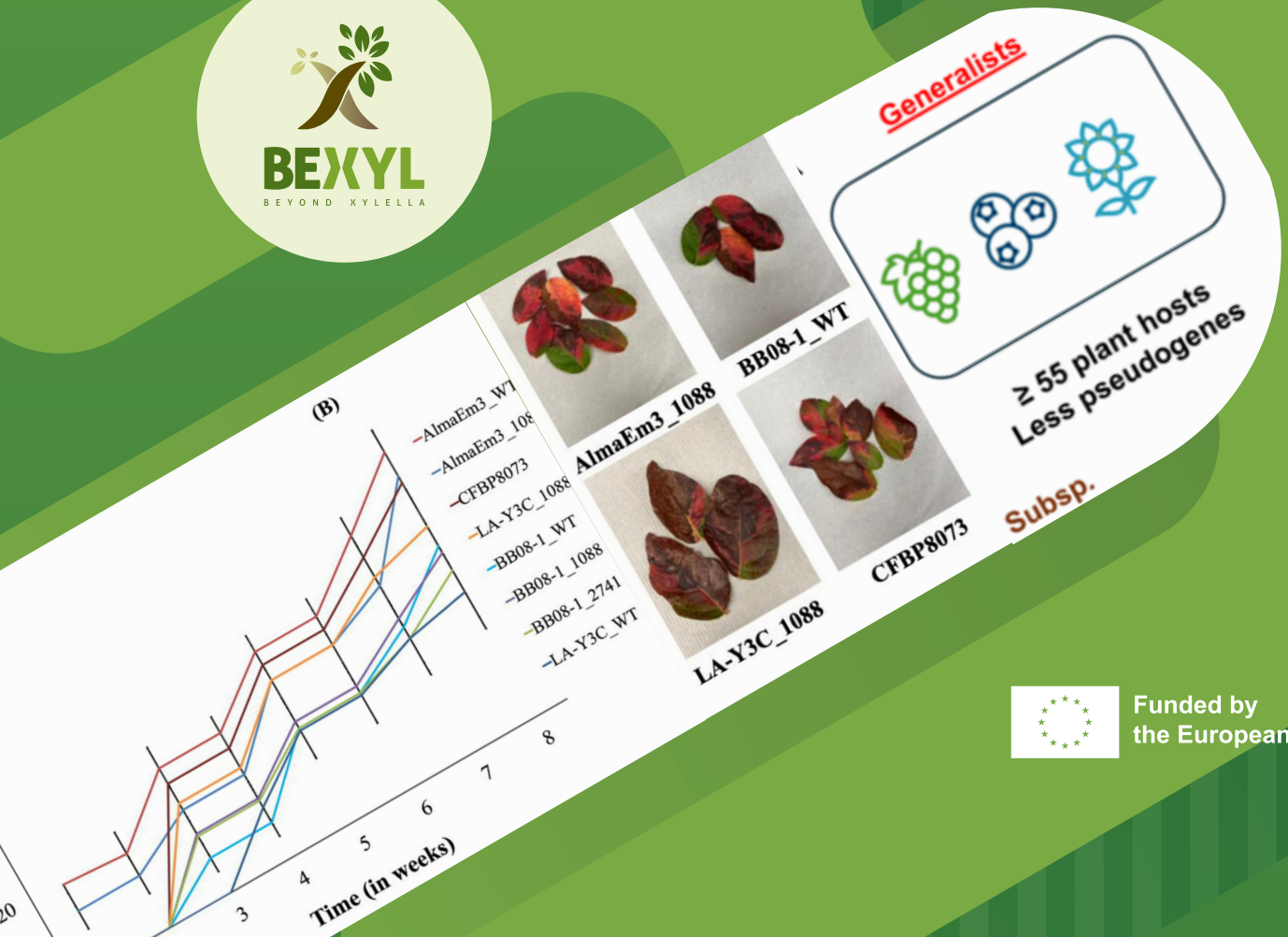
Beyond *Xylella*, Integrated Management Strategies for Mitigating *Xylella fastidiosa* impact in Europe

Practice abstract 12

What makes *Xylella fastidiosa* strains prefer some hosts and not others?

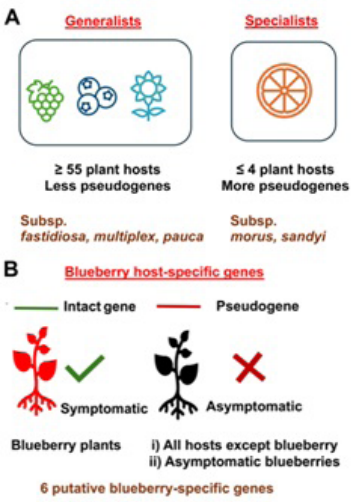


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What makes *Xylella fastidiosa* strains prefer some hosts and not others?

Although ***Xylella fastidiosa*** as a species can infect more than 700 plant species, observations over the years showed that specific strains of ***X. fastidiosa*** usually prefer one or a few plant hosts. The molecular basis of why a particular strain can cause disease in some plant hosts and not others remain unknown. This is very important to understand the risk posed by a new strain introduction in a specific region.

Assessing the host range of a strain is difficult since the evaluation of virulence in different hosts is laborious and takes long time. Therefore, we used bioinformatic analysis to gain knowledge on host specificity. For this study we focused on ***X. fastidiosa*** diseases in southern highbush blueberries that are very impactful in the southern US but have not been detected in Europe, where blueberry industry is growing.



Objective

We used different comparative genomics approaches and analysis of "junk" DNA (pseudogenes) to understand the basis of host selection in ***X. fastidiosa***. Bioinformatic analyses were complemented by experiments in the greenhouse to test virulence in blueberry and other hosts by specific ***X. fastidiosa*** strains isolated in Europe and the USA.

Research outcomes

We identified DNA regions in ***X. fastidiosa*** that could explain the preference for blueberries. By removing some of these genes we were able to show that they can influence the infection process. Moreover, based on the amount of junk DNA of a strain and comparison to the number of hosts they can infect, we were able to classify ***X. fastidiosa*** subspecies into either generalist (subsp. ***fastidiosa, multiplex*** and ***pauca***) or specialists (subsp. ***morus*** and ***sandyi***), suggesting the potential for host jumps.

Impact: Identifying gene(s) responsible for host specificity will improve surveys and inform potential for infection depending on the pathogen populations established in an area.

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