



R&D Webinar - BIODHYL Project Outcomes

Enhanced biocolonisation knowledge and optimisation of offshore renewable energy systems monitoring



With the financial support of:



Development of an integrative taxonomic approach including morphology and eDNA

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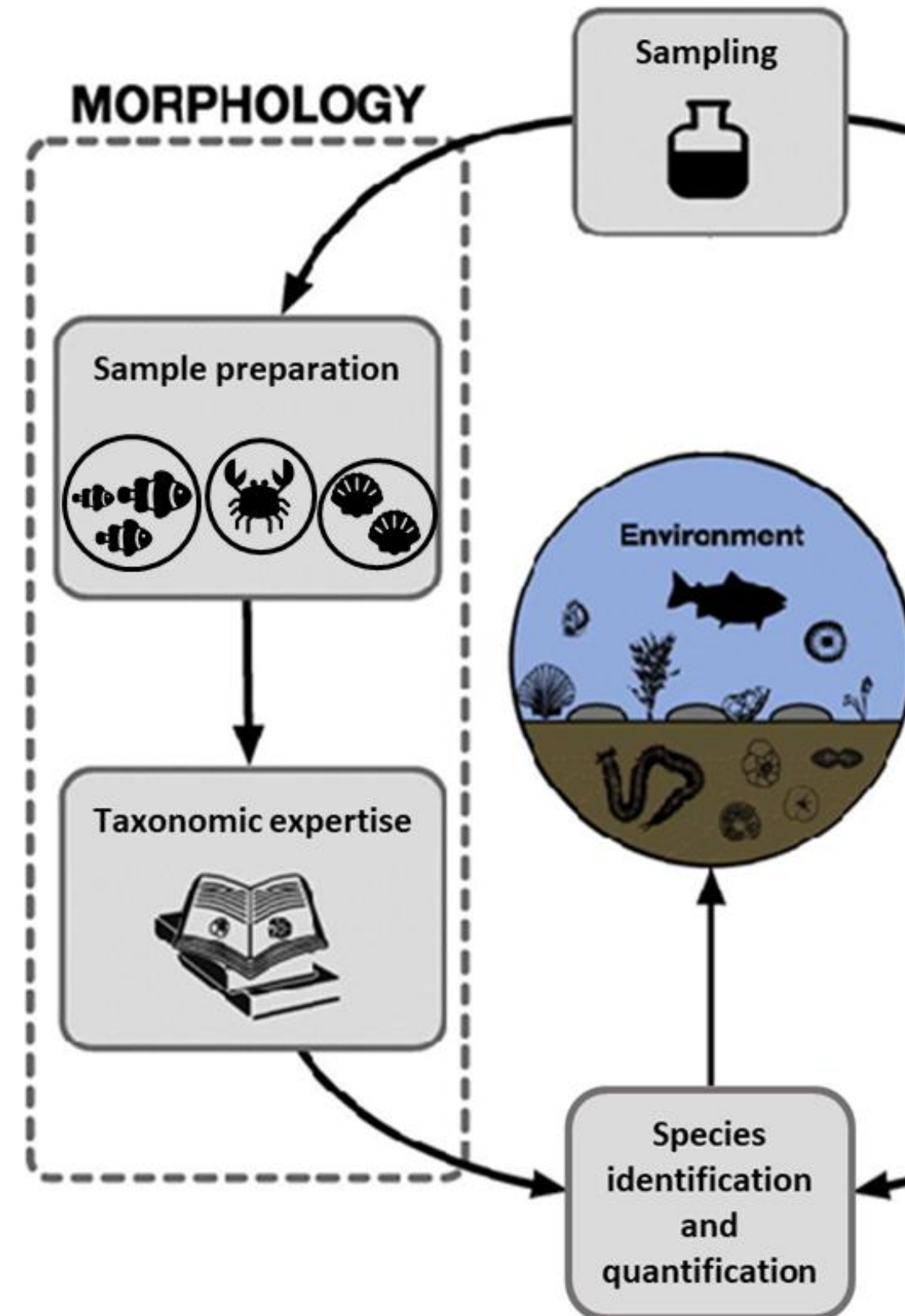
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Traditionally, studies of biofouling communities have been based on **morpho-taxonomic** approaches :

- ↳ quantitative data (abundance)
- ↳ biomass
- ↳ size of organisms

But

- ↳ time-consuming
- ↳ require strong taxonomic expertise
- ↳ tend to underestimate discrete, cryptic or small species



eDNA metabarcoding

emerged as a new approach (Rimet et al. 2025) capable of detecting :

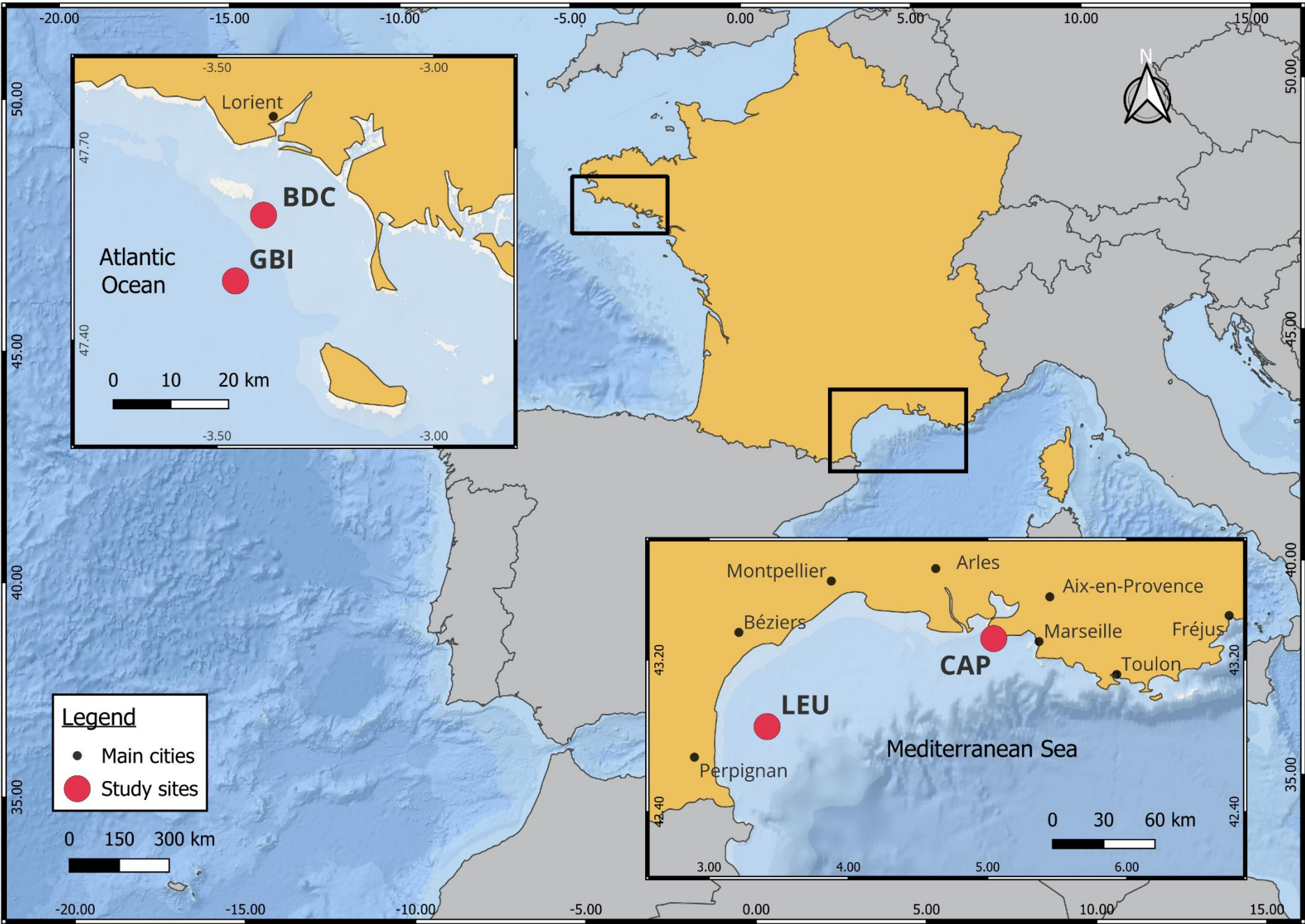
- ↳ a much wider range of taxa,
- ↳ rare species
- ↳ early stages of invertebrates
- ↳ microbes
- ↳ non-indigenous species

But

- ↳ Relative abundance or binary (+/-)
- ↳ Selectivity of primers (cf PCR)
- ↳ database accessibility and comprehensiveness

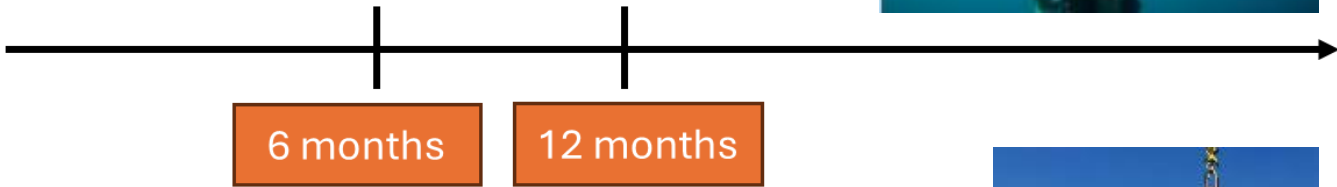
Combining **morpho-taxonomic** and **eDNA** metabarcoding approaches
to improve the characterisation of the diversity of biofouling community

- ↳ Validation of DNA extraction (Portas et al. 2022 – ABIOP+)
- ↳ Validation of genetic markers, associated primers and databases to cover the diversity of eukaryotes
COI (BOLD) and 18S rRNA (V7, PR2) genes
(Portas et al. 2022, 2023, 2024 – ABIOP+)
- ↳ How to proceed ? (Portas et al. in revision)



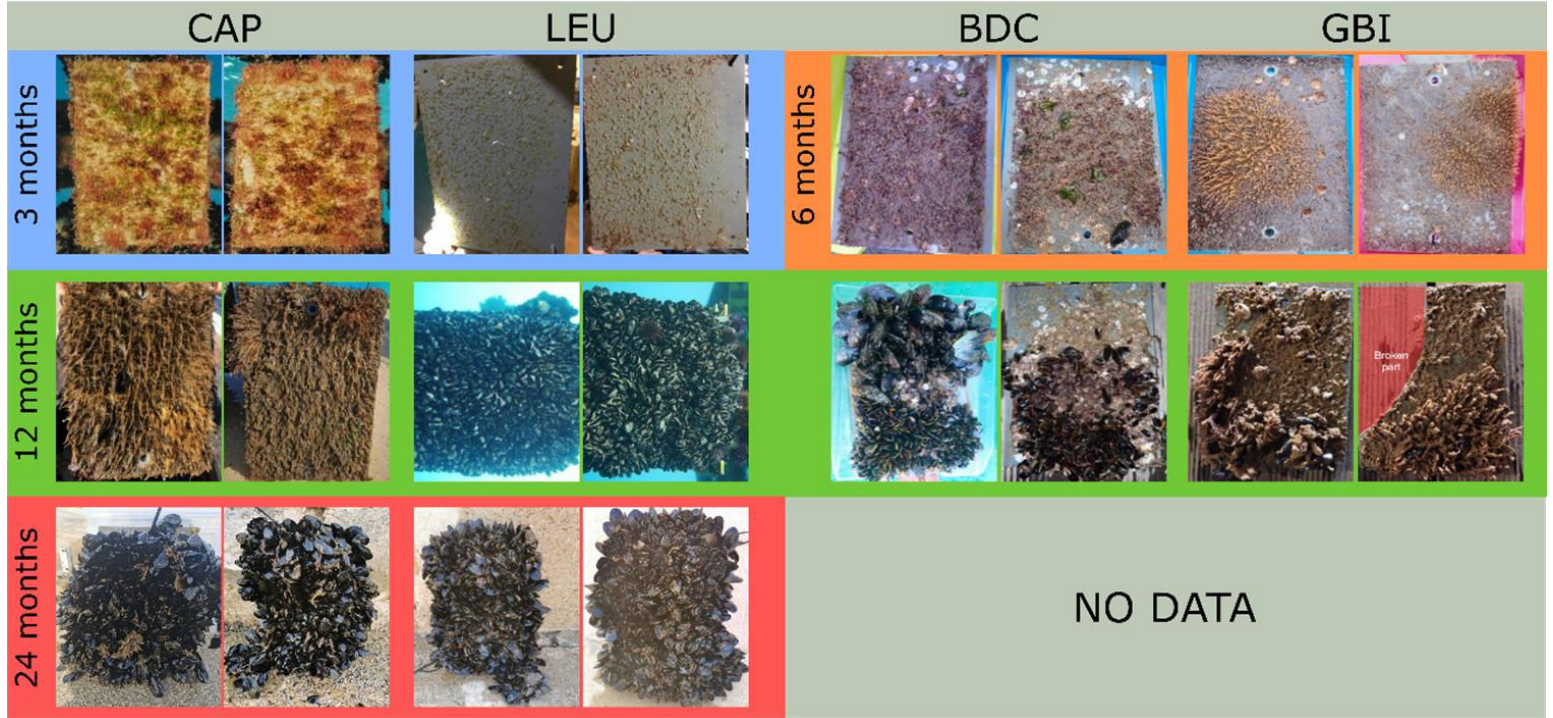
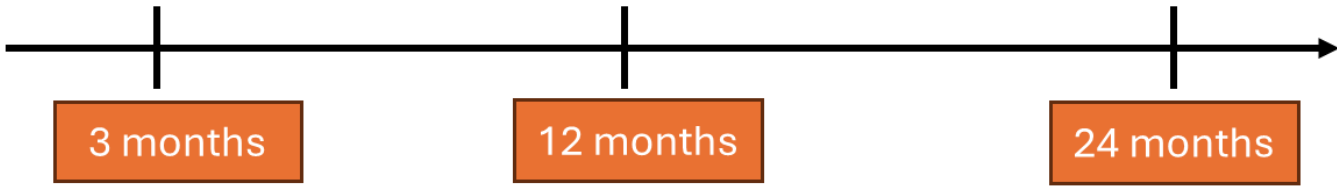
Atlantic :

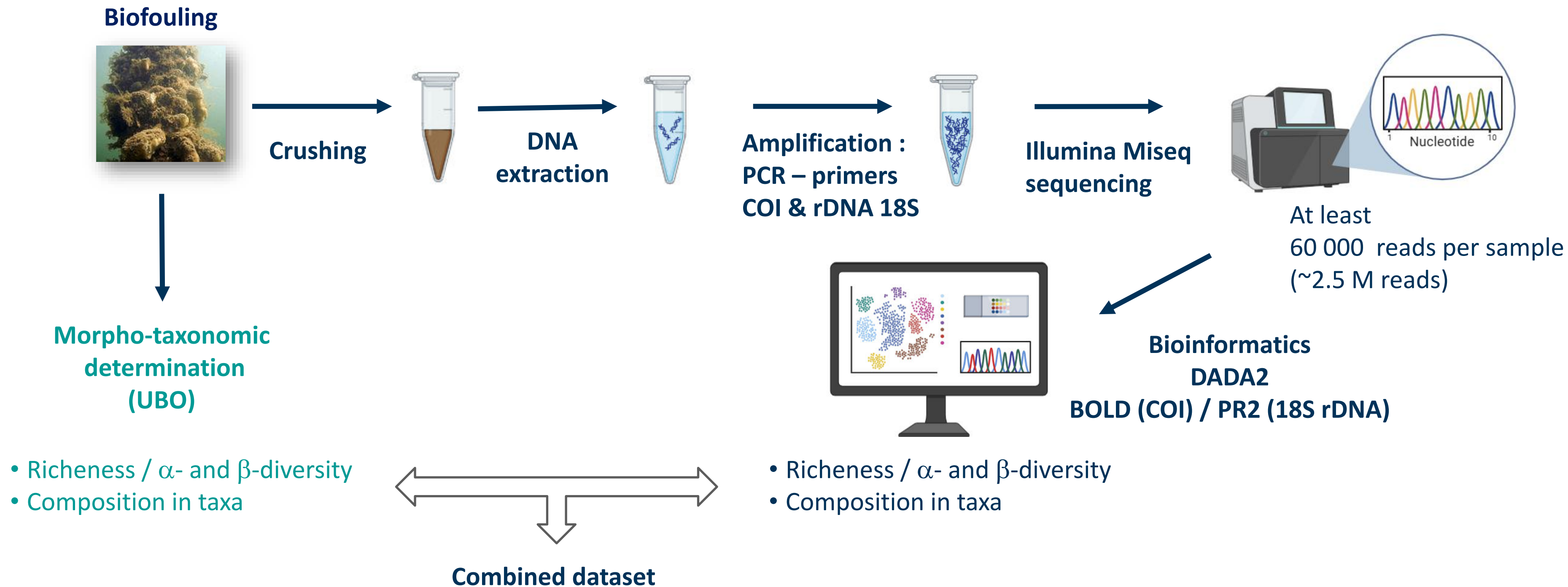
- Groix Belle-Île : APPEAL buoy
- Basse des chats



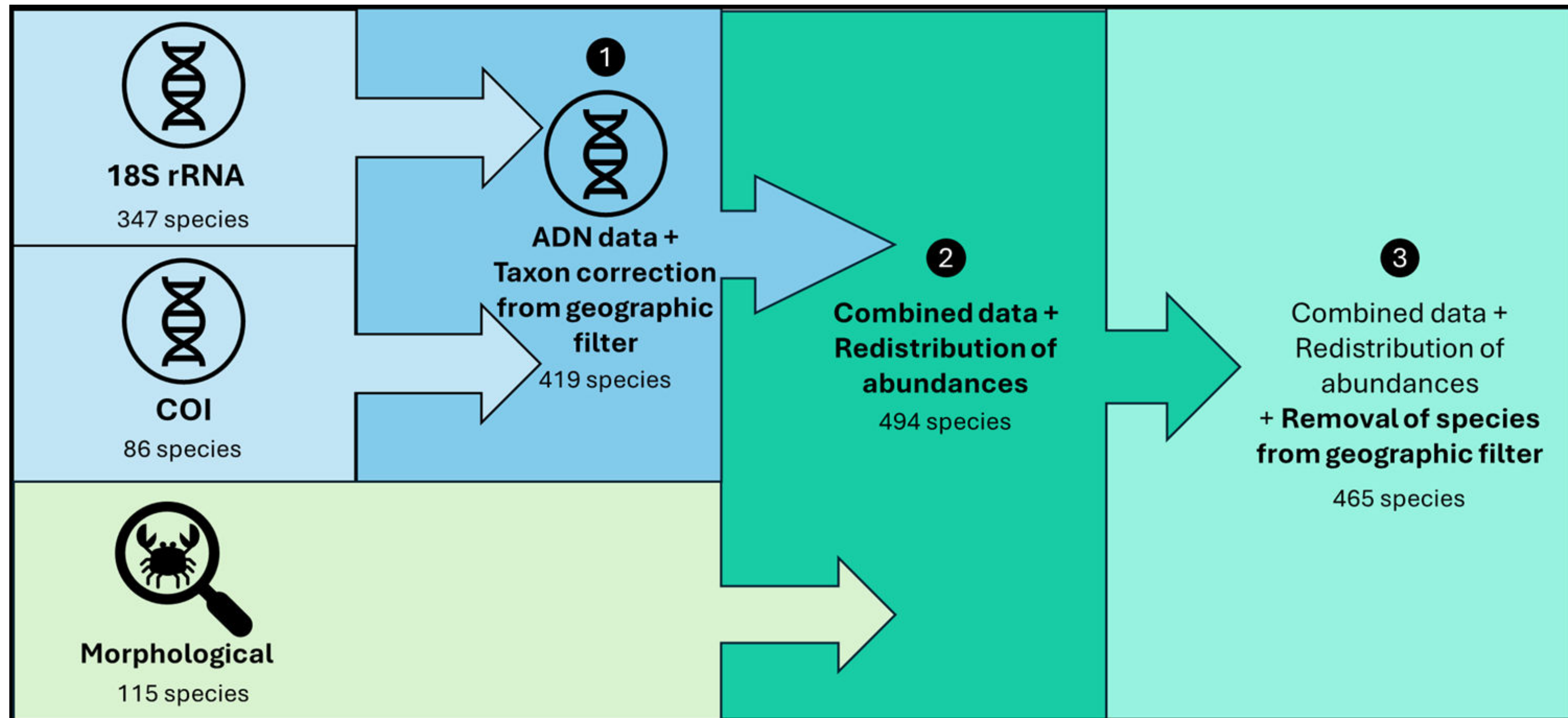
Mediterranean :

- Cap Couronne
- Leucate (BOB buoy)

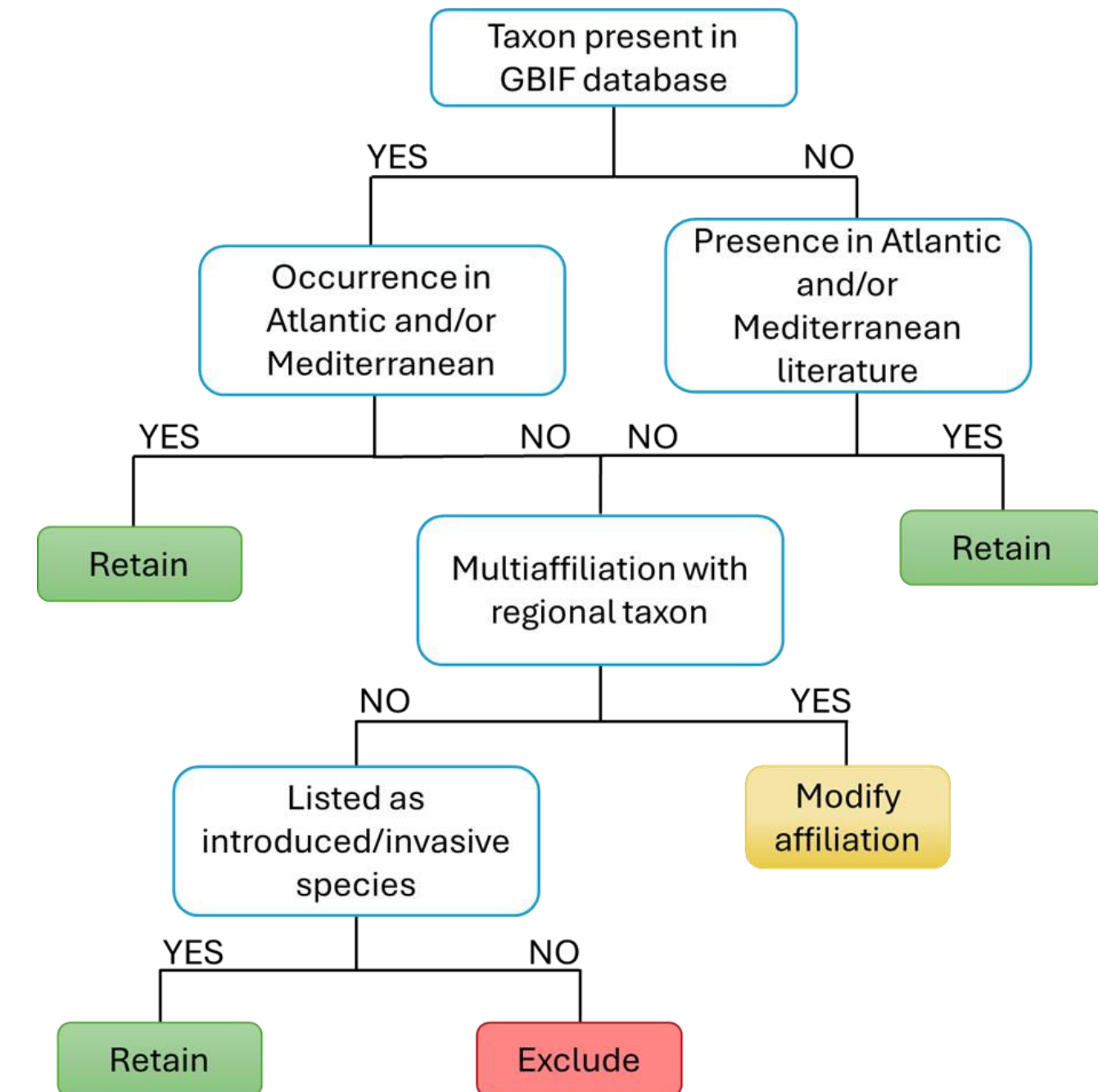
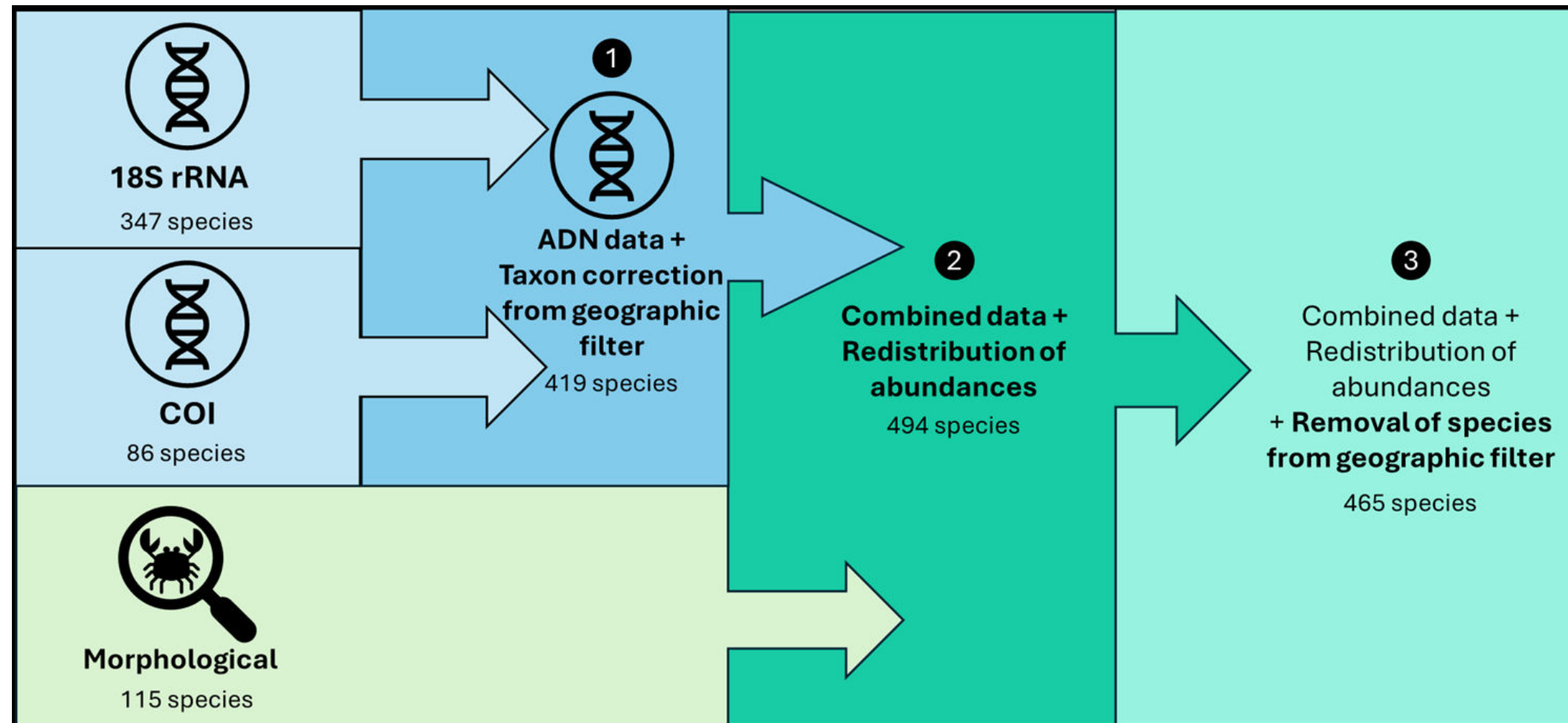


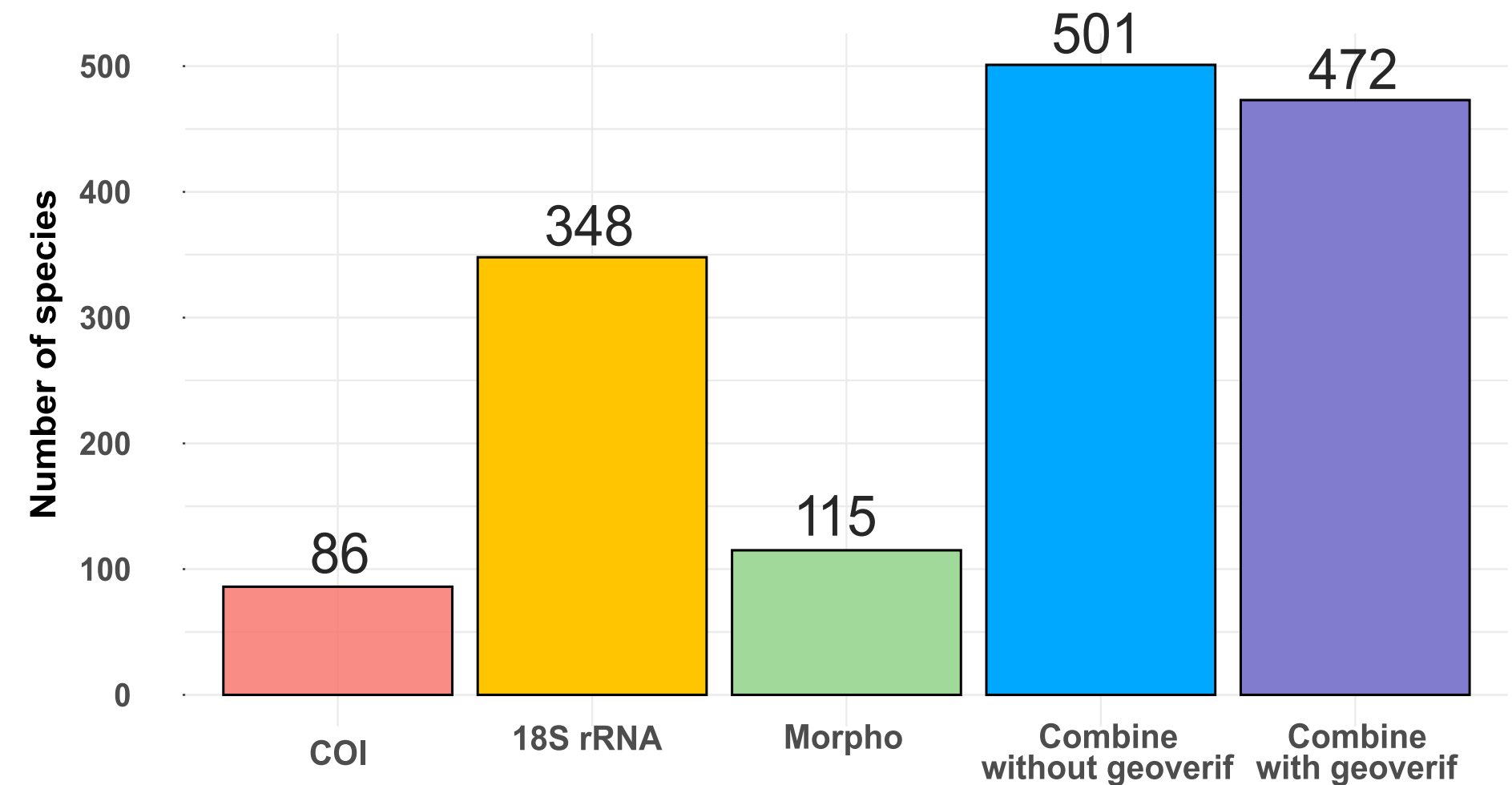
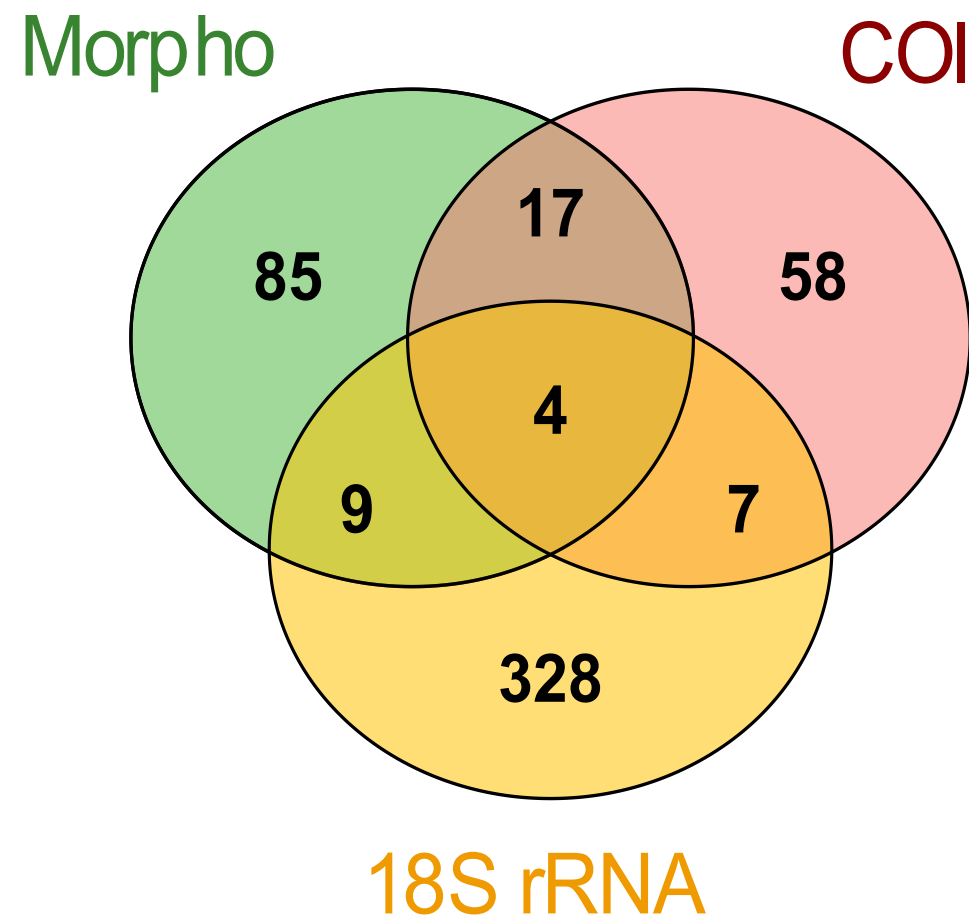


Workflow:

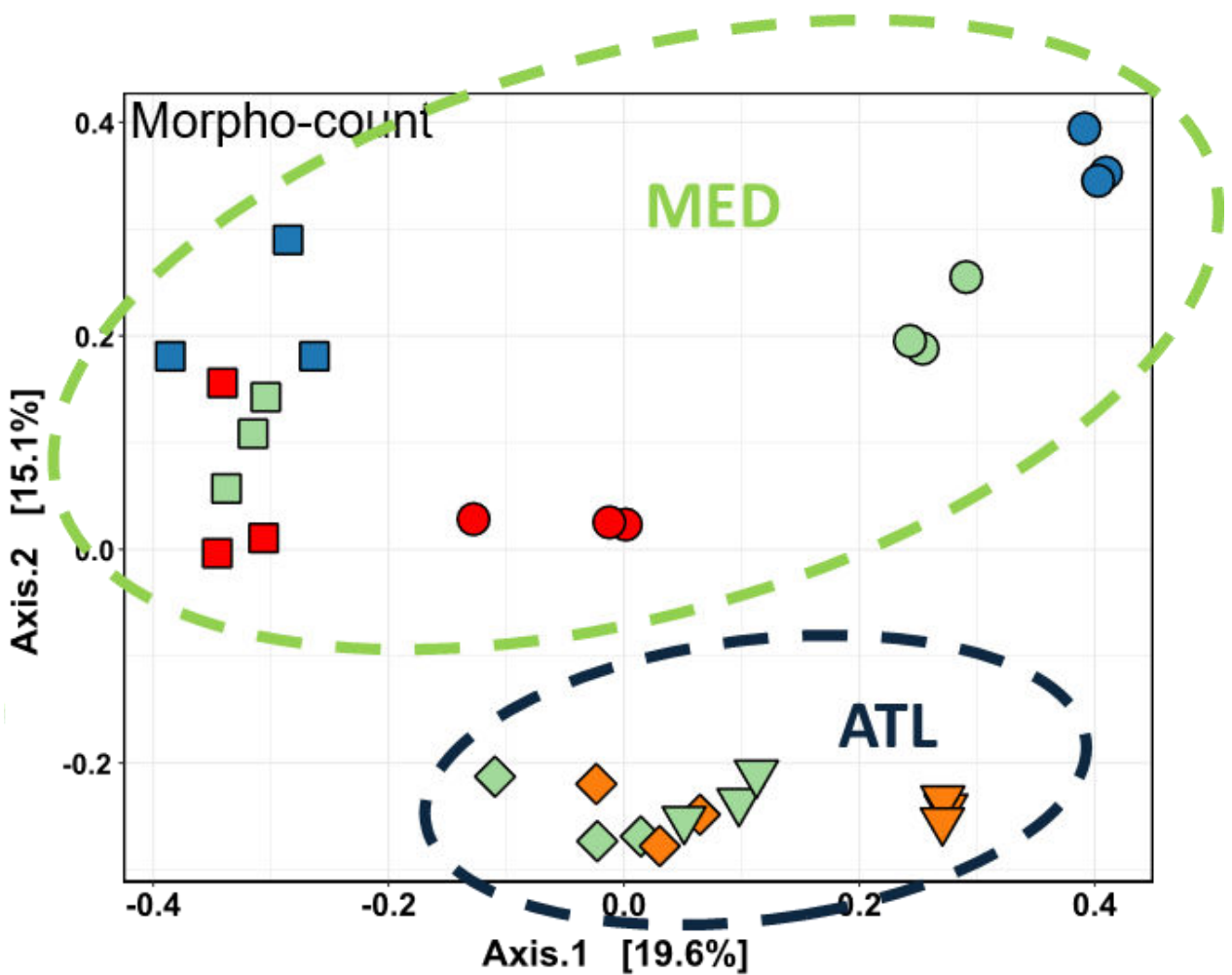


METHODS – COMBINED APPROACH

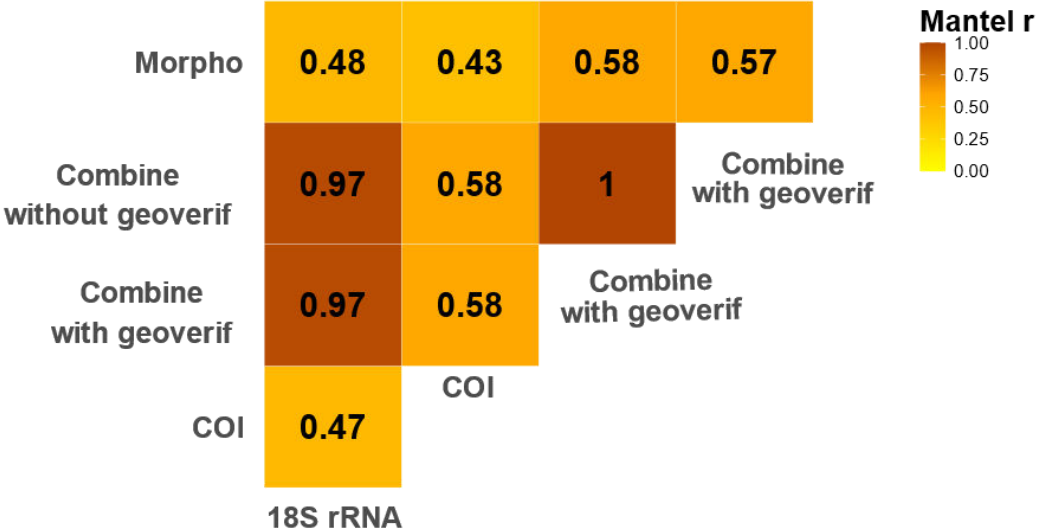
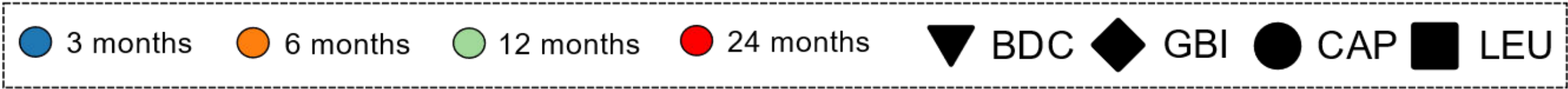




- 18S rDNA analysis identified a greater number of species than COI or morphological approaches
- The number of species shared among the three methods is low
- Each method detects different species
- Combining these methods allows for the identification of more species than using each method separately



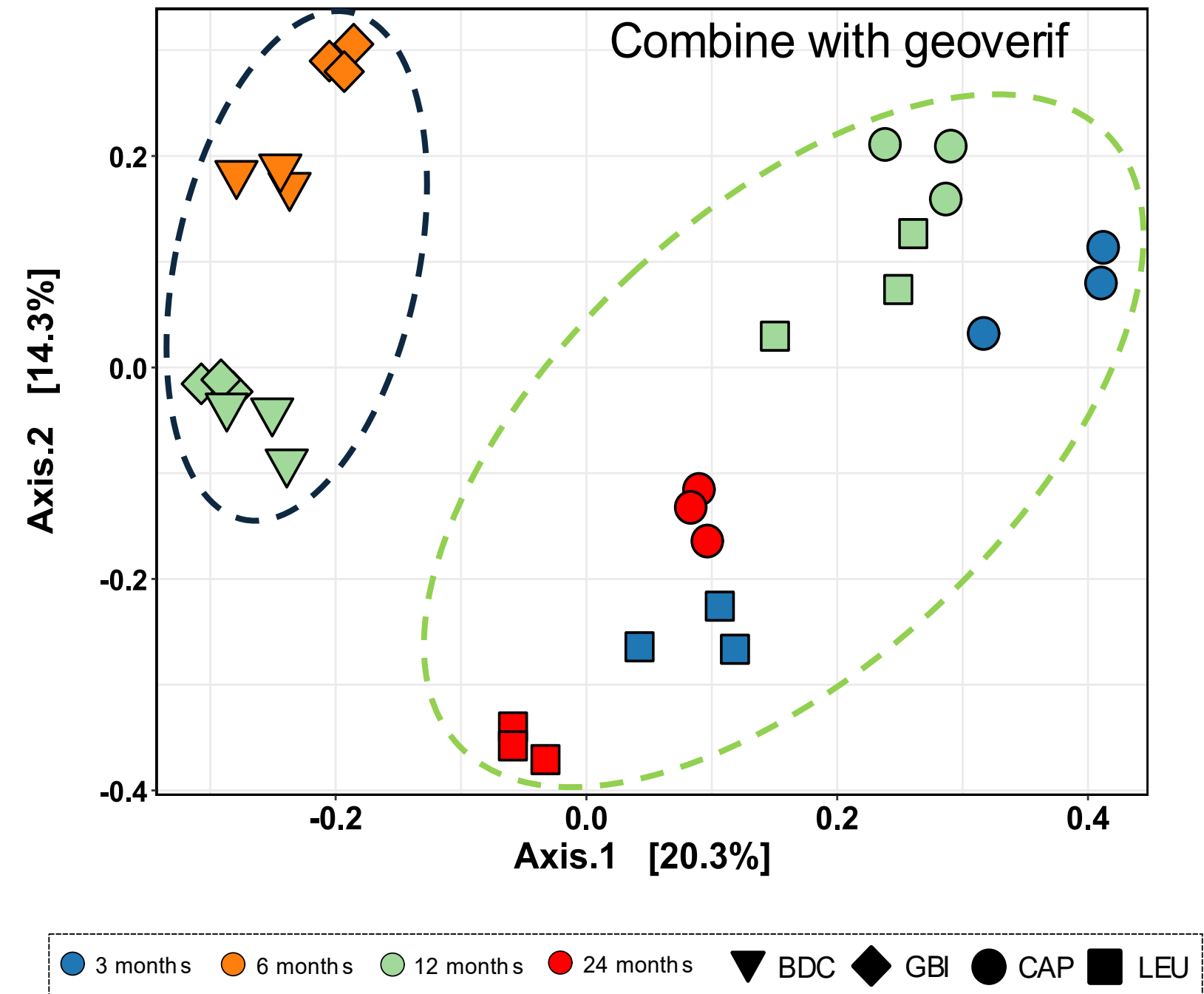
Permanova $p > 0.001$



Combined dataset:

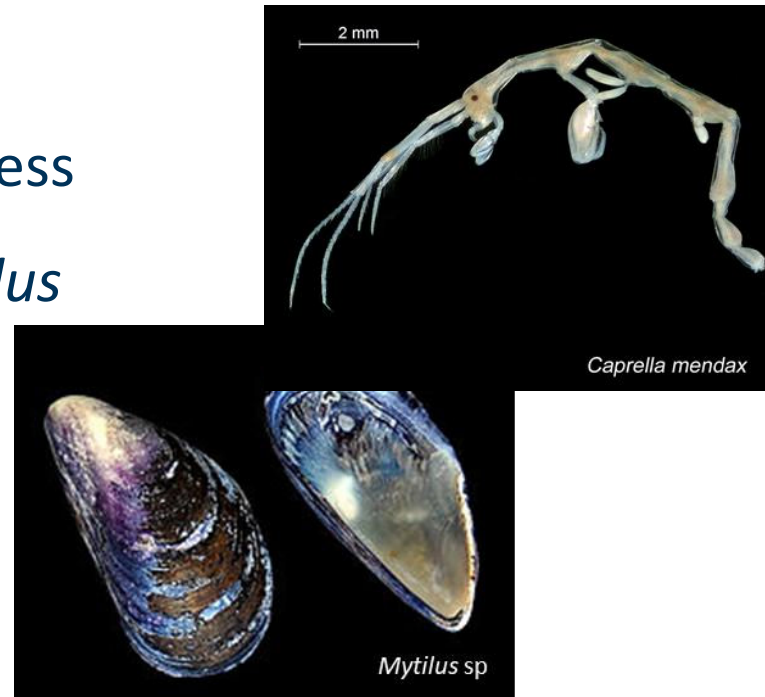
⇒ Confirm spatial dissimilarity ($p > 0.001$)

⇒ Improved temporal clustering



Huge differences

➤ Morpho-taxonomy: low richness
mainly *Jassa*, *Caprella* et *Mytilus*



➤ Molecular approaches= higher diversity

18S rDNA:

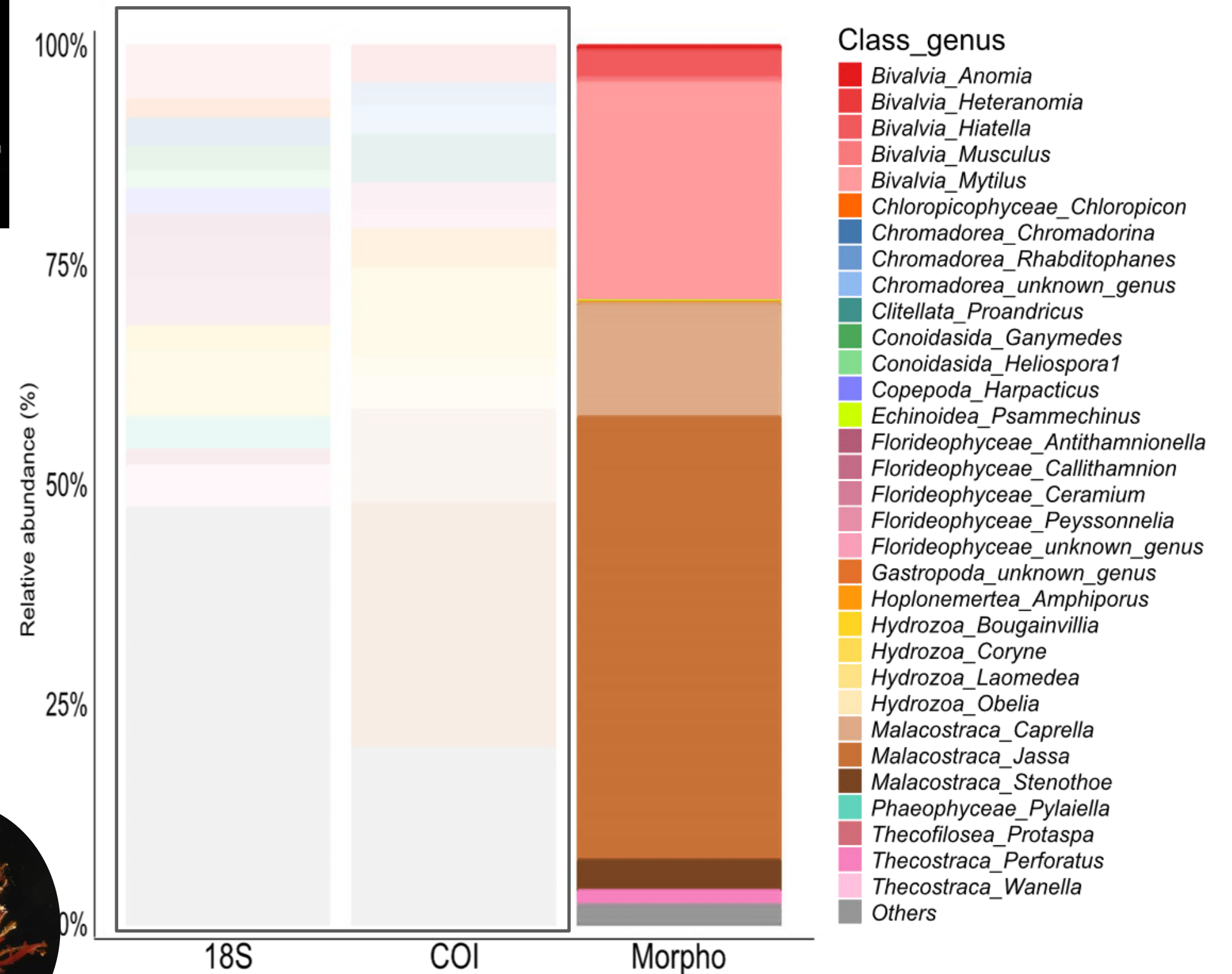
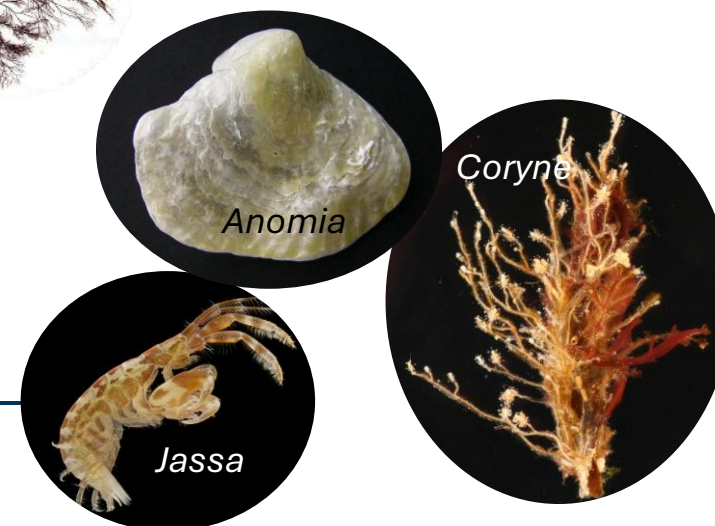
56% microeukaryotes (Others)

Floridophyceae



COI:

Bivalvia, Hydrozoa, Malacostra



Combined dataset:

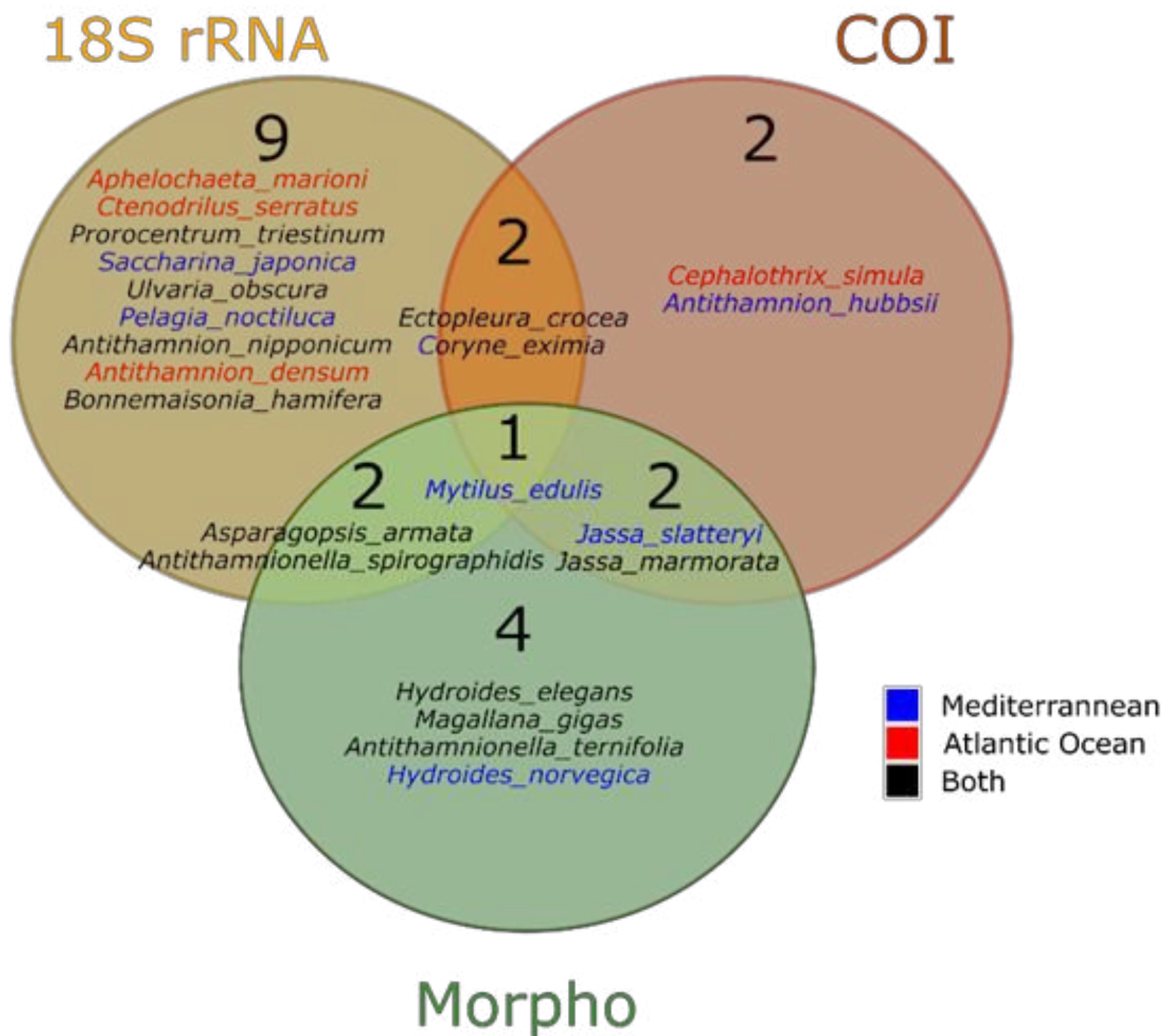


Non indigenous (NIS) species :

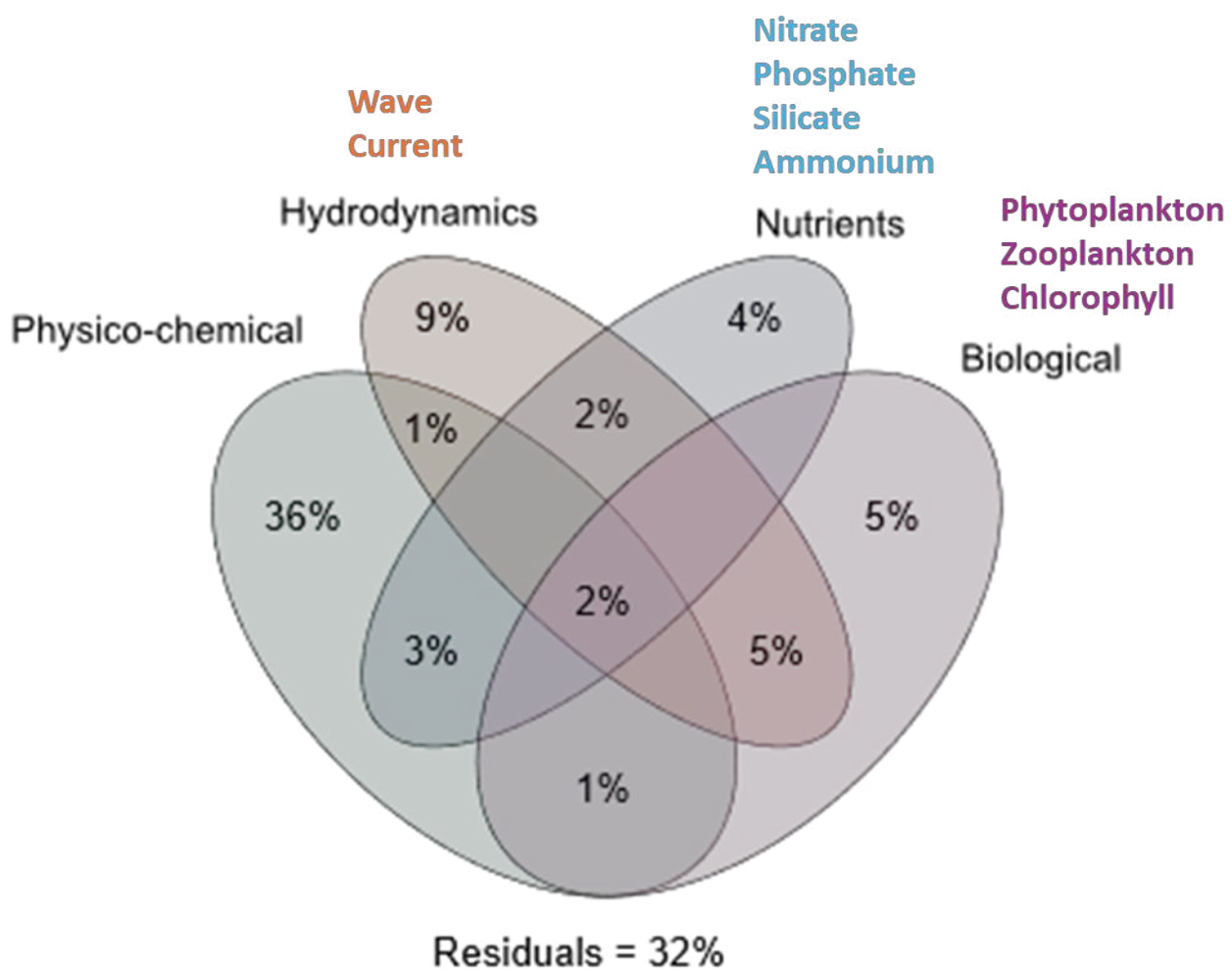
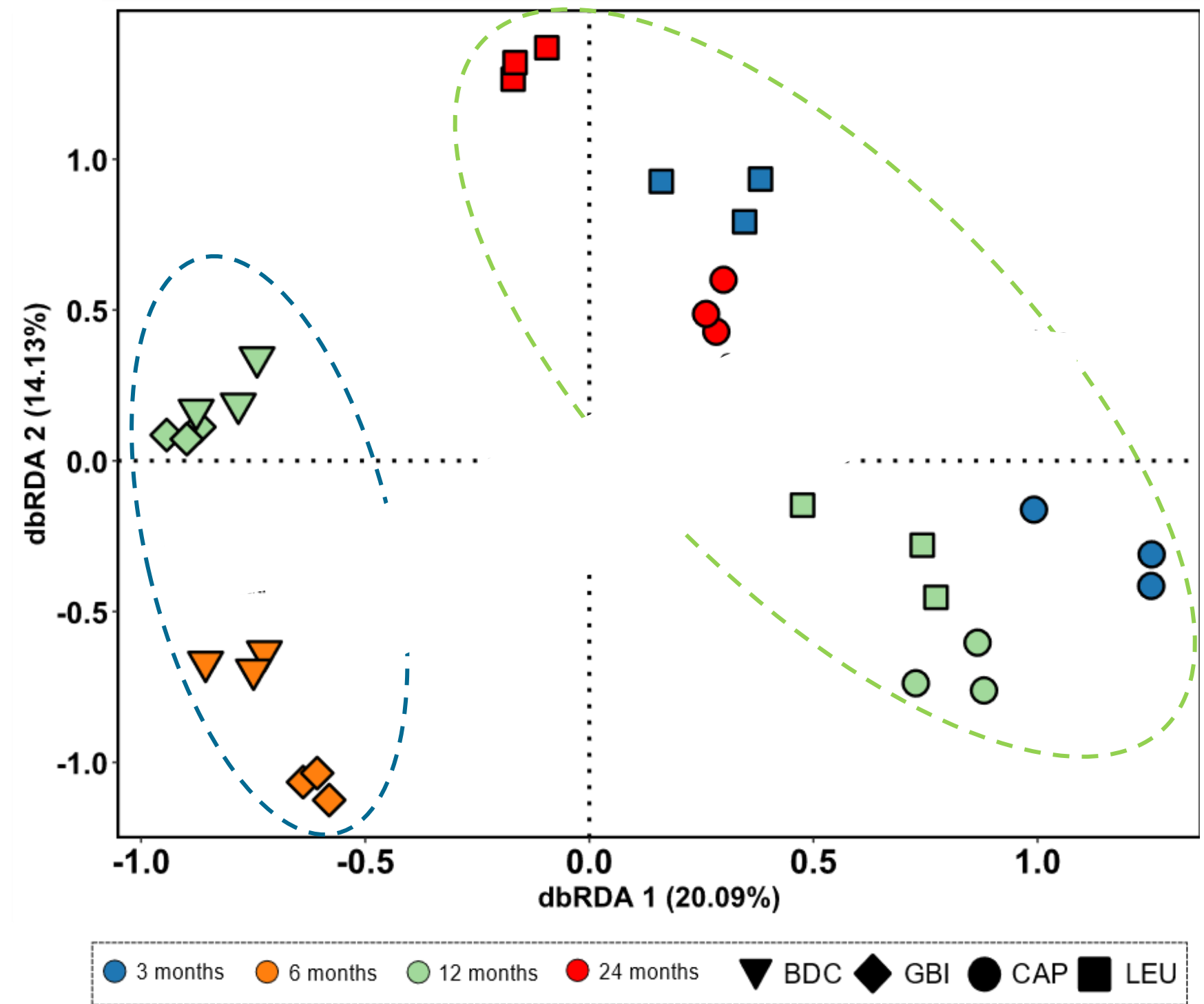
Morpho-taxonomy : 4

18S rDNA: 9

COI: 2



Based on Copernicus database



Variance partitioning

- ✓ Combination of morpho-taxonomic and molecular methods enables enhanced detection of biofouling communities in offshore environments
- ✓ Each method has its own advantages :
 - morpho-taxonomy providing quantitative data and visual confirmation of dominant macro-organisms
 - metabarcoding reveals a broader spectrum of biodiversity, including microeukaryotes and cryptic or early-stage taxa
- ✓ The integrative combination of these methods, with geographic filtering, corrected methodological biases and significantly improved taxonomic resolution and species detection in offshore environments
- ✓ The combination of these methods also improves the detection of NIS

Thank you for your attention!

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