Metabarcoding for the parallel identification of bats and their preys : focus on the greater horseshoe bat

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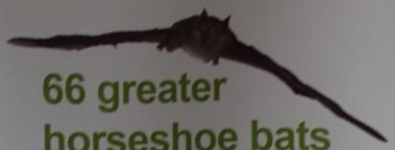
Galan et *al* 2017. BioRxiv doi: https://doi.org/10.1101/155721. Submitted in *Molecular Ecology Resources*



66 greater horseshoe bats

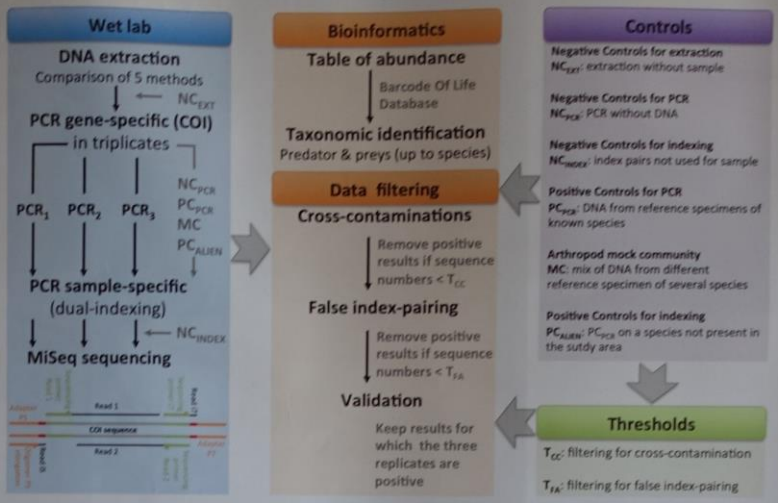
1 pellet/individual

12 localities

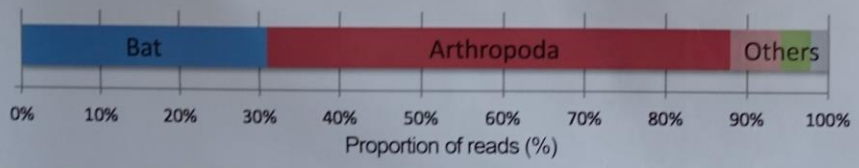
In Western France

Rigorous protocols

3 PCR replicates, positive and negative controls, several filters

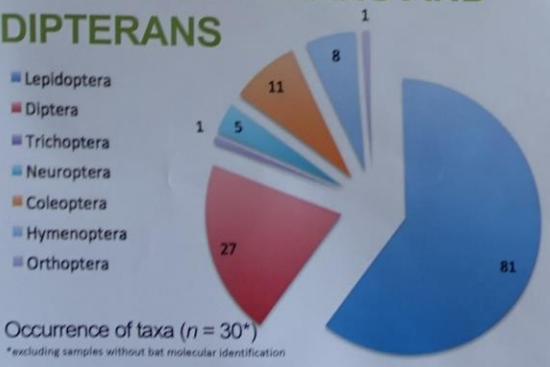


SUCCESSFUL DNA AMPLIFICATION OF BATS AND THEIR ARTHROPOD PREYS



- Greater horseshoe bat
- Arthropoda (Bold similarity > 97%)
- Arthropoda unclassified (Bold similarity score < 97%)
- Others (Blood meals, plants, fungi, ...)
- Unclassified

A DIVERSIFIED DIET, DOMINATED BY LEPIDOPTERANS AND DIPTERANS



Occurrence of taxa (n = 30*)

*excluding samples without bat molecular identification

...AND WHICH INCLUDES 16 PEST SPECIES


Cossus cossus


Peridroma saucia

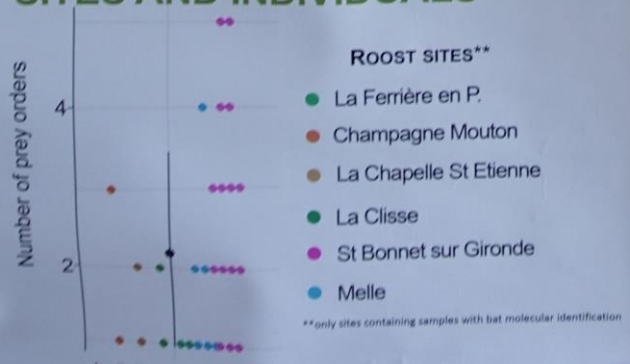

Agrotis segetum


Culex pipiens


Arhopalus rusticus


Anoxia villosa

WITH A HIGH VARIABILITY BETWEEN SITES AND INDIVIDUALS



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