The good, the bad and the ugly: insights from Odonata Barcoding


Abstract

DNA barcoding is currently an essential tool in a vast array of ecological and conservation studies (e.g. biodiversity monitoring, diet assessments). However, its applicability is still hampered by the lack of comprehensive reference collections. This knowledge gap becomes greater in invertebrates, especially from biodiversity hotspots like the Mediterranean Basin. Surprisingly, while dragonflies and damselflies are one of the best studied insect groups, no comprehensive barcoding of the European species has been made. These predatory insects are intimately connected to freshwater habitats, as their larval phase is completed in the water, being particularly sensitive to changes in the aquatic environment and constituting important bioindicators of ecosystem health.

Within InBIO Barcoding Initiative we barcoded 70 species of odonates, focusing mostly on species from Iberian Peninsula. Genomic DNA was extracted and the barcoding mitochondrial COI gene fragment (658 bp) was amplified. DNA barcodes were sequenced using either Sanger or high-throughput sequencing (Illumina).

Our results exhibited a scenario that illustrates some of the challenges posed by insect identification using DNA barcoding. While many species can be easily identified using the mitochondrial COI gene fragment, this is not true to all. Not all species possess a specific DNA barcode that allows the correct assignment of taxonomic names to unidentified specimens. For instance, two groups of Coenagrionid species share mtDNA haplotypes. Other species possess multiple copies of COI in the genome, impeding successful Sanger sequencing, which can be overcome using Next Generation Sequencing. These sequences are also likely to be detected in eDNA metabarcoding studies, and should therefore be documented and databased for more accurate estimation of taxa diversity and species identification. This data provides important insights into the diversity and taxonomy of odonates and guidelines to achieve a more reliable and useful Barcode reference database.

Barcoding pipeline

Material and methods

Sample DNA extraction DNA amplification DNA sequencing

Expected results

Phylogenetic tree Barcode gap genetic distance

The good

Clear divergence between species

The bad

No divergence between species (ex. mtDNA introgression)

Discussion

nuclear copies of mtDNA exist we are able to recover them they are also in the eDNA

Why not make the best of it?

Deposit Numts data in databases Opportunity to improve taxa assignment rate Avoid overestimation of taxa (biodiversity inventories, diet studies, etc...) Increase detection rate Targeted species: conservation concern or invasive

Odonata barcodes in numbers...

We obtained COI sequences for 413 specimens of 70 species

• 57 species had unique Barcodes
• 5 species shared COI haplotypes with at least another species
• 8 species exhibited Numts

Funding Sources/Acknowledgements