A compartmental model for Xylella fastidiosa diseases with explicit vector seasonal dynamics

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The bacterium *Xylella fastidiosa* (Xf) is mainly transmitted by the meadow spittlebug *Philaenus spumarius* in Europe, where it has caused significant economic damage to olive and almond trees. Understanding the factors that determine disease dynamics in pathosystems that share similarities can help to design control strategies focused on minimizing transmission chains.
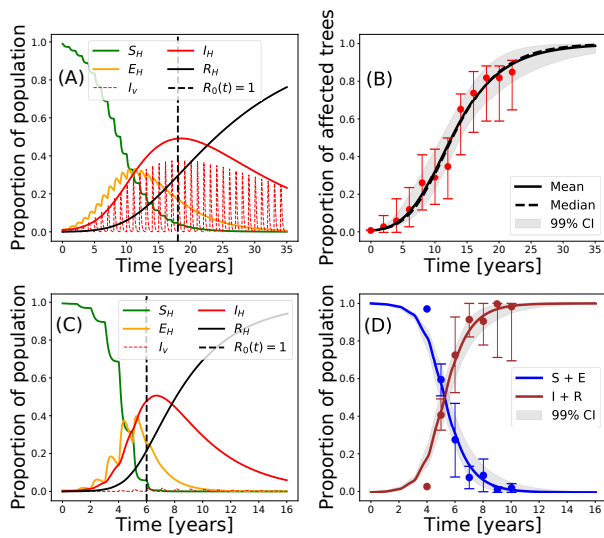

Fig. 1. (A) Simulation of the model with the best-fit parameters for ALSD. (B) Model fit to field data by means of the mean and median values of the posterior distributions of the parameters for ALSD. (C) Simulation of the model with the best-fit parameters for OQDS. (D) Model fit to field data by means of the mean and median values of the posterior distributions of the parameters for OQDS. The gray-shaded area corresponds to the 99% confidence interval. The error bars for the field data correspond to their 95% confidence interval obtained with a bootstrapping technique.

Several epidemic models have been already developed for Xf-diseases, but they lack a realistic description of some relevant processes [1]. Some of these models assume a simple general form for infected host dynamics or use a simplified S-I compartmental scheme for hosts, disregarding important features such as the latent period or the host mortality rate. Models that do take these features into account, however, do not explicitly model the population of vectors responsible for disease transmission [2]. Other more recent models have taken a step further in explicitly modeling the vector popu-

lation [3], but the characterization of its dynamics is still relatively simple, as it overlooks the known seasonal patterns of vector abundance. Several recent studies have provided new insights into the ecology and temporal dynamics of the transmission of Xf by *P. spumarius* in olive plants. However, these experimental data of the pathosystem have not been yet integrated at the population level . Thus, there is a need to continue advancing in the modeling of Xf diseases by developing more realistic models that can elucidate the fundamental processes involved in vector-host-pathogen interactions and help to design effective control strategies.

Here we introduce a compartmental model for Xf-caused diseases in Europe that accounts for the main relevant epidemiological processes, including the seasonal dynamics of *P. spumarius* [4, 5]. The model was confronted with epidemiological data from the two major outbreaks of Xf in Europe, the olive quick disease syndrome (OQDS) in Apulia, Italy, caused by the subspecies *pauca*, and the almond leaf scorch disease (ALSD) in Mallorca, Spain, caused by subspecies *multiplex* and *fastidiosa*. Using a Bayesian inference framework, we show how the model successfully reproduces the general field data in both diseases (Fig. 1). In a global sensitivity analysis, the vector-to-plant and plant-to-vector transmission rates, together with the vector removal rate, were the most influential parameters in determining the time of the infectious host population peak, the incidence peak and the final number of dead hosts. We also used our model to check different vector-based control strategies, showing that a joint strategy focused on increasing the rate of vector removal while lowering the number of annual newborn vectors is optimal for disease control.

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