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ICHTHYOLOGICAL DIVERSITY IN A TROPICAL NATURE RESERVE (ETANG DE SAINT-PAUL, REUNION ISLAND) FROM ENVIRONMENTAL DNA (eDNA) METABARCODING

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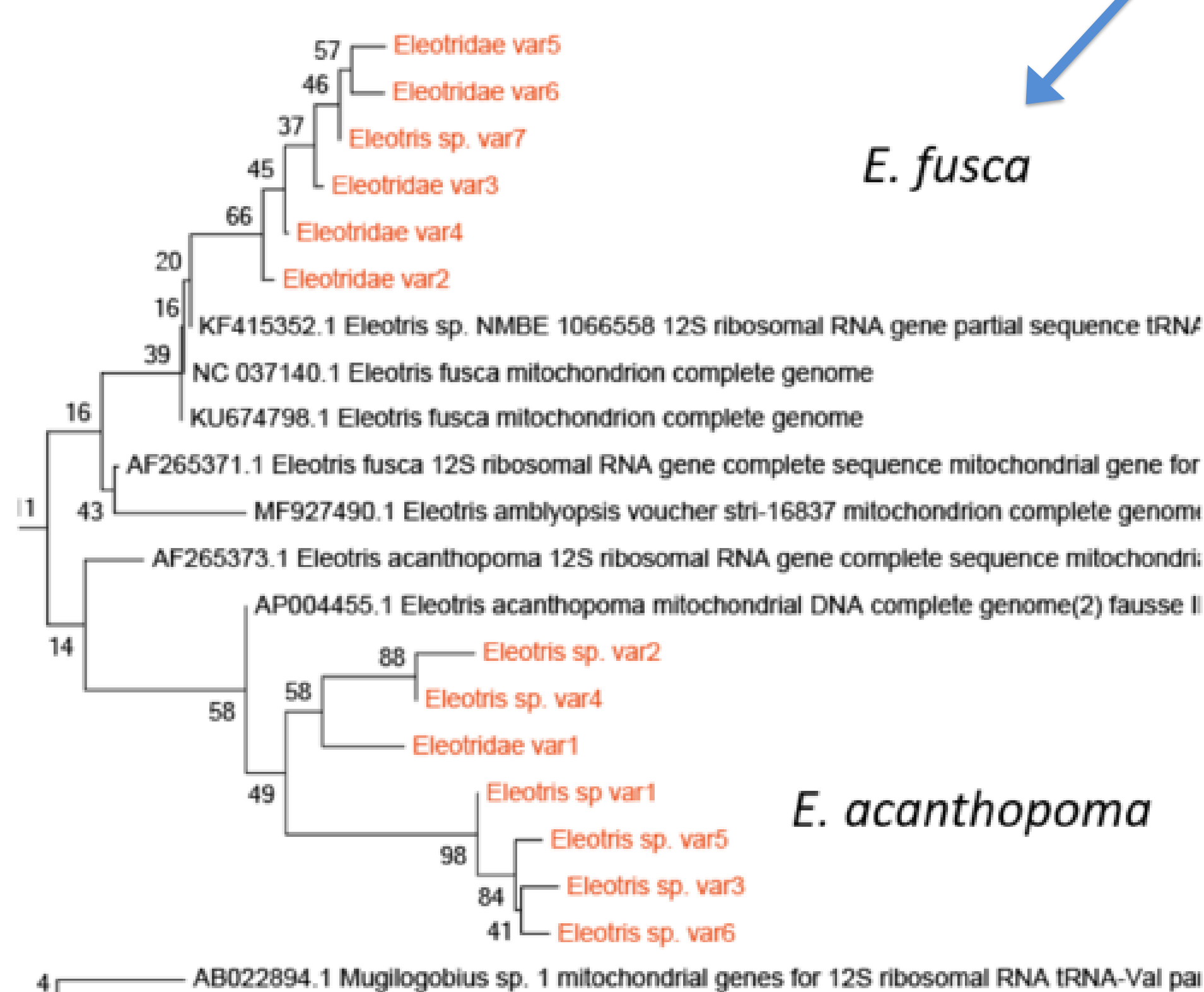
PROCESS

- SAMPLES:**
- 10 geographic localisation around the nature reserve.
- 2 L filtrate water by Pall-Acropack (0.45 μ).

- MOLECULAR:**
- 12 replicates per sample.
- Group-specific mitochondrial 12S primers (Spygen patent)
- Human blocking primers.

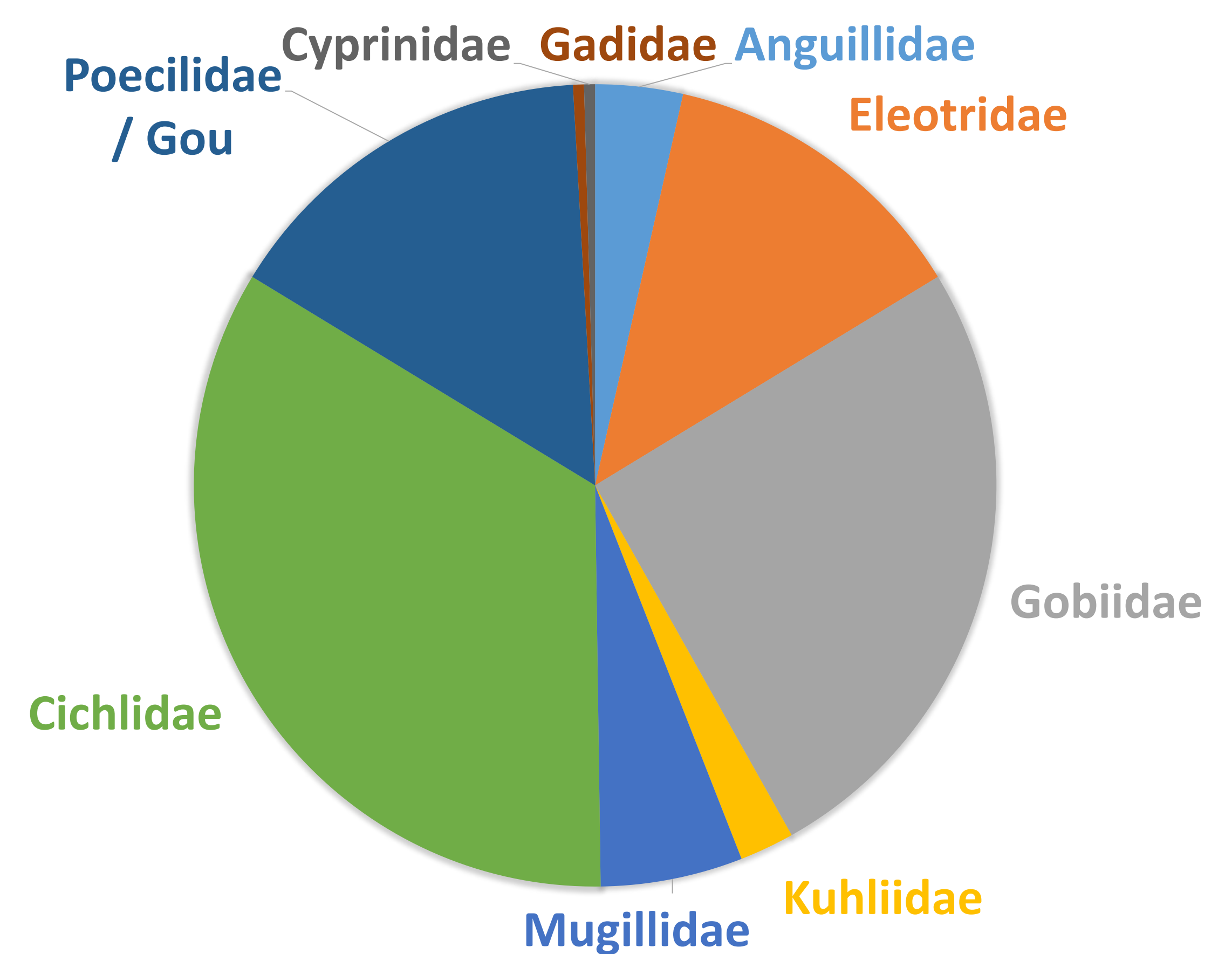
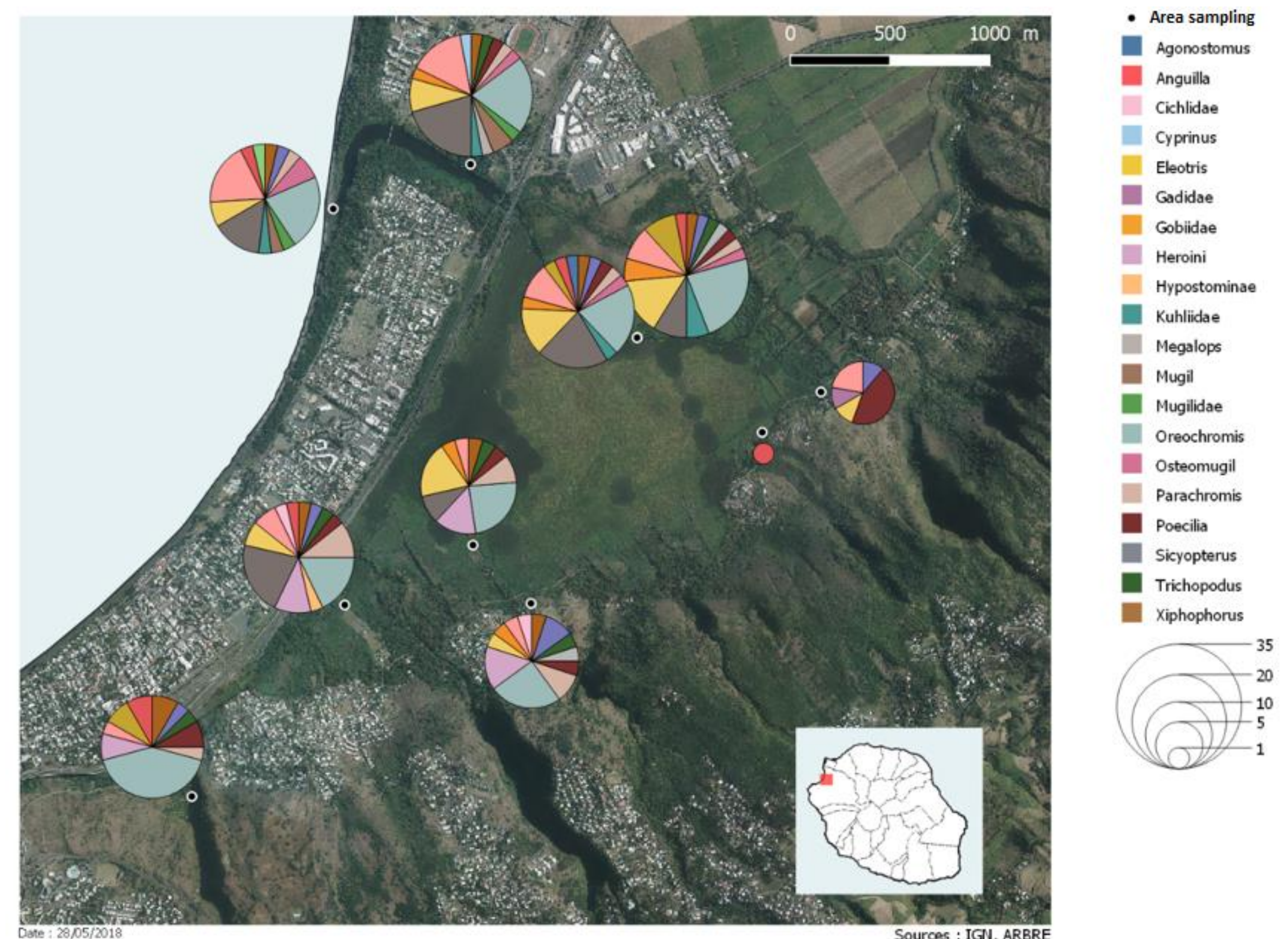
- BIOINFORMATICS:**
- Biofiltration by Obitools and alignment on reference genome on NCBI and SPYGEN database.
- Supplementary alignment by blast and Mega on NCBI and Bold database.
- Phylogenetic analysis on Mega and Non Metric Multidimensional Scaling (NMDS) analysis (R vegan package, using Jaccard index).

- RESULTS IMPROVE BY:**
- Confrontation of reference genome database.
- Phylogenetic analysis: Exemple *Eleotris*.



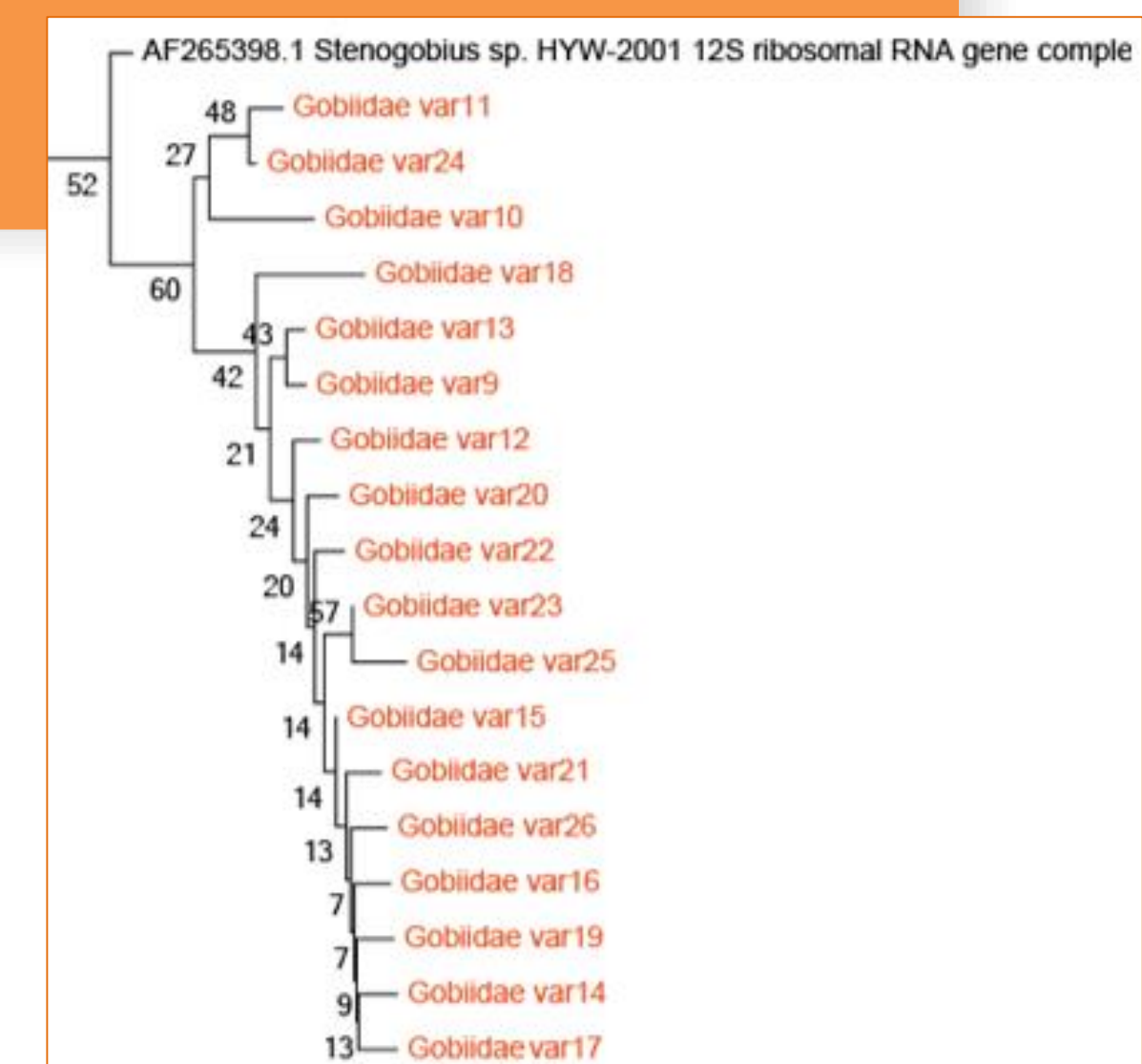
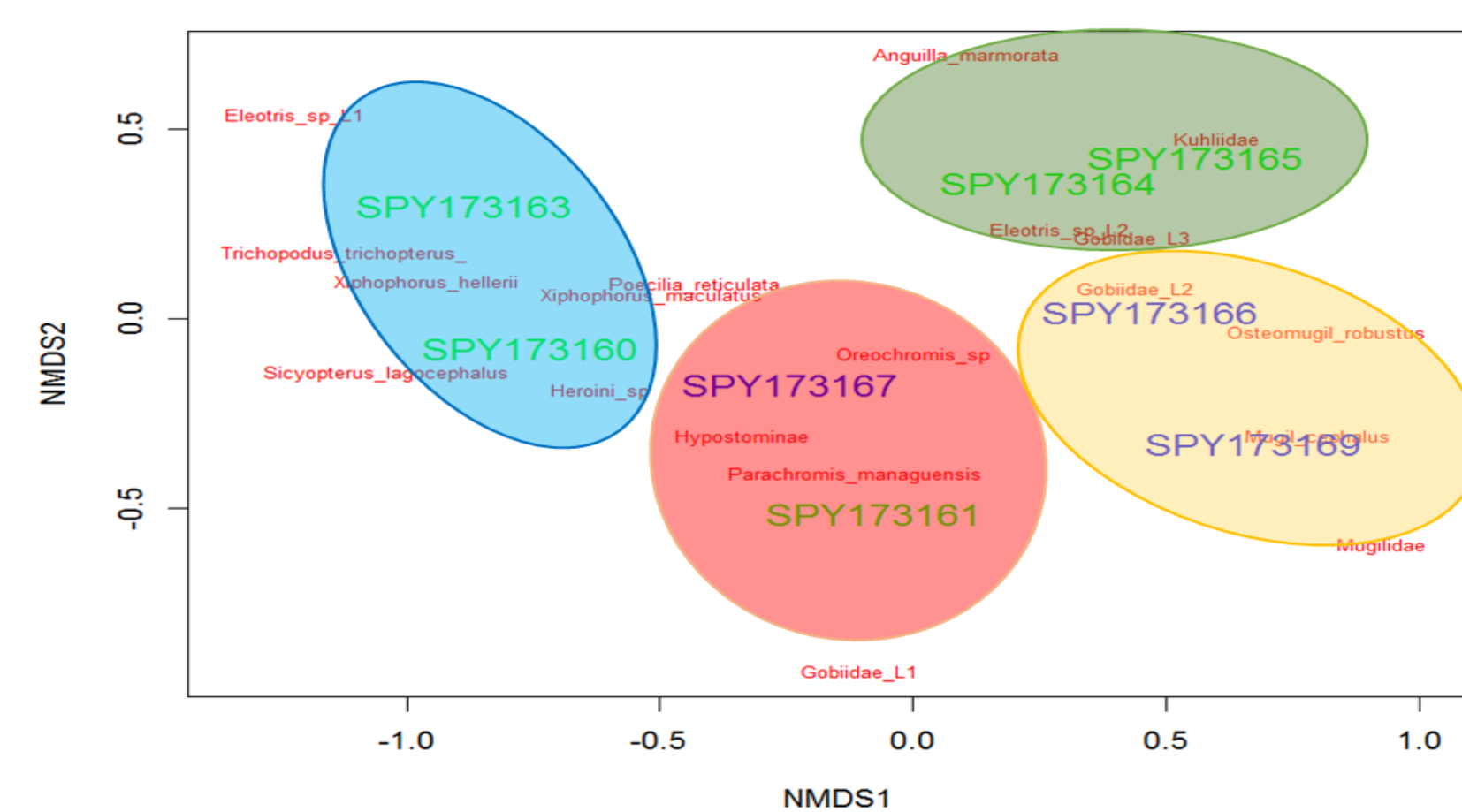
- CONCLUSION**
- ADNe detected expected fish diversity.
- ADNe reflect consistent fish assemblages at micro and macroscale.
- Accurate taxonomic assignment require enhancement of reference barcoding reference.

RESULTS



Need to be improve due to lack of reference genome:

- Lineage of Gobiidae (particularly *Stenogobius* and *Sicyopterus*).



Assemblies reflect different habitat uses between species

