ive and plum). The isothermal amplification method has been conceived to test, in one reaction, all the above sub-species. DNA from healthy plants was been used as negative control, and absence of cross-reaction has been ensured with closely related species (i.e. several *Xanthomonas* species). Flashdiag®XF has been designed for field use, and is adapted for users without laboratory experience. From a symptomatic plant leaf/petiole and in less than 1 h, the test will clearly indicate the presence or absence of *X. fastidiosa* for a given plant sample. In 2017, DNA samples from infected plants of olive, almond, oleander, cherry, *Polygala mirtifolia*, laurel, lavender and rosemary, collected by the University of Bari Aldo Moro, will be tested. In 2018, the kit will be tested on other host species. Field validation will be conducted by the end of 2017 on olive trees in Apulia (Italy), to test the kit in field conditions with a high number of samples. Flashdiag®XF aims to provide rapid diagnosis leading to efficient monitoring of *X. fastidiosa* in a field-based, user-friendly format.

This project was supported by the French Public Investment Bank (Bpifrance).

The emergence of *Xylella fastidiosa* in the Balearic Islands, Spain, is associated with several subspecies and sequence types of the bacterium. D. OLMO[1], M. MONTES-BORREGO[2], A. NIETO[1], F. ADROVER[1], A. URBANO[3], O. BEIDAS[4], A. JUAN[4], E. MARCO[5], M.M. LÓPEZ[5], I. NAVARRO[5], A. MONTERDE[5], J.A. NAVAS-CORTÉS[2], B.B. LANDA[2]. [1]*Serveis de Millora Agrària. Govern Balear. Eusebi Estada 145. 07009, Palma de Mallorca, Spain.* [2]*Department of Crop Protection, Institute for Sustainable Agriculture (IAS), Spanish National Research Council (CSIC), Alameda del Obispo s/n, 14004 Córdoba, Spain.* [3]*TRAGSA, Empresa de transformación Agraria, Delegación de Baleares. Pasaje Cala Figuera, 6. 07009, Palma.* [4] *Servicio de Agricultura. Conselleria de Medi Ambient, Agricultura i Pesca. C/Reina Constança, 4. 07006 Palma.* [5]*Instituto Valenciano de Investigaciones Agrarias (IVIA), Carretera Moncada-Náquera km 4,5, Moncada 46113, Valencia, Spain*

Xylella fastidiosa is a quarantine organism in the European Union (EU), that was first detected in Europe in Italy in 2013 where it is associated to a severe epidemic on olive trees. The bacterium has also been detected in France (2015) and Germany (2016). Due to the recent outbreaks and to different interceptions, mainly on ornamental coffee plants, the EU has implemented annual surveys in its member states to prevent new introductions or the spread of this harmful organism. During official surveys in late autumn 2016 in Mallorca Island, Spain, the bacterium was first detected in a garden centre near the locality of Manacor. Since then a total of 189 positive samples in 11 different host species have been found in different disease foci in the islands of Mallorca (124), Menorca (16) and Ibiza (49). Sequence analysis of the RNA polymerase sigma 70 factor sequence and multilocus sequence analysis (MLST)/typing revealed the presence of *X. fastidiosa* subsp. *fastidiosa* ST1 and *X. fastidiosa* subsp. *multiplex* ST6* (a new ST closest to 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. These results suggest that the emergence of *X. fastidiosa* in the Balearic Islands is likely due to several introduction events of diverse strains and different subspecies. Eradication measures were taken in the garden centre according to the Spanish contingency plan and EU legislation. Following the Commission Decision 2015/789/EU of establishing a 10 km radius delimiting buffer zone for each infection focus, 80% of the territory of Mallorca 50% of Menorca, and 90% of Ibiza are considered as demarcated areas. The best strategies to control the different outbreaks are under study.

This study was supported by funding from the European Union's Horizon 2020 research and innovation programme, under grant agreements No. 635646 POnTE (Pest Organisms Threatening Europe) and No. 727987 XF-ACTORS (Xylella Fastidiosa Active Containment Through a multidisciplinary-Oriented Research Strategy).

Fast and sensitive detection for *Xylella fastidiosa* through recombinase polymerase amplification. R. LI[1], P. RUSSELL[1], S. ZHANG[1], B. DAVENPORT[1], A. EADS[1], K. SCHUETZ[1], S. BERKANI[2], M. AMATO[2]. [1]*Agdia Inc., Elkhart, IN 46514, U.S.A.* [2]*Agdia-EMEA, 91350 Grigny, France. E-mail: Rugang.li@agdia.com*

Xylella fastidiosa (Xf), living and multiplying in host xylem systems, is regulated in many countries. Xf originates from the American continent. In recent years the pathogen has appeared in Mediterranean