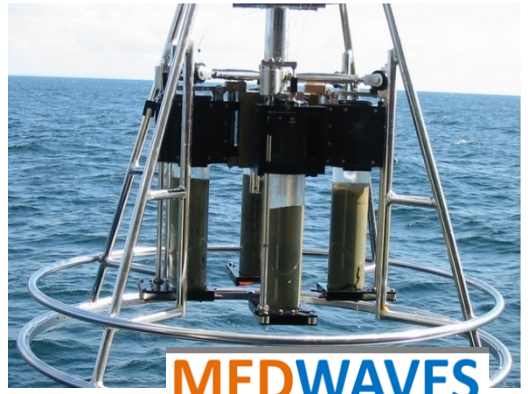
WP3: Resilient biodiversity

Jeannette Carlsson, Jens Carlsson, Marina Carreira, Telmo Morato, Sophie Arnaud-Haond

- Validate and refine current Global Open Ocean and Deep Seabed (GOODS) biogeographic classification scheme of biodiversity.
- Establish new indicators and methodological standards to assess biodiversity descriptors of Good Environmental Status (GES).
- **Test next-generation meta-barcode sequencing and eDNA technology tools as innovative standardised methods for integrated ecosystem approaches to assess biodiversity of deep-sea ecosystems.**
- Refine and develop novel evaluation frameworks for Regional Fisheries Management Organisations (RFMOs) including the North East Atlantic Fisheries Commission (NEAFC) to identify new ESBAs and help preserve Vulnerable Marine Ecosystems (VMEs) and Ecologically or Biologically Significant Areas (ESBAs) in order to assist the policy

CTD



Biodiversity assessment rely on the Species concept

- **Biological species concept**, according to Ernst Mayr (1940):

« groups of actually or potentially interbreeding natural populations, which are reproductively isolated from other such groups"

- ➔Hardly amenable to experimental tests for most cases, let alone the deep sea➔Looking for the best proxy:

Proxy for species delineation in biodiversity assessment?

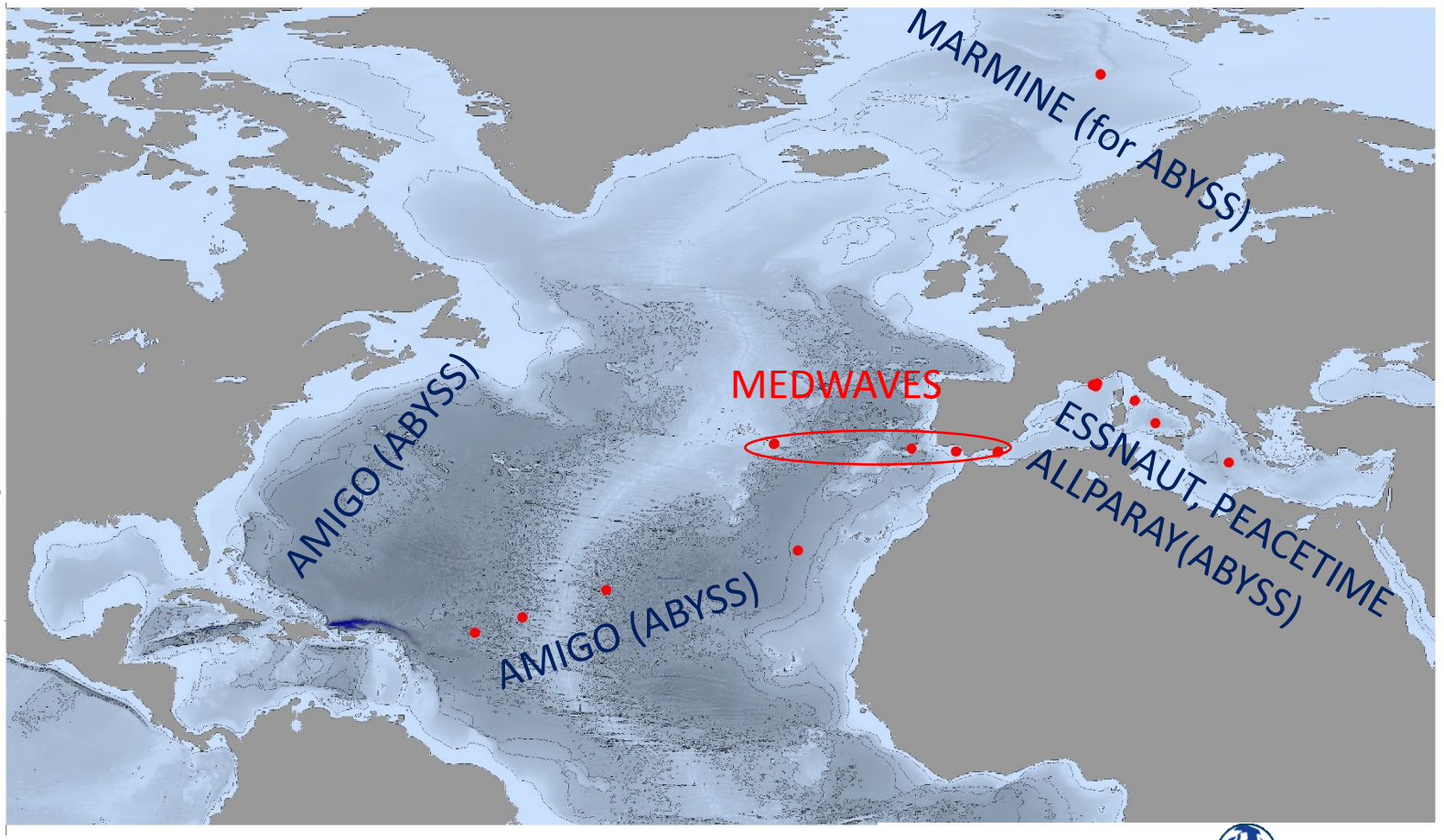
- Morphology, **Phenetic species concept**: A species is a set of organisms that look similar to each other and distinct from other sets (Ridley, 1993).

But phenotypic plasticity, synonymous species, cryptic species…

- Genetic divergence, **Evolutionary species concept**: A species is a lineage (an ancestral-descendant sequence of populations) evolving separately from others and with its own unitary evolutionary roles and tendencies (Simpson, 1961).

WP3: Samples collected for eDNA Integration with “Pourquoi Pas les Abysses” –ABYSS- Project

Cathy Liautard-Haag, Engineer



Miriam Brandt, PhD

Medwaves: Samples collected for eDNA

- Water Objectives:

→ Niskin for metabarcode to inventory communities

→ extended to 3 CTD per site, 3 to 4 depth to check for the effect of water masses on the composition of communities that can be detected

- Sediment Objectives:

→ 2 to 3 multicore per site for metabarcode to inventory communities

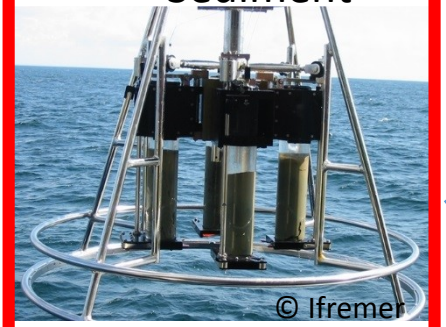
- State of progresses: All DNA extracted for sediment and water, being processed for metabarcoding with 5 barcode genes (protocol setup for Abyss), results hoped during summer

WP3: Development of a partnership with Total

A post-doctoral fellow to develop protocols for Environmental Impact Assessments

Environmental samples

Sediment



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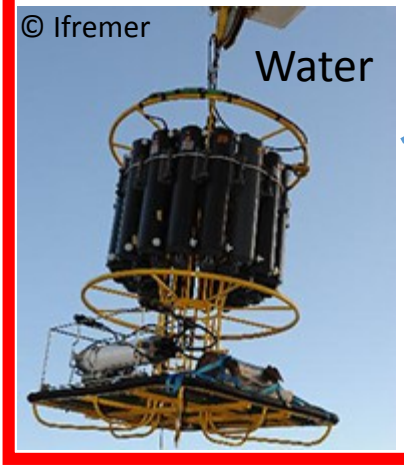
Water



1

DNA extraction

2

Barcode libraries

Massive sequencing

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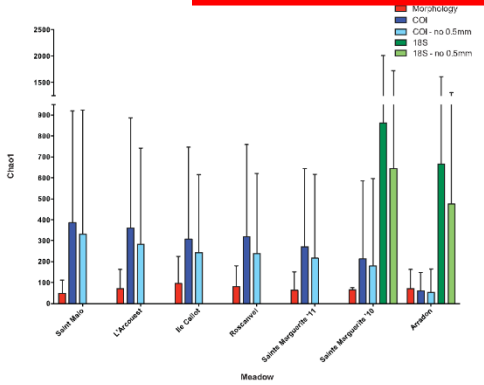
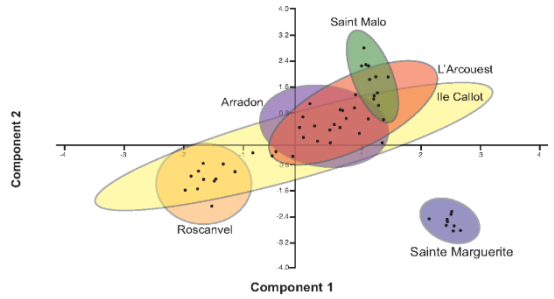
3

OTUs census diversities metrics





POURQUOI PAS LES ABYSSES

TOTAL
COMMITTED TO BETTER ENERGY

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frontiers in Marine Science

ORIGINAL RESEARCH
published: xx April 2017
doi: 10.3389/fmars.2017.00118

Cold-Water Coral Habitats in Submarine Canyons of the Bay of Biscay

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Publication of CoralFISH results, now also acknowledging Atlas

Contents lists available at ScienceDirect

Deep-Sea Research II

journal homepage: www.elsevier.com/locate/dsr2

Two “pillars” of cold-water coral reefs along Atlantic European margins: Prevalent association of *Madrepora oculata* with *Lophelia pertusa*, from reef to colony scale

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Thank You!

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This project has received funding from the European Union's Horizon 2020 research and innovation programme under grant agreement No 678760 (ATLAS). This output reflects only the author's view and the European Union cannot be held responsible for any use that may be made of the information contained therein.