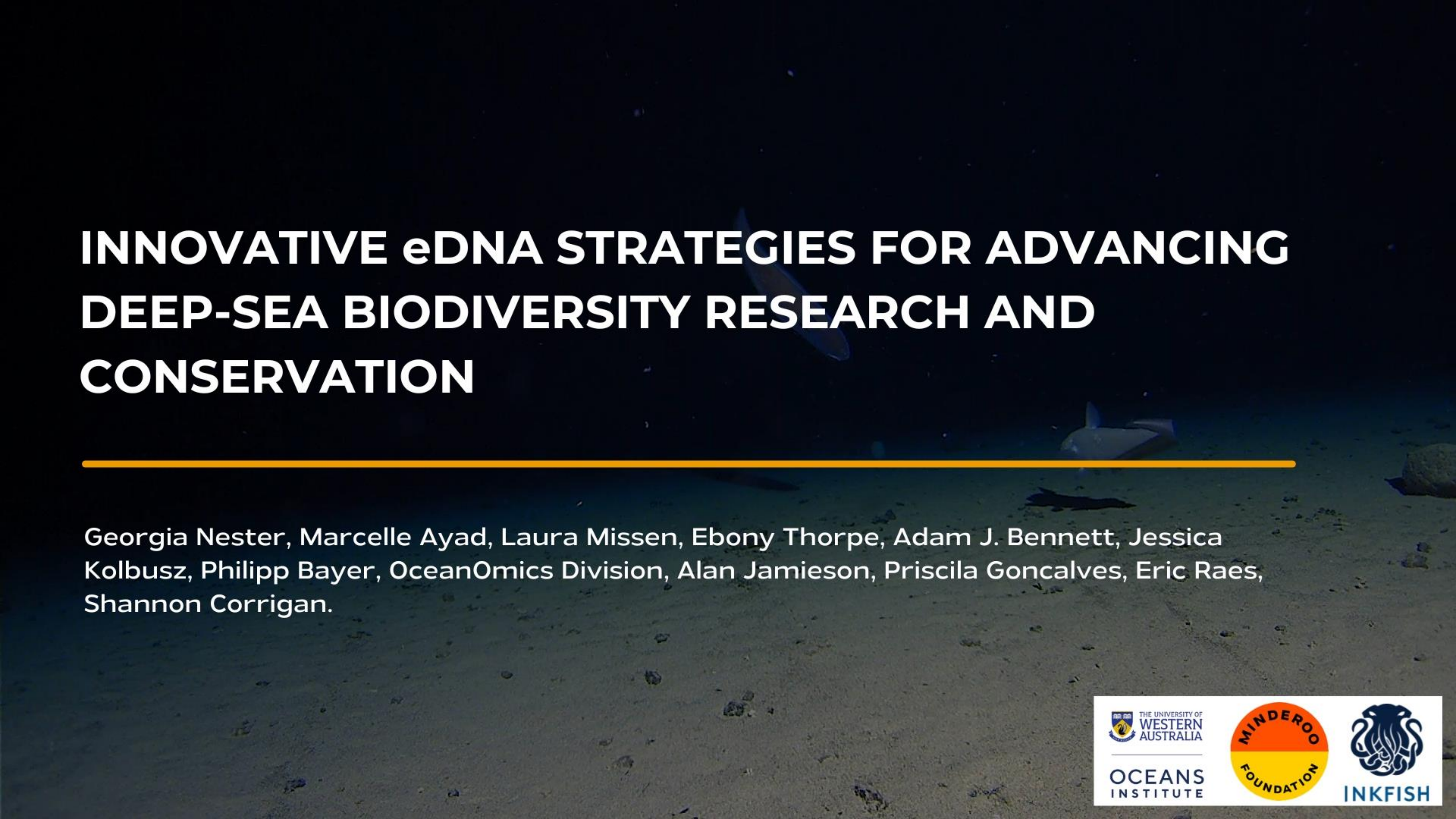
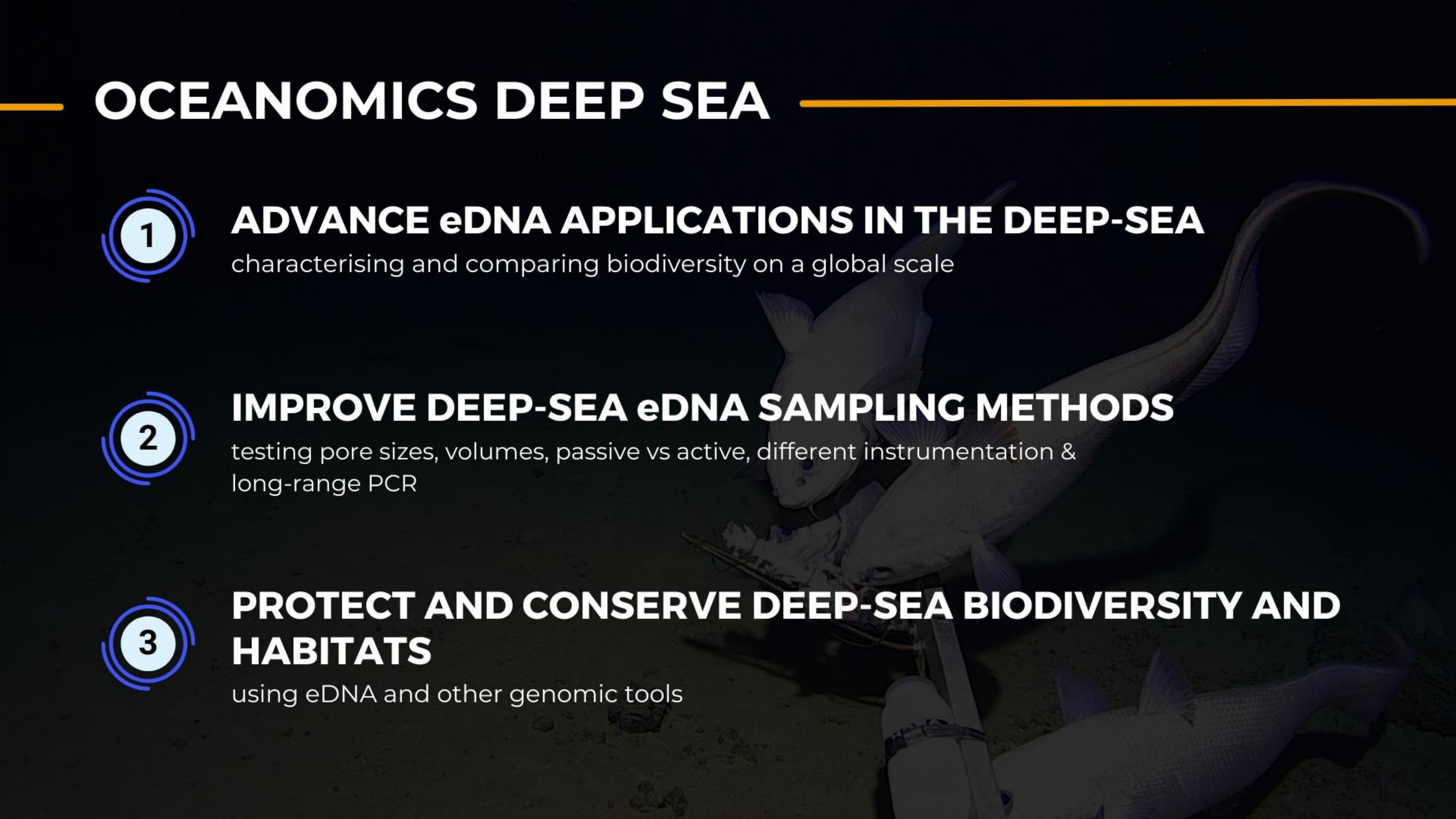


INNOVATIVE eDNA STRATEGIES FOR ADVANCING DEEP-SEA BIODIVERSITY RESEARCH AND CONSERVATION

Georgia Nester, Marcelle Ayad, Laura Missen, Ebony Thorpe, Adam J. Bennett, Jessica Kolbusz, Philipp Bayer, OceanOmics Division, Alan Jamieson, Priscila Goncalves, Eric Raes, Shannon Corrigan.

THE UNIVERSITY OF WESTERN AUSTRALIA
OCEANS INSTITUTE
MINDEROO FOUNDATION
INKFISH

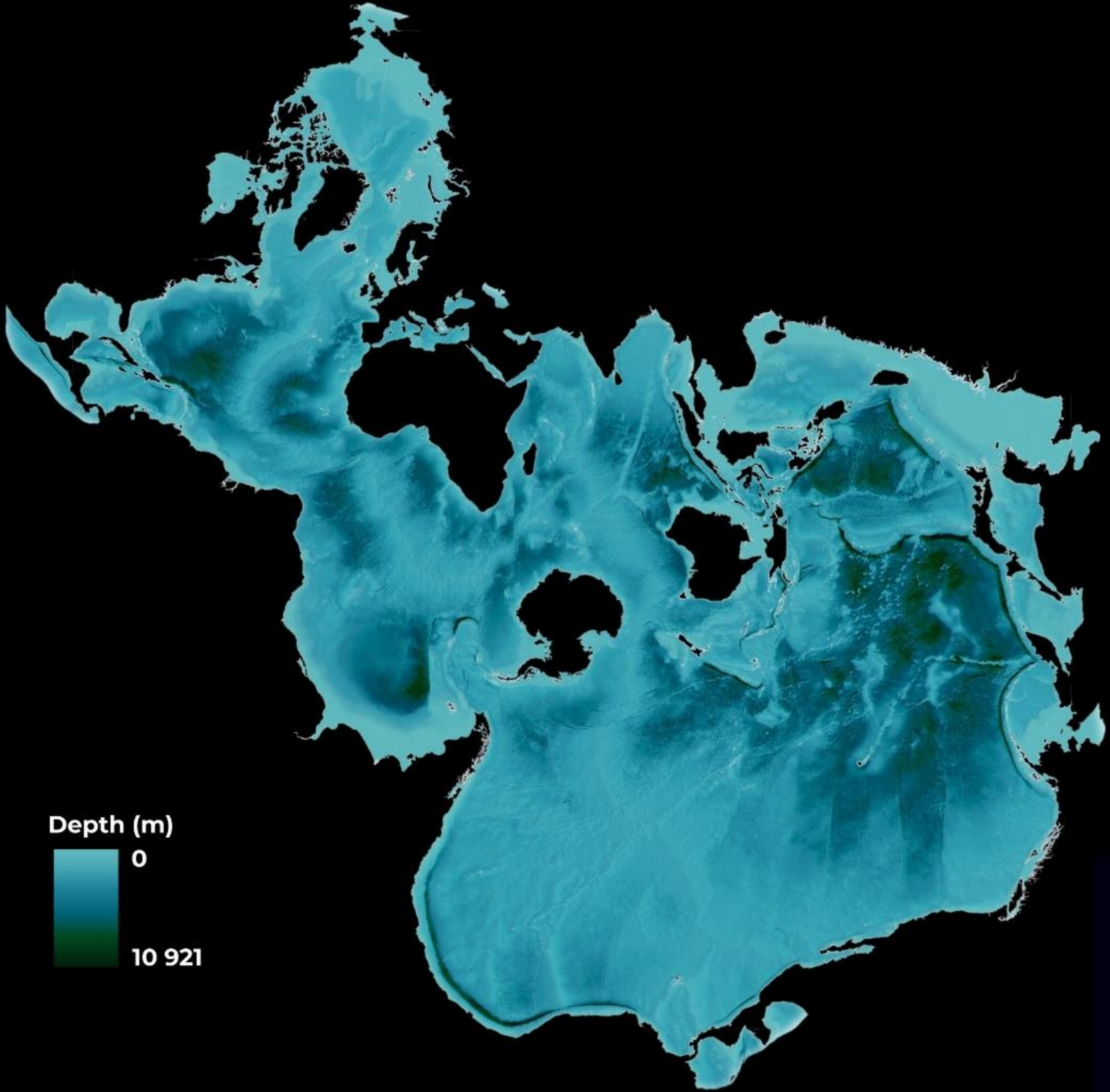
OCEANOMICS DEEP SEA



1. **ADVANCE eDNA APPLICATIONS IN THE DEEP-SEA**
characterising and comparing biodiversity on a global scale

2. **IMPROVE DEEP-SEA eDNA SAMPLING METHODS**
testing pore sizes, volumes, passive vs active, different instrumentation & long-range PCR

3. **PROTECT AND CONSERVE DEEP-SEA BIODIVERSITY AND HABITATS**
using eDNA and other genomic tools


Depth (m)
0
10 921


Konstantinov Ridge
Romanche Fracture Zone
Christmas Island
Gascoyne
Diamantina
Perth Canyon
Rio Grande Rise
East-Aus submarine canyons
South Orkney Trench
Falklands Escarpment
Tonga Trench
Nova-Canton Trough
Trans-Pacific Transit
Depth (m)
0
10 921
● Past voyage
● Upcoming voyage

CONDUCTED

- **Diamantina Fracture Zone**
- **Gascoyne region**
- **Perth Canyon**
- **Christmas Island**
- **East-Aus submarine canyons**
- **Trans-Pacific transit***
- **Nova-Canton Trough***
- **Tonga Trench***
- **South Orkney Trench***

UPCOMING

- **Falklands Escarpment***
- **Rio Grande Rise***
- **Konstantinov Ridge***
- **Romanche Fracture Zone***

***Inkfish voyages on RV Dagon**

9

locations explored

2,685

eDNA samples collected

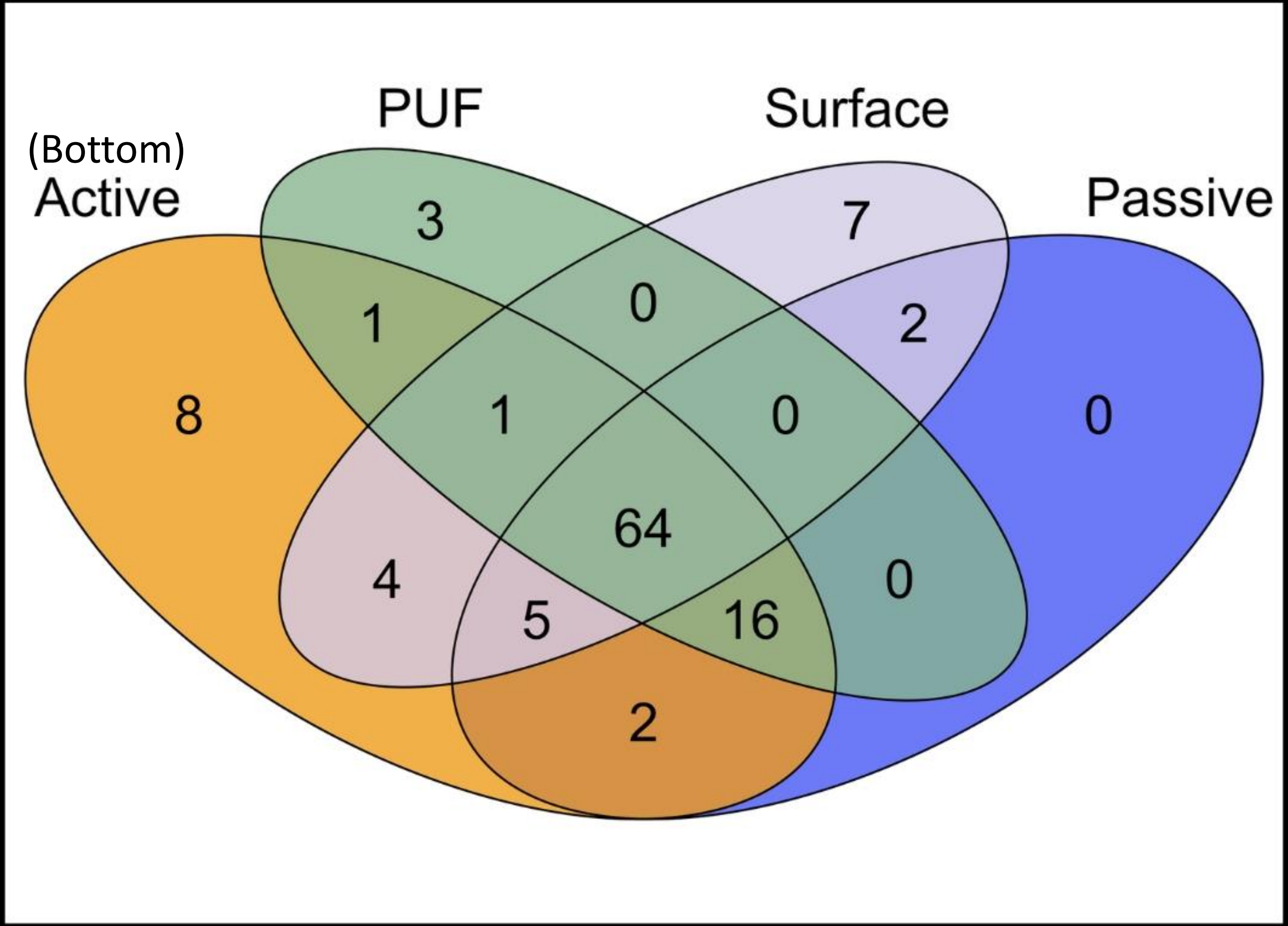
371

days at sea

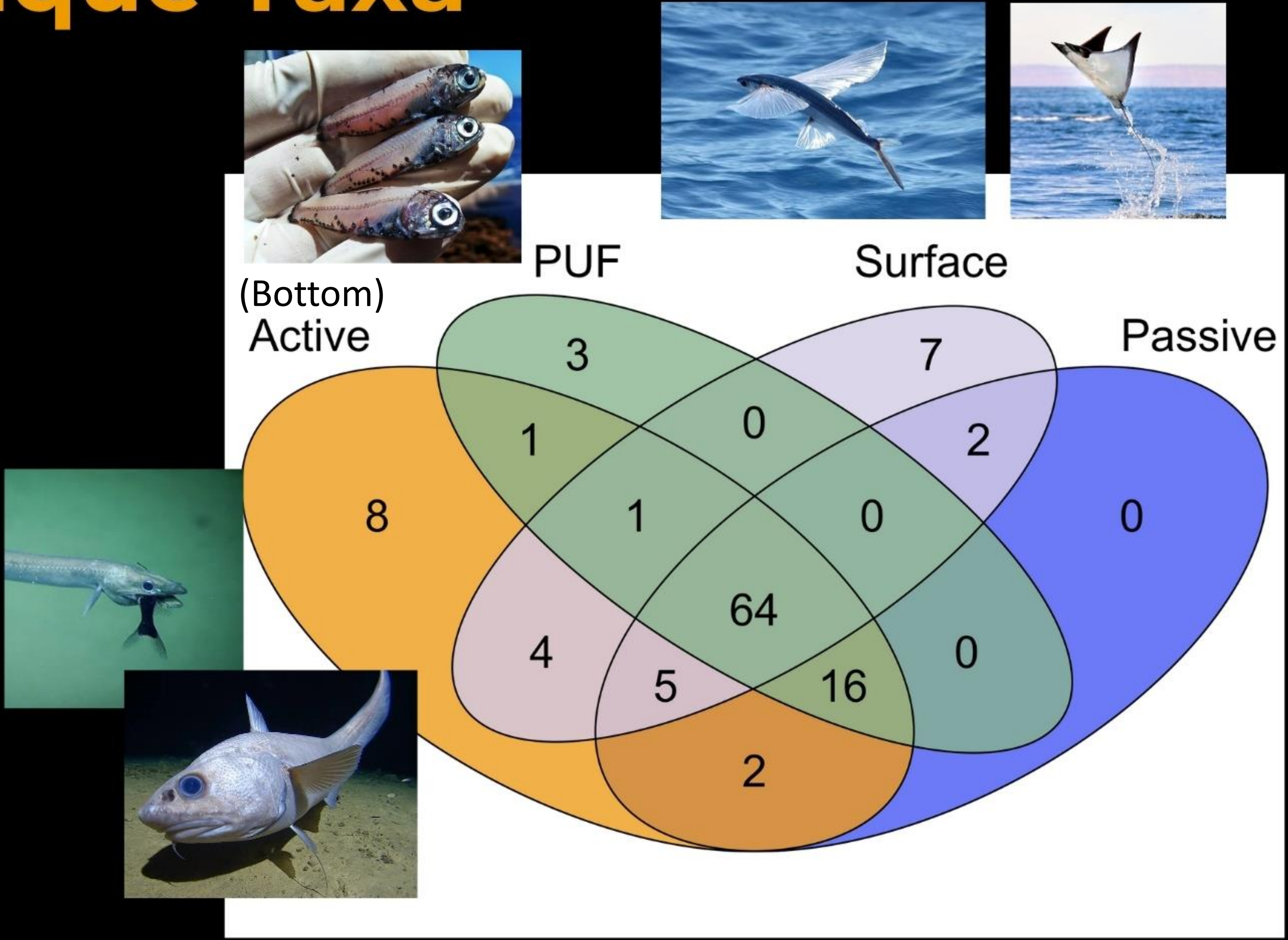
10,755m

reached - deepest eDNA sample in the Southern hemisphere

Unique Taxa (16S Fish)

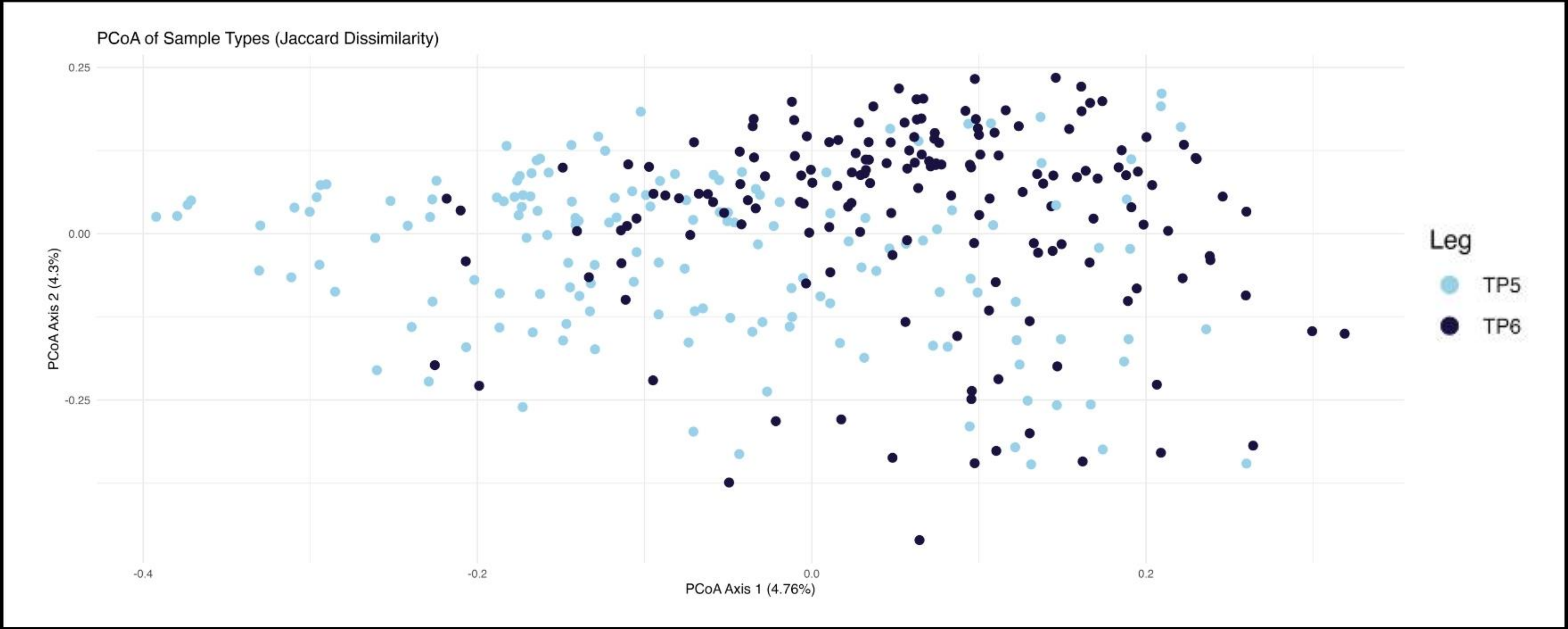


Unique Taxa



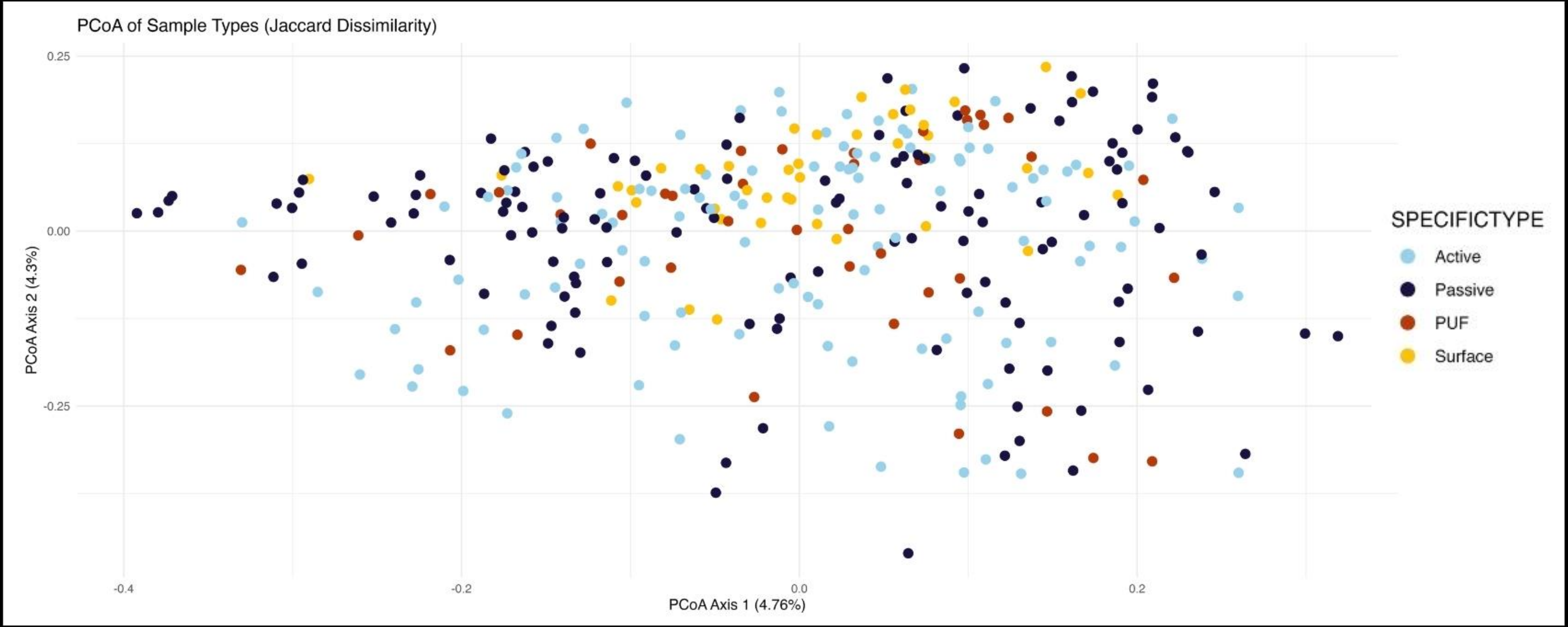
Biodiversity patterns

PERMANOVA results indicated Leg, site, and method were significantly different.



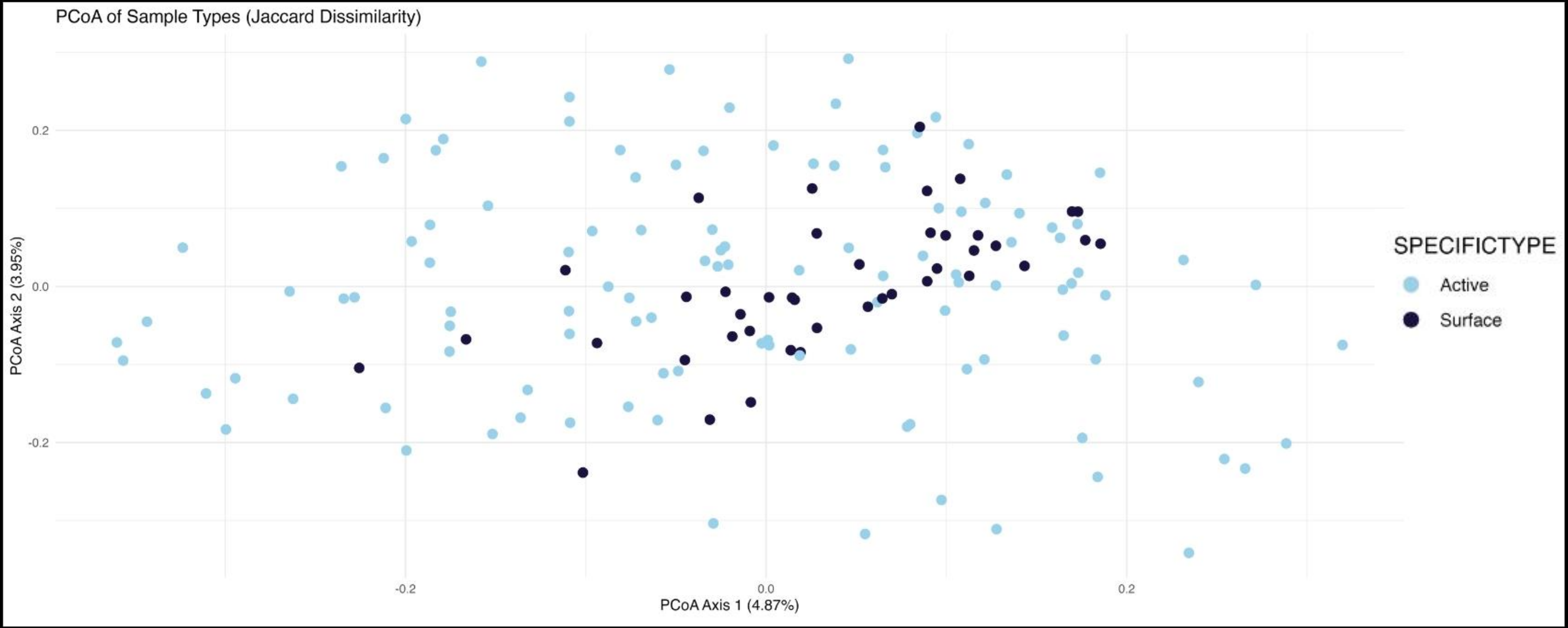
Biodiversity patterns

PERMANOVA results indicated Leg, site, and method were significantly different.

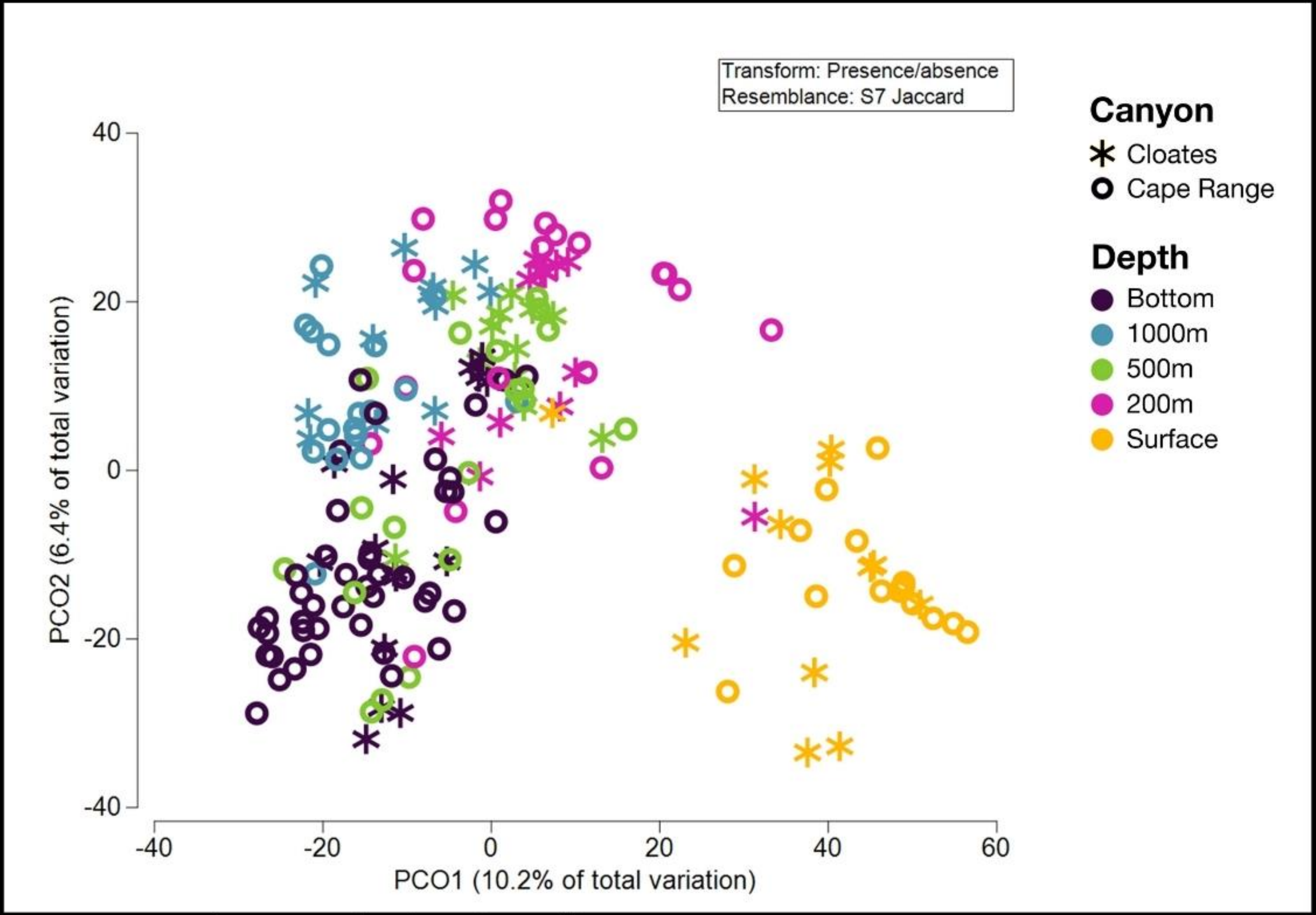


Biodiversity patterns

PERMANOVA results indicated Leg, site, and method were significantly different.



Biodiversity patterns



Nester et al., 2025 (submitted)

- Submarine canyons
- Same assay (16S Fish)
- Same depth range (max 5000m)

Factors influencing biodiversity patterns

- **Oceanographic Mixing:** Pacific currents (e.g., Equatorial Currents) mix surface/subsurface waters, homogenizing eDNA signals and blurring biogeographic patterns.
- **Vertical Transport:** eDNA moves between depths via marine snow or zooplankton migration, mixing surface and bottom signals.
- **eDNA Degradation/Persistence:** Variable degradation (temperature, UV, microbes) and long-distance transport can distort community patterns.
- **Tag-Jumping/Contamination:** Cross-contamination or tag-jumping during sequencing can introduce shared ASVs, masking true differences.
- **ASV-Level Noise:** High sensitivity to sequencing errors and rare taxa.
- **Sampling Method Differences:** Variability across methods (active, passive, PUF) may confound spatial patterns in nMDS despite PERMANOVA significance.


Coryphaenoides (grenadier)

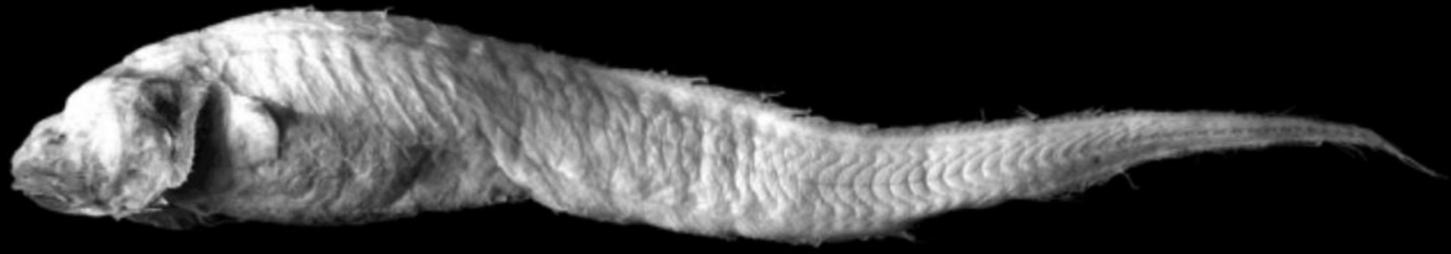

Cyclothone (bristlemouth)


Saccopharynx (whiptail gulper eel)

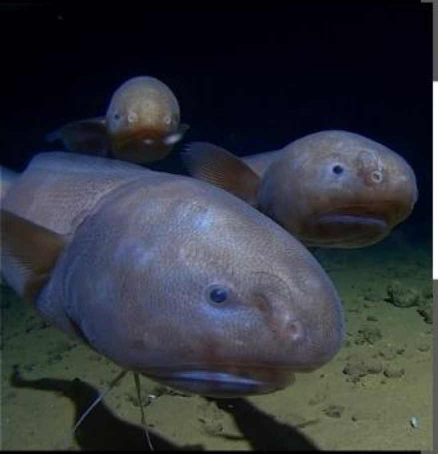

Idiacanthus (dragonfish)

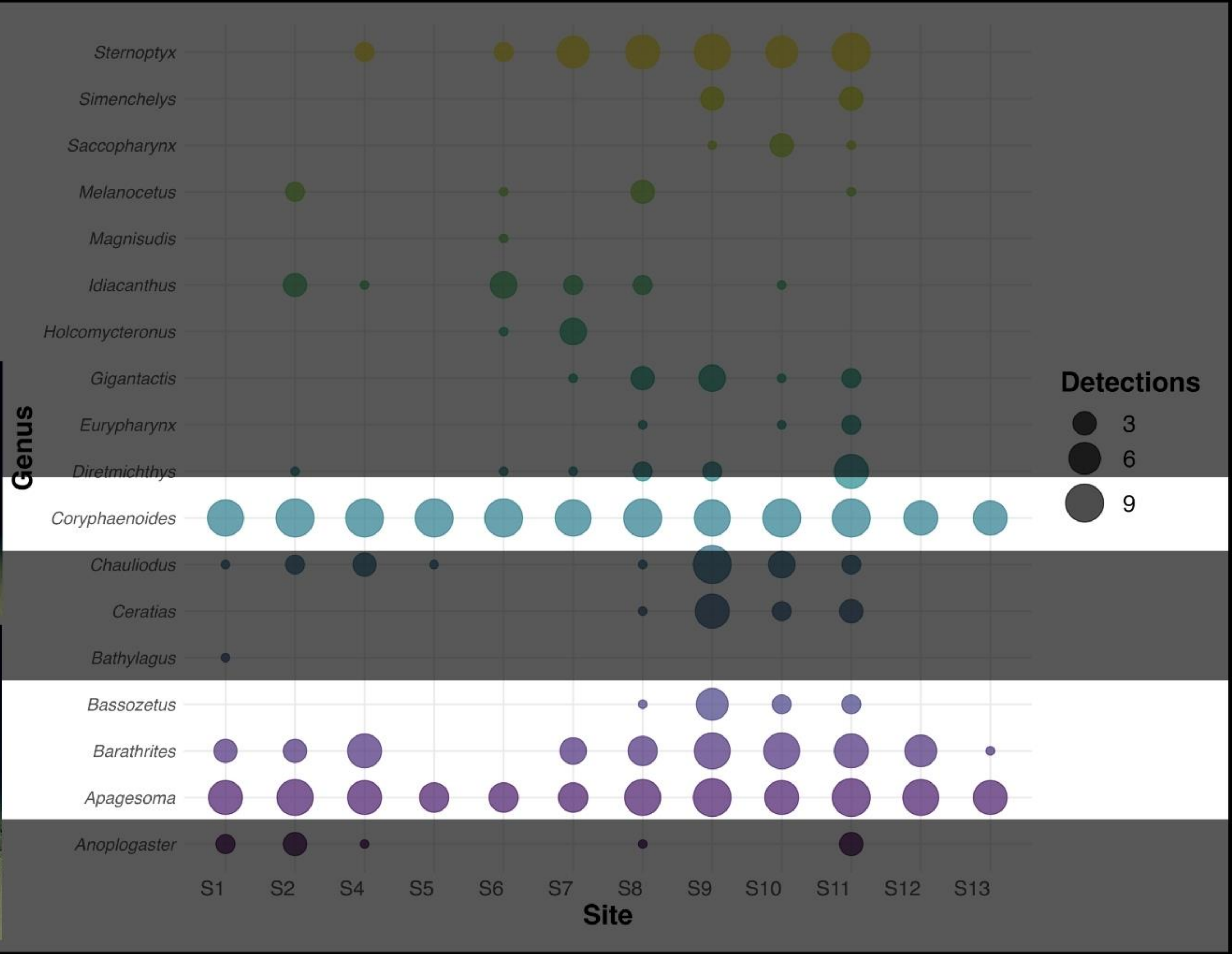

Eurypharynx (pelican eel)


Bassozetus (cusk eel)

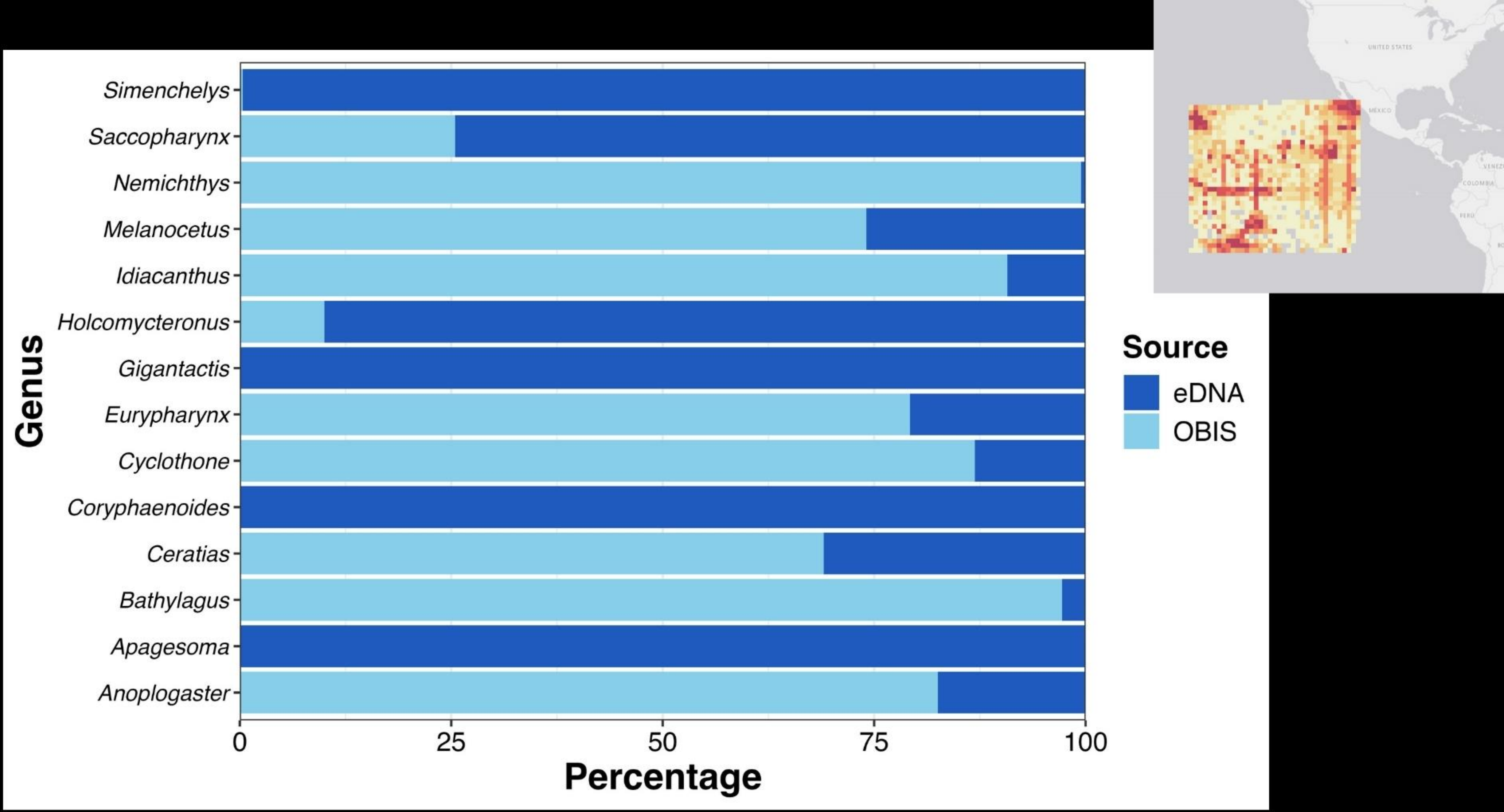

Apagesoma (cusk eel)

Images sourced from MUDSRC, MBARI, Fishes of Australia, Nautlius & Nielsen et al., 2008




Sternoptyx
Simenchelys
Saccopharynx
Melanocetus
Magnisudis
Idiacanthus
Holcomycteronus
Gigantactis
Eurypharynx
Diretmichthys
Coryphaenoides
Chauliodus
Ceratias
Bathylagus
Bassozetus
Barathrites
Apagesoma
Anoplogaster
Genus
S1
S2
S4
S5
S6
S7
S8
S9
S10
S11
S12
S13
Site
Detections
3
6
9

CONTRIBUTIONS OF eDNA TO GLOBAL DEEP-SEA DATABASES


Simenchelys
Saccopharynx
Nemichthys
Melanocetus
Idiacanthus
Holcomycteronus
Gigantactis
Eurypharynx
Cyclothone
Coryphaenoides
Ceratias
Bathylagus
Apagesoma
Anoplogaster
Genus
0
25
50
75
100
Percentage
Source
eDNA
OBIS
UNITED STATES
MÉXICO
COLOMBIA
PERU

KEY POINTS & FUTURE

- Delve into datasets further, exploring diversity and spatial patterns- oceanographic, lab or bioinformatic reasons for lack of seperation?
- Have looked at different volumes (2L, 10L, 20L, 36L) and pore sizes (0.45, 5, 8, 12µM)
- Explore other extraction methods to enhance sensitivity and enable long-range PCR for *Bassozetus* and *Coryphaenoides*
- Suite of targeted deep-sea primer sets
- Improve reference databases through genome sequencing of priority deep-sea taxa

ACKNOWLEDGEMENTS

OceanOmics Division, Minderoo-UWA Deep Sea Centre, crew aboard *RV Dagon, Pangaea Ocean Explorer,* and *RV Investigator*.

Research, field & technical collaborators: Matt Heydenrych, Sam Thompson, Olivia Stowell, Hayley Sims, Meg Cundy, Mel Stott, Devin Harrison, Dylan White-Kiely, Jimmy McIntyre

MINDEROO FOUNDATION

THE UNIVERSITY OF WESTERN AUSTRALIA

OCEANS INSTITUTE

INKFISH

CSIRO

WAM WESTERN AUSTRALIAN MUSEUM

Australian Marine Parks

illumina