

Oral Presentations

Session 1 - *Xylella fastidiosa*: a global threat.

***Xylella fastidiosa*, new risks from an old threat**

Almeida R.*

*University of California Berkeley; Berkeley CA (US)

Abstract: *X. fastidiosa* has long been considered a major threat to European flora. However limited interest had been paid to this exotic bacterium, as it had never been shown to be established in Europe. This changed significantly and rapidly after the detection of *X. fastidiosa* in southern Italy in 2013, followed by a series of reports primarily from France and Spain. In the span of just four years the status of *X. fastidiosa* at several Mediterranean regions went from absent to established. In addition, *X. fastidiosa* was introduced multiple independent times, and much of the known diversity of this pathogen is represented in these introductions. In this context, some of the emerging risks to European flora will be discussed.

Biology and pathogenicity of *Xylella fastidiosa* associated to olive quick decline syndrome

Saponari M.*, Boscia D., Altamura G., Loconsole G., Zicca S., D'Attoma G., Morelli M., Palmisano F., Saponari A., Dongiovanni E., Cavalieri V., Savino V.N., Martelli G.P.

*CNR, Istituto per la Protezione Sostenibile delle Piante, Bari (IT)

Abstract: A large program of mechanical inoculations and vector-mediated transmission experiments was launched in the past 2 years, and continuously implemented, in the attempt to disclose the role of the olive-infecting strain of *X. fastidiosa* in the olive quick decline disease (OQDS) and to ascertain the crop species under threat due to the expansion of the severe epidemic in southern Italy. Artificial inoculations were performed using the selected olive strain "De Donno" on different olive and grape cvs, stone fruit and citrus species, and ornamentals. These plant species, but including a larger number of olive cultivars, were also tested through field experiments set in the demarcated infected area, by exposing *Xylella*-free plants to the natural inoculum pressure and/or by caging naturally infected *Philaenus spumarius*. Comparison of the bacterial infection rates recovered upon mechanical inoculations and vector transmission (field experiments), showed perfect agreement regarding the susceptibility of the different host species: (i) high rates of systemically infected plants were obtained for olives, with some differences in relation to the cultivars, oleanders and *Poligala myrtifolia*; (ii) very low host colonization occurred for cherry and almond plants; (iii) no bacterial movement and host colonization could be detected in grapes, citrus, apricot, peach and plum. The pathogenicity of this strain has been also demonstrated; severe symptoms were detected on the most susceptible hosts.

Acknowledgment

This work was supported by the European Food Safety Authority (EFSA) in the framework of the "Pilot project on *X. fastidiosa* to reduce risk assessment uncertainties" (NP.EFSA.ALPHA.2014.07) and by the European Union's Horizon 2020 Research and Innovation Programme, under grant agreement No. 635646, POnTE (Pest Organisms Threatening Europe).

Emergence of *Xylella fastidiosa* in Balearic Islands, Spain: Current situation

Olmo D., Montes-Borrego M., Nieto A., Adrover F., Urbano A., Beidas O., Juan A., Marco E., López M.M., Moran F., Monterde A., Navas-Cortés J.A., Landa B.B.*

*CSIC, Instituto de Agricultura Sostenible, Cordoba (ES)

Abstract: During official surveys in late autumn 2016 in Mallorca Island, Spain, the bacterium was first detected in a garden center near the locality of Manacor. Since then, as of April 24, 2017, a total

of 189 positive samples in 11 different host species have been found in different foci in Mallorca (124), Menorca (16) and Ibiza (49) islands. Sequence analysis of the RNA polymerase sigma 70 factor sequence and MLST typing revealed the presence of *X. fastidiosa* subsp. *fastidiosa* ST1 and *X. fastidiosa* subsp. *multiplex* ST6* (a new ST with the closest being ST6) and ST7 in Mallorca island, *X. fastidiosa* subsp. *multiplex* ST6* in Menorca island and *X. fastidiosa* subsp. *pauca* ST80 (a new ST) in Ibiza island. *Polygala myrtifolia* was found to be infected by all subspecies and ST types. Altogether, these results suggest that the emergence of *X. fastidiosa* in Balearic Islands is likely due to several introduction events of diverse strains from different subspecies. Eradication measures were taken in the garden center according to the Spanish contingency plan and EU legislation. Following the Commission Decision 2015/789/EU of establishing a radius of 10 km to delimit the buffer zone for each infected foci 80%, 50% and 90% of the territory of Mallorca, Menorca and Ibiza islands, respectively, are considered as demarcated areas. Consequently, the best strategy to control the different outbreaks is under study.

Acknowledgment

This work has received funding from the European Union's Horizon 2020 research and innovation programme under grant agreement N. 635646 "Pest Organisms Threatening Europe POnTE" and grant agreement N. 727987 "*Xylella fastidiosa* Active Containment Through a multidisciplinary-Oriented Research Strategy XF-ACTORS".

Bibliography

- Minsavage GV, Thompson CM, Hopkins DL, Leite RMVBC, & Stall RE, 1994. Development of a polymerase chain reaction protocol for detection of *Xylella fastidiosa* in plant tissue. *Phytopathology* 84, 456–461.
- Yuan X, Morano L, Bromley R, Spring-Pearson S, Stouthamer R, & Nunney L, 2010. Multilocus sequence typing of *Xylella fastidiosa* causing Pierce's disease and oleander leaf scorch in the United States. *Phytopathology* 100, 601-11.

***Xylella fastidiosa* in France: current situation in Corsica and in the region of Provence-Alpes-Côte d'Azur.**

Poliakoff F.*, Legendre B., Olivier V.; Dousset C., Paillard S., Molusson D., Sainte- Luce A., Juteau V., Cuntly A.

*ANSES, Angers (FR)

Abstract: Since the first outbreak of *X. fastidiosa* on *Polygala myrtifolia* (*Pm*) in natural settings in 2015 in France, the national survey showed that disease is present in many ornamental host plant in environment of Corsica and French Riviera (PACA). *X. fastidiosa* has been detected on around forty plant species with a validated method based on Real-Time PCR (Harper *et al.*, 2010) associated to DNA extraction with QuickPick™ Plant DNA kit (Bio-Nobile) and KingFisher™ automate (Thermo Fisher Scientific). The sample preparation and isolation performed on modified PWG medium (EPPO, 2016) have been optimized and more than 40 *X. fastidiosa* strains were isolated from various ornamentals and trees. The characterization of isolates directly on plant or on pure strains is performed according to a multilocus sequence typing (MLST) (<http://pubmlst.org/X.fastidiosa/>). Following EPPO protocol PM 7/24 isolates were mostly allocated to sequence types ST6 and ST7 (subspecies *multiplex*). Modifications of the amplification protocol (Yuan *et al.*, 2010) proposed by Denancé *et al.* (2017) revealed infections linked to the subspecies *pauca*, *sandyi*, one recombinant and some mixed infections. EPPO protocol MLST confirmed four isolates in *Polygala myrtifolia* from PACA contaminated with subsp. *pauca* but not the identification of other contaminants. These contaminations could not be observed again in the immediate environment after plant eradication. Subspecies assignment directly from plant material is not always successful linked to PCR inhibitors depending of host plants. This study confirms the diversity of subspecies of *X. fastidiosa* in France. Nevertheless subspecies *multiplex* was found in the great majority.