

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

Jean-Claude Streito, Eric Pierre, Guénaëlle Genson, Maxime Bellifa, Marguerite Chartois, Xavier Mesmin, Pauline Farigoule, Astrid Cruaud, Jean-Yves Rasplus

▶ To cite this version:

Jean-Claude Streito, Eric Pierre, Guénaëlle Genson, Maxime Bellifa, Marguerite Chartois, et al.. A web-interface database for the identification of vectors of Xylella fastidiosa in Europe. 3rd European Conference on Xylella fastidiosa and XF-ACTORS final meeting, Apr 2021, Online Event, France. , 10.5281/zenodo.4680659. hal-03845933

HAL Id: hal-03845933 https://hal.inrae.fr/hal-03845933

Submitted on 16 Nov 2022

HAL is a multi-disciplinary open access archive for the deposit and dissemination of scientific research documents, whether they are published or not. The documents may come from teaching and research institutions in France or abroad, or from public or private research centers.

L'archive ouverte pluridisciplinaire **HAL**, est destinée au dépôt et à la diffusion de documents scientifiques de niveau recherche, publiés ou non, émanant des établissements d'enseignement et de recherche français ou étrangers, des laboratoires publics ou privés.

















3rd European Conference on Xylella fastidiosa and XF-ACTORS final meeting

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

Streito Jean-Claude¹, Pierre Éric¹, Genson Guénaëlle¹, Bellifa Maxime¹, Chartois Marguerite¹, Mesmin Xavier¹, Farigoule Pauline^{1,2}, Cruaud Astrid¹ & Rasplus Jean-Yves¹

¹CBGP, INRAE, CIRAD, IRD, Montpellier SupAgro, Univ. Montpellier, Montferrier-sur-Lez, France (<u>jean-claude.streito@inrae.fr</u>); ²AgroParisTech, Paris, France

















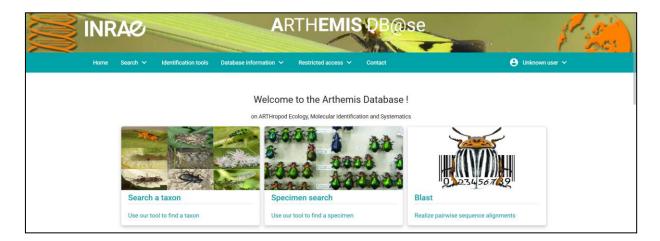
INTRODUCTION

Identification of vectors of Xylella fastidiosa (Xf) based on morphological characters can be difficult and sometimes impossible (eggs, nymphs).



We have developed a webinterface database of COI barcode.

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



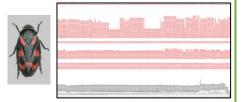


MATERIALS & METHODS

Sequencing

Sequences generated with a highthroughput 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 heteroplasms.

Data provided online

ARTHEMIS DB@se



- Metadata associated with records
- Pictures including habitus and genitalia
- Biological data



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



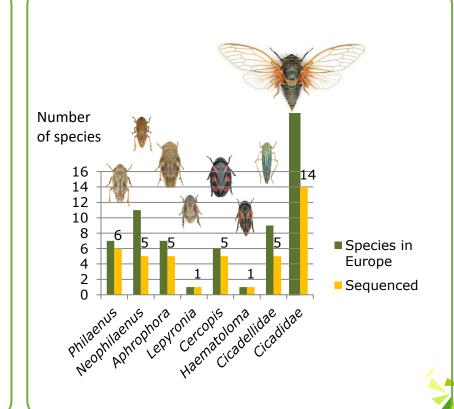
RESULTS

Database contents

- 681 barcodes sequences
- 74 species of potential vectors of Xf
- 536 sequences representing 42European 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. tesselatus 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

