Efficient monitoring of arthropod biodiversity in orchard ecosystems

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Introduction

There is a need for standardized monitoring protocols in order to follow up on the attempts to restore biodiversity. Monitoring arthropods on a regular base is challenging as surveys typically yield many different species, also per habitat, region and soil type. Their identification requires a high degree of specialization for the different taxa. New DNA techniques such as metabarcoding offer a promising alternative as a tool for arthropod biomonitoring.

Objective

In order to use metabarcoding as a tool to assess biodiversity in orchards we aimed at:

- performing a first proof of principle by comparing DNA results to identifications made by taxonomic specialists
- optimizing sampling protocols for DNA metabarcoding
- Test quantification of arthropods by comparing results
- testing three commonly used primer pairs for their suitability to amplify the "COI-B" region in arthropods in order to optimize species detectability.

Materials & Methods

Arthropod samples were taken in duplo in

- orchards (pitfall, beating net, Berleze, limb jarring)
- agricultural strip cropping (pitfall and Malaise)
- grasslands (pitfall)

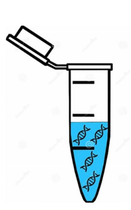
During sampling and sample processing special care was taken in order to avoid DNA polution and degeneration. For one of each paired sample, four taxonomic groups were identified by taxonomic experts (spiders, springtails, ants and beetles). The other sample was used for DNA analysis.

Figure 1 a-d. Different sampling techniques were used to cover arthropod subcommunities in agro-ecosystems. Limb jarring (a), beating net (b)) Malaize (c) pitfall trap (d).

DNA metabarcoding

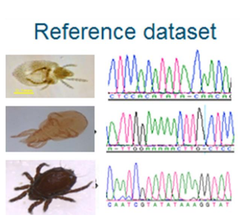
Below a simplified scheme to illustrate the process followed during DNA metabarcoding:

Step 1: Collecting arthropod bulk samples



Step 2: Extraction of DNA and sequencing

Step 3: Sequence processing using bioinformatics



Step 4: Comparison sequences with DNA database

Results

- Using DNA metabarcoding of samples taken in three agroecosystems we were able to identify 554 taxa of which the majority (83 %) at the species level, 10 % at genus level and 7 % at family level or higher.
- We found clear variability between locations and sampling type
- DNA-based identification resulted in a higher taxonomic resolution compared to morphological identification.
- DNA-based identification resulted in a higher number of identified species compared to morphological identification.
- We identified the primer pair mlCOIintF - HCO2198 as most promising primer set to amplify part of the COI gene in arthropods.

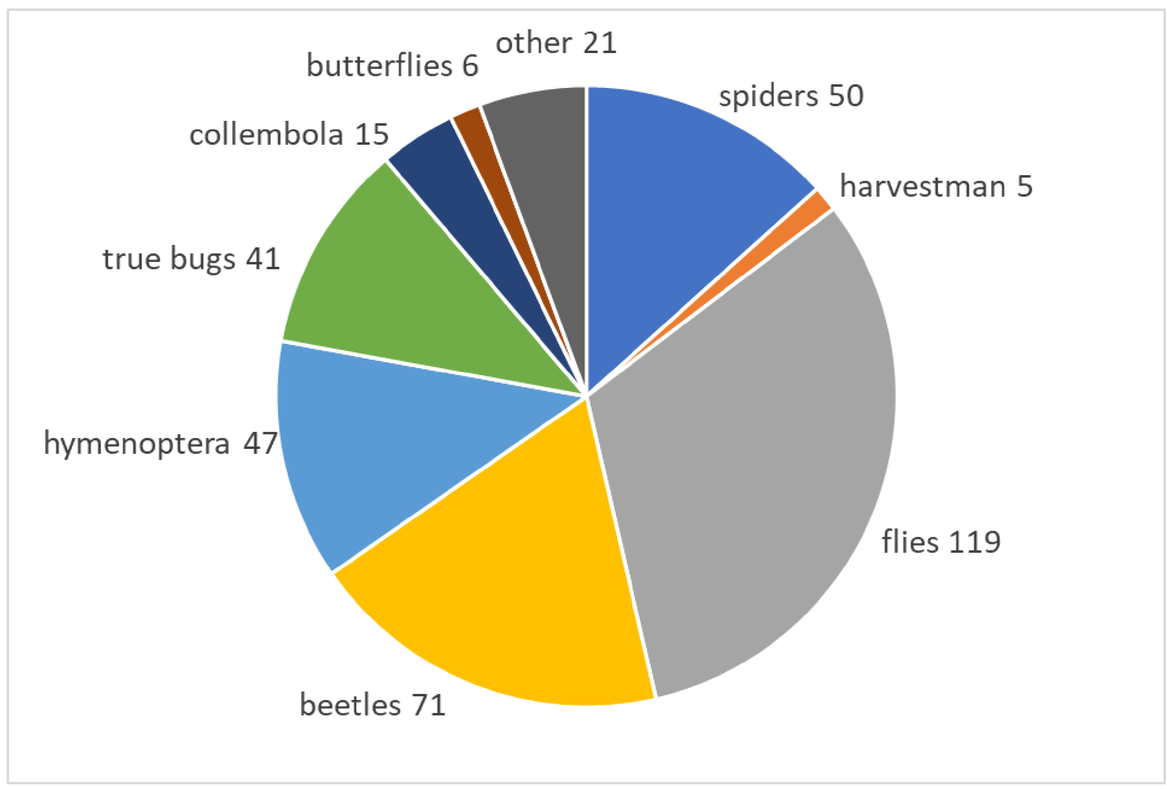


Figure 4. Sampling in experimental orchard Randwijk in 2019 resulted in identification of 375 different species, here grouped by (insect)order.

Conclusions

- DNA metabarcoding of arthropod samples offers more precise information on species diversity in the systems examined
- Identification of species is more cost-efficient and less dependent on specialized taxonomists
- The method provides a promising tool for arthropod biomonitoring in a variety of agro-ecological environments.

Perspectives

- In 2022 samples were taken at different orchard locations and in different management systems (biological and integrated). Results are expected end of 2022.
- First steps are taken to include quantitative information in the evaluation of samples
- Combination of Artificial Intelligence for quantification (camera and automatic identification) with DNA techniques is in development

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