

Harmonized protocol for monitoring and detection of *Xylella fastidiosa* in its host plants and its vectors.







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Research consortium

CNR (IT), BMLFUW (AT), ILVO (BE), BFSA (BG), CISTA (CZ), HCPHS (HR), Anses (FR), INRA (FR), BMEL (DE), SASA (GB), NFCSO (HU), CREA (IT), NVWA (NL), MINEZ (NL), INIAV (PT), FGBU-VNIIKR (RU), MKGP (SI), INIA (ES), UBT (AL), IAMB (IT), UNITUS (IT), IAV (MA), INHORT (PL), ARS (USA)

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Key outputs and results

- A common protocol for sampling and processing of plant/bacteria extract, with special emphasis on isolation of viable cells of *X. fastidiosa*.
- Harmonized and validated detection methods to determine prevalence of *X. fastidiosa* in plants and insects.

Goals

Xylella fastidiosa is a bacterial pathogen recently detected in association with olive trees showing rapid decline in Southern Italy. The disease was named: 'Olive quick decline syndrome' (OQDS). At the end of 2013 the disease was estimated to affect about 23.000 hectares of olive groves in Salento (Apulia), including centuries-old olive trees of special aesthetic, ecological, sociological and historical value.

The project has the objective to produce rapid and reliable detection protocols for monitoring *X. fastidiosa* and associated insect vectors in different plant species (symptomatic and asymptomatic plant material) and regions, with emphasis on improving sampling techniques, protocols for processing of samples (i.e., DNA extraction), and methods for isolating *X. fastidiosa* in culturing medium to fulfil quarantine and monitoring requirements.

The harmonized protocol would combine surveys to determine the prevalence of *X. fastidiosa* and spatio-temporal distribution of potential vectors (*Cicadellidae, Aphrophoridae, Cercopidae* and possibly *Cicadoidae*) occurring in grapevine, olive, almond, peach, plum crops and coffee and oleander plants present in the different European areas, as basic input for the design of suitable control strategies