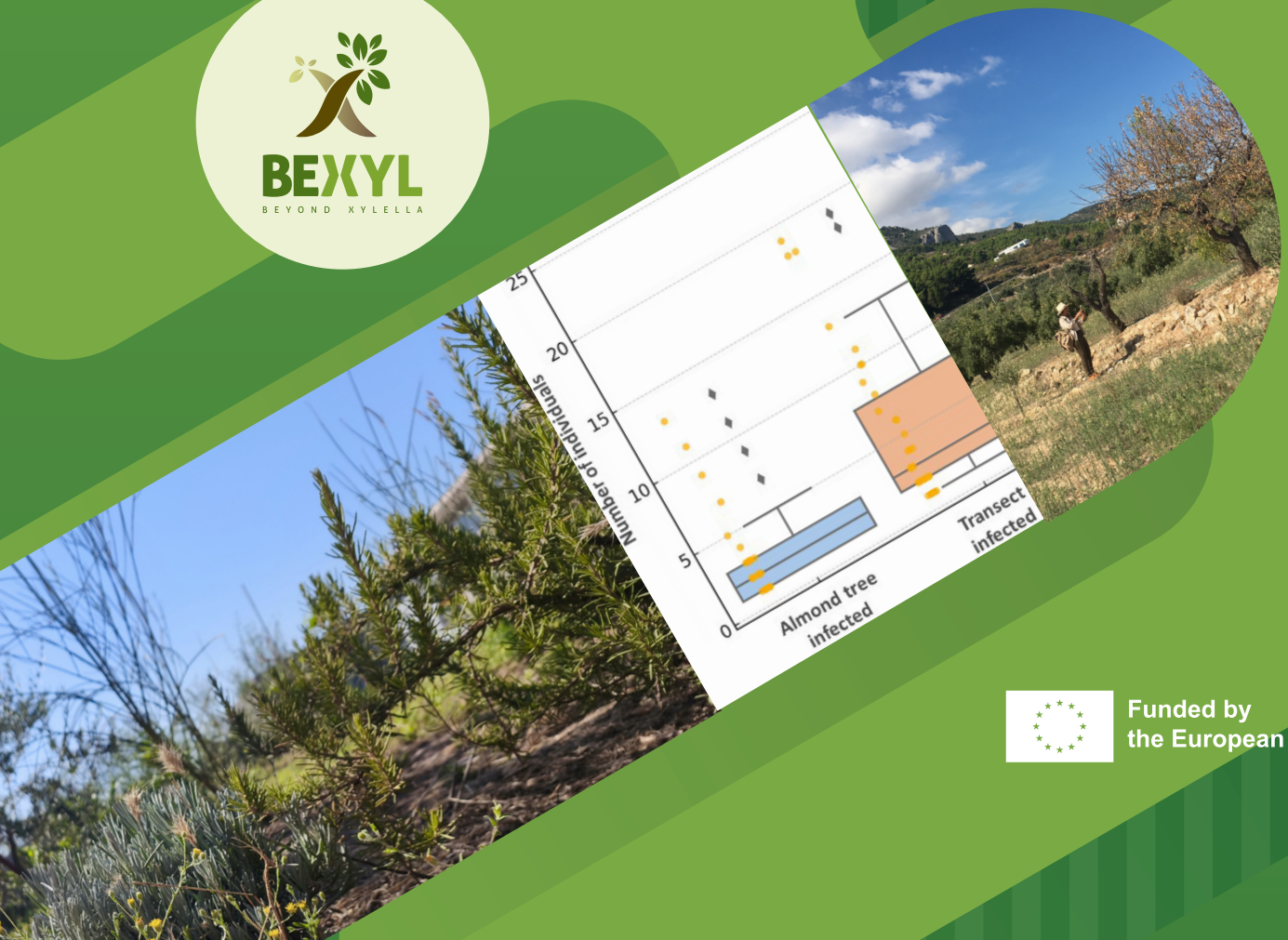
Beyond *Xylella*, Integrated Management Strategies for Mitigating *Xylella fastidiosa* impact in Europe

Practice abstract 13

Integrated spatial assessment of *Xylella fastidiosa* infection in the Iberian Peninsula

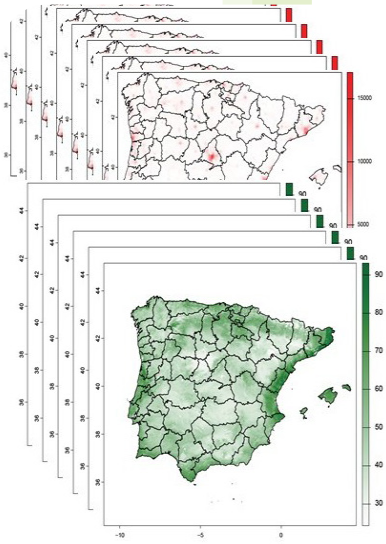
BEXYL
BEYOND XYLELLA



Funded by the European Union

Integrated spatial assessment of *Xylella fastidiosa* infection in the Iberian Peninsula

The **BeXyl** project addresses the urgent need to identify the most susceptible areas to be infected by the bacterium ***Xylella fastidiosa*** across Spain and Portugal, where it has already infested important fruit crops such as olive and almond plantations. ***X. fastidiosa*** is dispersed by two polyphagous spittlebugs that feed on 161 plant species reported to be infected by the pathogen. The aim of **BeXyl** is to map high-risk areas prone to infection for targeted prevention measures by considering the spatial explicit distribution of the pathogen, its vectors, susceptible crops and wild plant hosts.



How will BeXyl make a difference?

To identify areas highly vulnerable to ***X. fastidiosa*** infection in the Iberian Peninsula and the Balearic Archipelago, **BeXyl** will use bioclimatic, soil and land cover data to model the potential distribution of ***X. fastidiosa***, its two main vectors, ***Neophilaenus campestris*** and ***Philaenus spumarius*** (Hemiptera: *Aphrophoridae*) and hosts (both crop and wild plant species).

Then, we will integrate these results with ***X. fastidiosa*** climatic suitability, the distribution of susceptible crops, transport networks and garden center data as facilitators of the pathogen spread. We will also evaluate how infection prevalence and ***X. fastidiosa*** subspecies-host relationships affect the spatial variation in habitat vulnerability.

Impact: BeXyl will deliver an integrated framework useful for spatial surveillance aimed at identifying areas at high risk of infection by *X. fastidiosa*. Our approach can be applied to spatially explicit risk assessments of complex pathosystems, which need to address the interactions between native plant communities, vulnerable crops, and their vectors, as well as the overlap among areas able to host multiple pathogen strains.

Funded by the European Union