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## A web-interface database for the identification of vectors of *Xylella fastidiosa* in Europe

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European  
Commission



Xylella Fastidiosa Actor Containment Through a  
multidisciplinary-Oriented Research Strategy

3<sup>rd</sup> European Conference on  
*Xylella fastidiosa* and XF-ACTORS final meeting

# A web-interface database for the identification of vectors of *Xylella fastidiosa* in Europe

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# INTRODUCTION

- Identification of vectors of *Xylella fastidiosa* (Xf) based on morphological characters can be difficult and sometimes impossible (eggs, nymphs).
- **We have developed a web-interface database of COI barcode.**



<https://arthemisdb.supagro.inra.fr/>

INRAE ARTHEMIS DB@se

Home Search Identification tools Database information Restricted access Contact Unknown user

Welcome to the Artemis Database !  
on ARTHropod Ecology, Molecular Identification and Systematics

Search a taxon  
Use our tool to find a taxon

Specimen search  
Use our tool to find a specimen

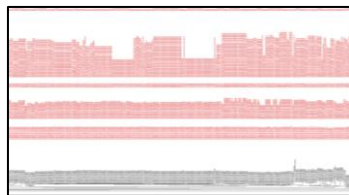
Blast  
Realize pairwise sequence alignments

# MATERIALS & METHODS

## Sequencing

- Sequences generated with a high-throughput approach involving two PCR steps to target *COI* and index samples followed by Illumina sequencing.

### Two-step PCR and Miseq sequencing

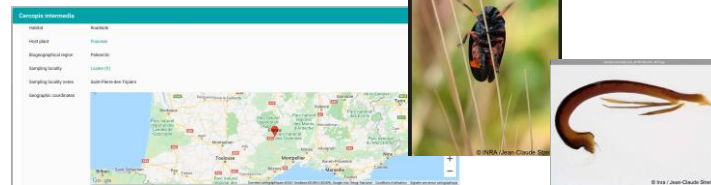


- Quality controls: i) non-destructive DNA extraction, vouchering and morphological re-examination by taxonomists; ii) bioinformatic controls to detect possible contaminants, PCR/sequencing errors, introgressions, NUMTs and heteroplasm.

## Data provided online



- Sequences : *COI* standards barcodes (Hebert et al., 2003)
- Metadata associated with records
- Pictures including habitus and genitalia
- Biological data



- Identification of a query sequence through BLAST comparison against our reference library.



My data

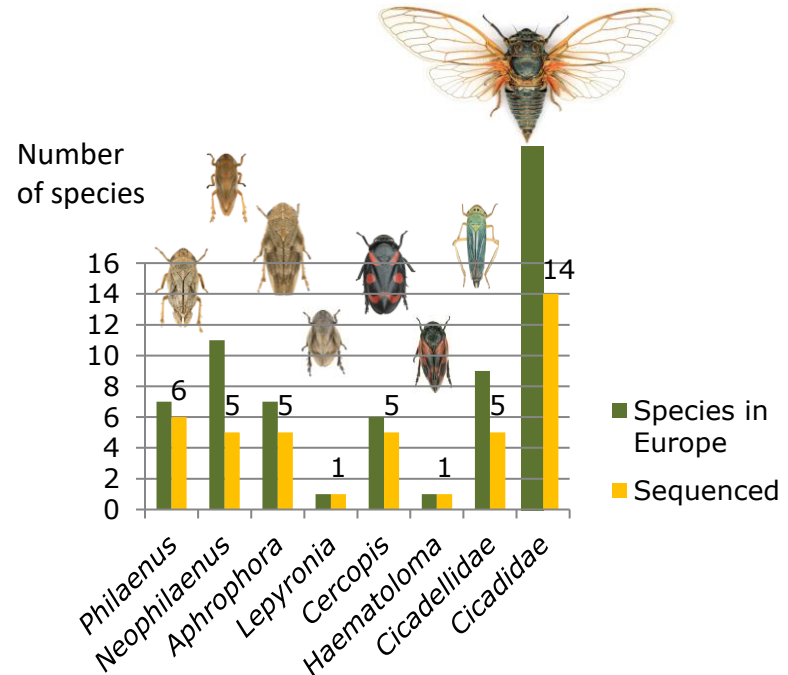
# RESULTS

## Database contents

- 681 barcodes sequences
- 74 species of potential vectors of Xf
- 536 sequences representing 42 European species
- 145 sequences representing 32 non-European species.
- All frequent species have been barcoded. Missing species do not represent an important threat for European agriculture.



## Database completion



# ISSUES AND CONCLUSION

## Can we rely on DNA barcoding and morphology to identify vectors of Xf ?

- *COI* allows reliable identification for 80% of the species, but we observed issues for the remaining 20%.
- *Philaenus spumarius* and *P. tessellatus* share the same *COI* but are also hardly distinguishable morphologically => possible synonyms ?
- It was also difficult to cross validate morphological and molecular results for some species within the genera *Neophilaenus* and *Aphrophora*?

*Identification of most of the vectors of Xf in Europe is possible using morphological characters and DNA barcoding.*  
***But more work has to be conducted to clarify the taxonomic status of some species***