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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Abstract

Grapevine trunk diseases cause yield losses and vine mortality in vineyards worldwide. However, there have been few quantitative studies evaluating grapevine dieback on a large spatial and temporal scale. Here, we consolidated and standardised databases from the 13 main wine regions of France, compiling records of leaf symptoms associated with esca and Eutypa dieback from 2082 plots and 36 cultivars over a 20-year period. This large dataset was used (1) for quantitative analysis of the prevalence (number of plots with at least one symptomatic plant) and incidence (percentage of symptomatic plants) of esca and Eutypa dieback; (2) to decipher the effects of cultivar, year and plot age on both the prevalence and incidence of esca leaf symptoms by temporal Bayesian modelling. Esca was present on a mean of 74 ± 2% plots annually, with an incidence of 3.1 ± 0.1%. Eutypa dieback occurred in 41 ± 3% of the plots, with an incidence of 1.4 ± 0.1%. Our modelling approach revealed that the cultivar had a significant impact on the prevalence of esca, but not on its incidence when prevalence is greater than zero. Esca prevalence remained stable, whereas esca incidence was higher than the mean value in six of the years after 2012. We also found a significant non-linear effect of plot age, with 10- to 30-year-old plots significantly more susceptible, depending on the cultivar. This study clearly illustrates the importance of considering extensive and continuous monitoring to improve our understanding of the impact and evolution of crop diseases.

I) Introduction

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

Dieback of grapevine (*Vitis vinifera* L.) is caused by various abiotic and biotic factors, including diseases affecting grapevine wood. Trunk diseases, such as esca, Eutypa dieback, and Botryosphaeriaceae dieback, are the most widespread globally (Guerin-Dubrana et al. 2019; Mugnai et al. 1999). These diseases cause vine destruction leading to yield losses (Bertsch et al. 2009; Gramaje et al. 2018; Mondello et al. 2018), although these can be overestimated in some regions (Dewasme et al. 2022). The current epidemic spread of trunk diseases in Europe can be traced back to the early 1990s (Mugnai et al, 1999; Reisenzein et al, 2000; Surico et al, 2000). In the first few years of the 21st century, until at least 2008, the incidence of grapevine trunk diseases, including esca in particular, appears to have increased (Bruez et al. 2013). This increase is a matter of great concern to vine growers, particularly in the wake of the sodium arsenate ban introduced in France in 2001, as this was the only effective treatment for esca (Mugnai et al., 1999). Several factors may be associated with variation in the incidence of trunk diseases. These factors include cultivar (Murolo and Romanazzi, 2014), year (Dewasme et al. 2022) and plot age (Fussler et al. 2008). Cultivar is a major factor underlying differences in the incidence of esca disease between vineyards and vine-growing regions, as shown by the considerable variability of the proportion of symptomatic plants per cultivar in France during the monitoring of 46 cultivars planted in a common garden vineyard over a period of seven years (Gastou et al. 2024), in Italy during the

monitoring of 67 cultivars for one year (Murolo and Romanazzi, 2014) and in Spain, during the monitoring of 47 cultivars for three years (Chacón-Vozmediano et al. 2021). Indeed, certain cultivars, such as Merlot, only rarely display esca leaf symptoms whereas others, such as Sauvignon Blanc, are frequently affected. Moreover, strong interannual variability has been observed within vineyards (Calzarano et al. 2018; Dewasme et al. 2022). The age of the vines significantly influences their response to biotic and abiotic stresses, determining their tolerance or susceptibility. As a result, the incidence and expression of symptoms of stress increase linearly with plant age (Pandey et al. 2015). The effect of vineyard age on esca incidence is unclear. A few studies have reported an absence of correlation between plot age and esca incidence (Bruez et al. 2013; Péros et al. 2008), but others have reported a significant age effect for plots aged from 10 to 21 years (Kovács et al. 2017). By contrast, other studies have suggested that the relationship between plot age and symptom expression is quadratic rather than linear, with disease incidence highest at intermediate ages (Fulchin et al. 2019; Fussler et al. 2008). Incidence appears to be higher in vineyards of between 15 and 25 years of age than in vineyards of other ages, as shown in a study of 22 cultivars (Fussler et al. 2008) and, more recently, in a study of 5 cultivars (Fulchin et al. 2019). However, in these studies, age was considered as a categorical ordered variable (e.g. 'young' if the plot was less than 7 years old and 'old' if more than 11 years old, Romanazzi et al. 2009, or 0-15, 15-25, 25-40, and over 40 years old, Fussler et al. 2008). No study has ever addressed age as a fully continuous quantitative variable, probably due to a lack of long-term, large-scale monitoring.

Distinguishing between the effects of year and plot age requires large-scale and long-term monitoring, to ensure that the variables are not correlated, or at least no more than weakly correlated. Large-scale monitoring is essential to improve pest surveillance for plants, particularly 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 a
94 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**

1) French database of grapevine trunk disease observations

The database contains 12587 observations of esca leaf symptoms and Eutypa dieback, in the main wine-producing regions in France. This database is stored in the information system of the French Epidemiological Plant Health Surveillance Platform (ESV Platform). The observations were obtained from two sources: (i) regional surveys conducted from 2003 to 2022, and (ii) the historical "National Grapevine Trunk Diseases Survey", which tracked the progression of grapevine trunk diseases throughout France from 2003 to 2008 (Fussler et al. 2008; Grosman and Doublet, 2012; Bruez et al. 2013). The historical and regional surveys were conducted by experts from diverse public or private agronomic institutes or associations in each of the regions (see the Acknowledgements section).

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

132 For 63% of the plots monitored for esca, annotation was also available for Eutypa dieback
133 symptoms. Eutypa dieback was monitored between April and May (Table S1) to score plants
134 presenting stunted shoots with necrotic leaves as shown in Mondello et al. (2018). In total, 7073
135 observations were available for this disease, spread over 1310 plots located in 592 municipalities
136 (2.2 ± 2.4 (mean ± SD) plots per municipality), 39 provinces, 10 wine regions, and 7 administrative
137 regions. All cultivars other than Meunier, Sciaccarellu, Vermentinu, and Niellucciu were
138 monitored for Eutypa dieback, with data available only for esca leaf symptoms for these
139 exceptions.

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

144 The number of vines with esca or Eutypa dieback symptoms on leaves was recorded on a defined
145 number of vines in the plots described above. A mean of 420 ± 530 vines was observed per plot
146 (see supplementary materials, Table S2). One plot of Cabernet Sauvignon was monitored in its
147 entirety as part of an experiment, accounting for the large mean number of vines observed for this
148 cultivar (Table S2). The definitions of disease prevalence and incidence proposed by Nutter et al.
149 (2006) were used.

150

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

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

156 of plants presenting esca leaf symptoms (as described by Lecomte et al. 2012) or Eutypa dieback
157 leaf symptoms (as described by Sosnowski et al. 2007) by the number of plants monitored in the
158 plot concerned (included dead or missing vines).

159

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

162 In addition to the descriptive analysis of the whole database, a statistical model was developed to
163 estimate the effect of cultivar, year and plot age on both prevalence and incidence of esca leaf
164 symptoms at plot scale. In this modelling approach, only esca was used, as Eutypa dieback is
165 affecting almost exclusively the Ugni Blanc cultivar and presents a decreasing incidence over time,
166 in contrast to esca (Figure 3). To optimise model identifiability, we applied some criteria to select
167 the data used in this approach. We selected observations (one plot in a given year) from plots under
168 50 years old (older plots excluded), for which at least five years of observation were available (not
169 necessarily consecutive), and cultivars for which at least 300 observations were available.
170 The application of these criteria resulted in a database of 5161 observations (from the 12587
171 observations initially identified) spread over 12 cultivars (Table 1). On average, a plot was
172 monitored for 9 ± 4 [5, 20] years. Mean plot age ranged from 18 to 32 years (Table 1). Mean plot
173 age tended to increase from 2003 to 2013, remaining stable thereafter (Figure 4).

174

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

there being at least one vine with esca symptoms in the plot. Thus, a zero-inflated binomial distribution parameterised to exclude zero with a logit link was used for the incidence. Both the prevalence and incidence components included cultivar and plot identity as independent random effects and the year as an autoregressive process of order 1 (AR1). These effects account for interannual dependence arising from underlying meteorological or environmental factors and agricultural practices affecting esca symptoms. Finally, the incidence component included plot age as an AR1 process specific to each cultivar. We describe below the "full" model including all explanatory variables. Intermediate models with fewer explanatory variables were also estimated and compared to the full model on the basis of two information criteria: the deviance information criterion and the widely applicable information criterion (DIC and WAIC) (Table 2).

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

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

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

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

$$\alpha_0[plot(i)] \sim Normal\left(0,\ \sigma^2_{plot0}\right)$$

$$\gamma_0[cultivar(i)] \sim Normal(0, \sigma^2_{cultivar0});$$

$$\delta_0[2003] \sim Normal\left(0, \sigma^2_{year0}(1-\rho^2_{year0})^{-1}\right)$$

$$\delta_0[t] = \rho_{year0}\left[\delta_0[t-1]\right] + \varepsilon_0[t],\ t = 2004, \dots, 2022$$

$$\varepsilon_0[t] \sim Normal\left(0, \sigma^2_{year0}\right)$$

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

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

$$n_i|y_i = 1 \sim ZIB^+(n_i^{tot},\ \omega_i),\ i \in S$$

$$logit(\omega_i) = \beta_1 + \alpha_1[plot(i)] + \gamma_1[cultivar(i)] + \delta_1[year(i)] + \tau_{cultivar(i)}[age(i)]$$

$$\alpha_1[plot(i)] \sim Normal\left(0,\ \sigma^2_{plot1}\right)$$

$$\gamma_1[cultivar(i)] \sim Normal(0, \sigma^2_{cultivar1})$$

$$\delta_1[2003] \sim Normal\left(0, \sigma^2_{year1}(1-\rho^2_{year1})^{-1}\right)$$

$$\delta_1[t] = \rho_{year1}\left[\delta_1[t-1]\right] + \varepsilon_1[t],\ t = 2004, \dots, 2022$$

$$\varepsilon_1[t] \sim Normal\left(0, \sigma^2_{year1}\right)$$

$$\tau_{cultivar1}[1] \sim Normal\left(0, \sigma^2_{age1,cultivar}(1-\rho^2_{age1,\,cultivar})^{-1}\right),\ cultivar = 1,\ \dots,\ 12$$

$$\tau_{cultivar1}[z] = \rho_{age1,cultivar}\left[\tau_{cultivar}[z-1]\right] + \varepsilon_{age1,cultivar}[z],\ z = 2, \dots, 49$$

$$\varepsilon_{age1,cultivar}[z] \sim Normal\left(0, \sigma^2_{age1,cultivar}\right)$$

In the model, β_0 and β_1 are the intercepts of prevalence and incidence, respectively. The parameter μ_0 takes into account the different numbers of plants monitored per plot (note that n_i^{tot} was standardised to ensure robust estimation). The autoregressive parameters ρ_{year0}, ρ_{year1}, $\rho_{age1,cultivar}$ (all of which have absolute values < 1) correspond to the correlation coefficients for the prevalence

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

III) Results

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

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

Only 10% of the 2075 plots monitored over the 2003-2022 period contained no symptomatic vines (1861 of 2075 plots contained at least one vine presenting symptoms). The annual prevalence of esca ranged from 54% in 2010 to 84% in 2017, with a mean of 74 ± 2% (mean ± SEM, standard error of the mean) plots containing at least one symptomatic plant (Figure 3a). During the monitoring period, for all years considered together, the prevalence of esca in the regions ranged from 100% of the plots containing at least one vine with esca (Corse and Jura & Savoie) to 78% (Champagne) (data not shown).

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

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

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

280 **1.2) Variability of the prevalence and incidence of Eutypa dieback**

281 In total, 1296 plots were monitored for Eutypa dieback over the 2003-2022 period, and 31% were
282 Eutypa-free (895 of the 1296 plots contained vines displaying Eutypa dieback). The annual
283 percentage of plots with Eutypa dieback (i.e, the prevalence) ranged from 20% in 2016 to 61% in
284 2005, with a mean value of 41 ± 3% (mean ± SEM) (Figure 3b). During the monitoring period,
285 the regional prevalence of Eutypa dieback ranged from 96% in Charentes to 40% in the Sud Ouest
286 region.

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

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

301

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

304 The two model selection criteria considered (DIC and WAIC) supported the full model (Table 2),
305 suggesting that all the explanatory variables considered had a significant impact on esca dynamics.
306 We therefore consider only the full model hereafter. The model fit was satisfactory for both the
307 prevalence and incidence components. Specifically, the area under the ROC curve (AUC) for esca
308 prevalence was 0.93. Pearson's r for the correlation between adjusted and observed values of esca
309 incidence was 0.83 ($p < 0.001$).
310
311 The model included the number of vines monitored as a covariable to account for the sampling
312 effort in each plot used to determine incidence. As expected, the mean effect was positive (0.33),
313 confirming that increasing the number of plants inspected in a plot increases the likelihood of at
314 least one plant being symptomatic. The associated probability of direction was 0.95 (μ_0, Table 3).
315 The identity of the plot had a significant impact on both the prevalence and incidence of esca
316 symptoms. For prevalence, 13% of the individual plot effects were negative (i.e. associated with a
317 q-97.5% < 0), < 1% were positive (q-2.5% > 0) and the remaining 87% were associated with
318 individual effects including zero (the mean value) in their 95% credible intervals. For incidence,
319 25% of the plots were negative, 30% were positive and the remaining 45% were associated with
320 individual effects including zero in the 95% credible interval. These values correspond to the
321 percentage of plots characterised by an esca prevalence or incidence lower than, higher than or not
322 significantly different from the overall mean, respectively.
323
324 Cultivar had a significant impact on the prevalence of esca symptoms but a much weaker effect
325 on esca incidence. Indeed, cultivar was significant if WAIC was used (64436 without the cultivar
326 effect vs. 64418 for the full model) but not with the DIC (37835 without the cultivar effect vs.
327 37842 for the full model, Table 2). The individual effects of each of the 12 cultivars considered
328 are shown in Figure 6. Chardonnay, Merlot and Pinot Noir all had a prevalence of esca below the
329 overall mean (mean = 0, q-97.5% < 0) whereas Gewurztraminer and Cabernet Sauvignon had a

330 prevalence above the overall mean (q-2.5% > 0) (Figure 6a). No such differences were observed
331 for the incidence of esca. The 12 estimated 95% credible intervals included zero, meaning that
332 esca incidence did not differ between cultivars, provided that esca was observed (prevalence > 0;
333 Figure 6b). However, the probability of direction (*pd*) showed that cultivars such as
334 Gewurztraminer, Riesling and Melon had a strong tendency to have a high incidence whereas
335 Merlot and Chardonnay had a low incidence (*pd* > 0.90, Figure 6a, b).
336
337 Unlike the effect of cultivar, the effect of year did not affect the prevalence of esca symptoms, but
338 their incidence. However, the 95% credible interval [0.25, 0.89] of the hyperparameters ρ_{year0} of
339 the AR1 process modelling the effect of year on esca prevalence suggests that esca prevalence is
340 strongly correlated across successive years. No such significant correlation was detected for esca
341 incidence (the 95% CI of ρ_{year1} was [-0.20, 0.71]) (Table 3; Figure 6c, d). An analysis by year
342 showed that the prevalence or incidence (if esca was recorded in the plot) of esca was significantly
343 lower than the mean value (=0) in the first year (2003) and that esca incidence was lower in 2022.
344 The prevalence and incidence of esca tended to be below the mean value in 2004, as was the
345 incidence in 2005 (probability of direction, *pd* > 0.95). In 2017, the prevalence and incidence of
346 esca were significantly higher than the mean. Moreover, esca incidence has remained above the
347 mean value since 2012, including the years 2013, 2014, 2016, 2017, and 2021. However, *pd* values
348 showed that between 2010 and 2012, prevalence tended to be high (pd > 0.92, as shown in Figure
349 6c, d).
350
351 The hyperparameters $\rho_{age1,cultivar}$ of the AR1 process, modelling the effect of plot age on esca
352 incidence for each cultivar, were strictly positive, suggesting a positive correlation between plot
353 age and incidence (Table 3). A pattern of the effect of age on esca incidence common to all
354 cultivars is emerging. Indeed, in most cultivars, esca symptoms peak at an intermediate age. With

355 the exception of Merlot, all cultivars had an incidence of esca above the mean value for plots aged
356 between 10 and 40 years (in red, Figure 7). Conversely, the youngest plots (under 10 years old)
357 sown with these cultivars had an esca incidence below the mean value (in blue, Figure 7). Finally,
358 Cabernet Franc, Cabernet Sauvignon, Gewurztraminer, Merlot and Pinot Noir had incidences
359 significantly below the mean value after the age of 30 years. Overall, when age had a significant
360 positive effect on esca incidence (when esca prevalence > 0), esca occurred at ages between 9 and
361 45 years, with a peak of susceptibility between 9 and 24 years, depending on the cultivar (Figure
362 8). Even though the cultivars with the lowest incidence had a narrower age range for peak
363 incidence (Cabernet Franc, Cabernet Sauvignon, Chardonnay, Pinot Noir), a pattern remained in
364 the relationship between cultivar susceptibility (from left to right, according to modelling, Figures
365 6 and 8) and the age ranges for susceptibility to esca and peak incidence.

366

367 **IV) Discussion**

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

380 our case study, focusing on the prevalence of esca leaf symptoms is particularly relevant when
381 comparing a wide range of cultivars with different levels of susceptibility, including some for
382 which no leaf symptoms were reported on a large number of plots. Once the presence of leaf
383 symptoms is confirmed in a plot, analyses of the variation of incidence are then required to identify
384 the factors driving leaf symptom expression, as esca is characterised by fluctuating expression
385 between years and plots. This approach showed that since the incidence of esca leaf symptoms
386 was significantly higher than the mean value in six of the years since 2003, all occurring after
387 2012.

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

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

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

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

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

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

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

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

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

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

499

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Competing interests

The authors declare that they have no competing interests.

Data availability statement

We agree to archive an anonymized version of the trunk disease dataset in the public repository 'INRAE dataverse' if the manuscript is accepted.

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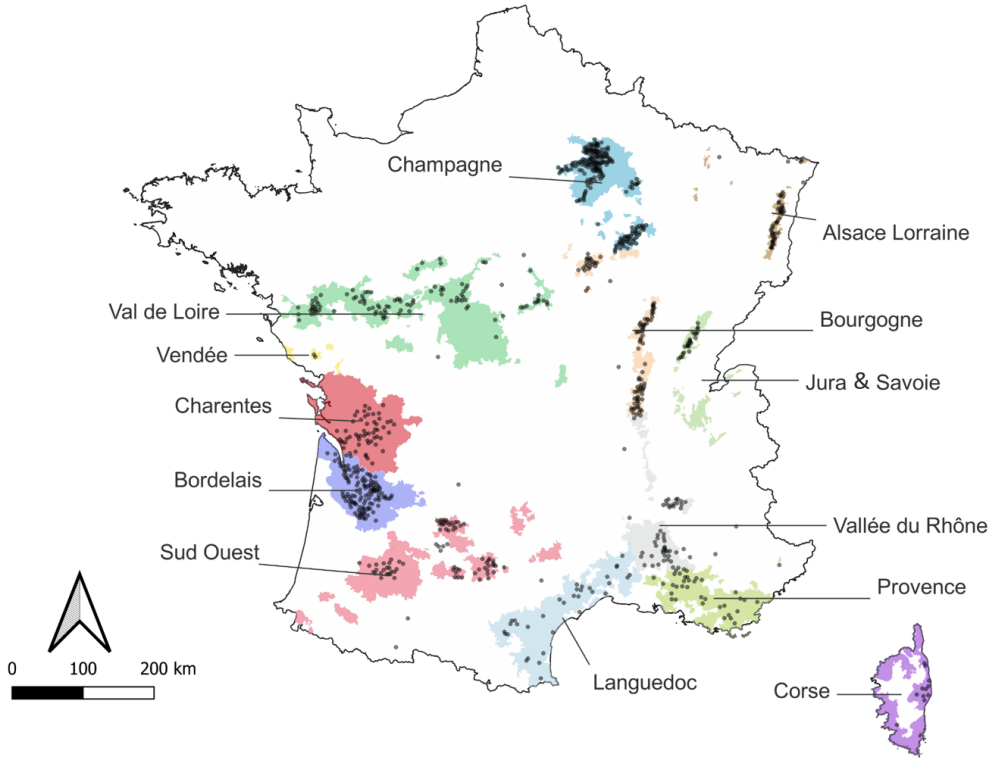
721 **Figures**



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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.

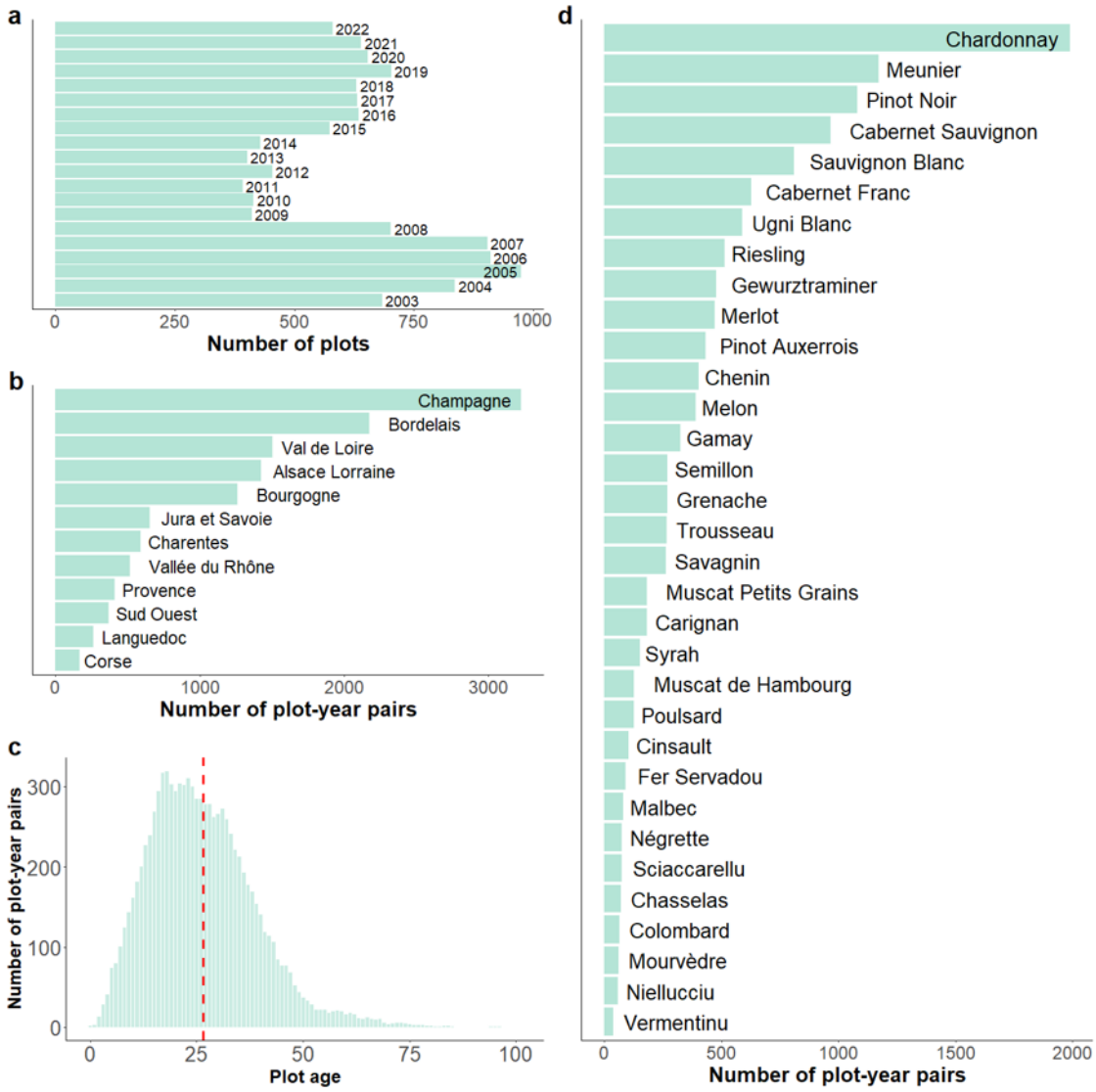

Figure 2: Number of plots or observations (plot-year pairs) monitored in France for grapevine trunk diseases between 2003 and 2022 and recorded in the database, by year (a), wine region (b), plot age (c), and *Vitis vinifera* cultivar (d). An observation corresponds to one plot monitored in a given year.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

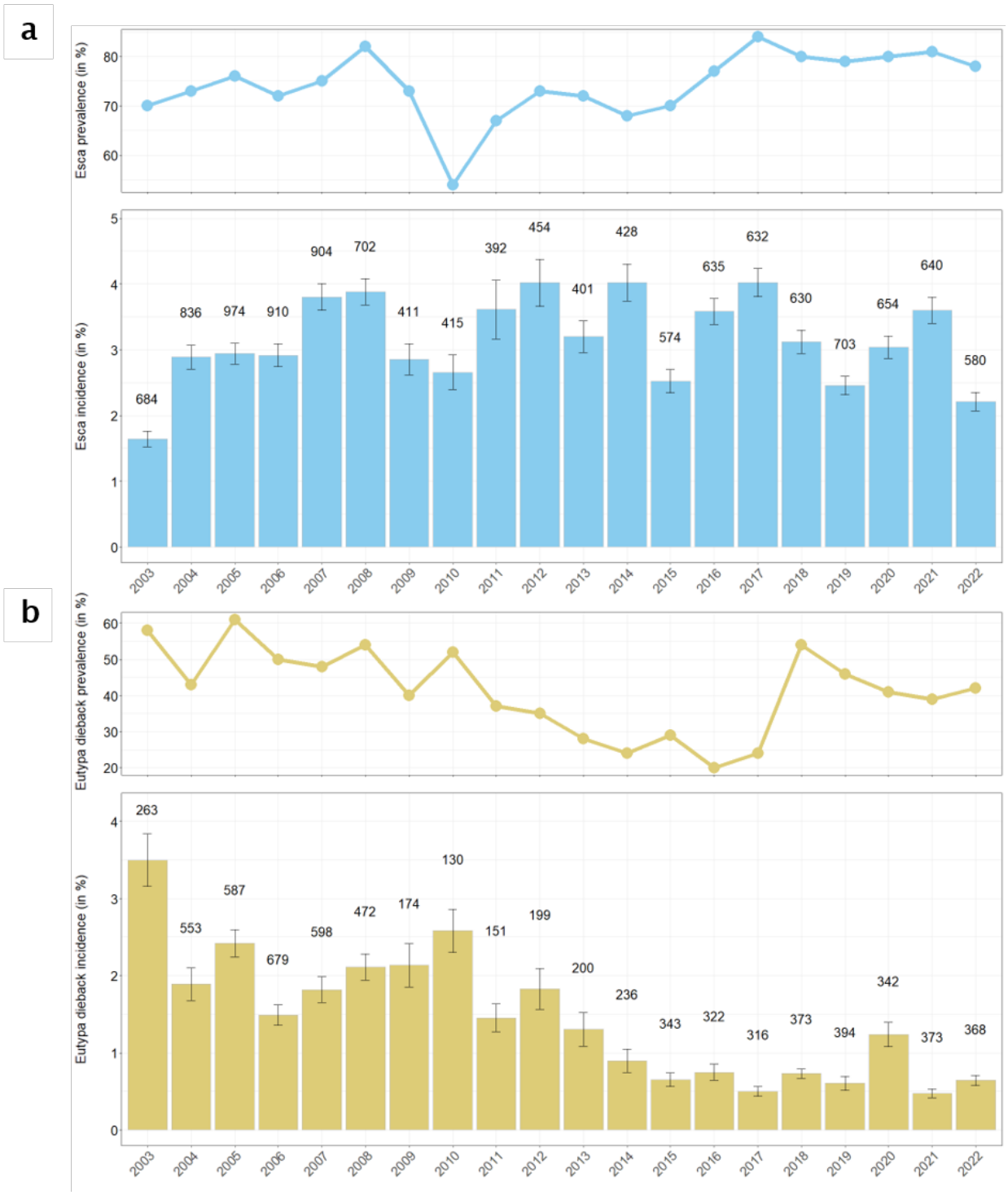

Figure 3: The mean prevalence and incidence of grapevine trunk diseases per year in France over the 2003-2022 period. The prevalence (shown as curves in the top panel) was determined as the number of plots with at least one symptomatic vine recorded per year. The incidence (represented by bar charts in the bottom panel) was determined as the percentage of symptomatic vines observed per plot each year. The numbers displayed correspond to the number of plots monitored for the

incidence of (a) esca (blue dots, lines and bars) and (b) Eutypa dieback (mustard dots, lines and bars). The error bars indicate the standard error of the mean.

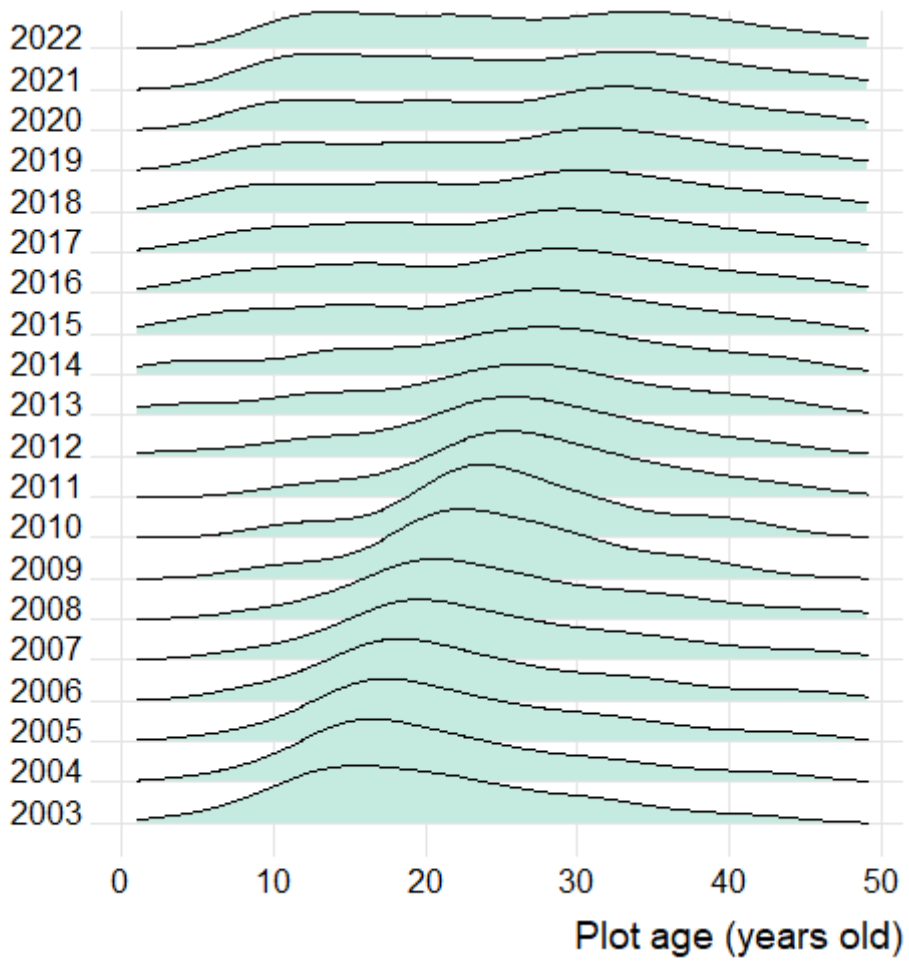

Figure 4: Distribution of plot age (range: 1 to 49 years) for each year for the 12 *V. vinifera* cultivars used in the modelling approach.

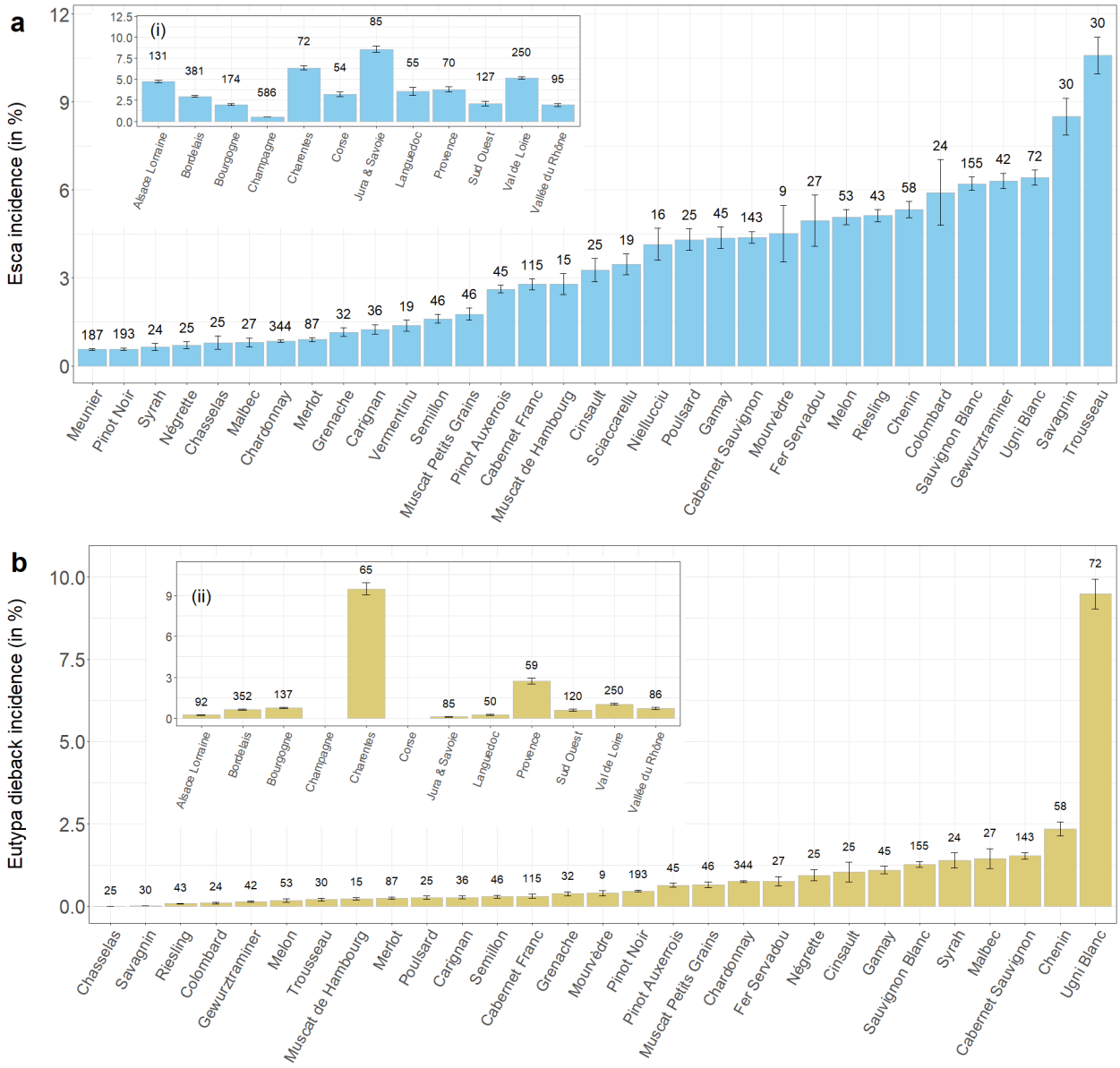

Figure 5: The mean incidence of grapevine trunk diseases by cultivar and wine region (inset, i : esca; ii : Eutypa dieback) in France over the 2003-2022 period. Numbers represent the number of plots monitored for the incidence of (a) esca (blue bars) and (b) Eutypa dieback (mustard bars). The error bars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

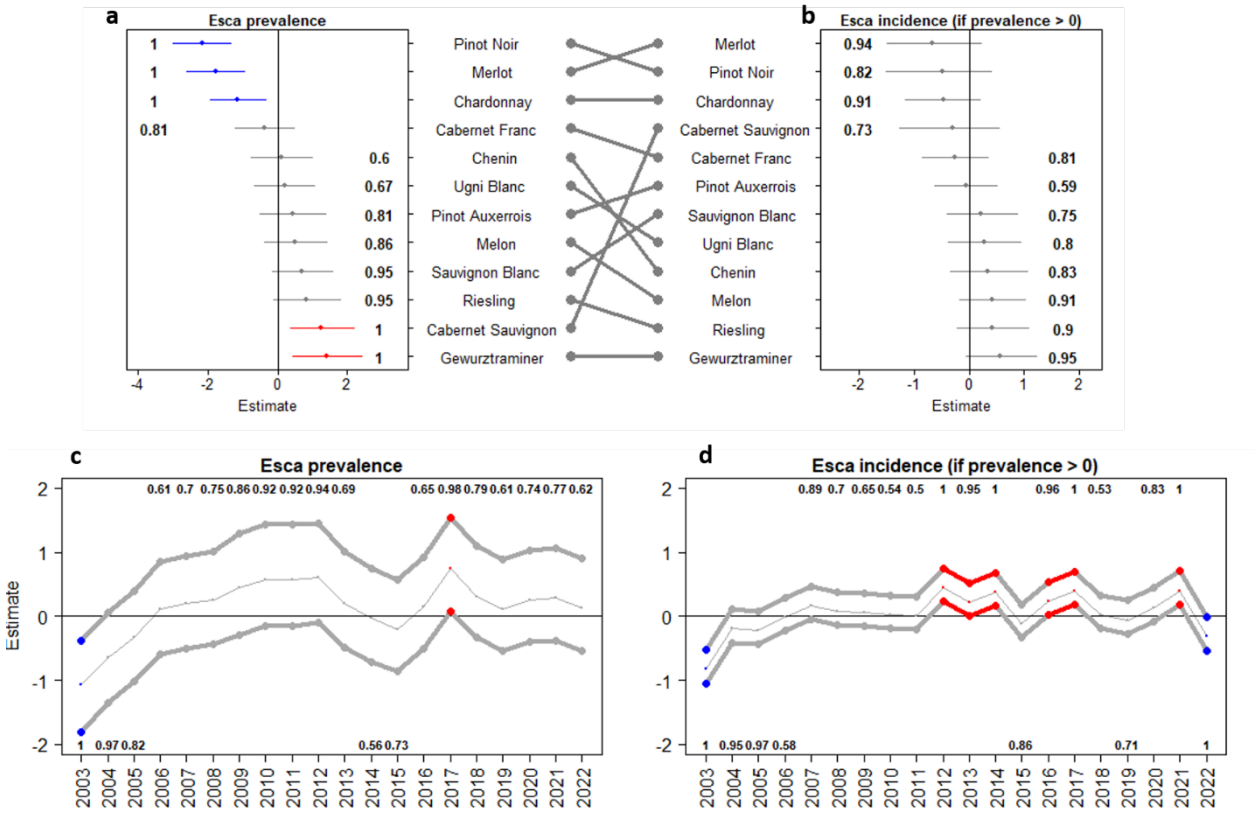

Figure 6: Effects of cultivar (upper panels, means in descending order) and year (lower panels) on esca prevalence (left panels) or esca incidence if esca was observed in the plot (right panels). In the upper panels, black points represent the posterior median (50th percentiles, middle) and vertical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

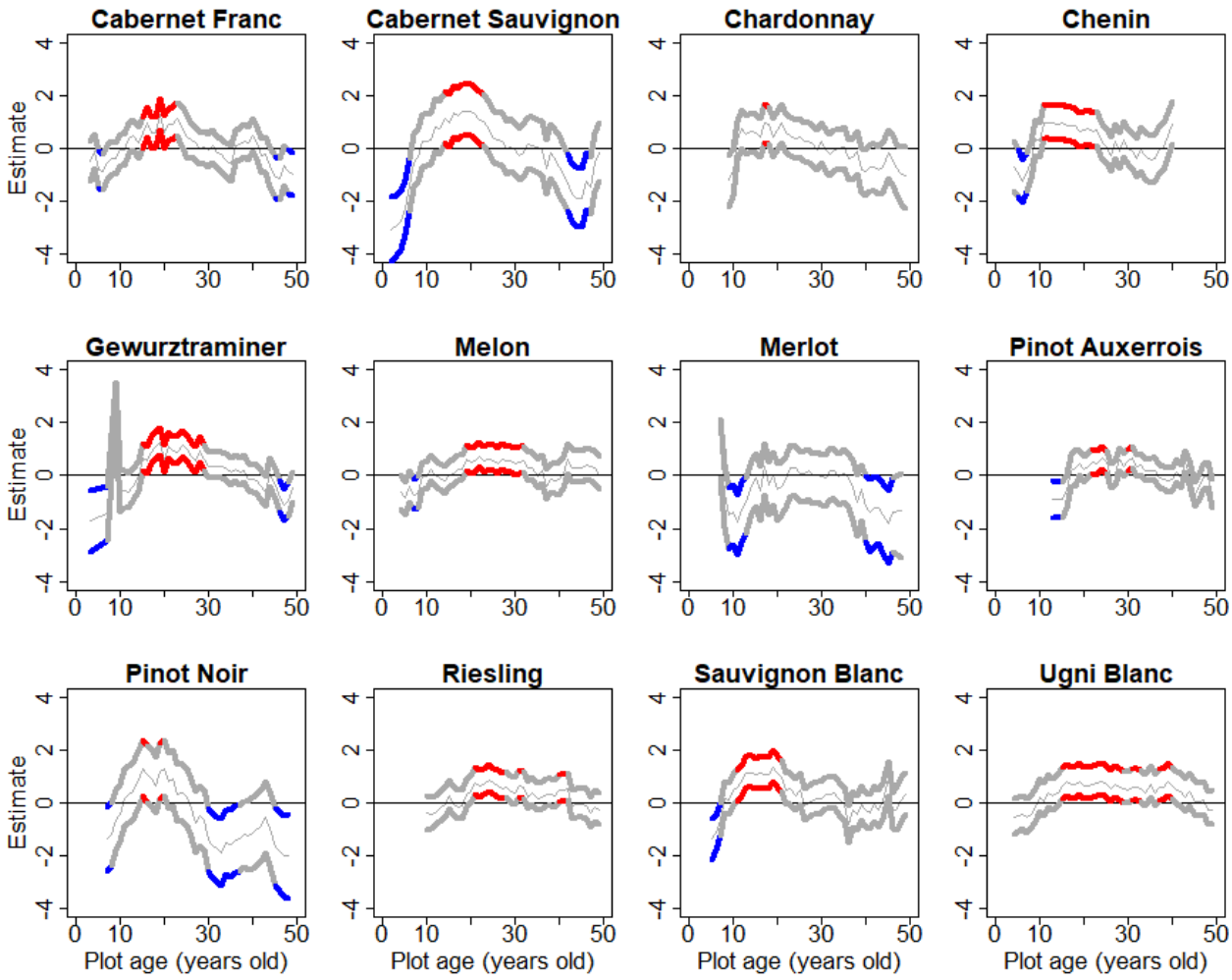

Figure 7: Impact of plot age (in years), by cultivar, on standardised estimates of the esca incidence for the plots in which esca was observed. The posterior median (50th percentiles, middle), lower (2.5th percentiles) and upper (97.5th percentiles) limits of the credible interval are shown. Estimates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

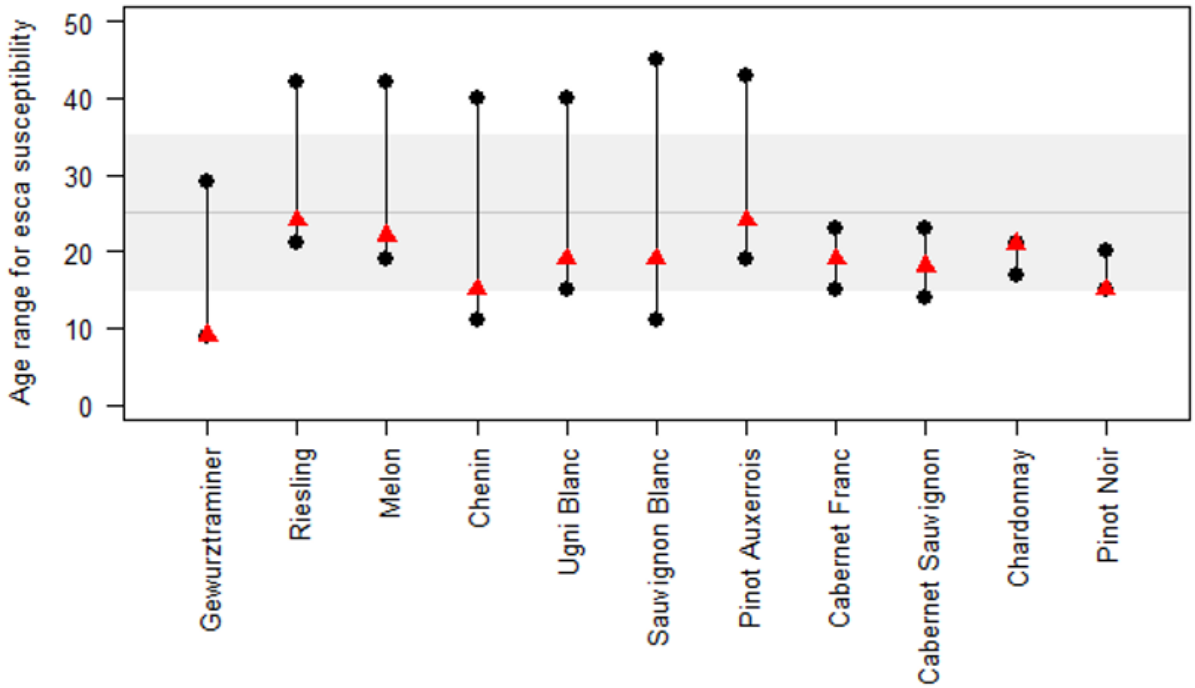

Figure 8: Range of ages during which vines are susceptible to esca (black points) and peak (red triangle) susceptibility for cultivars with significant and positive results between the first and the last plot age. The cultivars are ordered by estimated mean incidence and only cultivars with an age significantly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

794 **TABLES**

795 Table 1: Summary statistics for plot age and number of plots (total and per year) monitored for the
796 12 *Vitis vinifera* cultivars retained for statistical modelling. Maximum plot age was fixed at 49
797 years.

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

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Table 2: Deviance information criterion (DIC) and widely applicable information criterion (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

Table 3: Summary statistics for the parameters of the full model of the prevalence and incidence of esca leaf symptoms. For both model components (prevalence and incidence for plots with a prevalence of 1), the table summarises the posterior mean, standard deviation (SD), 0.025, 0.5, 0.975 quantiles (quant.) and mode for intercepts (β_0: intercept for esca prevalence; β_1: intercept for esca incidence), the number of vines monitored (μ_0), the variance of the independent random effects associated with cultivars and plots ($\sigma^2_{cultivar0}$, $\sigma^2_{cultivar1}$, σ^2_{plot0} *and* σ^2_{plot1}), the correlation coefficients and variance of the AR1 process associated with year (ρ_{year0} and ρ_{year1}) and the correlation coefficients and variance of the AR1 process associated with age for each cultivar ($\rho_{age1,cultivar}$ and $\sigma^2_{age1,cultivar}$ to be detailed).

	Mean	SD	0.025quant.	0.5quant.	0.975quant.	Mode
Esca prevalence						
β_0	2.75	0.47	1.83	2.75	3.69	2.74
μ_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
σ^2_{plot0}	0.36	0.04	0.29	0.36	0.44	0.36
ρ_{year0}	0.64	0.16	0.25	0.67	0.89	0.72
σ^2_{year0}	5.11	2.40	1.84	4.65	11.08	3.82
Esca incidence (when prevalence > 0)						
β_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
σ^2_{plot1}	1.25	0.09	1.09	1.25	1.43	1.25
ρ_{year1}	0.30	0.24	-0.20	0.32	0.71	0.36
σ^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