

Degree-day-based model to predict egg hatching of *Philaenus spumarius*, the main vector of the bacterium *Xylella fastidiosa* in Europe

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The meadow spittlebug *Philaenus spumarius*, with a body length of 5-7 mm, is a polyphagous insect belonging to the spittlebug family *Aphrophoridae* that is the main vector transmission in Europe of the diseases induced by the bacterium *Xylella fastidiosa*. Among them one can mention the Olive Quick Syndrome Disease (OQSD) that has devastated the olive tree plantations in Apulia (Italy), the Almond Leaf Scorch Disease (ALSD) that devastated almond-tree plantations in Mallorca and Alicante, and Pierce's Disease that is a threat to Mediterranean European vineyards.

P. spumarius is a univoltine species that overwinters in the egg stage, with its nymphs emerging in late winter or spring. Predicting the time of egg hatching is essential for determining the precise times for deploying control strategies against insect pests, and in our case it is the most effective strategy to manage the diseases produced by *X. fastidiosa*. In this work we have built a tool to forecast egg hatching in the Iberian Peninsula through a growing degree-day (GDD) model. In order to fit the model we monitored eggs from oviposition to egg hatching, together with environmental conditions, at four field locations that were located at different altitudes in

central Spain.

The model was then used as a decision-support tool to calculate the optimum timing for applying control actions against *P. spumarius*. So we simulated controls at different times and our results [1] suggest that controlling nymphs at two different dates would target the highest percentages of nymphal populations present in the field. The predictions of the model can be checked in an easy way in this web page [2], that implements the GDD model using semihourly temperature data from Aemet stations. Our model represents a first step for predicting the emergence of nymphs and adopting timely control actions against *P. spumarius*. These actions could limit disease spread in areas where *X. fastidiosa* is present.

[1] C. Lago, À. Giménez-Romero, M. Morente, M.A. Matías, A. Moreno, and A. Fereres, *Environmental Entomology*, nvad013 (2023). <https://doi.org/10.1093/ee/nvad013>

[2] <http://pseggs.ifisc.uib-csic.es/>