ARPHA Conference Abstracts 9: e203363
doi: 10.3897/aca.9.e203363

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Conference Abstract

Integrated assessment for evaluating the areas at risk of infection by *Xylella fastidiosa* in the Iberian Peninsula

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Received: 09 Jun 2026 | Published: 09 Jun 2026

Citation: Gonzalez-Moreno P, Galan-Diaz J, Hernandez-Lambraño R, Vilà M (2026) Integrated assessment for evaluating the areas at risk of infection by *Xylella fastidiosa* in the Iberian Peninsula. ARPHA Conference Abstracts 9: e203363. https://doi.org/10.3897/aca.9.e203363

Abstract

The spread of certain economically important agricultural pathogens depends on complex biotic interactions with dispersal vectors and several host plant species. Therefore, evaluating the areas at risk of infection requires considering all interacting species at play. The bacterium *Xylella fastidiosa* (*Xf*) is one of the most threatening plant pathogens in the world. In the Iberian Peninsula, where it has already infested important fruit crops such as olive and almond plantations, *Xf* is dispersed by two polyphagous spittlebugs that can feed on 161 plant species reported to be infected by the pathogen. The aim of this study is to map high-risk areas prone to *Xf* infection for targeted prevention measures by considering the spatial explicit distribution of the pathogen, its vectors, susceptible crops and wild plant hosts.

We used bioclimatic, soil and land cover data to model the potential distribution of *Xf* vectors and hosts (both crop and wild plant species) in the Iberian Peninsula and the Balearic Archipelago. Then, we integrated these results with *Xf* climatic suitability, the

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distribution of susceptible crops, transport networks and garden center data to identify areas highly vulnerable to *Xf* infection. We also evaluated how infection prevalence and *Xf* subspecies-host relationships affect the spatial variation in habitat vulnerability.

Two regions of the Iberian Peninsula emerged as most vulnerable to *Xf* infection. On the one hand, the Balearic Archipelago and East of Spain appeared as highly vulnerable due to the high environmental suitability for *Xf* and its plant hosts, which are spatially intermingled with susceptible fruit crops such as almond trees. On the other hand, the SW of the Iberian Peninsula was also at high risk due to strong environmental suitability for *Xf* and its vectors , which indicates high potential of natural spread. Host range diversity influenced the distribution of areas of high risk of infection.

Our spatial analysis delivers an integrated framework useful for spatial surveillance aimed at identifying areas at high risk of infection by plant pathogens dispersed by insects. S patially explicit risk assessments of complex pathosystems, need to address the interactions between n ative plant communities and vulnerable crops with their vectors, as well as the overlap among areas able to host multiple pathogen strains.

Keywords

agricultural biosecurity, plant pathology, risk assessment, species distribution models, *Xylella fastidiosa*, vector-borne diseases

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Presented at

Neobiota 2026, the 14th International Conference on Biological Invasions

Grant title

BeXyl project (grant ID 101060593) EU-Horizon Europe

Conflicts of interest

The authors have declared that no competing interests exist.