



Introduction and adaptation of an emerging pathogen to olive trees in Italy

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The invasive plant pathogen *Xylella fastidiosa* currently threatens European flora through the loss of economically and culturally important host plants. Previously absent from Europe, and considered a quarantine pathogen, *X. fastidiosa* was first detected in Apulia, Italy in 2013 associated with a devastating disease of olive trees. Although the biology of *X. fastidiosa* has been studied for over a century, there is still no information on the determinants of specificity between bacterial genotypes and host plant species, which is particularly relevant today as *X. fastidiosa* is expanding in the naïve European landscape. We analyzed the genomes of 79 *X. fastidiosa* samples from diseased olive trees across the affected area in Italy as well as genomes of the most genetically closely related strains from Central America. We provided insights into the ecological and evolutionary emergence of this pathogen in Italy. We showed the pathogen was recently introduced, and we generated a list of candidate genes that could play a major role in the adaptation of *X. fastidiosa* to new environments.

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