

***Xylella fastidiosa* and olive: the complex host-pathogen-microbiota interactions**

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Since the mid-19th century *Xylella fastidiosa* (*Xf*) has been extensively documented as a harmful pathogen threatening important crop species in the Americas, but infections in olives have been reported only recently. It occurred in 2013, when the bacterium was found associated with a severe and deadly disease: the olive quick decline syndrome (OQDS). This new pathosystem (olive-*Xylella*) emerged from an inadvertent introduction of a novel hitherto undescribed *Xf* genotype (from central America) in an area (the Salento peninsula, Apulia) with an extensive presence of susceptible host plants (mainly olives), with suitable environmental conditions (mild winter) and abundant populations of an efficient insect vector, the spittlebug - *Philaeenus spumarius*. Because of the alarming phytosanitary scenario determined by this Italian report of *Xf* in olive, surveillance programs begun in all EU Member States, leading to the discovery of several *Xf*-outbreaks, caused by different strains and subspecies, in other Italian region (Tuscany and Lazio) and EU countries, i.e. France, Spain, Portugal. However, recent genomics studies suggest that *Xf* was introduced into these European countries 20 or more years ago, i.e. years before the first discovery of *Xf* in olives in southern Italy.

The management of this quarantine pathogen in olive, a novel host where it causes a detrimental disease, posed major challenges to the scientific community and severely impacted the socio-ecological system and thus the local society as a whole, as olive represents not only a major crop but a tree of historical value.

The lack of effective cure for infected plants implies that, once a new foci is identified, the application of quarantine measures is enforced, including the removal of infected plants, a controversial and debated action. In addition, the large extension of the affected territory in Apulia, determined the establishment of the so called “demarcated infected area” in which the eradication of the infections is no more pursuit, whereas containment measures aiming to reduce the spread and the impact of the infections are supported. Several research programs have been therefore funded to find practical solutions to cope with the bacterium in areas where infections are entrenched, including the evaluation, among the other, of antimicrobial formulations, bacterial antagonists and the search for genetic traits of resistance in the olive germplasm. A relevant amount of information have been gained in the past few year on olive-*Xylella* interactions, fulfilling several knowledge gaps and opening the route for new innovative investigations.

There is for example an unprecedented interest in characterizing the microbial communities that thrive in the olive xylem, to isolate potential biocontrol agents. In particular, the study of the microbiome of infected plants showed that an overt dysbiosis, and the tendency of *Xf* to occupy the whole ecological niche of the endophytic microbiome occur in the susceptible cultivar Cellina di Nardò and Kalamata, whereas a greater microorganisms diversity is maintained in the resistant cultivars Leccino or FS17. Albeit differences in the microbiomes of the susceptible versus resistant cultivars were observed, so far none of the species isolated from resistant trees proved to be efficient in inhibiting *Xf in vitro*.

As in other crop species, phenomena of resistance to *Xf* have been documented in olive, even if in a very limited number of cultivars. Indeed, the discovery of traits of resistance in the cv Leccino and FS17 represents a major breakthrough for the implementation of management strategies. The recent availability of the Leccino genome and the production of several cross-bred progenies harboring at least one resistant parental, will facilitate and boost in the near future more in depth investigations on the genetic and physiological mechanisms determining the lower bacterial population and symptom expression in the resistant cultivars. Up to date, extensive or targeted gene expression studies indicated that Leccino senses the bacterium by cell wall receptors and manages to contain the induced drought stress by modulating genes involved in the sugar metabolism and water flux across membranes. Conversely, the bacterial movement through the xylem network is likely enhanced in the susceptible Cellina di Nardò because of its facilitated exploitations of the pit membranes interconnecting xylem vessels. Overall, both molecular and physiological studies show that Leccino is more resilient to the infection and that this feature seems to be efficiently transferred to the progeny.