



Detection of recombination events in *Xylella fastidiosa* genomes of different Spanish strains

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Xylella fastidiosa (Xf) has the capacity of uptaking extracellular DNA from the environment and incorporate it into its genome by homologous recombination, process known as Natural Competence. The process of genetic acquisition and recombination of extracellular DNA could be related to the acquisition of new traits such as antibiotic resistance and virulence factors, giving rise to the origin of new pathotypes. We took a step forward in comparative genomics analysis of Spanish populations of Xf by determining the complete genome of several isolates from Alicante, Mallorca and Ibiza and established potential recombination events that may have occurred with isolates from other places in the world. For this purpose, we used combined Illumina and Oxford Nanopore sequencing platforms and combined assembly approaches to obtain complete circularized genomes. Our results showed that olive and almond isolates belonging to subspecies *pauca* ST80 from Ibiza (Balearic Islands), the only place where this ST has been detected, showed an unusual level of recombination, being so far the isolates showing the highest number of recombination events among all the Xf isolates sequenced to date. On the other hand, we have confirmed the high degree of homology among genomes from Xf strains from Mallorca and California belonging to subspecies *fastidiosa* ST1 and subspecies *multiplex* ST81 isolated from almond and grapes, and we have also identified specific long-size genomic rearrangements in isolates of Xf subspecies *multiplex* ST6 from Alicante, compared to their homologous strains from the Americas. Research is now underway to determine the source and the functionality of these recombinant genes and their role in pathogenicity.

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