a shotgun metagenomic DNA sequencing approach that avoids the limitations of amplicon sequencing. Data obtained (28,333,924 and 29,096,610 reads from *Xf*-infected and healthy plants) were analyzed by MetaPhlAn, a metagenomic abundance estimation tool which maps reads to a set of selected marker sequences. Libraries from xylem tissues revealed a complex community in which small symbiotic bacteria of insects, i.e. *Candidatus* Zinderia insecticola and *Candidatus* Carsonella ruddii represented the 31% and 22% of the total population. *Xf* reaches in infected plants the 12% of the total microbial community. Studies are ongoing to characterize the microbial communities in the xylem sap of tolerant and susceptible olive cultivars, to envisage a control strategy based on the manipulation of these resident communities and to identify endosymbiont(s) which may be used to reduce the severity of symptoms. To this end, the evaluation of an endosymbiont bacterium for its potential to colonize *Xf*-infected olive tissues is underway.

RAPID SCREENING TESTS FOR DIFFERENTIATING *XYLELLA FASTIDIOSA* ISOLATES.

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The bacterial pathogen *Xylella fastidiosa* (*Xf*) is characterized by a wide plant host range and insect vectors, and on the basis of phylogenetic studies it was subdivided into different subspecies. Results from strain typing, phylogenetic analyses, and other data comparisons have shown that phylogenetic clusters exhibit host-based genetic relationships. Until now, different molecular tests can be used for the differentiation of *Xf* isolates, among which MLST/MLSA represents the most common method to determine classification and phylogenetic placement of novel isolates. *Xf* outbreaks in EU motivated the search for accurate and faster approaches for detection and identification of the bacterium in different plant matrices. Because MLST/MLSA requires several PCR reactions and sequencing analyses, we have developed two independent approaches for rapid taxonomic assignment of uncharacterized isolates: (1) single-nucleotide primer extension (SNuPE) method for the multiplex amplification of six *Xylella* DNA sequences (targeting all subspecies and three genotypes within *Xf* subsp. *pauca* including the type-isolate infecting olive in Italy); (2) high-resolution melting analysis of the amplicon recovered from the gene encoding the conserved HL protein. Both assays proved to clearly differentiate *Xf* isolates currently known to occur in the Italian and France outbreaks. Indeed, validation on a larger panel of isolates covering the different subspecies consistently allowed to rapidly differentiate the isolates in different clusters. In conclusion, these approaches represent a useful tool for pre-screening and selection of infected samples to be further analyzed by MLST or whole genome sequencing.

TRANSMISSION OF *XYLELLA FASTIDIOSA* TO DIFFERENT HOST PLANTS BY NATURALLY INFECTED *PHILAENUS SPUMARIUS*.

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The meadow spittlebug *Philaenus spumarius* (Hemiptera, Aphrophoridae) has been identified as a vector of *Xylella fastidiosa* (*Xf*) in southern Italy where the bacterium has established in the Salentinian Peninsula. This species is one of the most common potential vectors in Europe, but limited information is available on spittlebugs as vectors of *Xf*. In this work, eleven transmission experiments were performed in 2015 from late spring to late autumn, when adult spittlebugs were present in the *Xf*-infected olive groves. Insects were collected by sweeping net on the olive canopies of two selected *Xf*-infected olive groves and transferred in groups of five on to the following recipient plants: olive, oleander, citrus, grapevine, GF677 (*Prunus persica* x *Prunus amygdalus*) and periwinkle. Following an inoculation access period (IAP) of 7-days, the insects were recovered from the cages in order to estimate i) the survival rates ii) the presence of *Xf* by real-time qPCR in single insects. Transmissions were determined by testing with qPCR the recipient plants. The results showed that the proportion