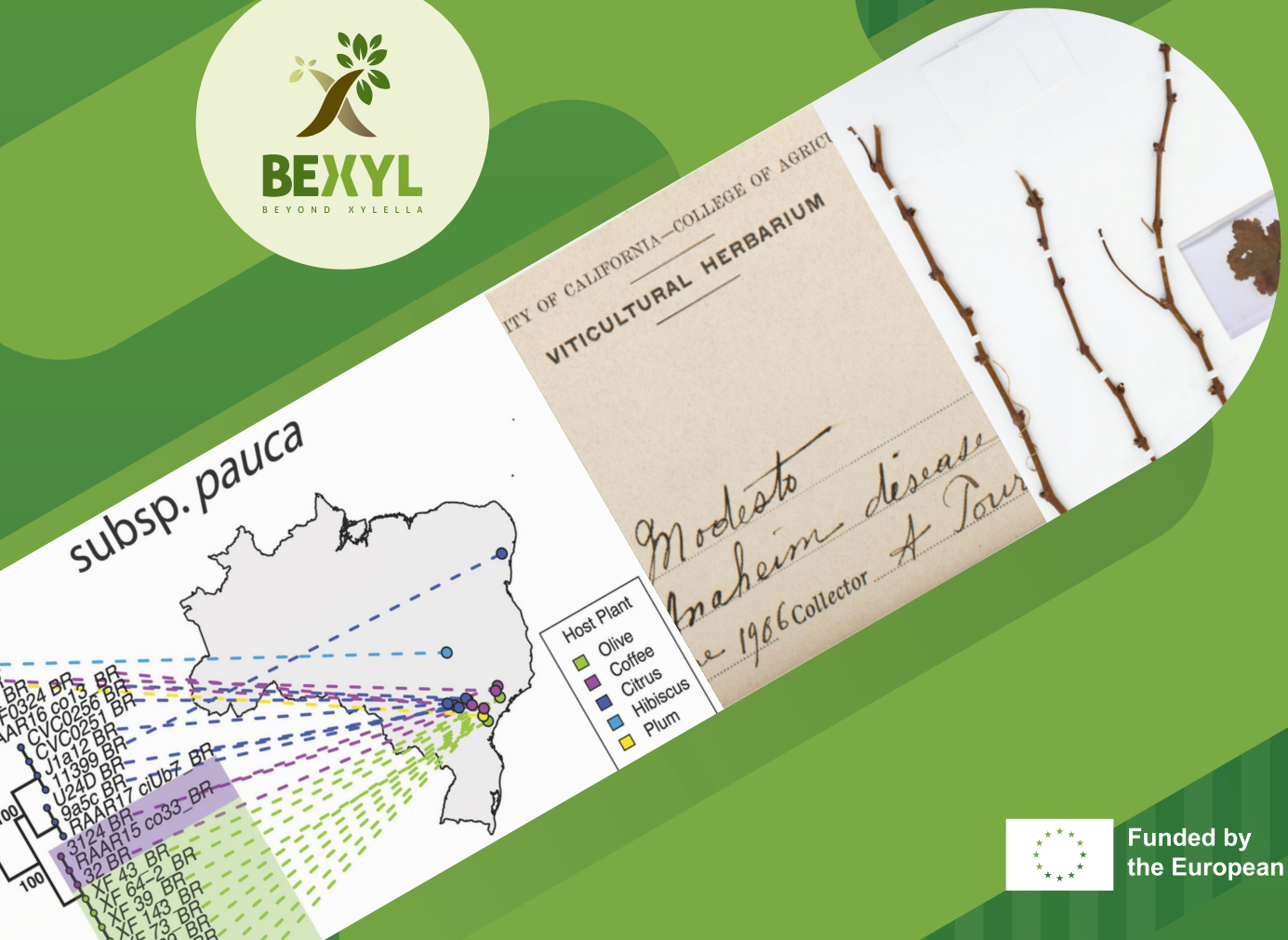
Beyond *Xylella*, Integrated Management Strategies for Mitigating *Xylella fastidiosa* impact in Europe

Practice abstract 7

Reconstructing the spread and host adaptation of *Xylella fastidiosa*

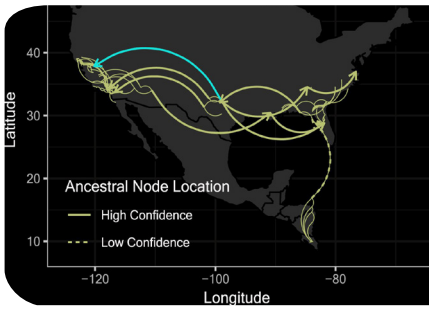
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Reconstructing the spread and host adaptation of *Xylella fastidiosa*

The repeated movement of plant pathogens across geographic boundaries has created opportunities for host jumps, driving the emergence of novel plant diseases worldwide. The **BeXyl project** focuses on ***Xylella fastidiosa***, a highly diverse bacterial pathogen capable of infecting hundreds of plant species and causing severe agricultural impacts. By combining population genomics, historical DNA, and comparative analyses across multiple host shifts, we investigated how introduction events and evolutionary processes shape **host adaptation** and **disease emergence**.



How will BeXyl make a difference?

Objective: We intend to understand the genetic and evolutionary mechanisms underlying plant host shifts and geographic spread in ***Xylella fastidiosa***. This included reconstructing the timing and routes of pathogen introduction, determining whether host jumps are accompanied by adaptive genetic changes, and assessing whether similar host shifts arise through convergent or independent evolutionary pathways. Collectively, our work links historical invasion events with contemporary patterns of disease emergence.

Outcomes: Selected Comparative population genomics identified genes and small genetic changes (SNPs) associated with host shifts, including adaptation to grapevine in the U.S.A. and independent shifts of the bacterium from coffee to olive in Brazil and Italy. Sequencing of a **1906 herbarium specimen** enabled time-calibrated phylogenetic analyses, placing the initial introduction of ***Xylella fastidiosa*** into the U.S.A. in the early 18th century and supporting a single Central American origin followed by regional spread. Notably, parallel olive host shifts in Italy and Brazil occurred through distinct, non-convergent genetic changes, highlighting multiple evolutionary routes to host specialization.

BeXyl work advances understanding of how *Xylella fastidiosa* adapts to new plant hosts following introduction into novel environments. By revealing that similar disease outcomes can arise through independent genetic solutions, the findings challenge assumptions about predictability in pathogen evolution. The integration of historical specimens with modern genomics provides a powerful framework for resolving long-standing questions about disease origins and spread. Overall, these insights inform plant biosecurity efforts and improve our ability to anticipate and manage emerging plant diseases in an increasingly connected world.

For more specialized information, see: Donegan et al. (2023), Donegan et al. (2024) and Kahn et al. (2025).

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