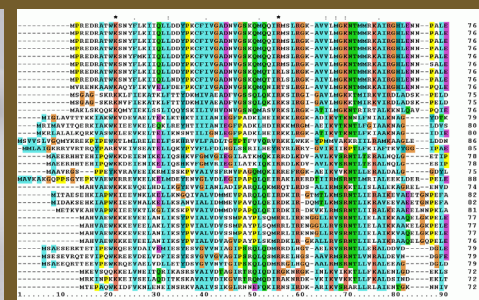


DNA sequences for reliable identification of arthropod species of plant health importance



Funding

Non-competitive funding mechanism. Each funder only pays for the participation of their own national researchers. Total funding € 77 000

Research consortium

SASA (GB), AGES (AT), DAFM (IE), MPI (NZ), EPPO (Int), USAMV (RO)

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Goals and objectives

Classical insect and mite taxonomy is a highly specialised skill. Taxonomists generally operate within a few areas of expertise and have limited opportunities to pass on their knowledge to the next generation or colleagues in other countries. DNA sequencing is increasingly used to complement classical taxonomic methods for the rapid and accurate identification of arthropod species and is of particular use to researchers and diagnosticians involved in plant protection. However, this method relies heavily on the accuracy and availability of sequences on public databases which although useful for biodiversity studies can be less reliable at the species level.

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Ideally, all barcode sequences should have been derived from a vouchered specimen, which was initially identified by a taxonomic expert however this is not always the case. Errors can also be compounded if any newly generated molecular identification is based upon a previous misidentification.

The project aims to make information from arthropod collections more accessible. In particular, the project will focus on validated genomic sequences and their associated metadata such as collection site, information on the specimen, images, and nucleic acid extraction methods.

Key outputs and results

The project partners will:

- Identify existing collections and databases
- Develop guidelines for validation of sequences
- Review the EPPO Q-bank

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