

Exploring the changing dynamics of pelagic metazoan communities in the Beagle Channel: Insights from an integrated research approach



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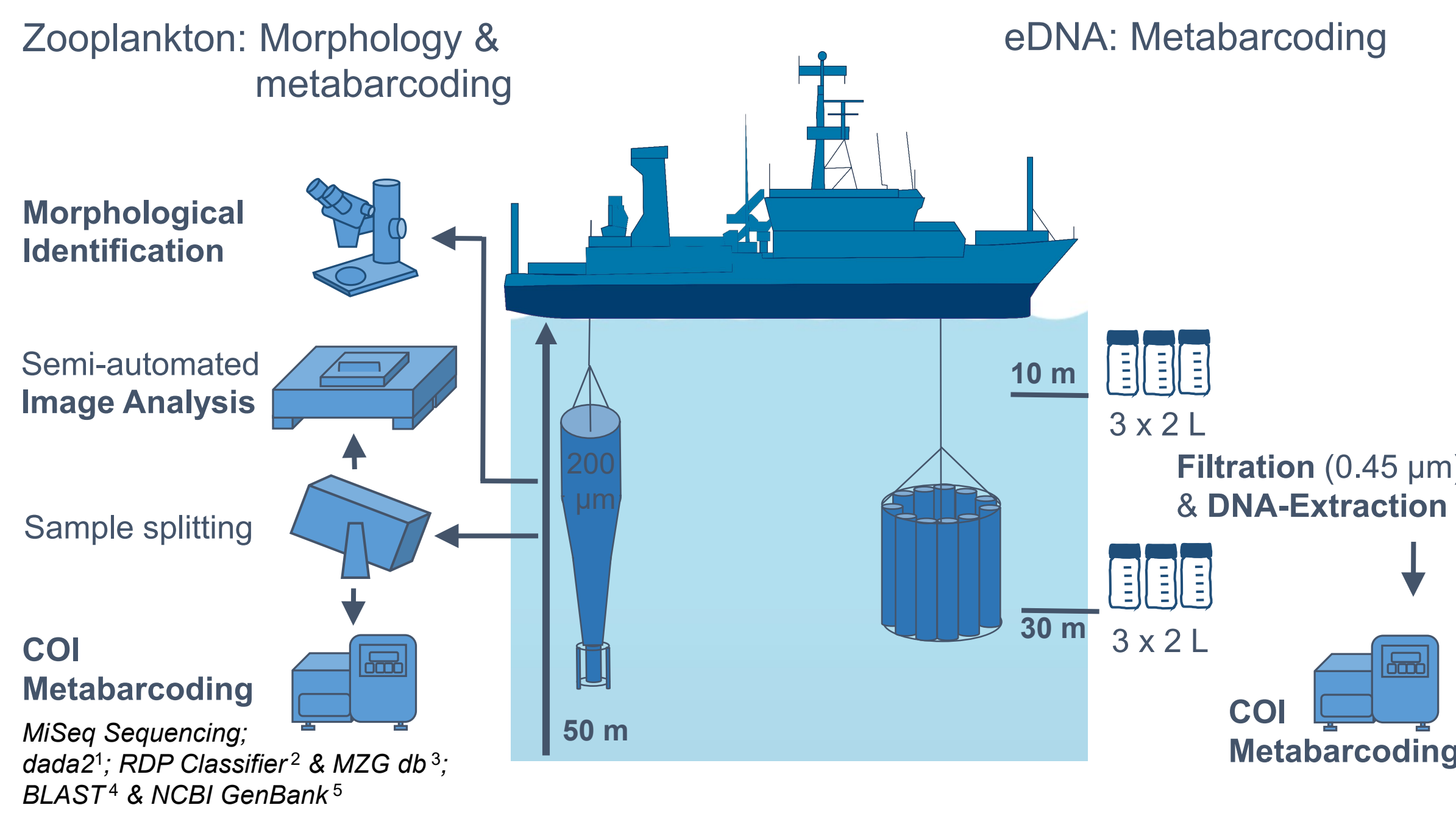
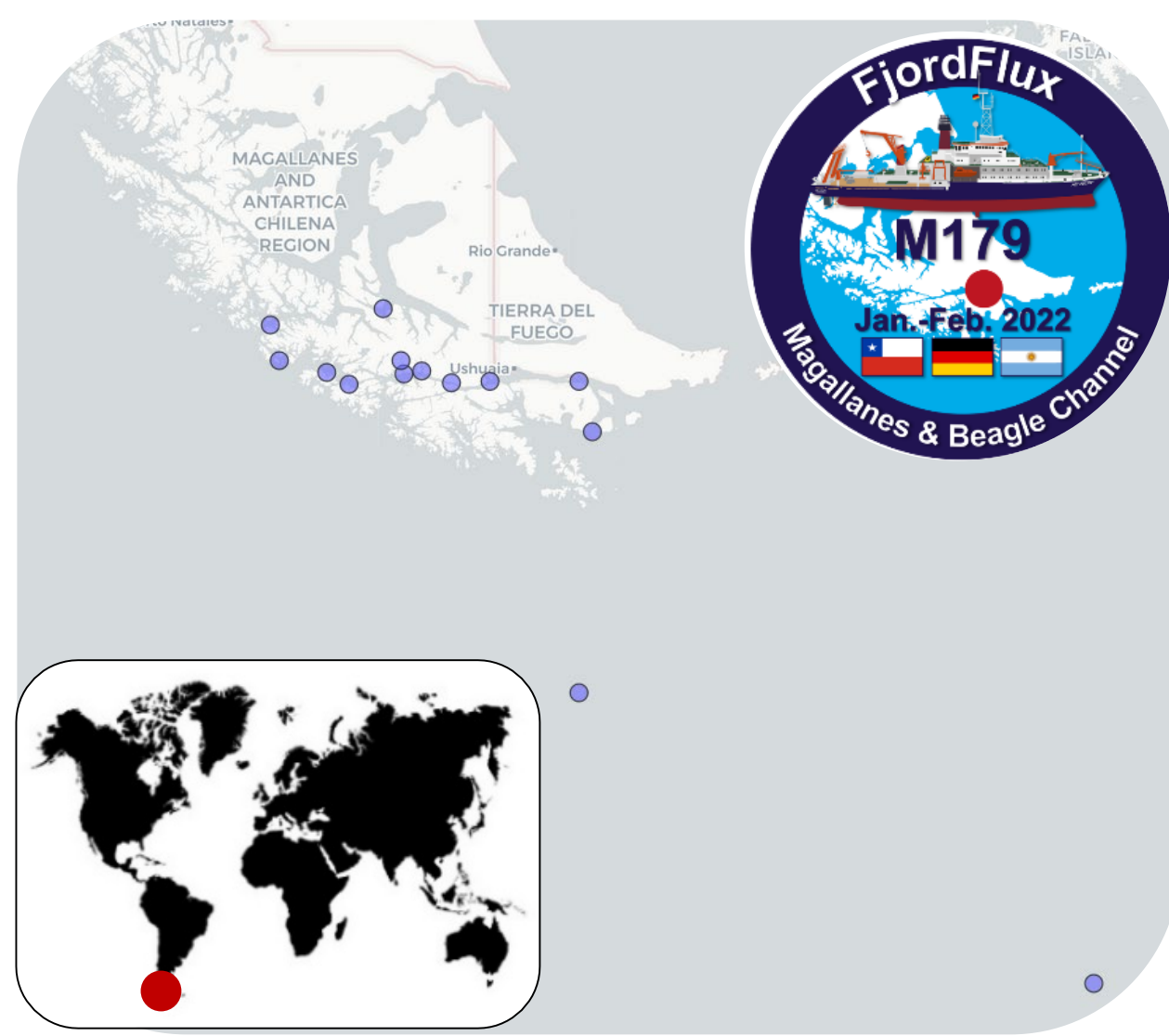
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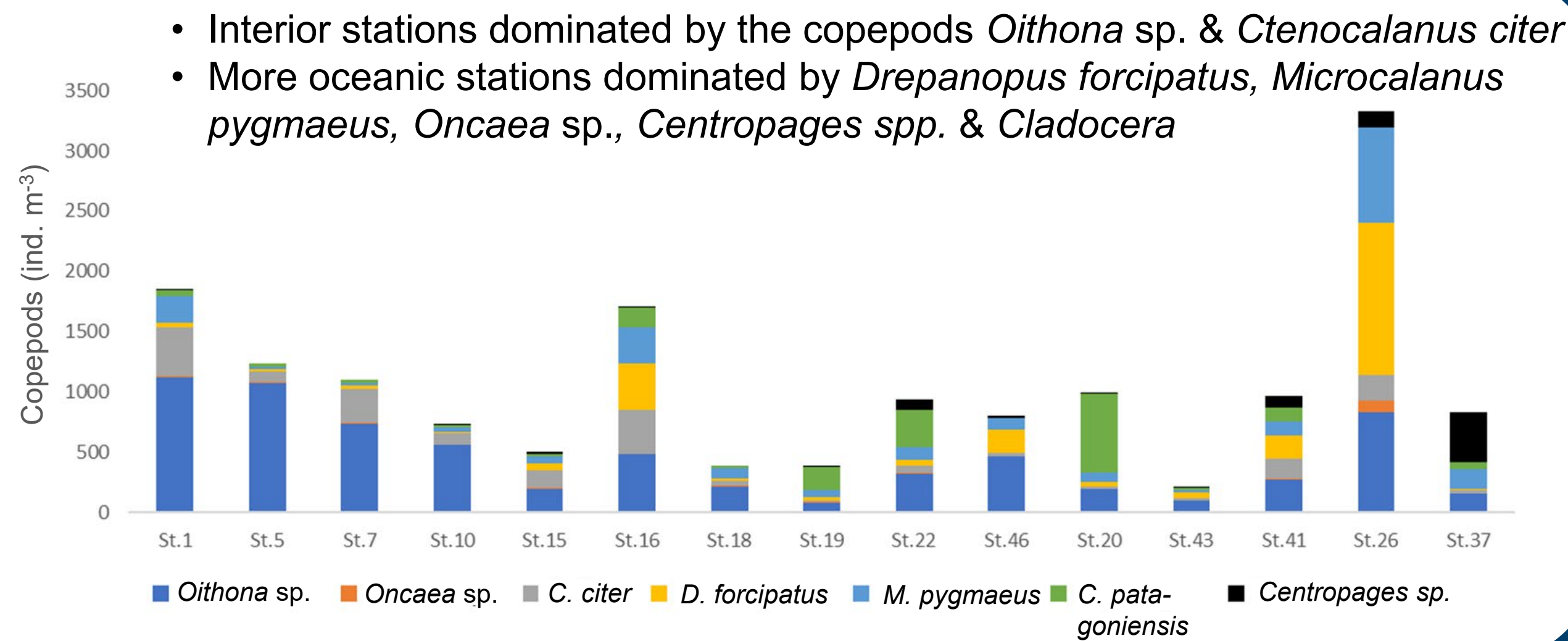
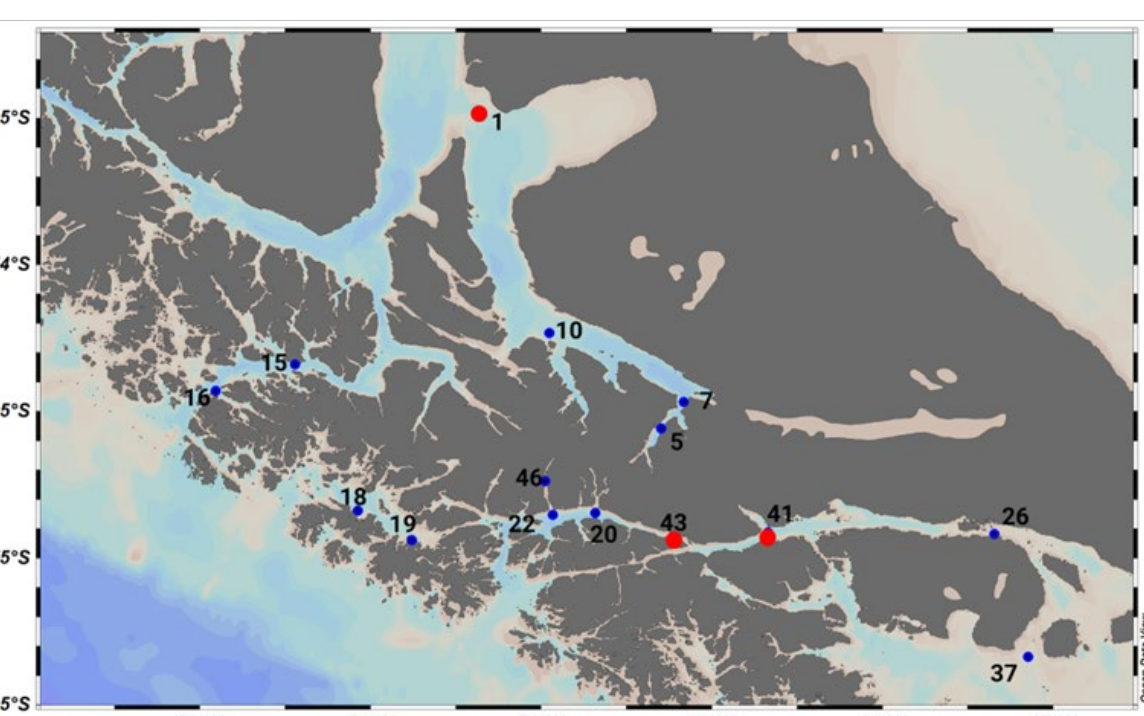
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Our Approach



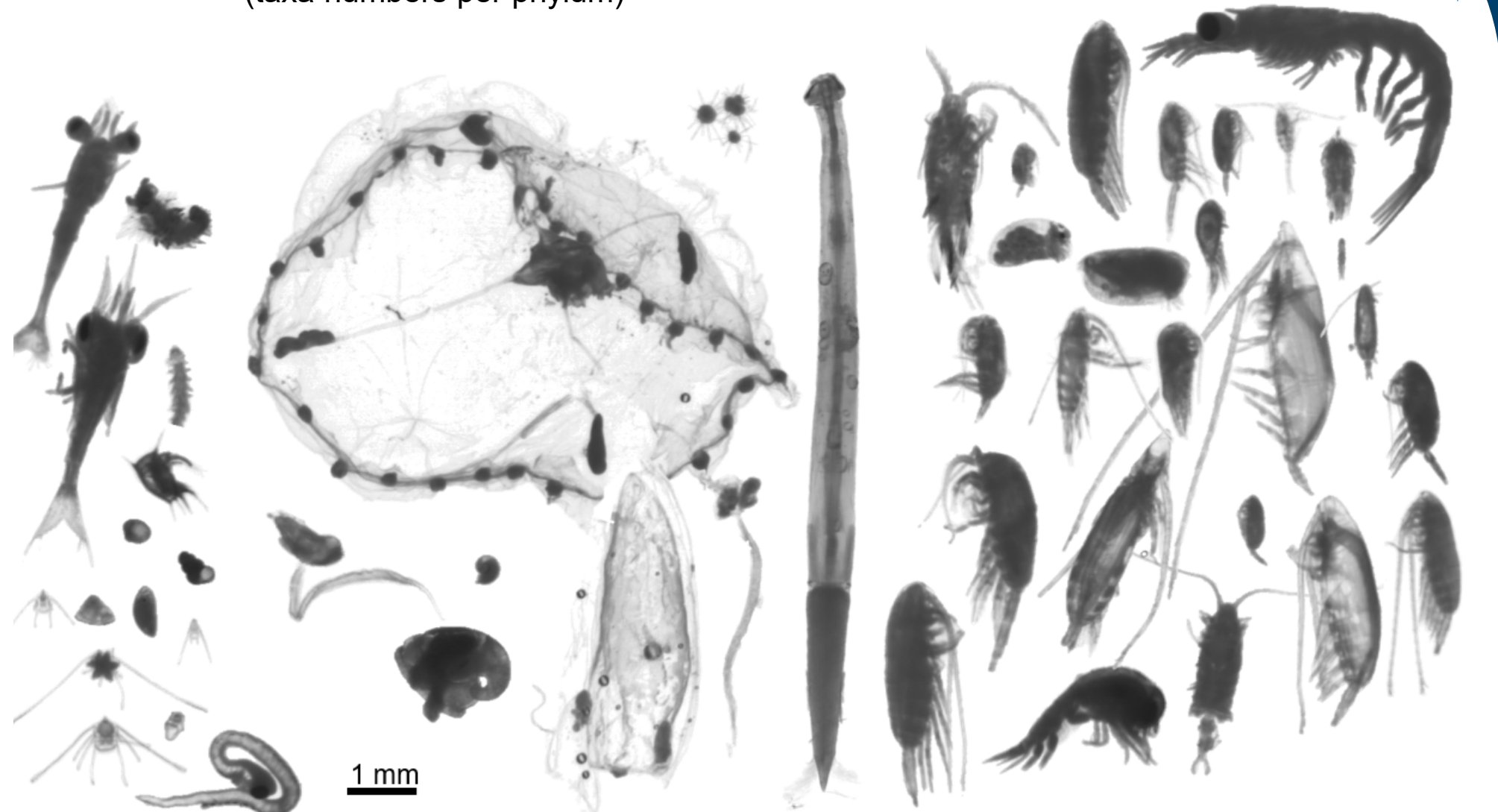
The **Beagle Channel system** in Patagonia is currently considered to be in a "pristine" state. However, it is facing growing threats from climate change & anthropogenic pressures. During the Fjordflux cruise (RV Meteor, M179) conducted in early 2021, we sampled the **pelagic metazoan community** along an east-west transect within the Beagle Channel, encompassing areas with varying degrees of deglaciation & eutrophication. Our primary objective was to analyze biodiversity & abundance using an **integrative approach**. Zooplankton was sampled by vertical tows (WP2, 0-50m) and analyzed by morphology (stereomicroscope & image analysis (ZooScan)) & molecular genetic multi-species analysis (COI metabarcoding). To capture zooplankton diversity beyond what nets could provide, water samples from 10 & 30 m were analyzed based on environmental DNA (eDNA) COI metabarcoding.

Zooplankton



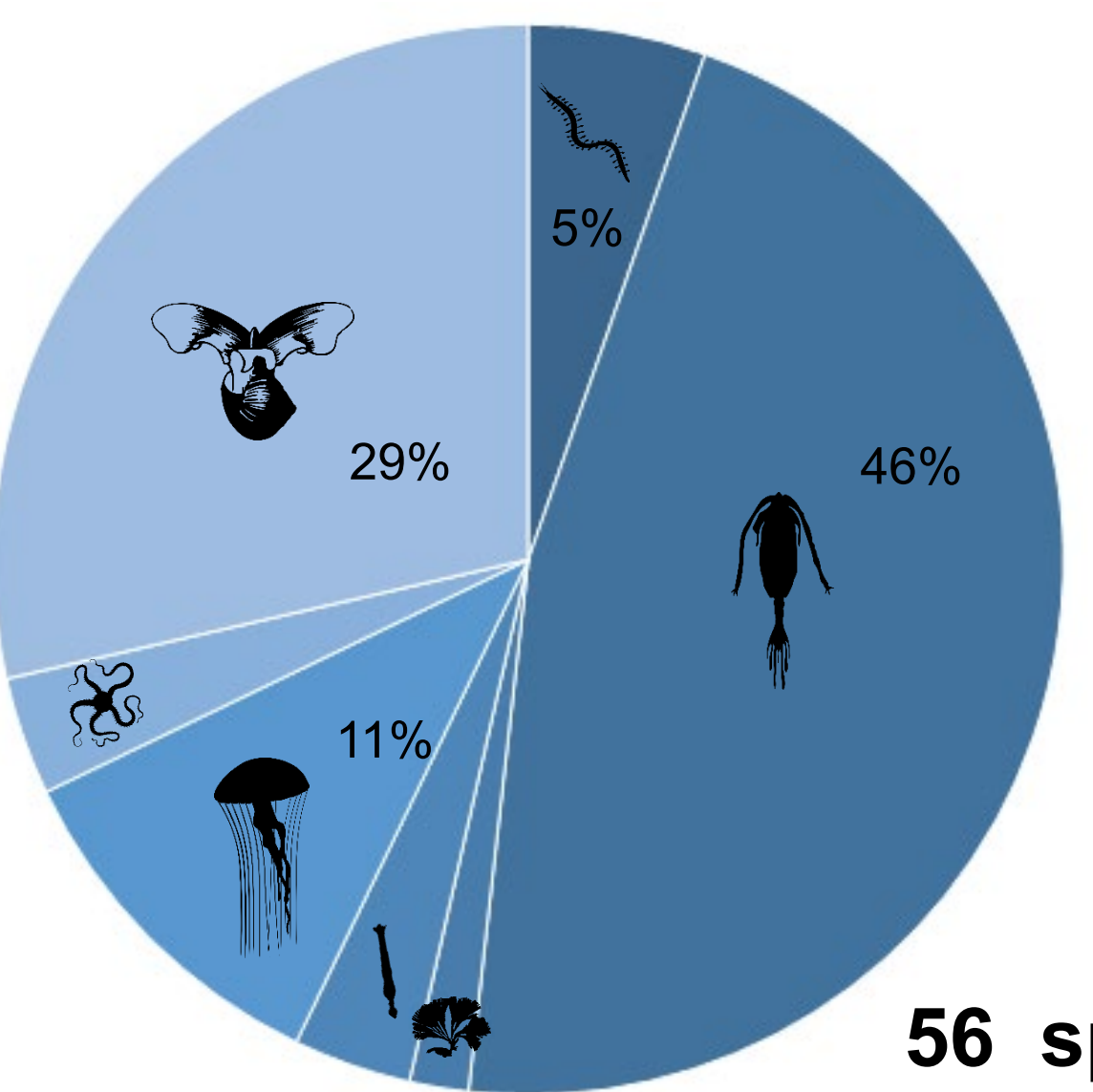
Zooplankton

(taxa numbers per phylum)



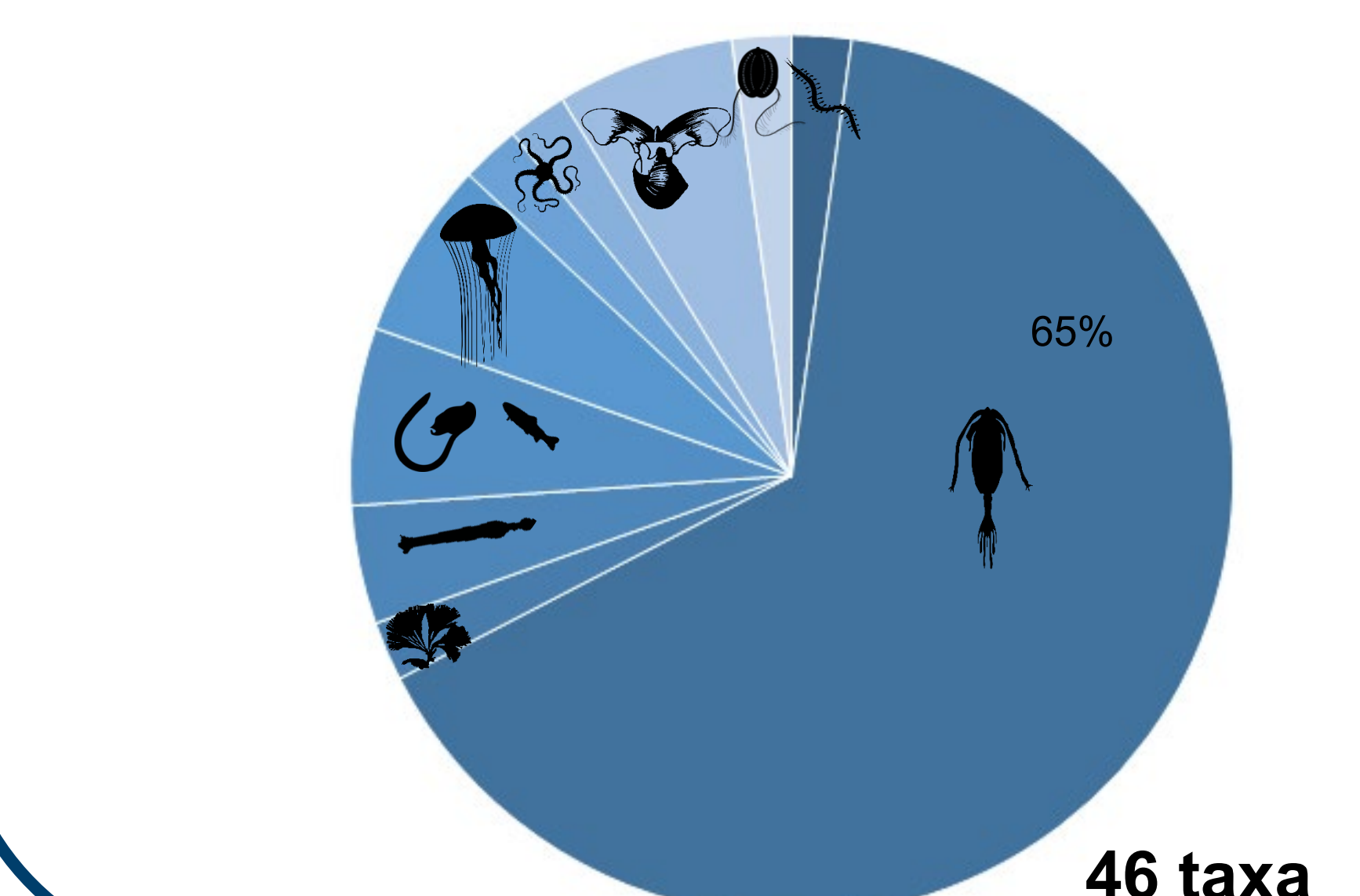
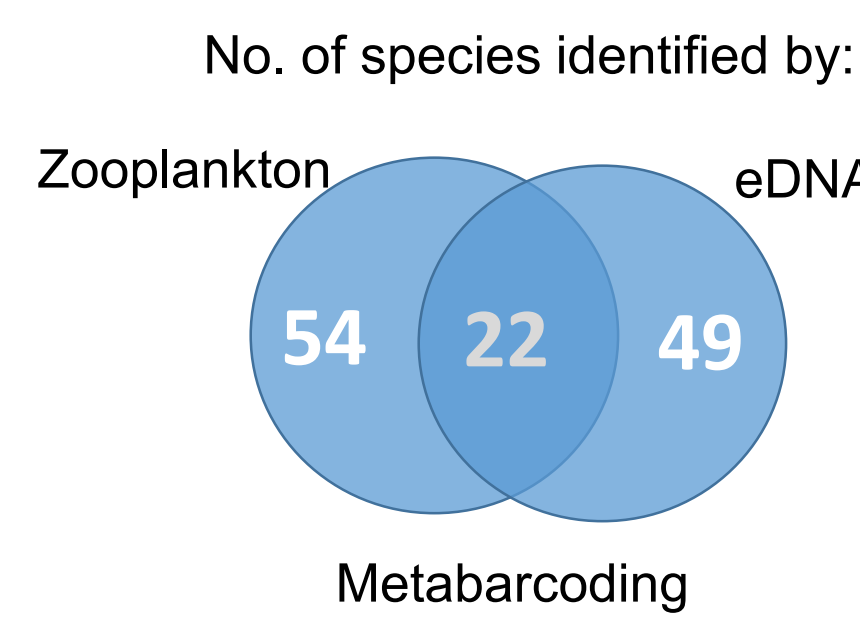
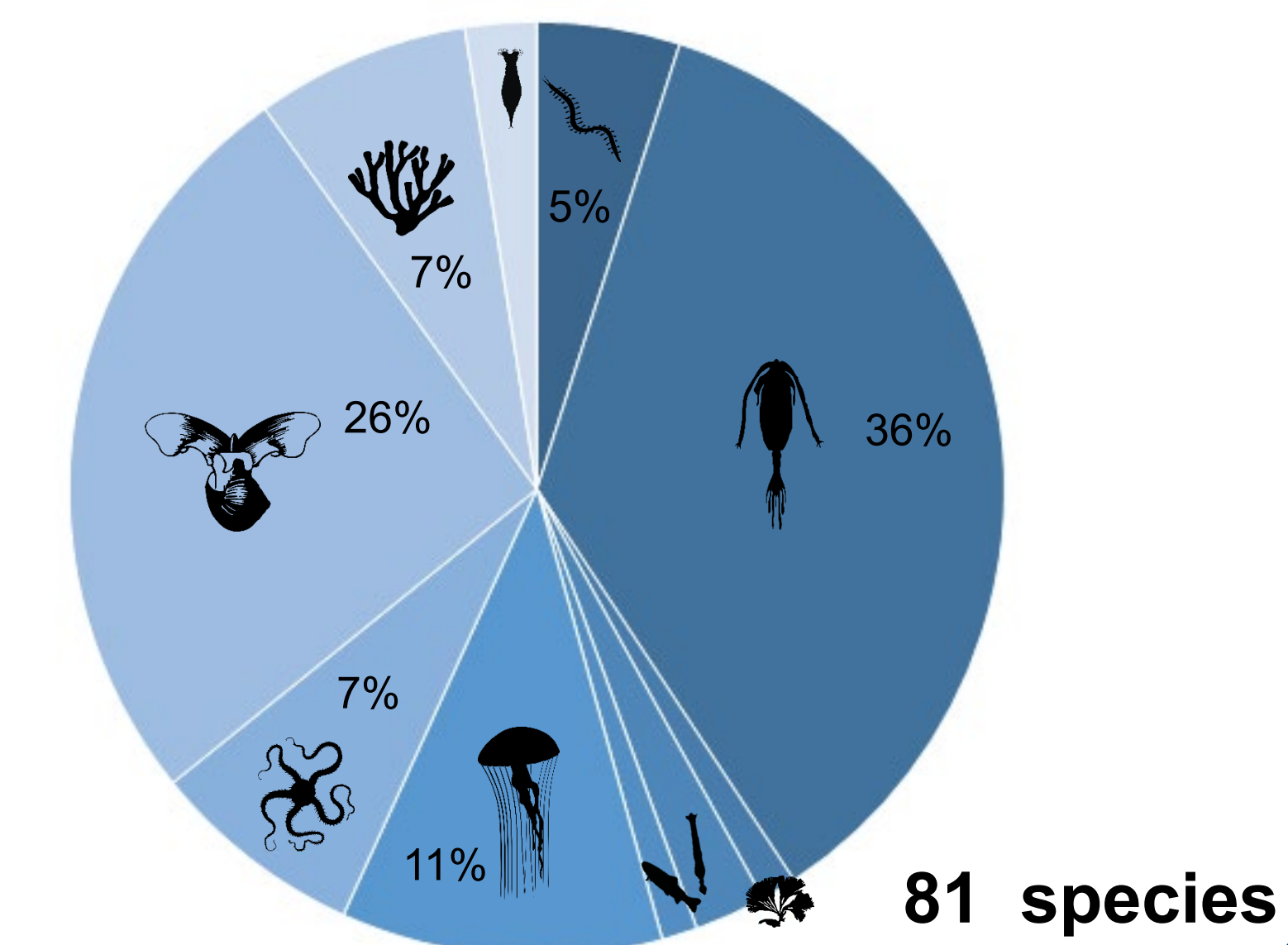
Zooplankton

(species numbers per phylum)



Zooplankton + eDNA

(cumulative species numbers per phylum)



Integrated Outcomes

Identification of holoplanktonic crustaceans by **morphology only** (in blue), **metabarcoding only** (in red) & **both approaches** (in black).

- | | | |
|-----------------------------------------|--------------------------------------|------------------------------|
| <i>Acartia</i> sp. | <i>Neocalanus tonsus</i> | <i>Themisto gaudichaudii</i> |
| <i>Calanoides acutus</i> | <i>Metridia lucens</i> | |
| <i>C. patagoniensis</i> | <i>Paraeuchaeta antarctica</i> | <i>Euphausiacea</i> |
| <i>Calanus australis</i> | <i>Paracalanus</i> cf. <i>parvus</i> | <i>Euphausia lucens</i> |
| <i>C. propinquus</i> | <i>Rhincalanus gigas</i> | <i>E. vallentini</i> |
| <i>C. simillimus</i> | <i>Subeucalanus longiceps</i> | <i>Thyssanoessa gregaria</i> |
| <i>Candacia</i> sp. | | <i>T. macrura</i> |
| <i>Centropages brachiatus</i> | <i>Oithona similis</i> | <i>Ostracoda</i> |
| <i>Clausocalanus brevipes</i> | <i>Oncaeidae</i> | <i>Evadne nordmanni</i> |
| <i>C. laticeps</i> | <i>Harpacticoida</i> (2 taxa) | <i>Podon leuckartii</i> |
| <i>Ctenocalanus citer</i> | | |
| <i>Drepanopus forcipatus</i> | | |
| <i>Microcalanus</i> cf. <i>pygmaeus</i> | | |

- **High identification success** of holoplanktonic **Crustacea** in all approaches
→ Crustacea are the most species-rich (diverse) group
- All approaches detected fewer Calanoida species in a similar study from Nov 1994 (30 species⁵ vs. 18 species (this study)) in the upper 50 m
- **Molecular approaches detect:**
→ More species, especially benthic & meroplanktonic species (i.e. Mollusca, Echinodermata, Bryozoa, Decapoda, Cnidaria)
→ *Calanoides propinquus*: This species has identical COI sequences with *C. simillimus*, so its presence is not clear
- **Molecular approaches did not detect**
→ *Centropages brachiatus*: No COI data available in sequence reference data bases
→ *Microcalanus* cf. *pygmaeus*: Potential primer bias as COI sequence data are available in sequence reference data bases

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