

Determining the diet of predatory mites through metabarcoding

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Mites in Agroecosystems

Phytophagous mites

Feed on plant tissue,
includes virus vector;
Can reach pest status

Tetranychidae, Eriophyidae,
Tenuipalpidae, Tarsonemidae



Predatory mites

Feed on other mites
and also on small
insects - thrips,
whiteflies

Phytoseiidae, Ascidae,
Blattisociidae



Pest management measures based on ecological interactions

How can we determine the diet of predatory mites?

- Laboratory essays (pre-defined potential preys)
- Molecular methods
 - Traditional / High throughput sequencing-based

Metabarcoding approach



Objectives

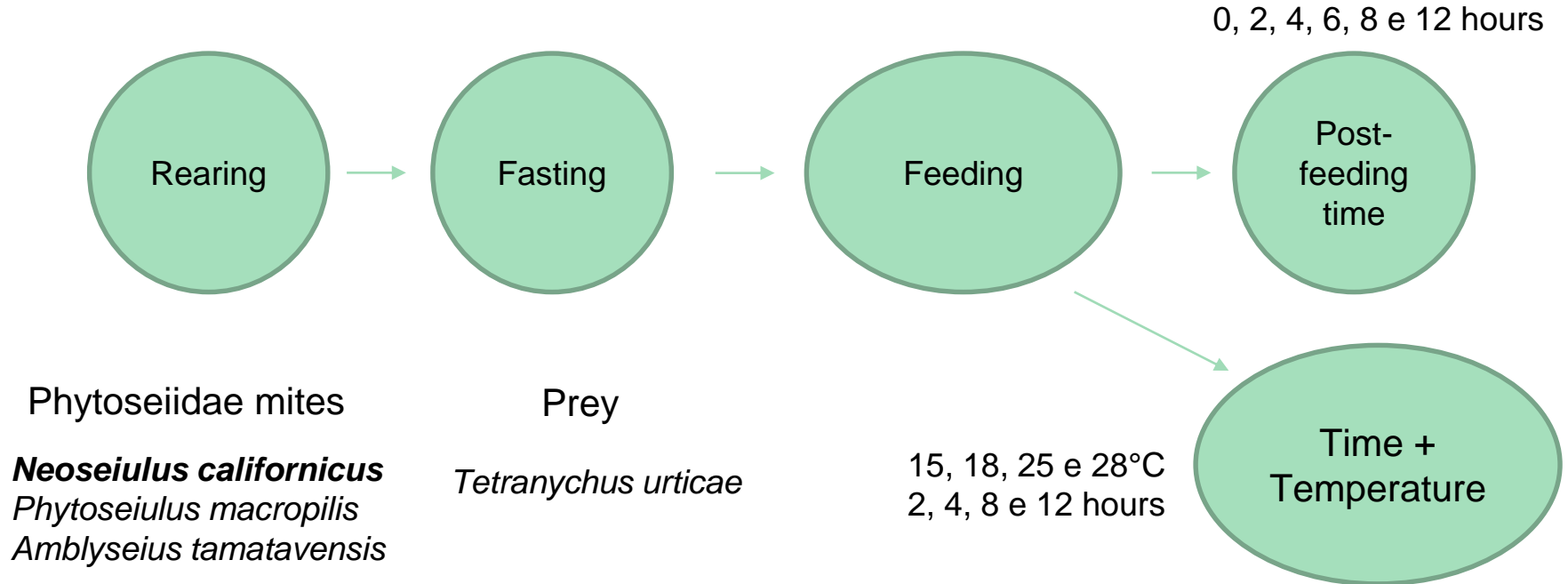
1) To determine the effect of biotic and abiotic parameters on the detectability of preys on predatory mites through metabarcoding.

- Taxon
- Temperature
- Post-feeding time
- Multiple preys

2) To understand the interactions on communities involving predatory mites on soybean-cowpea intercropping system, with and without weeding

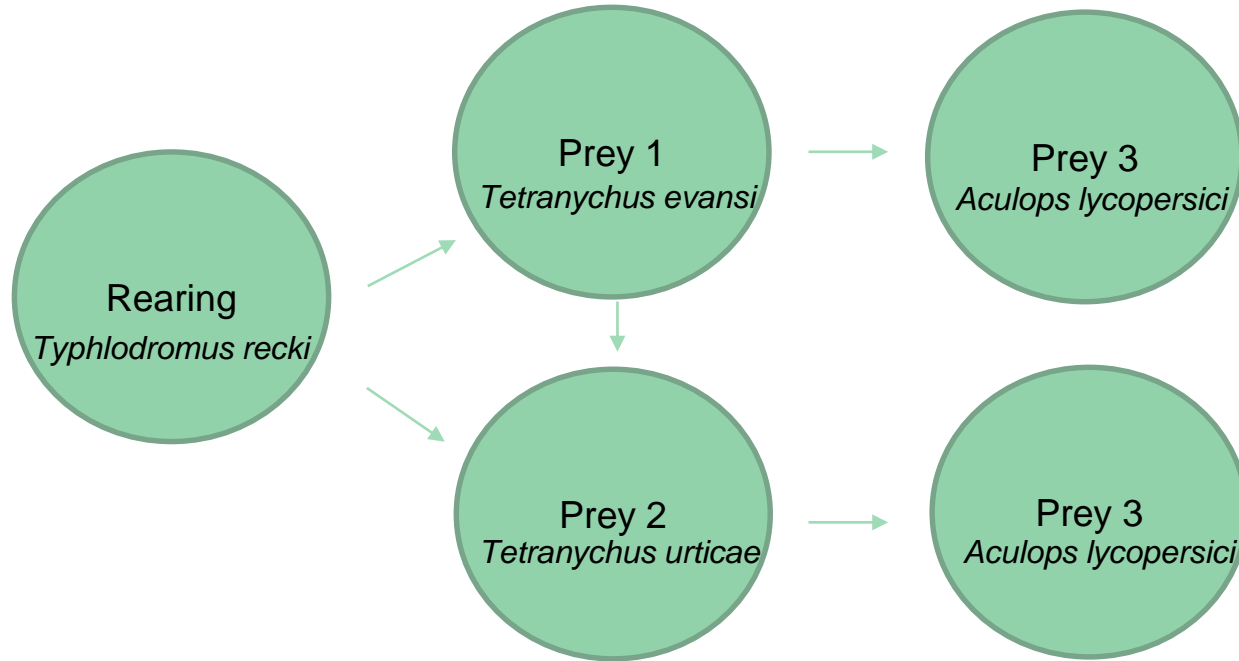
Methodology

- Controlled feeding essays – post-feeding time and temperature*



Methodology

- Controlled feeding essay with multiple preys – at *Centre de Biologie pour la Gestion des Populations* (CBGP)





Predators

- *P. macropilis*
- *A. tamatavensis*
- *N. californicus*
- *T. recki*

Preys

- *T. urticae*
- *T. ludeni*
- *T. evansi*
- *A. lycopersici*

Methodology

Field sampling

- Soybean & Cowpea bean (production and experimental areas)
 - intercropping
 - with weeding X without weeding
- Predatory mites and potential preys



Methodology – Metabarcoding using MiniCOI group-specific primers

Samples

- Lab essays
- Field samples



DNA extraction

Individually extracted



PCR & Sequencing

- CO1 and MiniCO1
- Sanger (taxonomical ID)
- NovaSeq (diet analysis)



Data assigning

Sequence reference databank
Taxon ID

Data analysis

Bioinformatics



Methodology

Field

275 predators

ID & diet



Lab essays

150 specimens - controlled time

160 specimens - controlled time
& temperature

95 multi-preys

Molecular

6 plates sequenced in HTS (Lab and field)

30M sequences/plate

Metabarcoding data analysis

- Primers removal
- Taxonomic assignment
- Sequence ID



- Data clean-up
- Removal of false-positives



- Analysis and data interpretation in progress



Jean-François Martin



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APPLICATION

Methods in Ecology and Evolution BRITISH ECOLOGICAL SOCIETY

metabAR: An R package for the evaluation and improvement of DNA metabarcoding data quality

Lucie Zinger¹ | Clément Lionnet² | Anne-Sophie Benoiston¹ | Julian Donald^{3,4} |
Céline Mercier² | Frédéric Boyer²

Thank you!

Merci !



UnB



CAPES



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la science pour la vie, l'humain, la terre



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