

Xylella fastidiosa and its insect vectors



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Research consortium

SASA (GB), AGES (AT), INRA (FR), JKI (DE), EVPM (EE), NEBIH (HU), CIHEAM-IAMB (IT), NVWA (NL), NIB (SI), FERA (GB), INIAV (PT), AUT (AL), UiB (ES), ARC (EG),

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Objectives and key outputs

Vectors of *Xylella fastidiosa* are relatively well known in South and North Americas, but our knowledge needs to be improved in the European countries where the disease has been recently detected. Therefore there is a requirement for the evaluation of methods to reliably sample for vector species in the environment both to aid their study but also to potentially provide a sentinel network for the reliable detection of this pathogen and its vectors.

The project will:

- Survey potential vector species associated with *X. fastidiosa* hosts
- Evaluate sampling methods for vector species in the environment
- Validate non-destructive DNA extraction methods already developed in potential vectors and Improve non-destructive extraction methods to other insect
- Develop real-time assays for known and suspected vector species (including North American species) to provide taxonomic support (especially nymphs) and rapid sample screening
- Improve detection of *X. fastidiosa* in potential vectors
- Identify potential cultural and chemical control methods related to vector lifecycle.