28	2.23	1.19
$\rho_{age1,Melon}$	0.77	0.13	0.45	0.80	0.94	0.85
$\sigma^2_{age1,Melon}$	6.04	2.92	2.14	5.46	13.39	4.42
$\rho_{age1,Merlot}$	0.74	0.13	0.44	0.76	0.93	0.81
$\sigma^2_{age1,Merlot}$	1.62	0.80	0.52	1.47	3.59	1.18
$\rho_{age1,Pinot Auxerrois}$	0.66	0.14	0.33	0.69	0.88	0.73
$\sigma^2_{age1,Pinot Auxerrois}$	4.83	2.20	1.82	4.41	10.30	3.67
$\rho_{age1,Pinot Noir}$	0.91	0.05	0.80	0.92	0.97	0.94
$\sigma^2_{age1,Pinot Noir}$	0.97	0.50	0.30	0.87	2.22	0.68
$\rho_{age1,Riesling}$	0.80	0.10	0.55	0.82	0.94	0.86
$\sigma^2_{age1,Riesling}$	6.85	3.45	2.27	6.15	15.53	4.90
$\rho_{age1,Sauvignon Blanc}$	0.82	0.08	0.64	0.84	0.94	0.86
$\sigma^2_{age1,Sauvignon Blanc}$	2.17	0.99	0.74	2.01	4.54	1.67
$\rho_{age1,Ugni Blanc}$	0.90	0.06	0.76	0.91	0.97	0.93
$\sigma^2_{age1,Ugni Blanc}$	5.37	2.89	1.61	4.77	12.66	3.67

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