Admixture and fast speciation in species complexes of phytophagous Hymenoptera and Orthoptera: A MuseOMICS approach

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DFG Priority Programme "Taxon-Omics: New Approaches for Discovering and Naming Biodiversity" (SPP 1991)
Project HA7255/2-1 "A MuseOMICS approach to scrutinise DNA barcode failure:
testing the causes for taxonomic incongruence patterns in phytophagous Hymenoptera and Orthoptera
through hybridization capture using RAD probes"

evolution MONTPELLIER 2018 August 19-22, 2018 Montpellier, France

Background:

DNA barcoding studies conducted at the ZSM between 2009 and now produced overall good congruence between traditional taxonomy and barcodes, but also detected some cases of increased incongruence.

E.g. **Orthoptera**: Many species were not distinguishable by DNA barcodes, even across genera (Hawlitschek et al. 2017).

- Hemimetabolan
- Large genomes (up to 14 gb)
- Barcode sharing detected in 41% of N=70 species

E.g. **-Symphyta-**: High amount of para- and polyphyletic species (Schmidt et al. 2017).

- Holometabolan
- Small genomes (ca. 500 mb)
- Barcode sharing detected in >20% of N=822 species

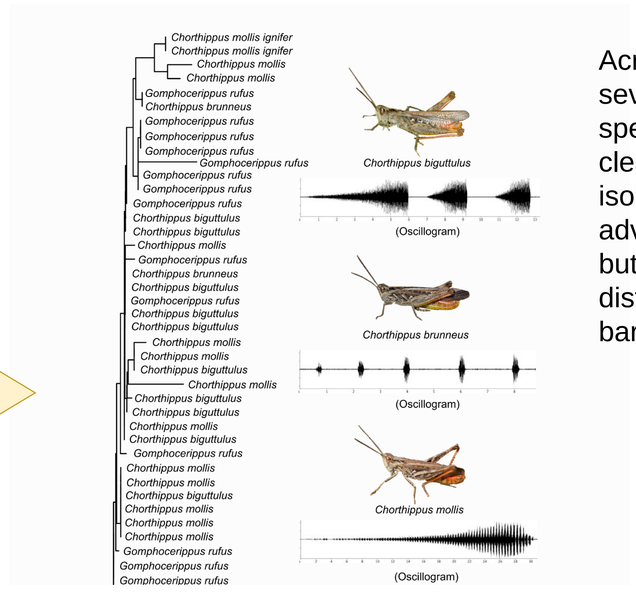
Possible reasons:

Operational bias (taxonomy, misidentification)

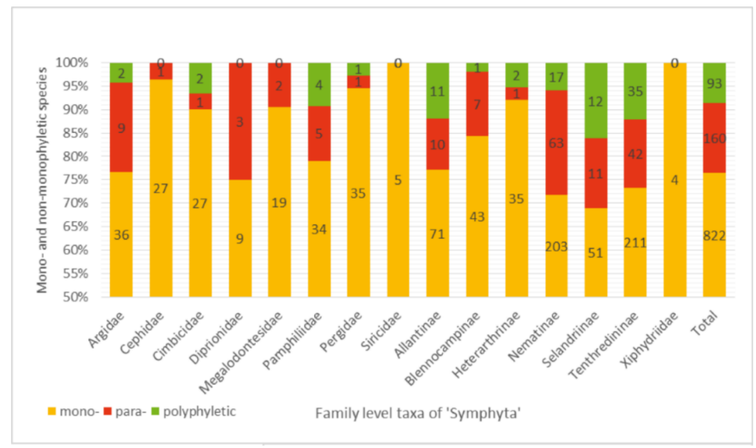
Pseudogenes (numts)

Wolbachia infection

Hybridization, incomplete lineage sorting



Acrididae comprises several complexes of species that are clearly reproductively isolated by advertisement calls, but cannot be distinguished by DNA barcoding.



Most families of -Symphyta- exhibit high degrees of barcode incongruence, with para- as well as polyphyletic operational taxonomical units.

Questions and Goals:

Is the mitochondrial (COI) haplotype sharing reflected in genomic admixture?

If yes, what is the degree and geographic structure of this admixture?

We use SNPs generated in RAD sequencing to answer these questions. Sampling fresh material is difficult especially in Hymenoptera, but museum collections house extensive sampling of all relevant species that will be available to a MuseOMICS approach.

Preliminary data shows that complexes of closely related species are very common in our study groups. We expect to detect more of these complexes in addition to possible hybridization and its importance in speciation.

What is the importance of NUMTs and *Wolbachia*?

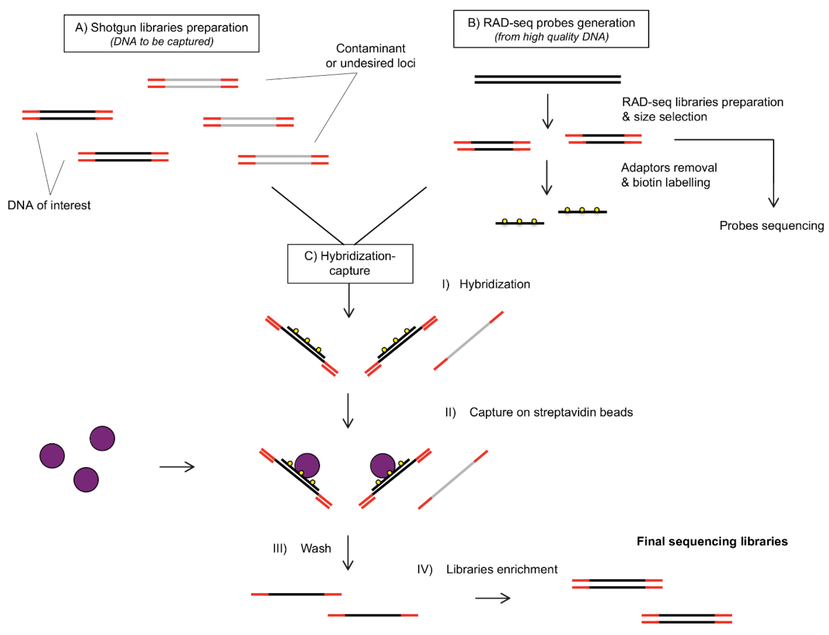
Shedding more light on the influence of nuclear mitochondrial pseudogenes and *Wolbachia* infections is a secondary goal of the project.

What are the taxonomic consequences?

Disentangling species complexes and detecting hybrids will very likely have wide-ranging consequences on the taxonomy of the study groups.

Methods:

Fresh samples are processed in ddRAD sequencing. Older samples (10 – 100 ya) are processed in **hyRAD sequencing** (figure from Suchan et al. 2016).



The application of the ddRAD protocol to low-quality DNA is often difficult because the hyRAD protocol uses a ddRAD library as probes for capturing fragments homologous to the RADtags from a shotgun library. This will also work if one of the restriction sites of the target fragment is lost and therefore will allow working with low-quality DNA.

SNPs generated in RADseq (ddRAD and hyRAD) allow detailed study of evolutionary processes in species complexes of Hymenoptera and Orthoptera.

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Acknowledgements:

We thank the following colleagues and collaborators:

Amelie Höcherl
Arne Lehmann
Burcin Yildirim
Carmen Argudo
Frank Glaw
Georg Waeber
Gerhard Haszprunar
Gerlind Lehmann
Günther Wöss
Inge Illich
Jason Brozio
Jérôme Morinière
Jochen Wolf
Kathleen Webster
Marina Querejeta
Marko Prous
Olga Schmidt
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