
Using genomic approach to assess phage therapy against the plant pest *Xylella fastidiosa*

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Résumé

Xylella fastidiosa is a Gram-negative plant-pathogenic bacterium emerging in Asia and Europe. Long-known in the Americas, this xylem-limited bacterium is associated with several socio-economically important plant diseases and it is transmitted by xylem-feeding insects. Nowadays, *X. fastidiosa* has been introduced in various places of the Mediterranean regions probably through commercial exchanges (Jacques et al. 2016). Listed as a quarantine pest in Europe, three subspecies of *X. fastidiosa* were recently detected in Europe. First, the subspecies *pauca*, the causal agent of Citrus Variegated Chlorosis (CVC) affecting Citrus and Coffee trees in the USA, has been associated with the Leaf Scorch of Olive trees in Italy since 2013. Another strain from this subspecies was also recently detected in Mallorca, Spain. *X. fastidiosa* subsp. *multiplex*, including strains causing diseases in Oleander and Polygala, has been detected in the south of France and in Corsica (2015) and in Spain (2016). And, finally, the subspecies *fastidiosa*, the causal agent of the Pierce's disease on Grapevines in the USA, was detected on oleander in Germany and in Sweet Cherry plants in Spain (2016).

Bacteria frequently acquire new genes and functions through horizontal gene transfer. We are particularly interested by integrated forms of temperate phages, since in many cases prophages contribute to the host fitness and physiology, as well as to bacterial virulence (Fortier et al., 2013). Prophages are also involved in various mechanisms behind resistance to infection by other phages, which is an obvious disadvantage considering phages as biocontrol agents (Bondy-Denomy et al., 2016). Interestingly, despite their relative small sized-genomes, *X. fastidiosa* species host numerous prophages suggesting the latter may contribute to the host physiology (Varani et al. 2013).

*Intervenant

Important goals of our project are: (i) to identify prophages genes in *X. fastidiosa* genomes; (ii) to make a link between prophages and host range specificity of virulent phages, and (iii) to determine phage contribution to strain subsets emergence. Using a bioinformatics approach, we analyzed 39 genomes from six subspecies (*pauca*, *multiplex*, *fastidiosa*, *sandyi* and *morus*) representing at best the know diversity of *X. fastidiosa*. With this genomic approach we hope to bring some light in the understanding of the contribution of integrated-phage genomes in the fitness and pathogenicity of *X. fastidiosa*.