

From seascape genomics to community ecology: comparing the physical factors structuring genetic diversity within a bioengineer species of the coralligenous habitats with those structuring the species composition of the coralligenous community

Aurélien DE JOUDE , Romain DAVID , Caroline ROCHER , Marjorie SELVA , Anne Haguenauer , Stéphane SARTORETTO , Jean-Pierre FERAL , Anne CHENUIL

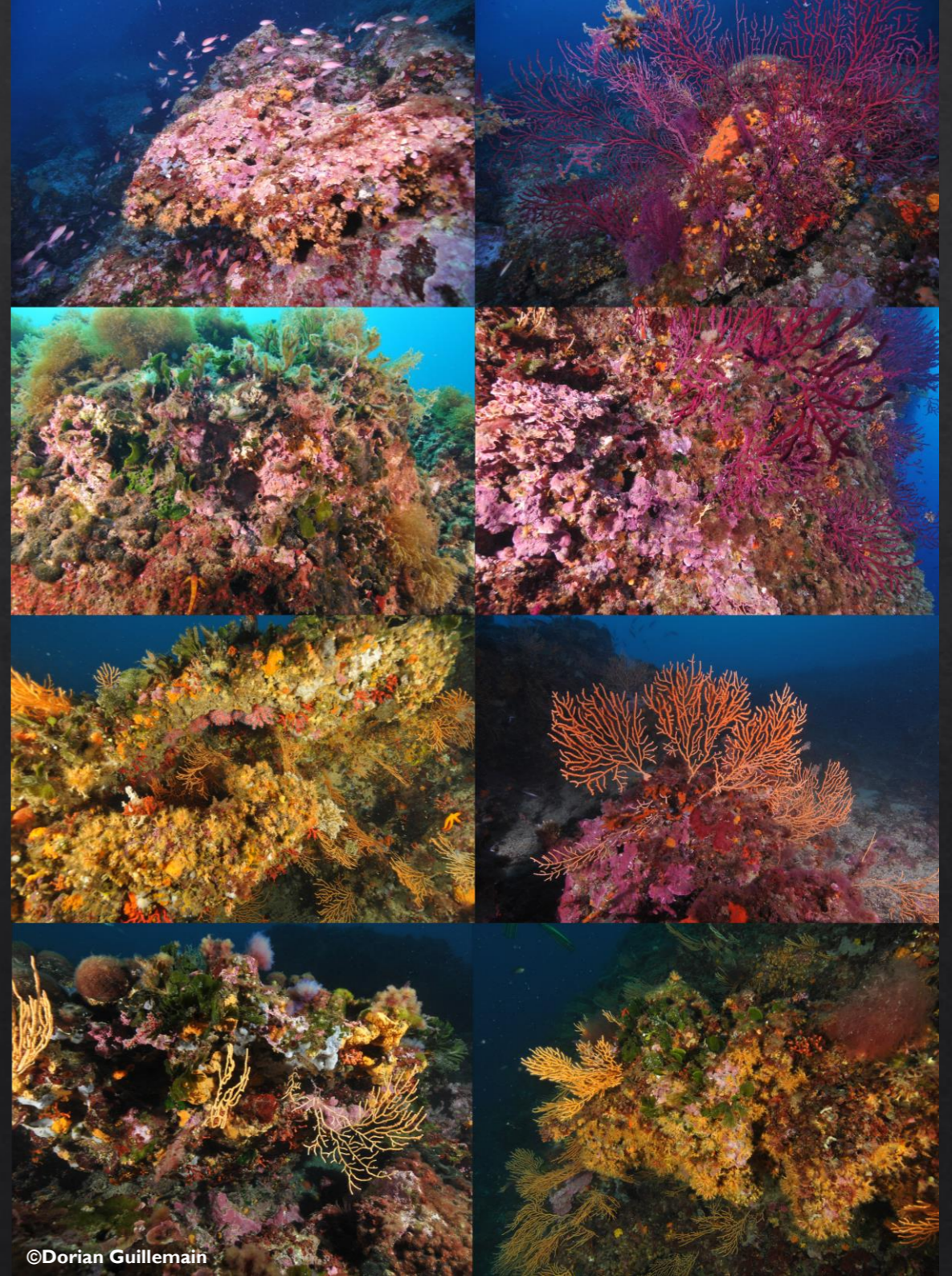
IMBE team Biodiversity Origin and Evolution



Coralligenous habitats

❖ Definition

- ❖ **Bio-concretion** of calcareous red algae (*Peyssonneliaceae* & *Corallinaceae*)
- ❖ Dim light
- ❖ Marine invertebrates



Coralligenous habitats

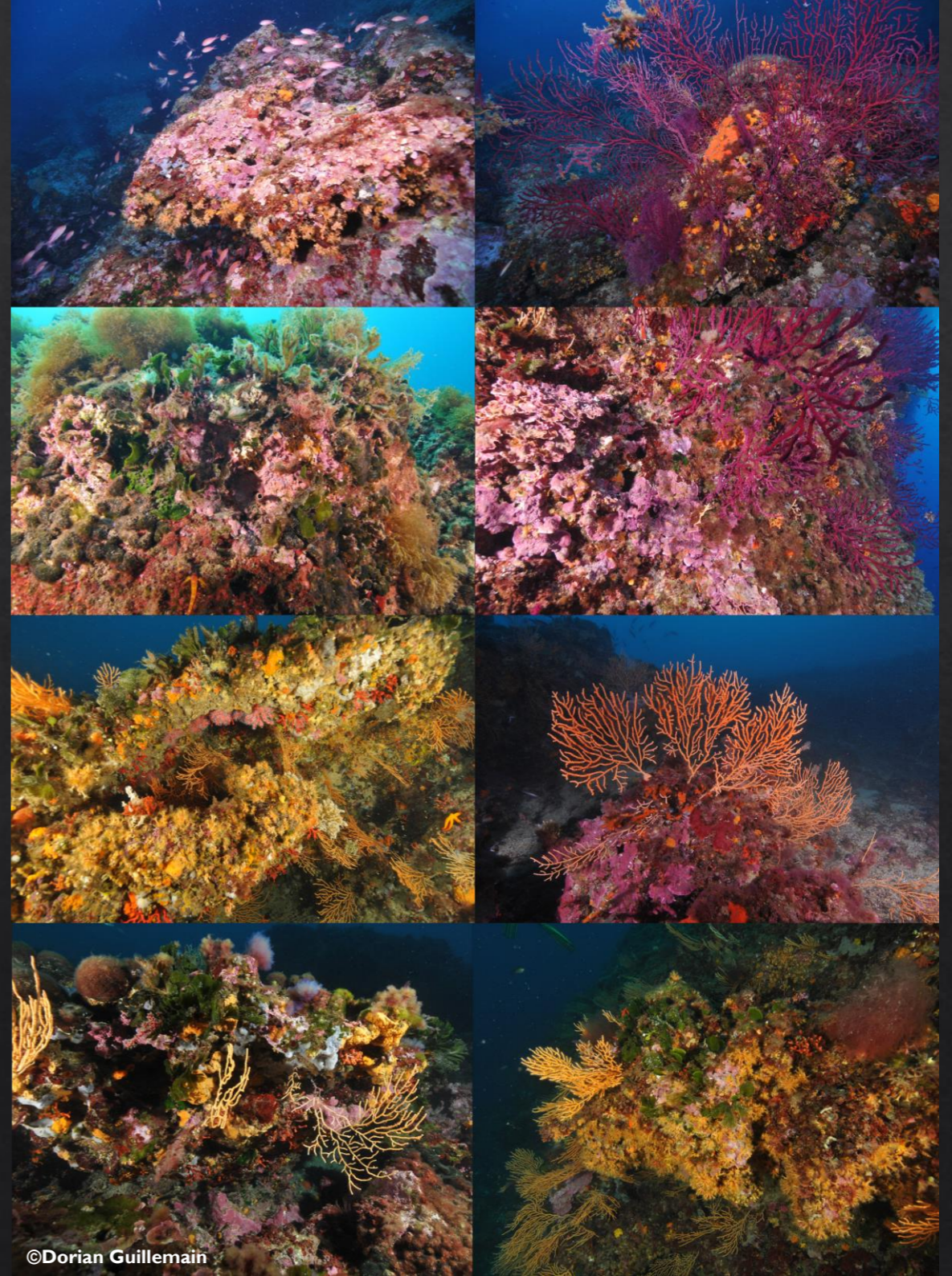
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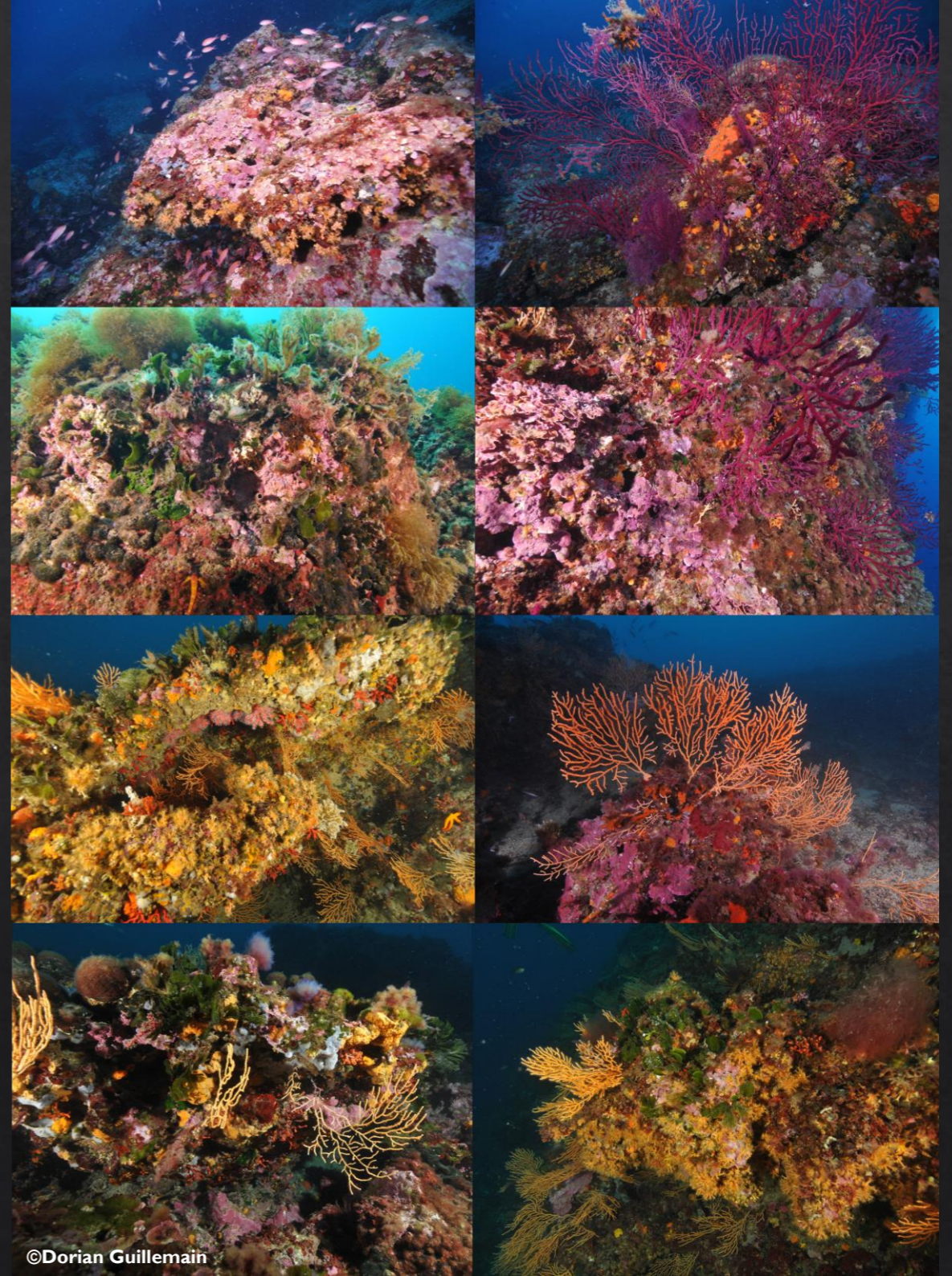
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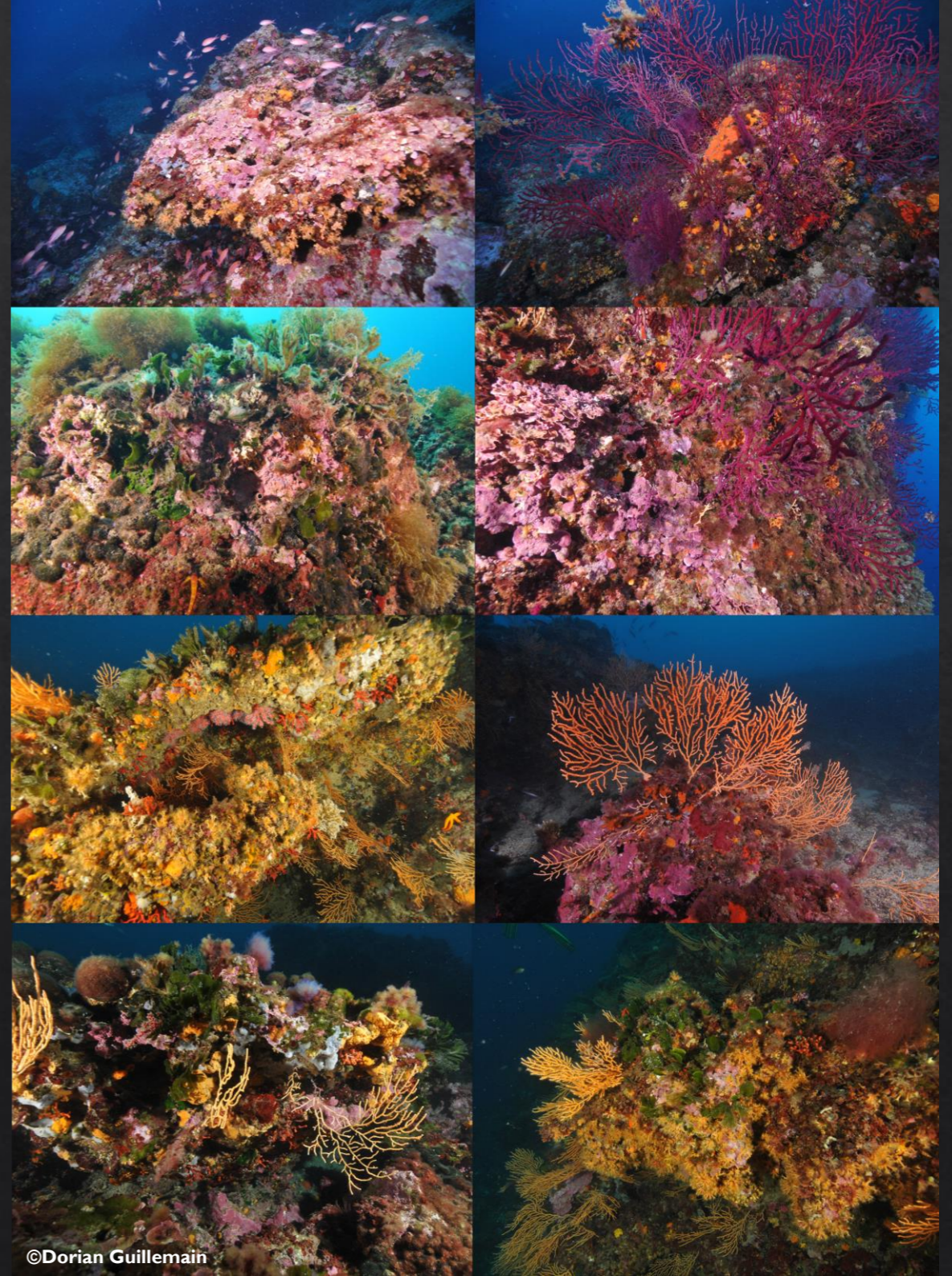
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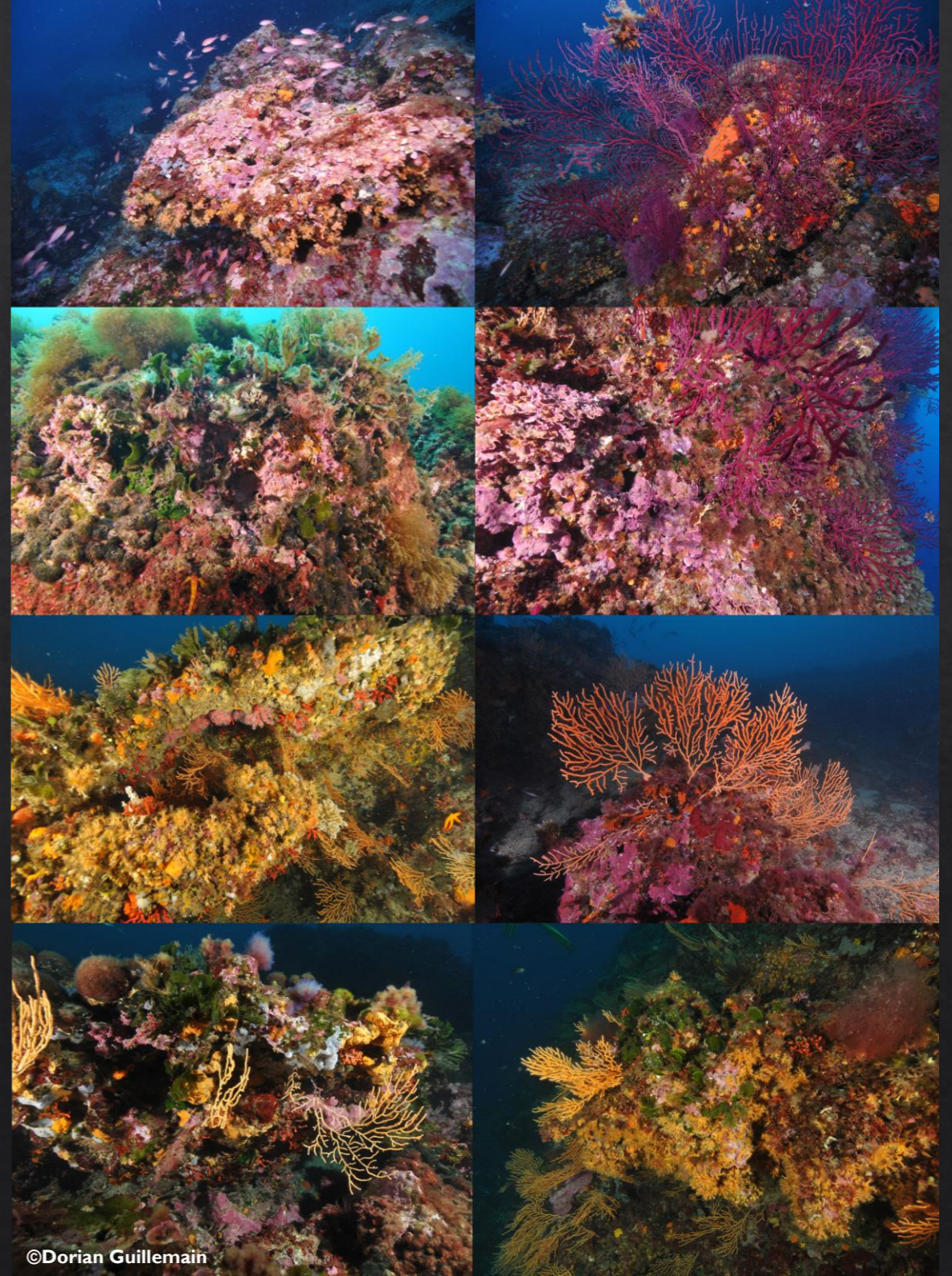
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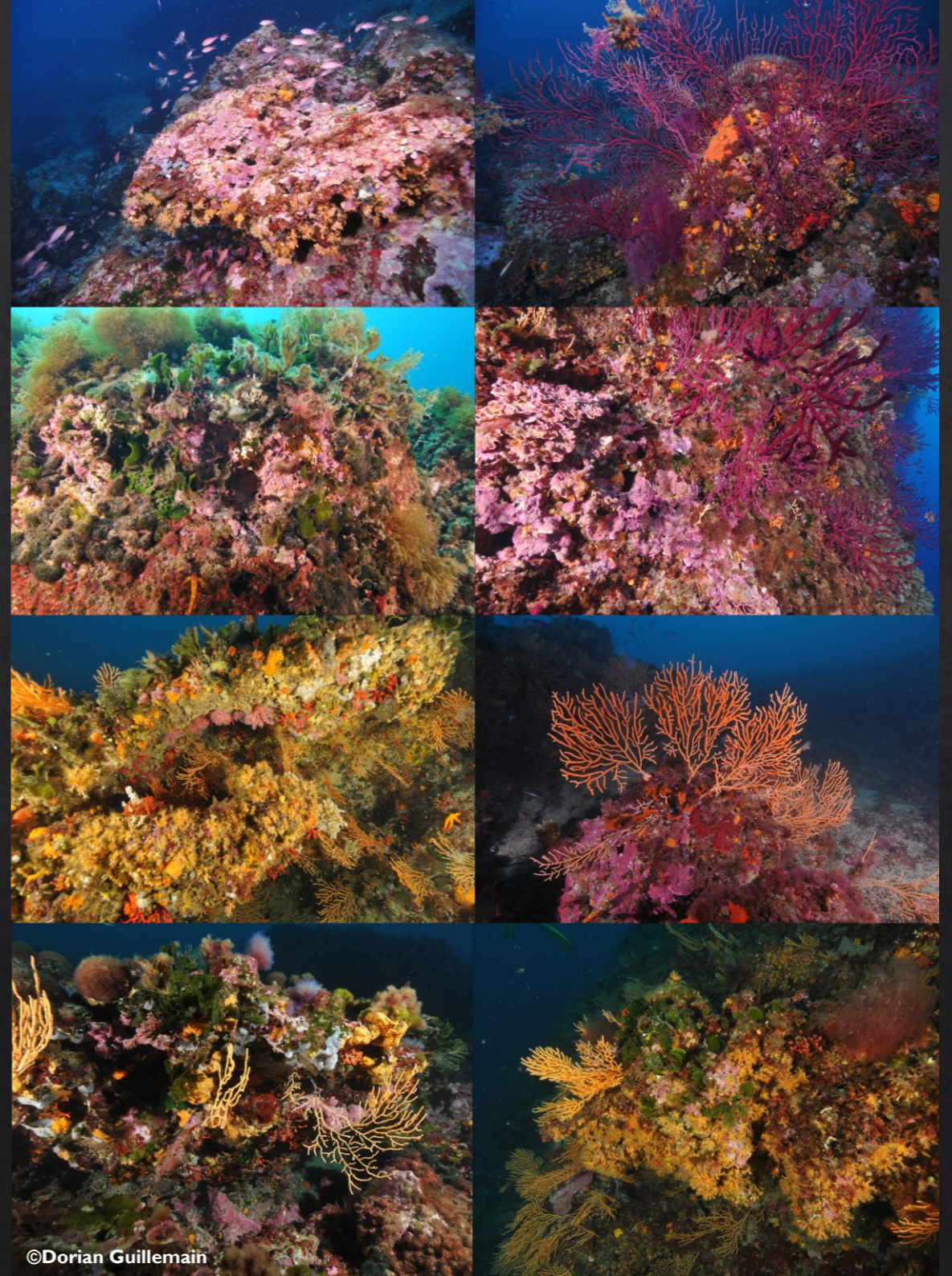
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- ❖ **No protection policies dedicated to these habitats**



Ecosystems engineering species in the marine realm

- **Definition:**
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➤ **Priority targets for conservation**

***Major engineering species of coralligenous habitats :
Calcareous Red Algae***

➤ ***Crustose red algae : 2 families Corallinaceae & Peyssonneliacea***

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Corallinaceae

Lithophyllum spp.



Mesophyllum spp.



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Lithophyllum stictaeforme and *L. cabiochae* in coralligenous habitats



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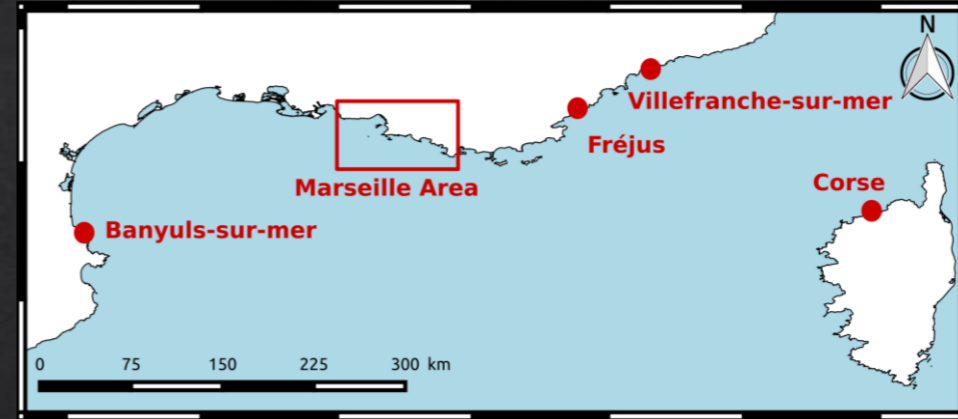
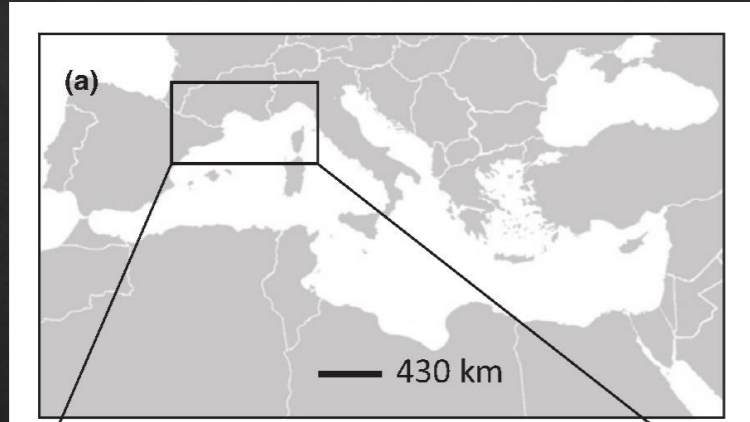


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- ◇ **Cryptic diversity ?**

Material & Methods : sampling

➤ **Sampling by scuba diving** in 5m long segments with at least one meter between each individuals

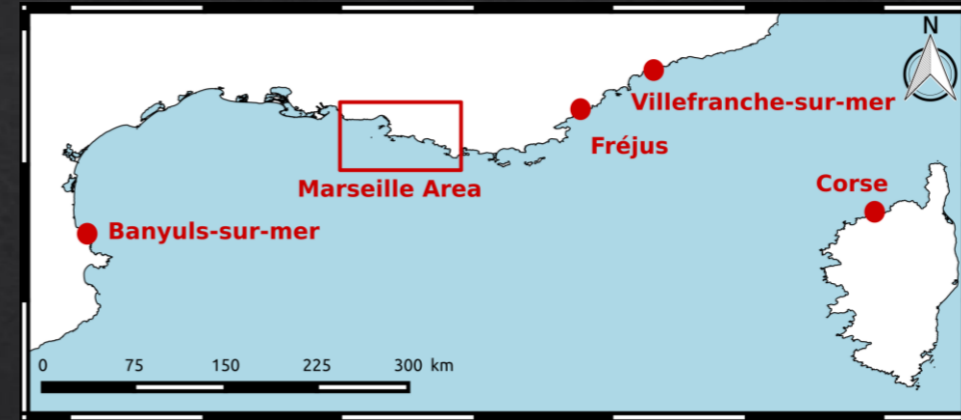
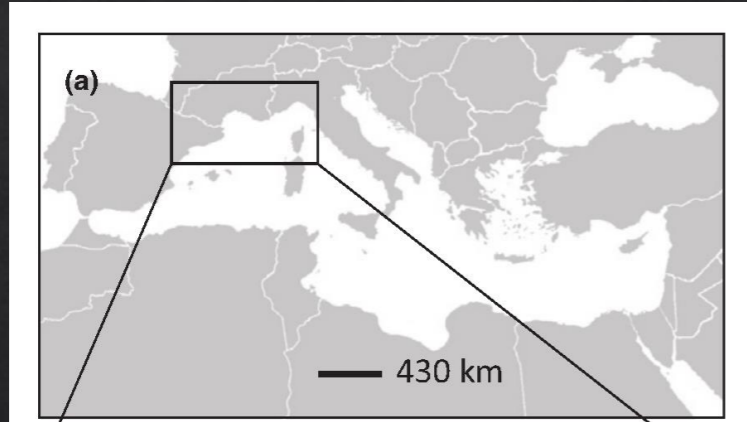
507 individuals on 13 sites



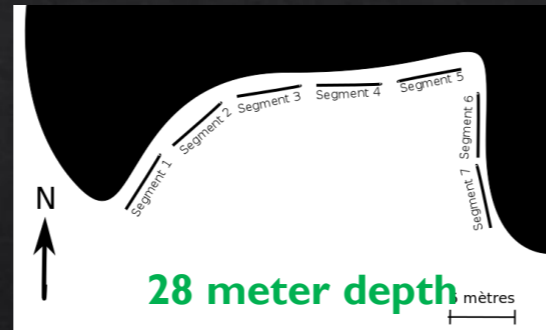
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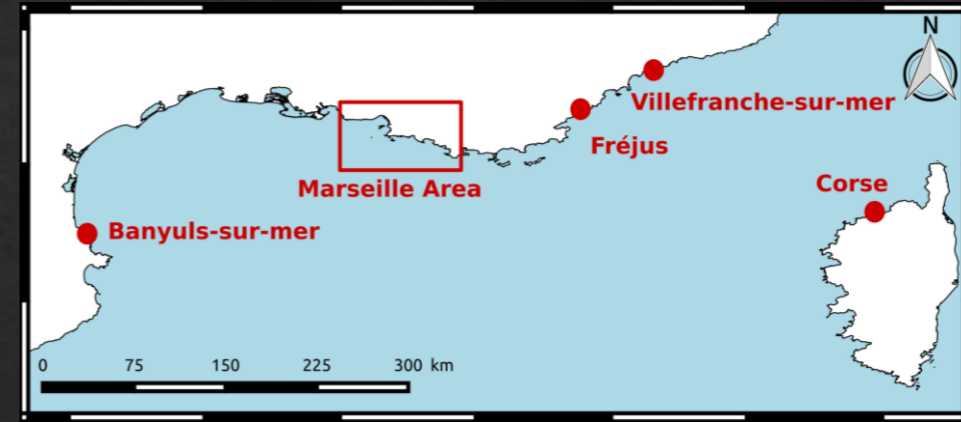
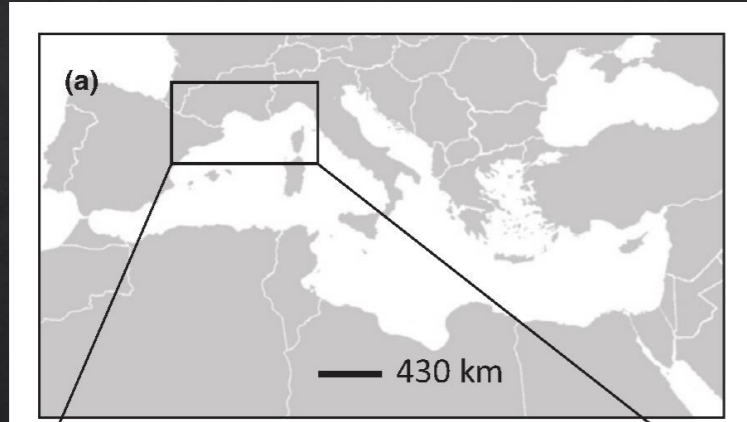
- **Depth and topological** data were recorded on each segment



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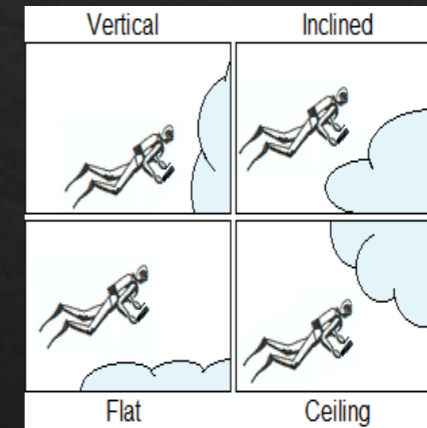
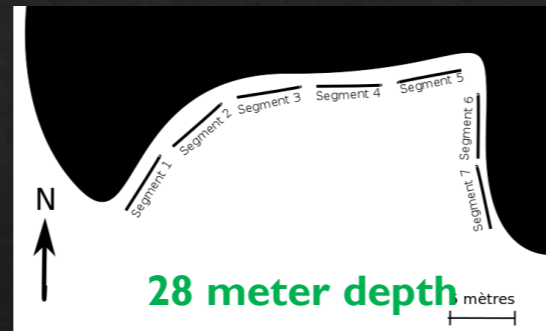
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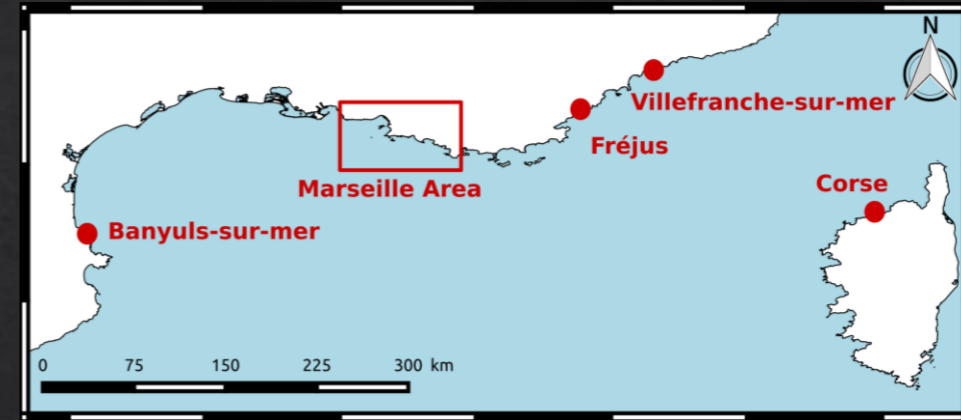
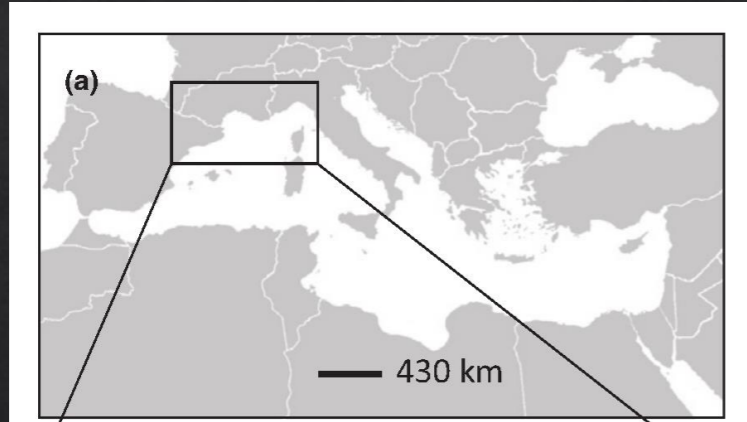
- **Inclination**



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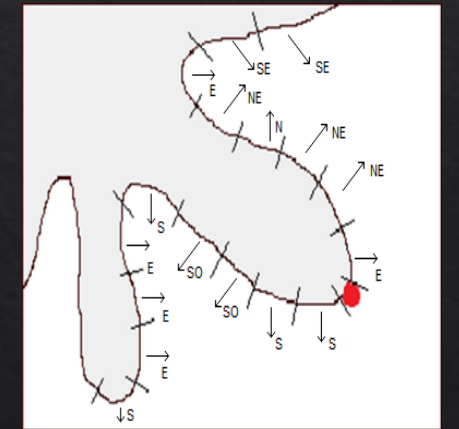
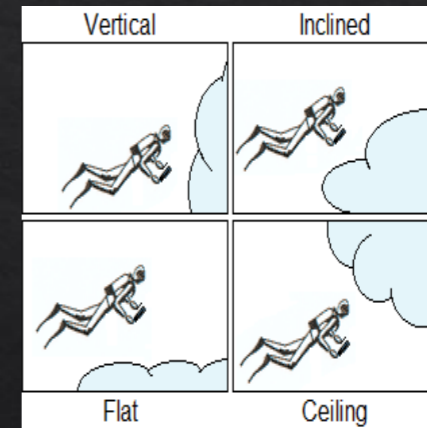
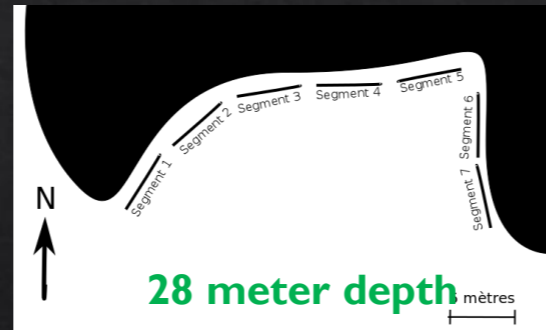
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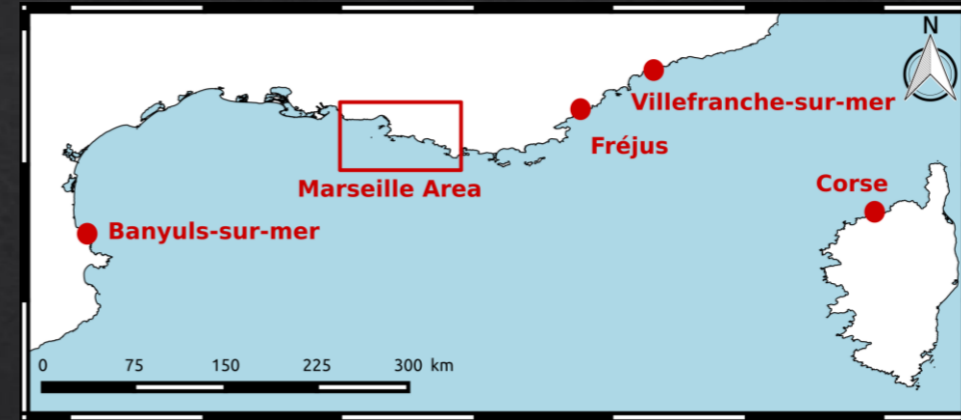
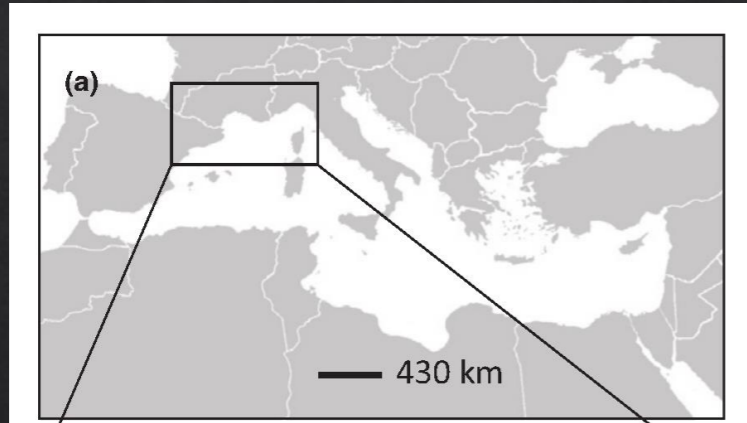
- Inclination
- Orientation



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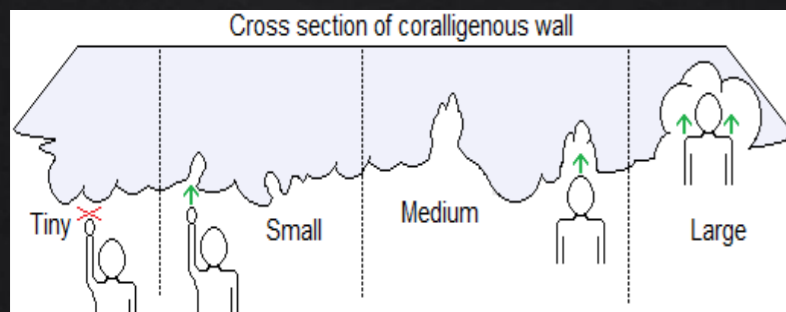
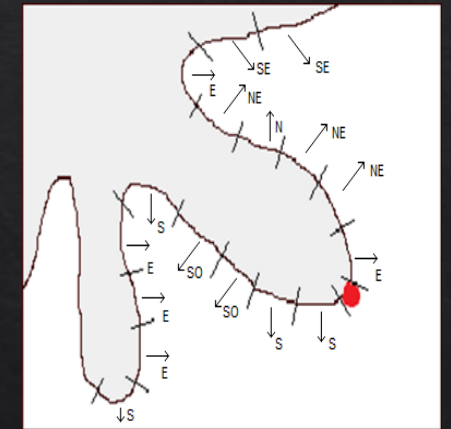
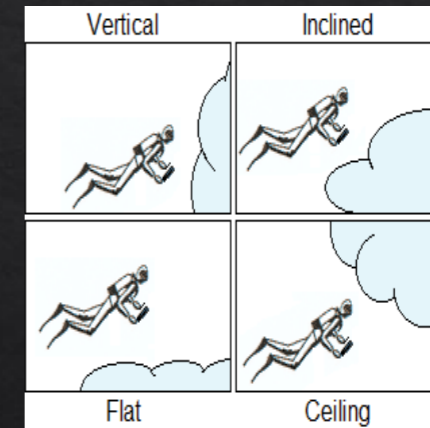
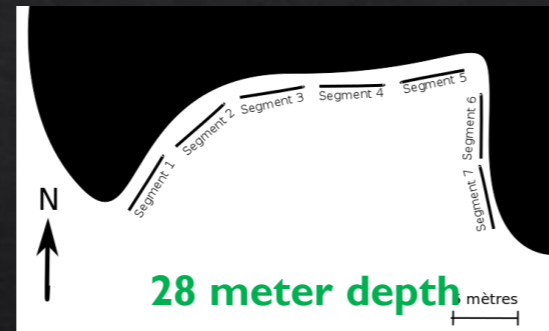
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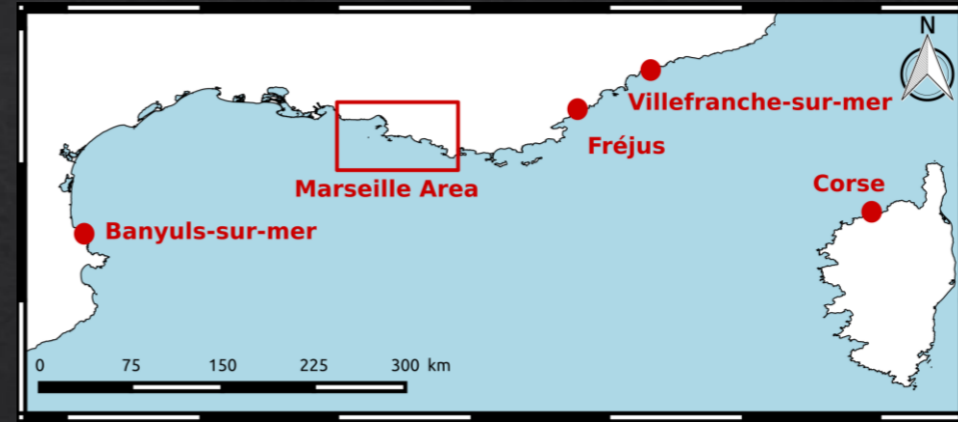
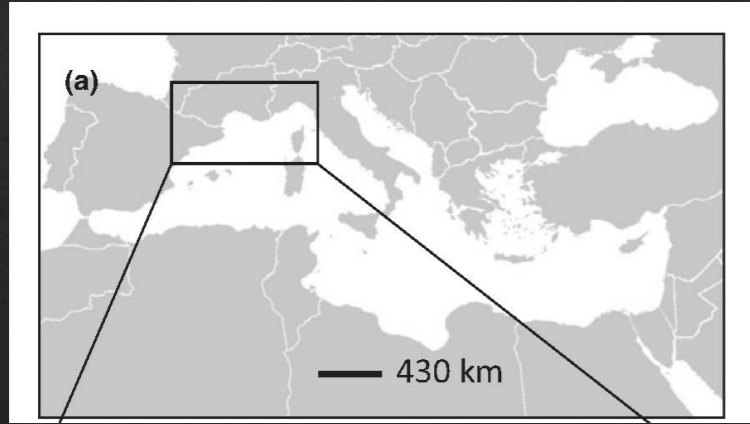
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- Rugosity



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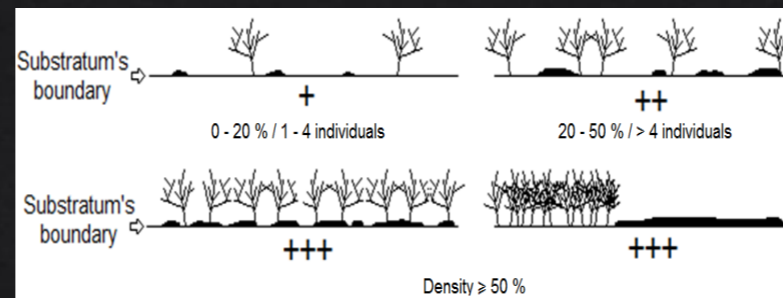
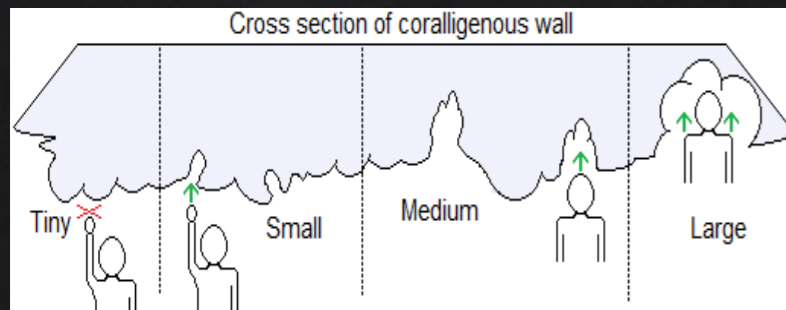
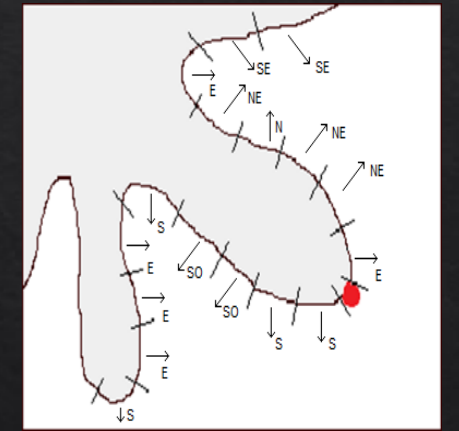
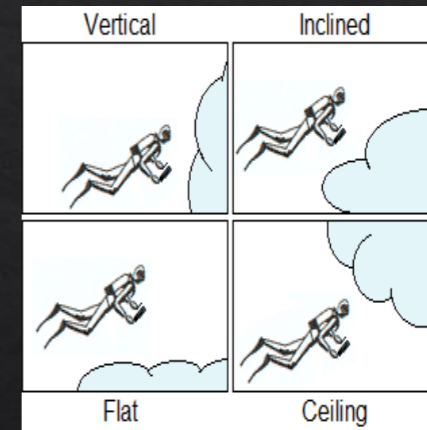
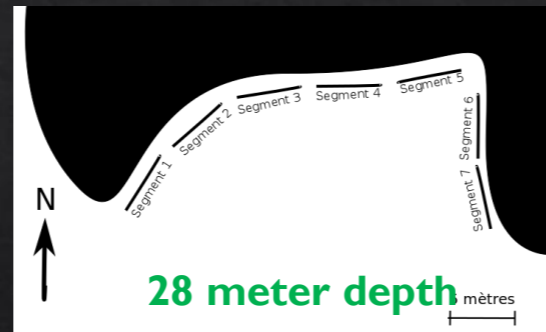
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- Inclination
- Orientation
- Rugosity
- Most abundant species



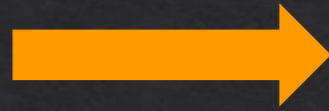
Material & Methods : genetics & genomics

- Barcoding approach using different markers : *psbA*, 28S and COI

DNA Extraction

PCR for each maker

Phylogenetic analyses



Intra specific diversity or cryptic species ?

Species identification of each individual

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- **Population genomics approach : Genotyping by capture sequencing**

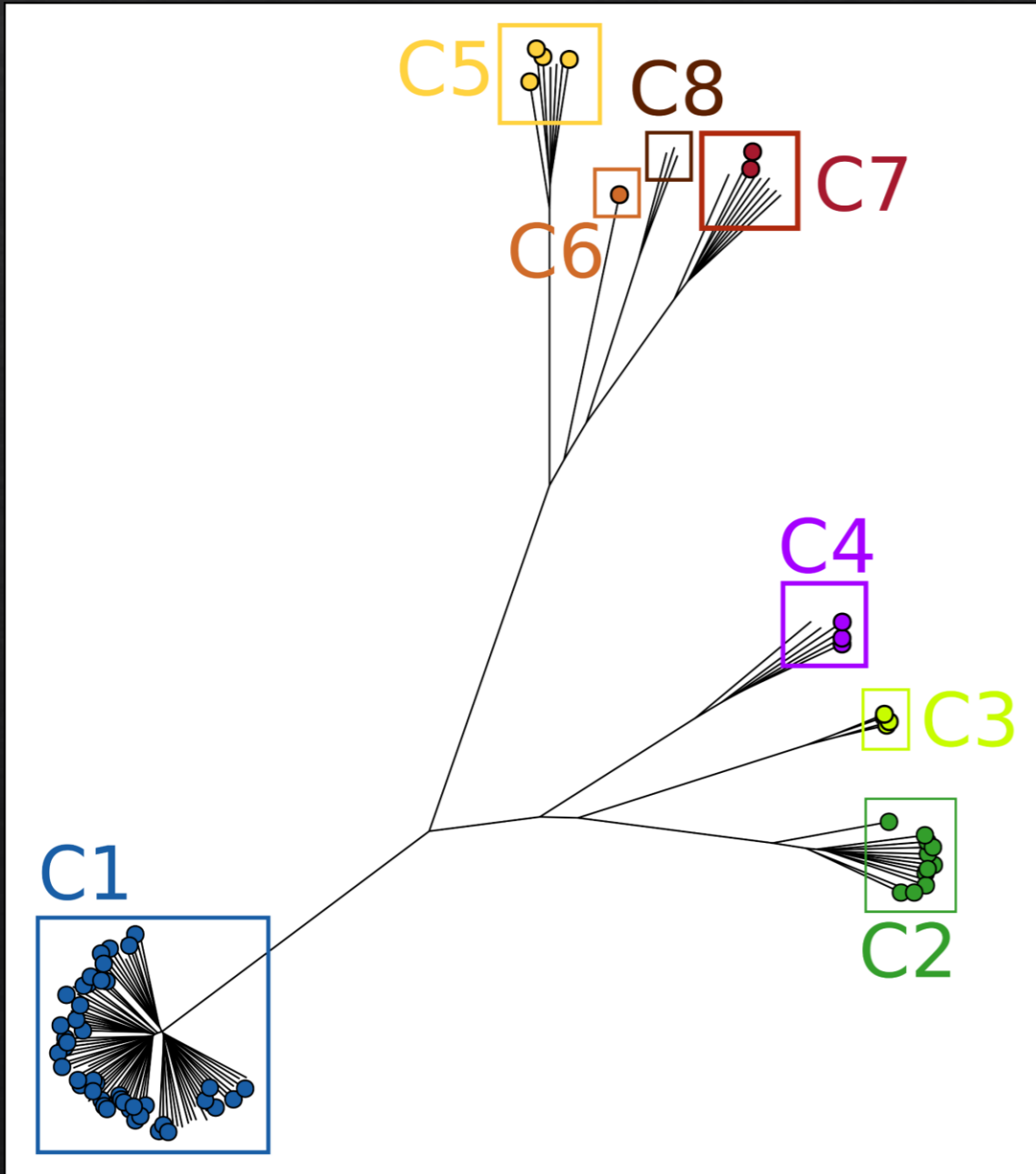
RNA extraction, sequencing and assembling to build a reference transcriptome
Probe design based on the reference transcriptome
DNA extraction
Capture reaction & sequencing



Combine with the barcoding approach
species delimitation

Genetic diversity and connectivity
Local adaptation

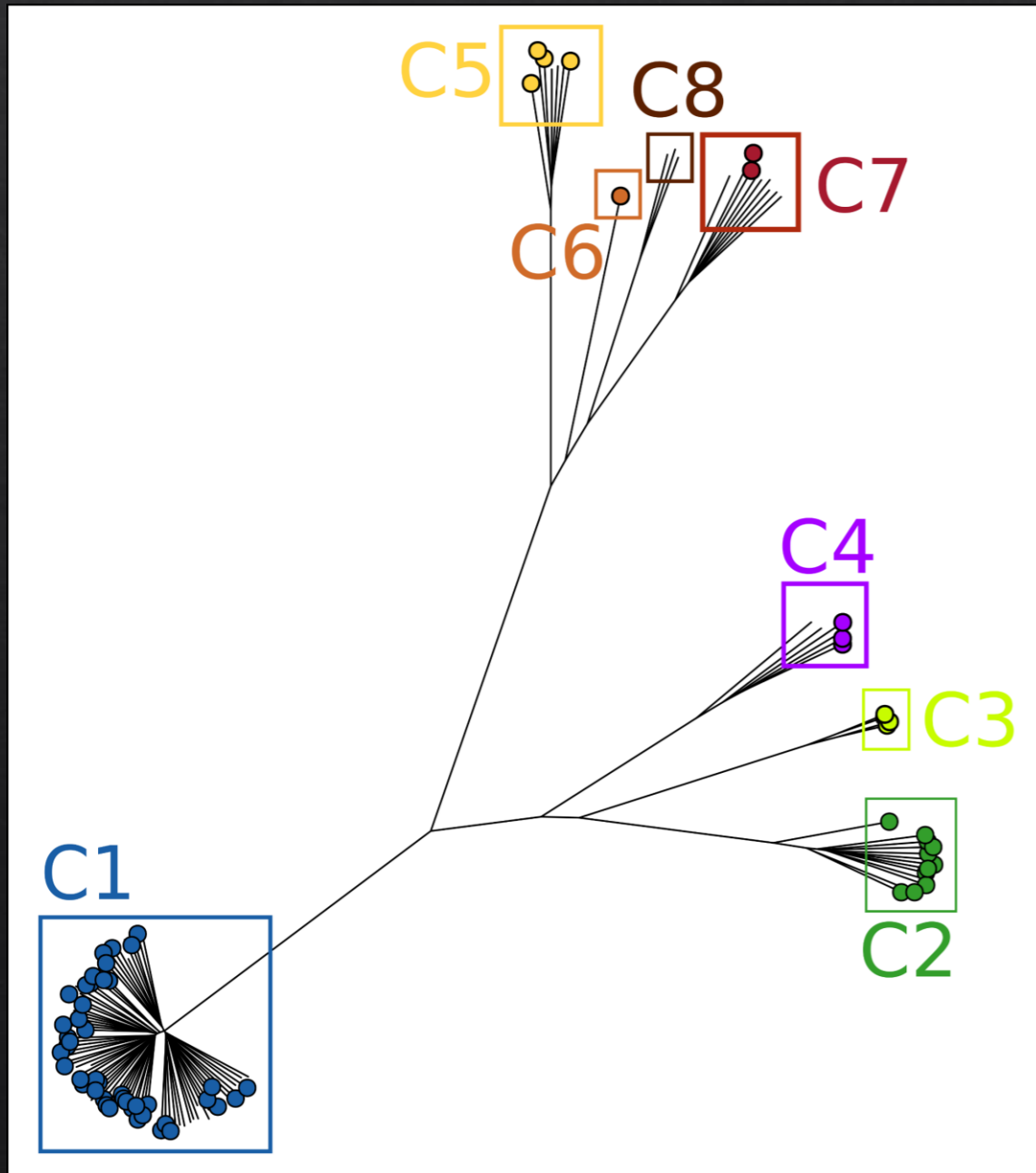
Results : *Lithophyllum stictaeforme/cabiochae* cryptic species complex in coralligenous habitats



Barcoding & Population genomics

- 3 Barcodes
- ~5000 SNPs

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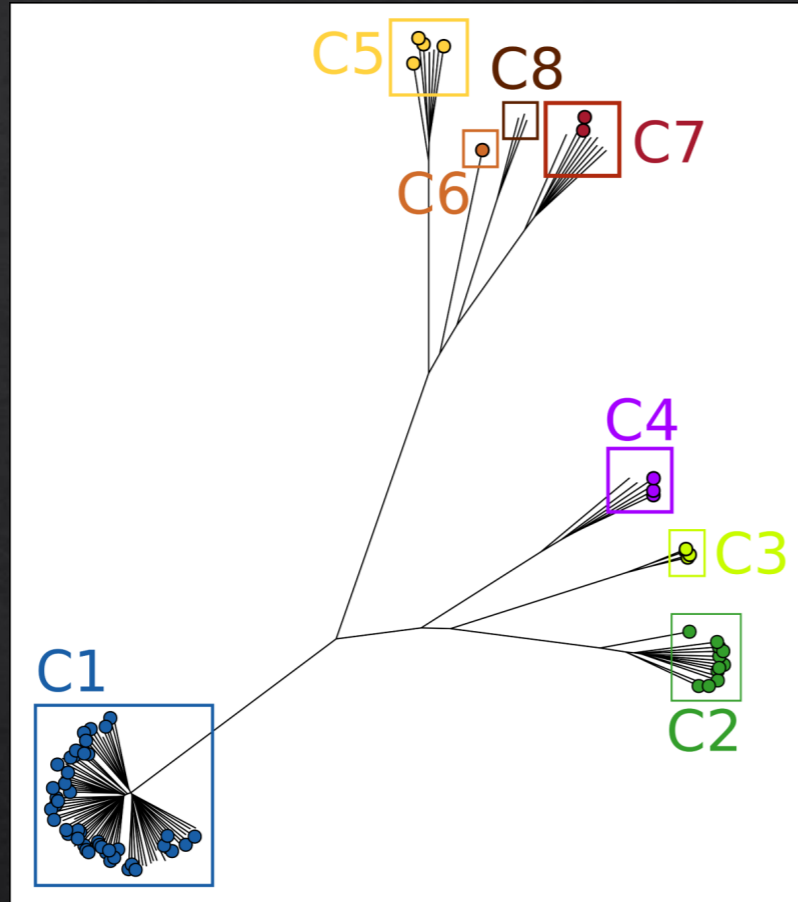
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Cryptic species = distinct biological species belonging to one given nominal species

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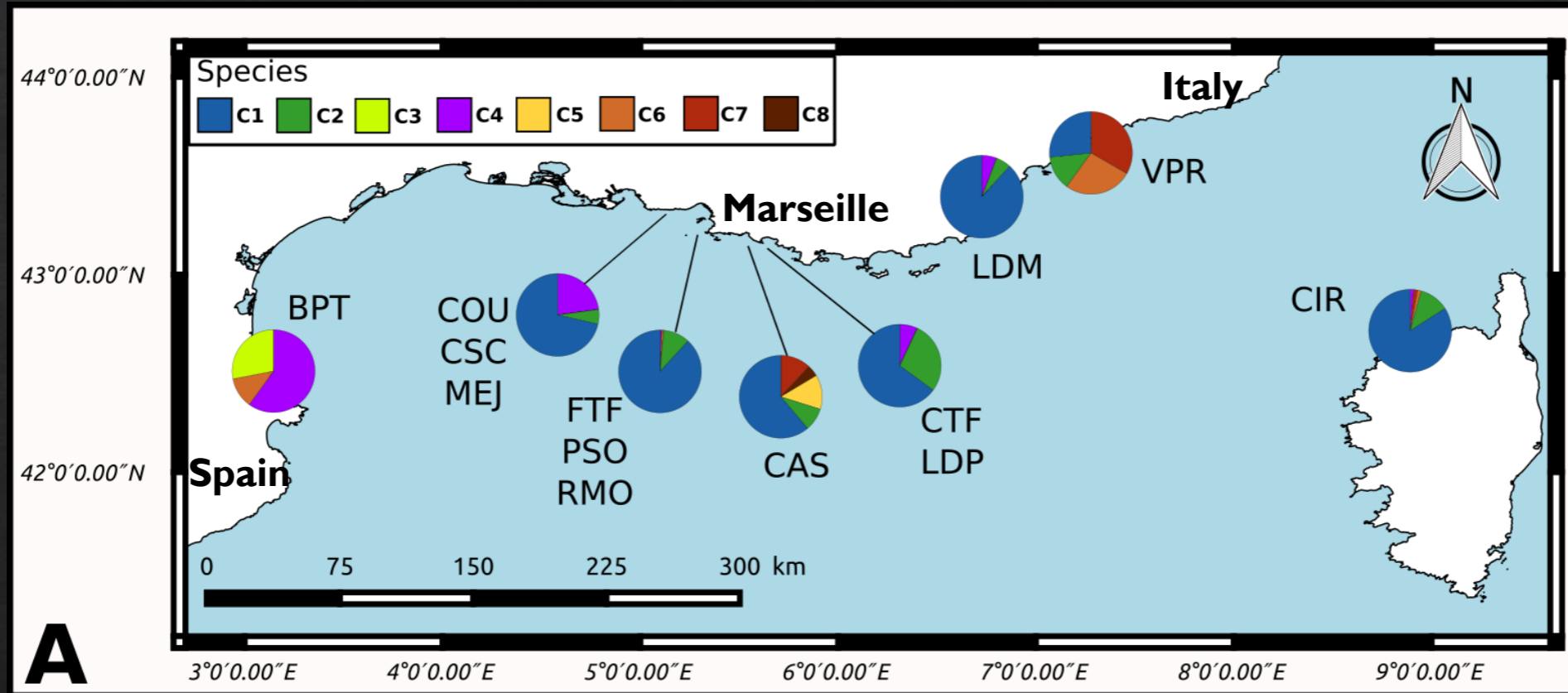
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- Distribution of these species along the French Mediterranean coastline ?
- Distribution along a depth gradient ?
- Ecological differentiation ?

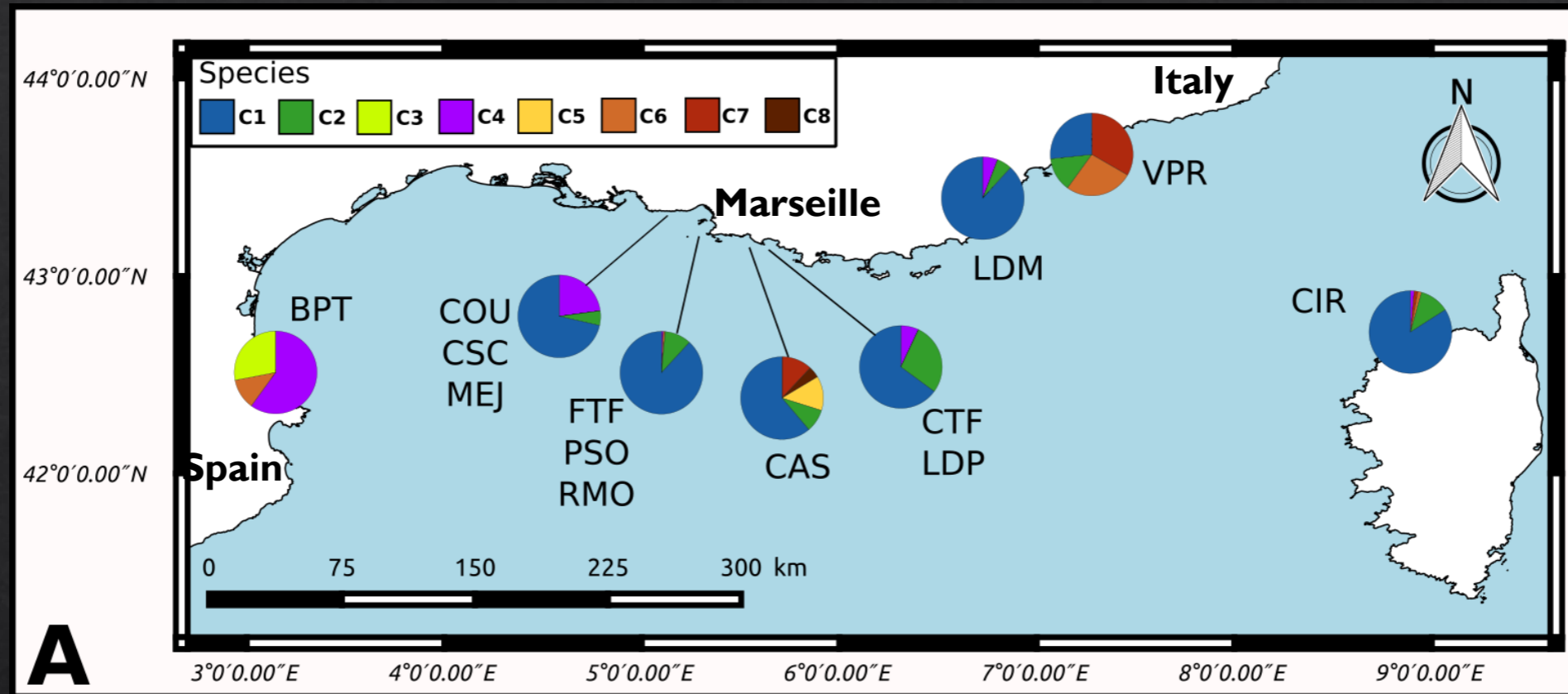
Distribution along the French Mediterranean coast

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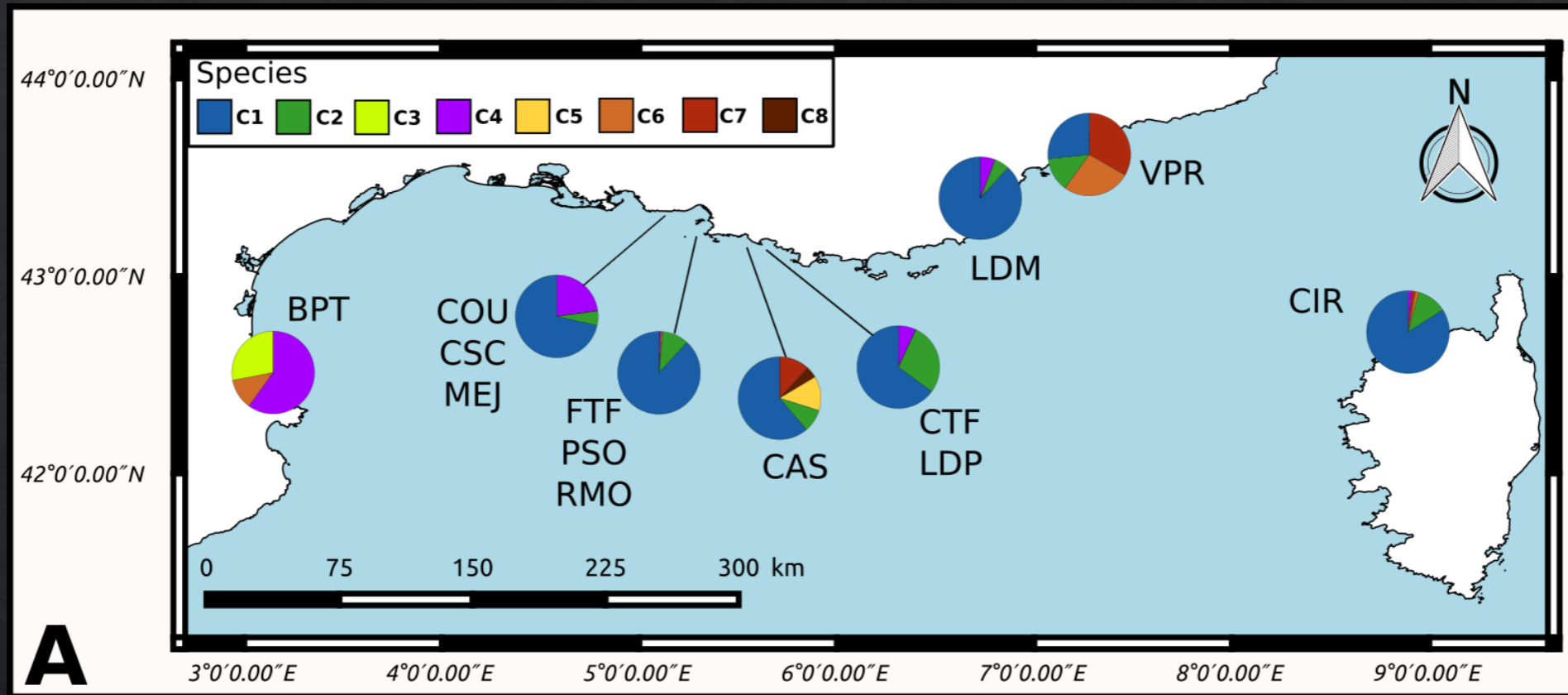


- Different communities in different sites
- C1 everywhere except in BPT
- C3 only found in BPT

- C6 & C7 very abundant in VPR
- C8 & C5 only found in CAS
- Community from Corsica are close from Marseille communities

Distribution along the French Mediterranean coast

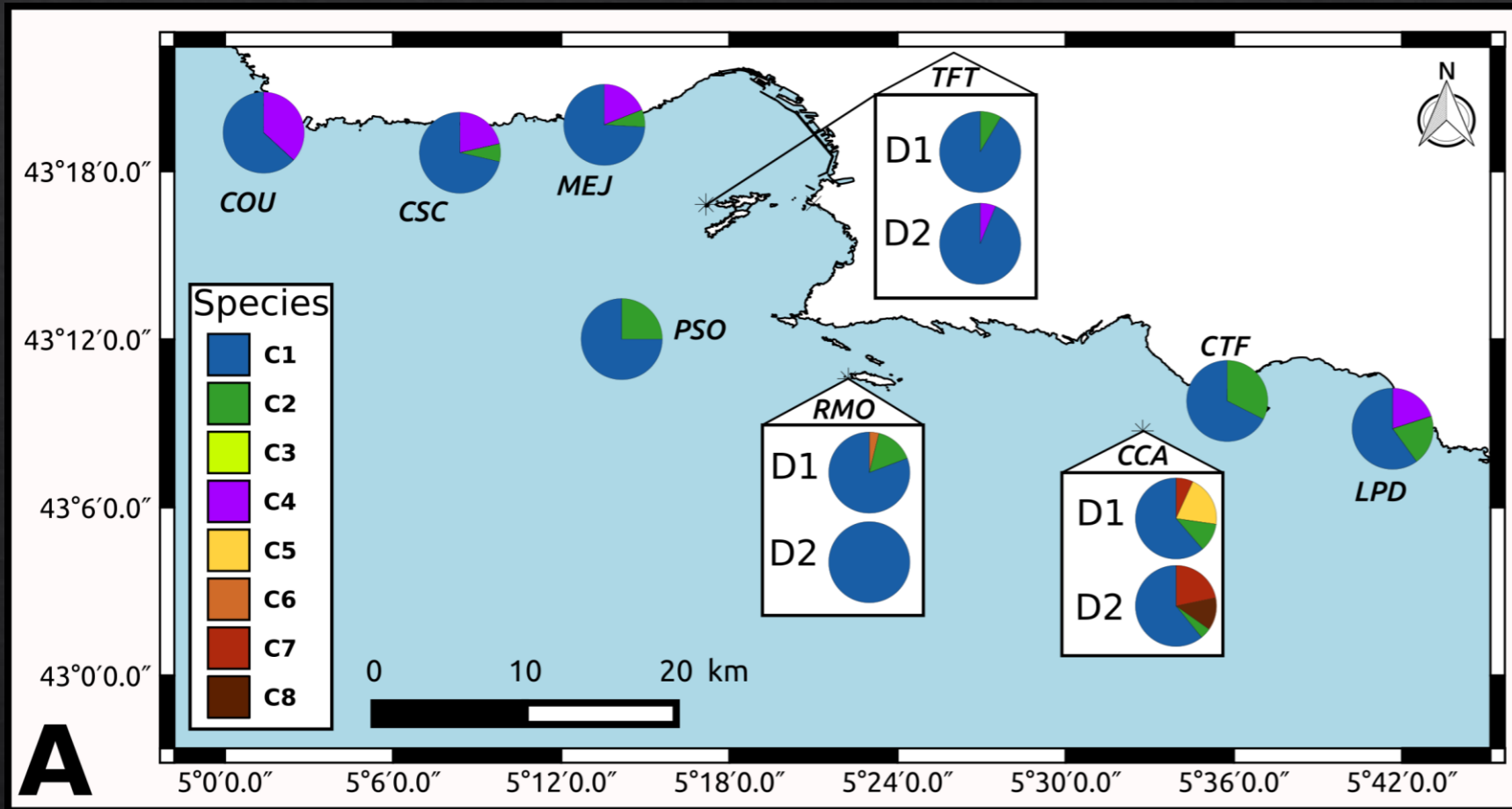
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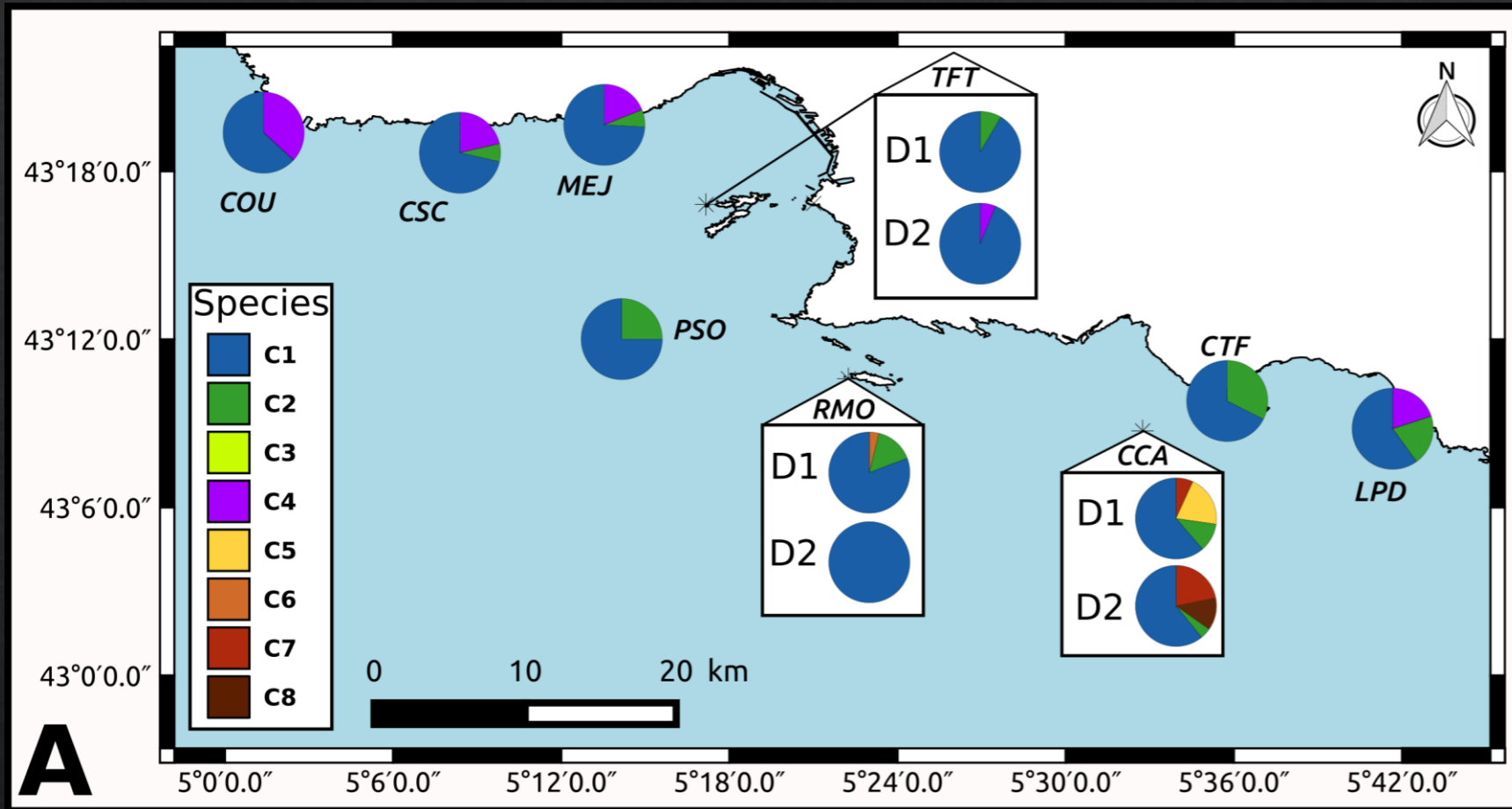
**Environmental conditions different in different sites ?
Or/and connectivity breaks ?**

Distribution in the Bay of Marseille



- **D1 : 28 to 32 meters depth**
- **D2 : 40 to 45 meters depth**

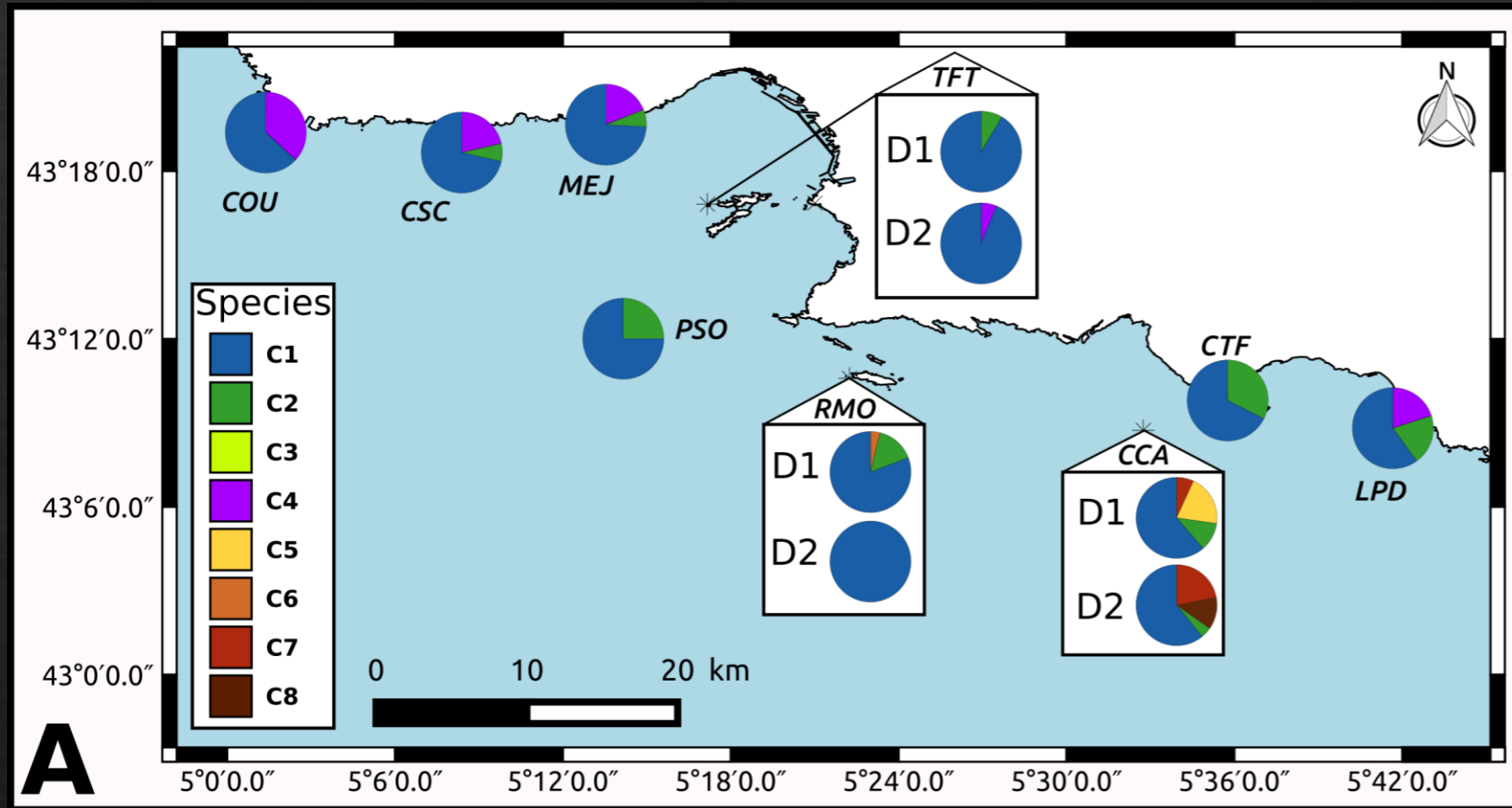
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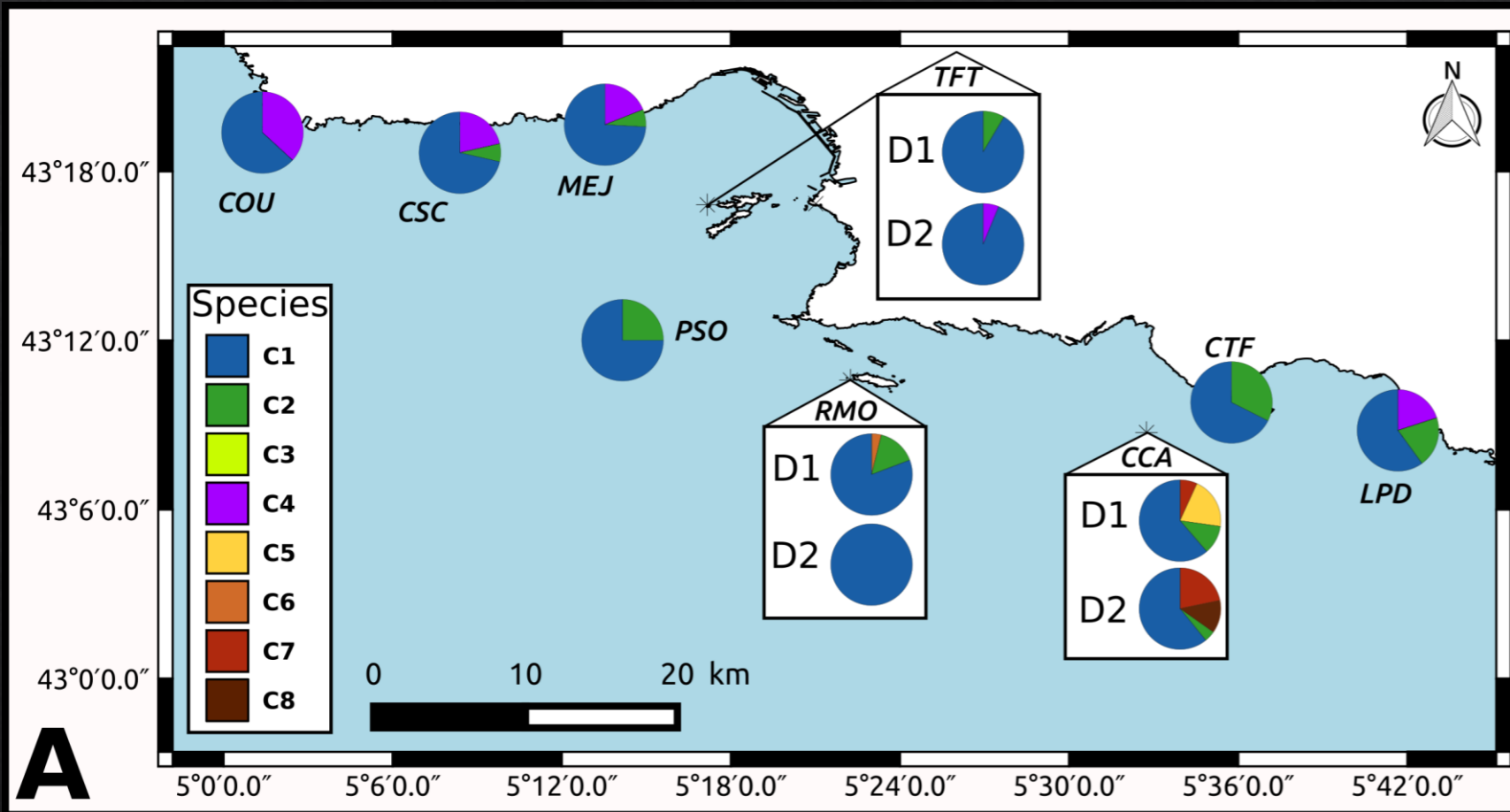


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- **Different communities at different depths in CCA and RMO**

Distribution in the Bay of Marseille



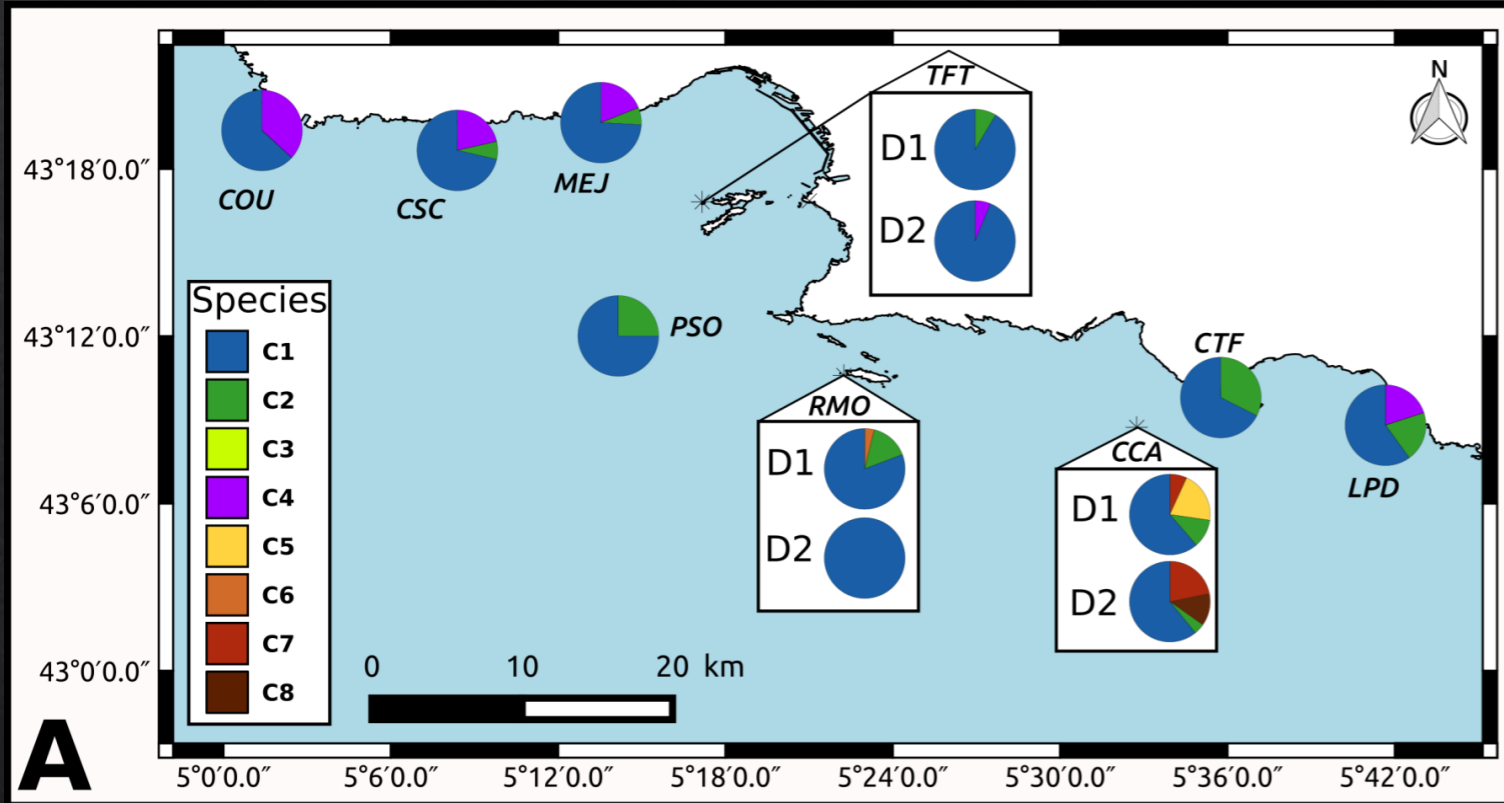
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Is the community differentiation between the two depth due to a lack of migration ?

Genetic structure in the most abundant species

~3000 SNPs from capture sequencing



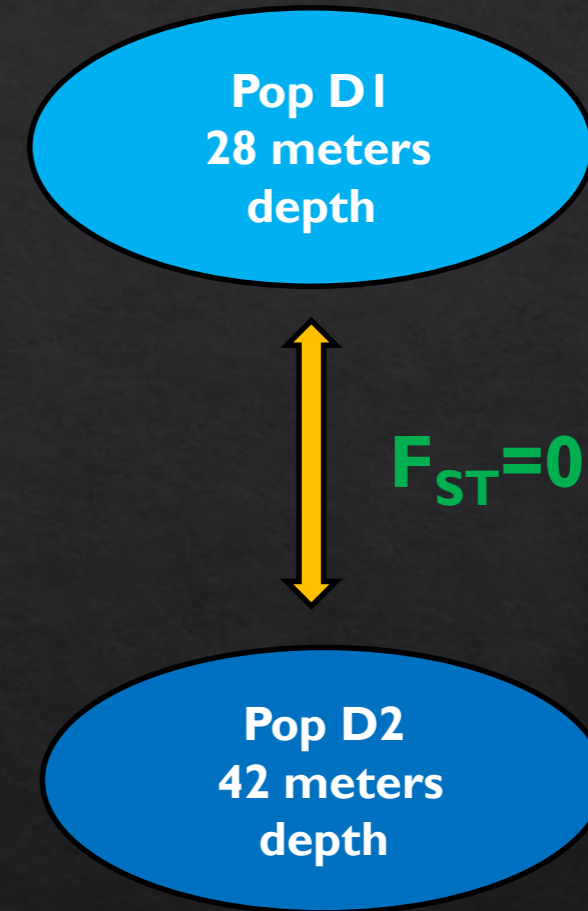
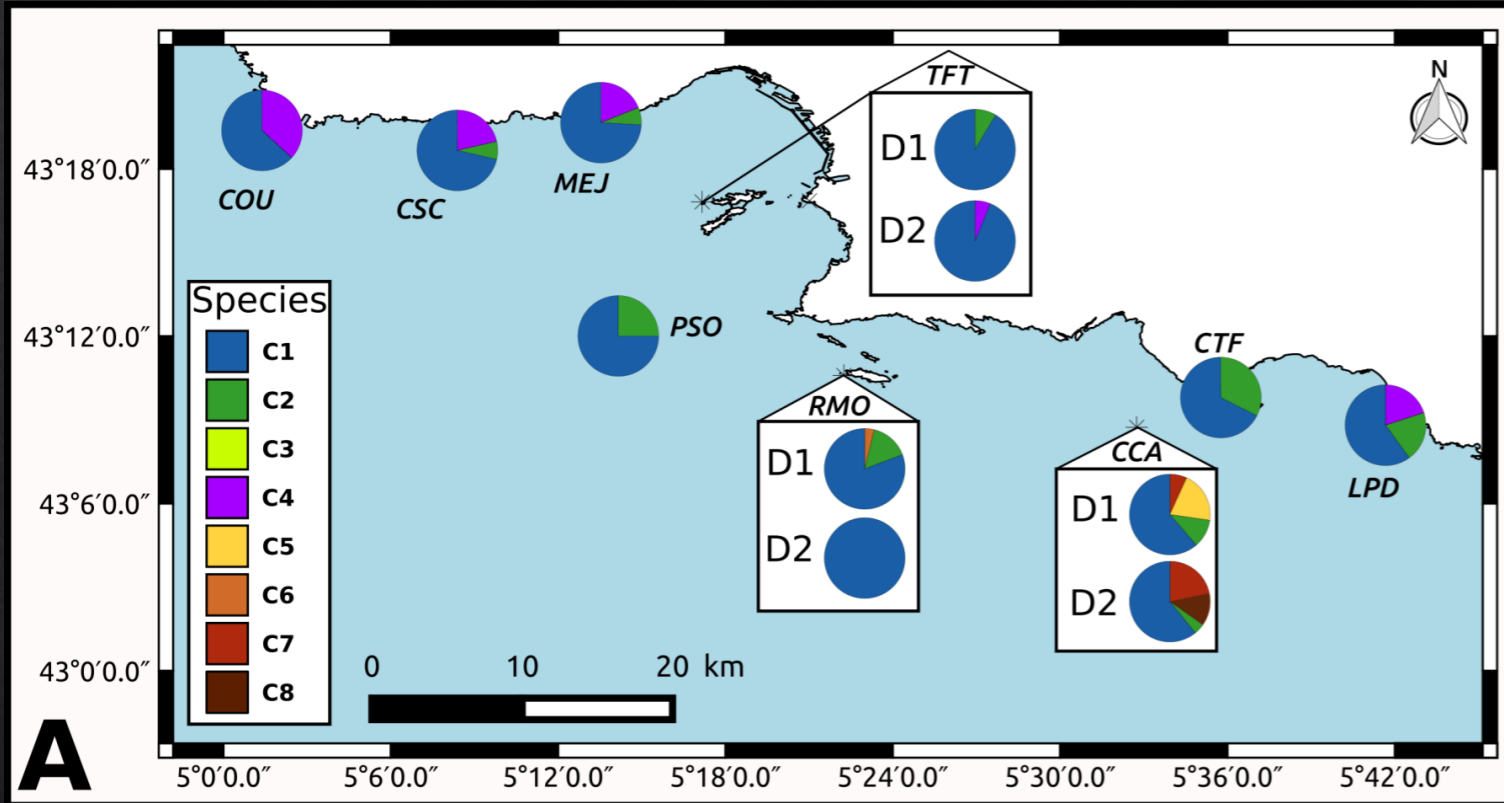
Pop D1
28 meters
depth

$F_{ST}=0$

Pop D2
42 meters
depth

Genetic structure in the most abundant species

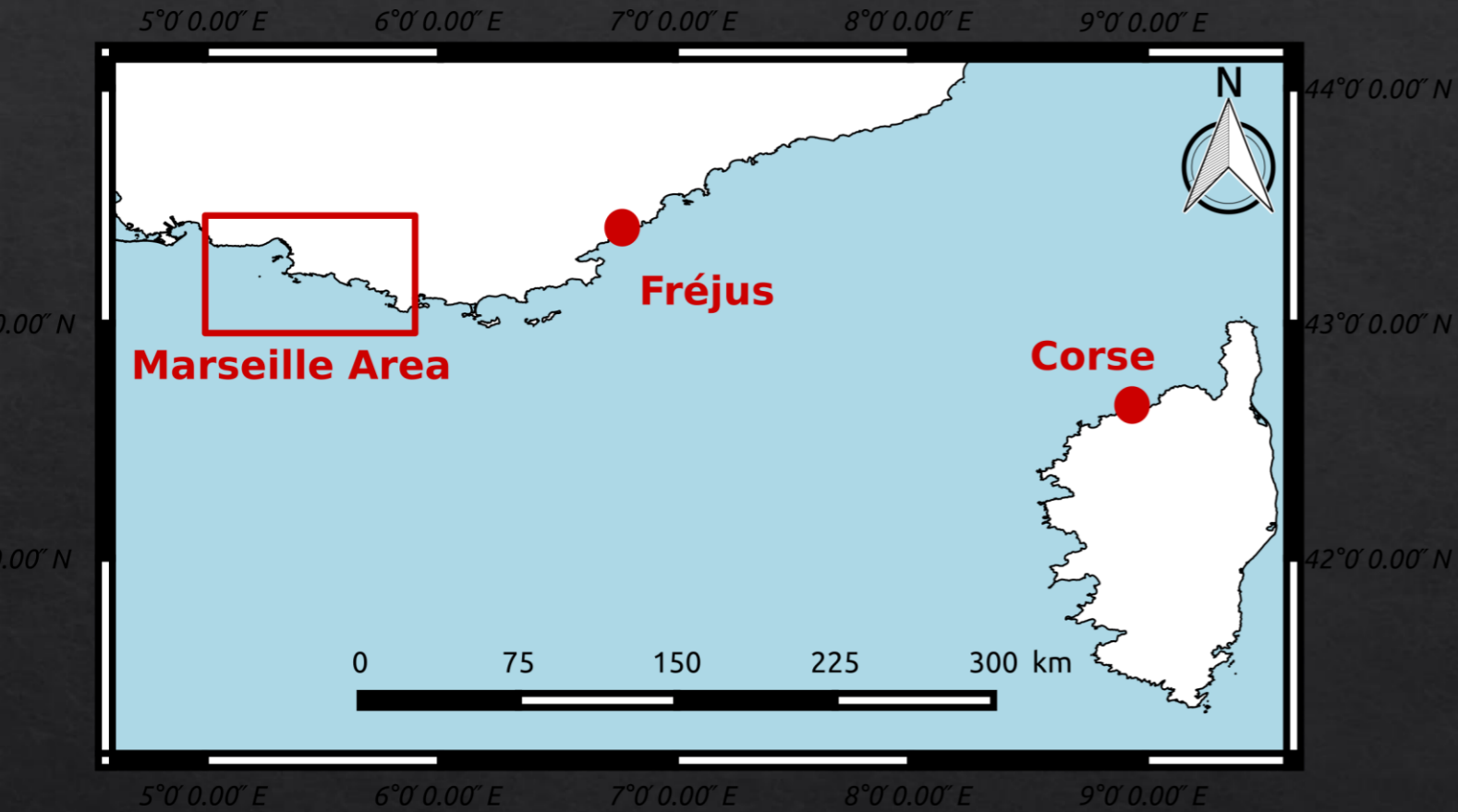
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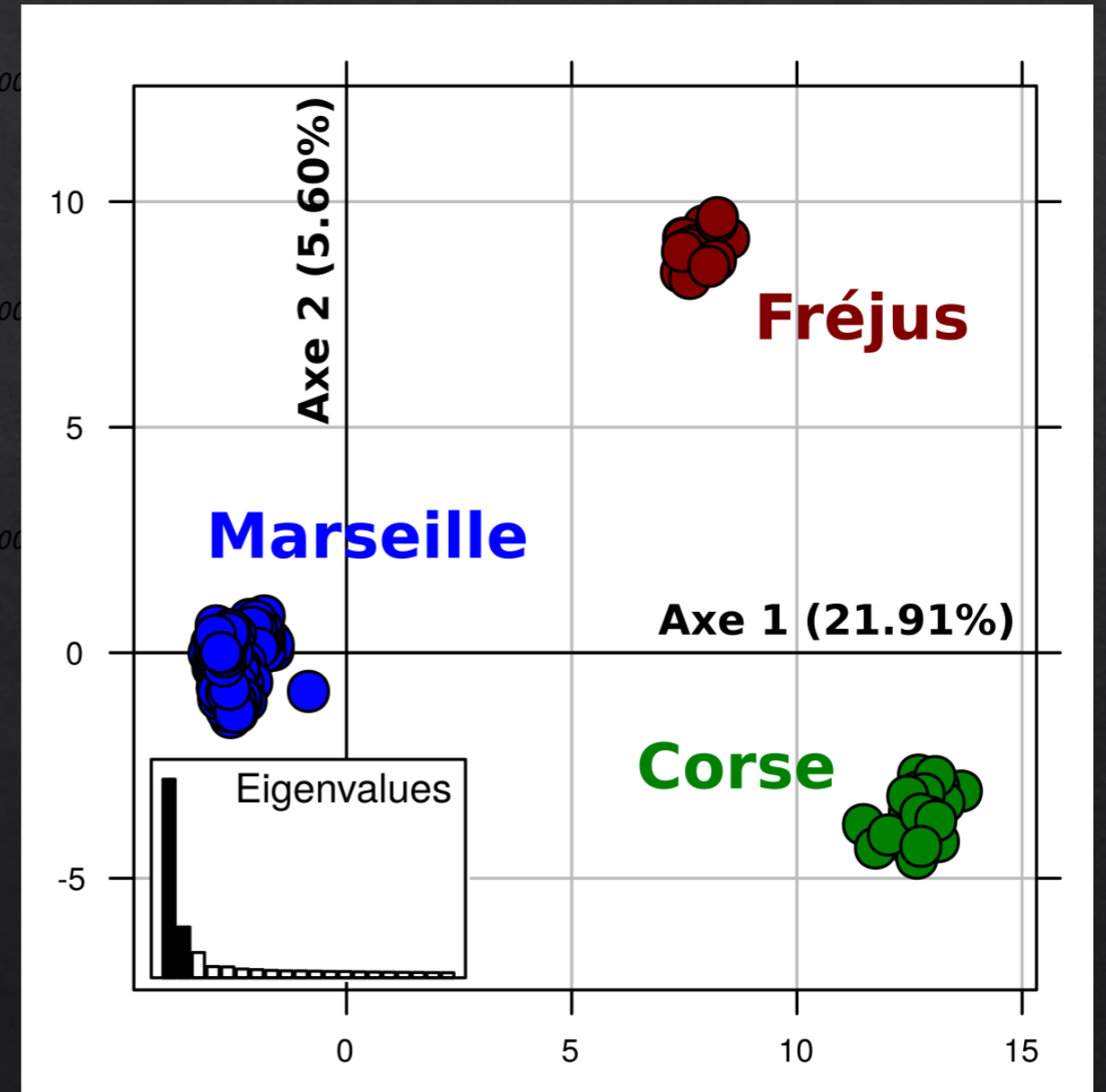
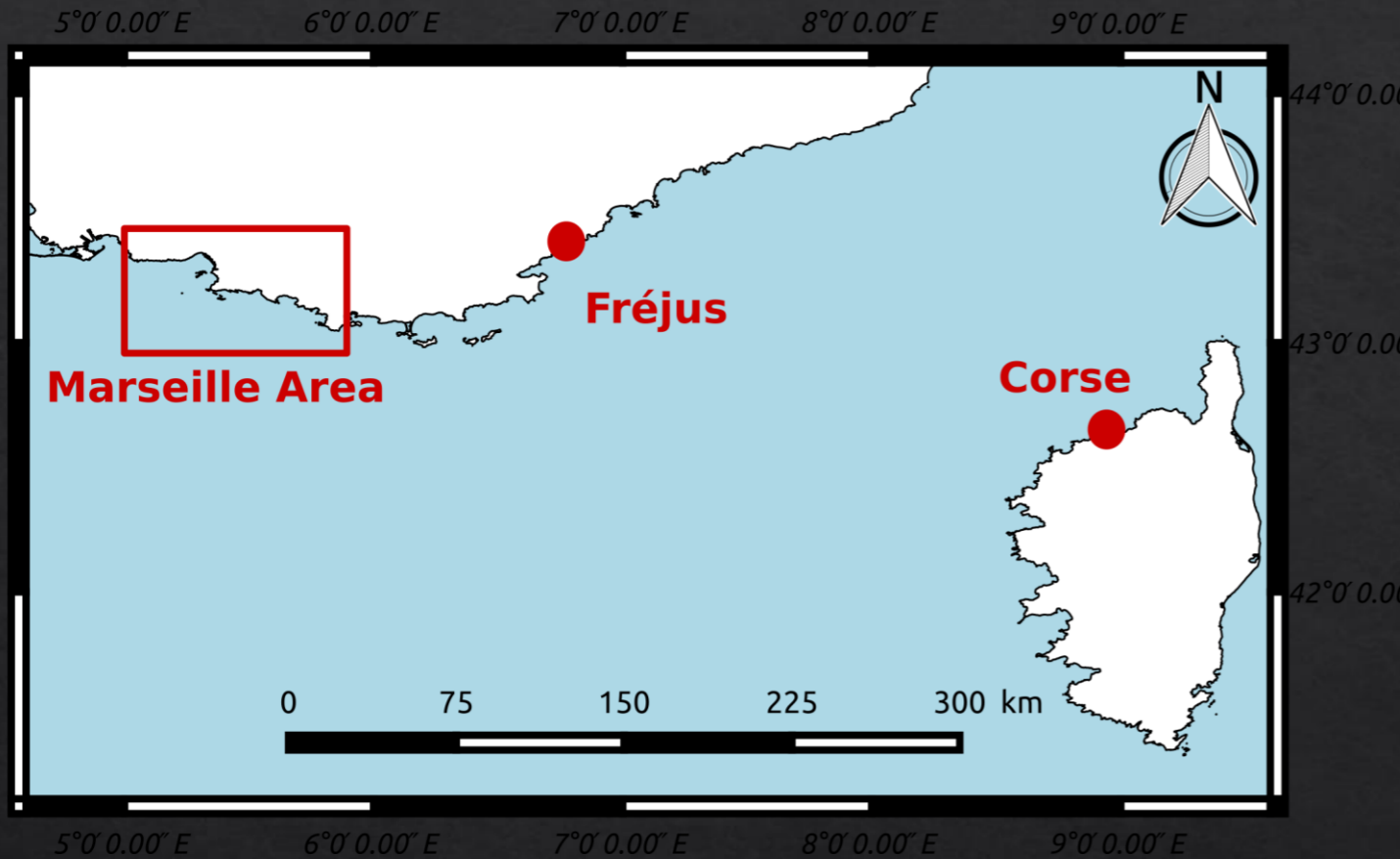
- No genetic differentiation between population of different depth at the same
- Migration is possible between two depth at the same site
- **Community differentiation probably due to a selective effect**

What about genetic structure in the most abundant species ?

Genetic structure in the most abundant species

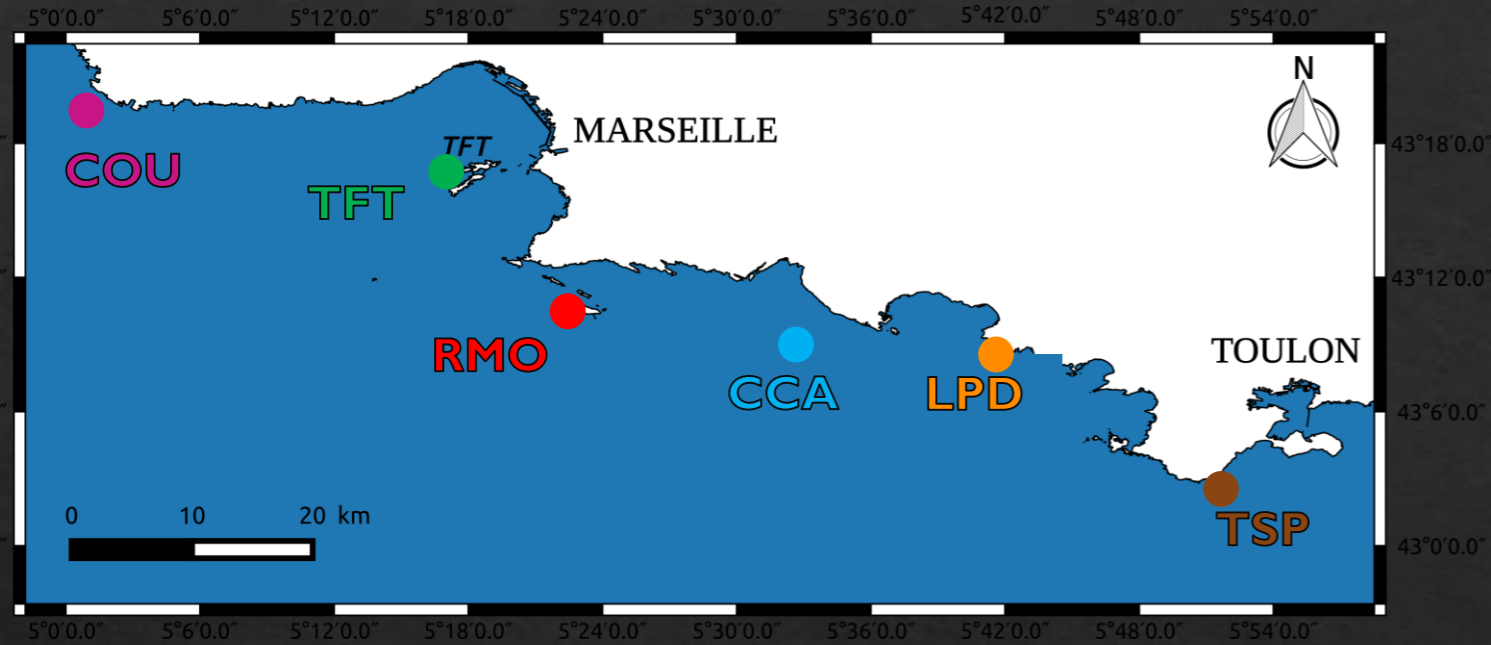


Genetic structure in the most abundant species

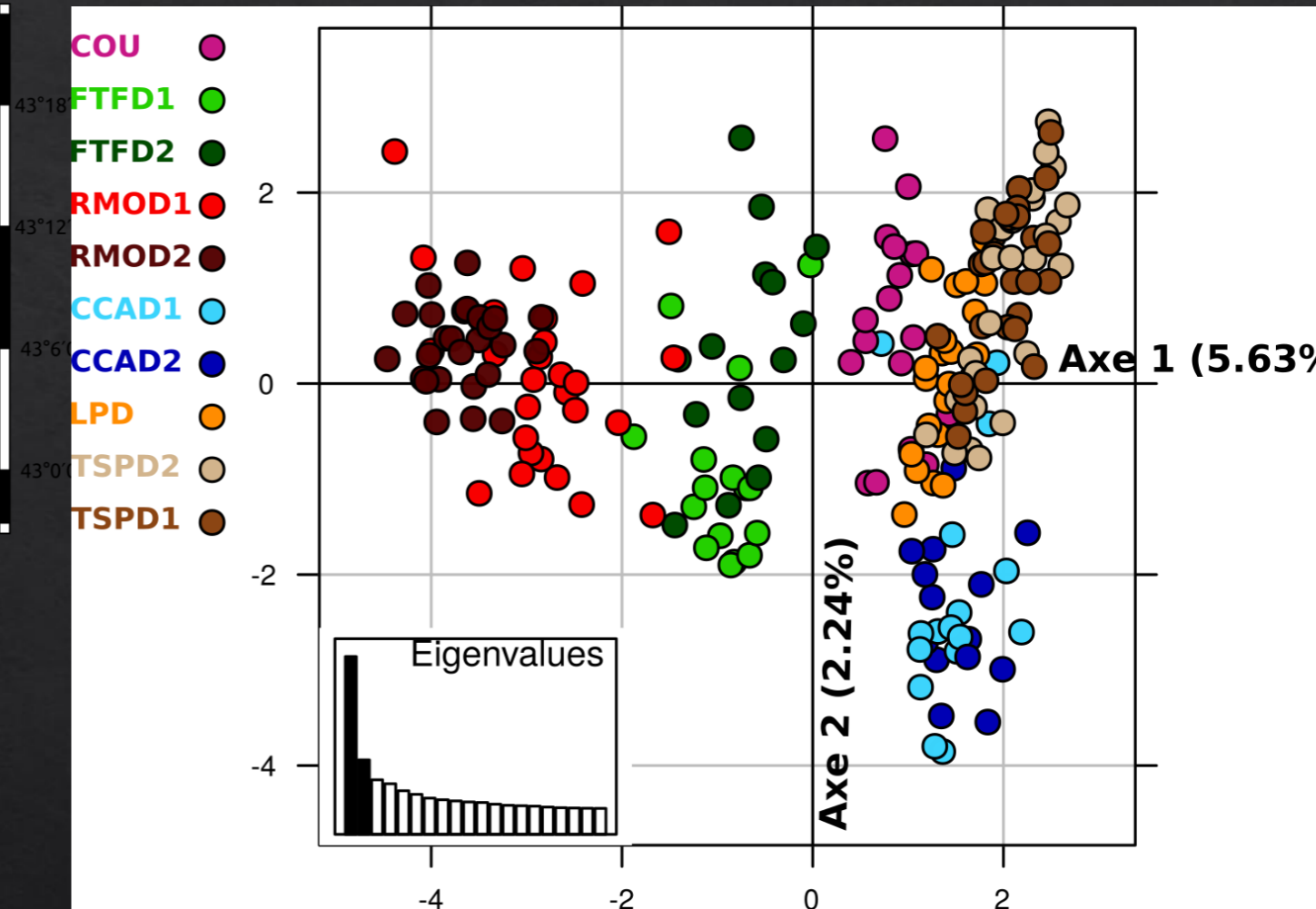
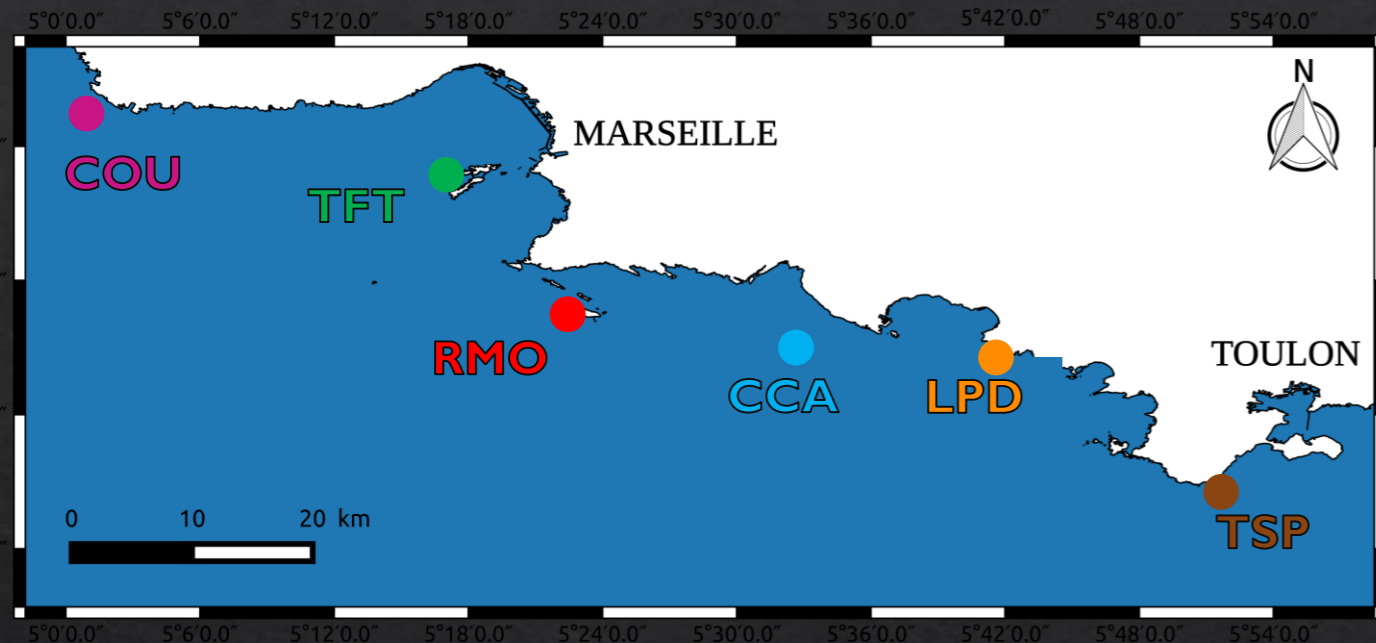


➤ Strong genetic structure at large spatial scale

Genetic structure in the most abundant species

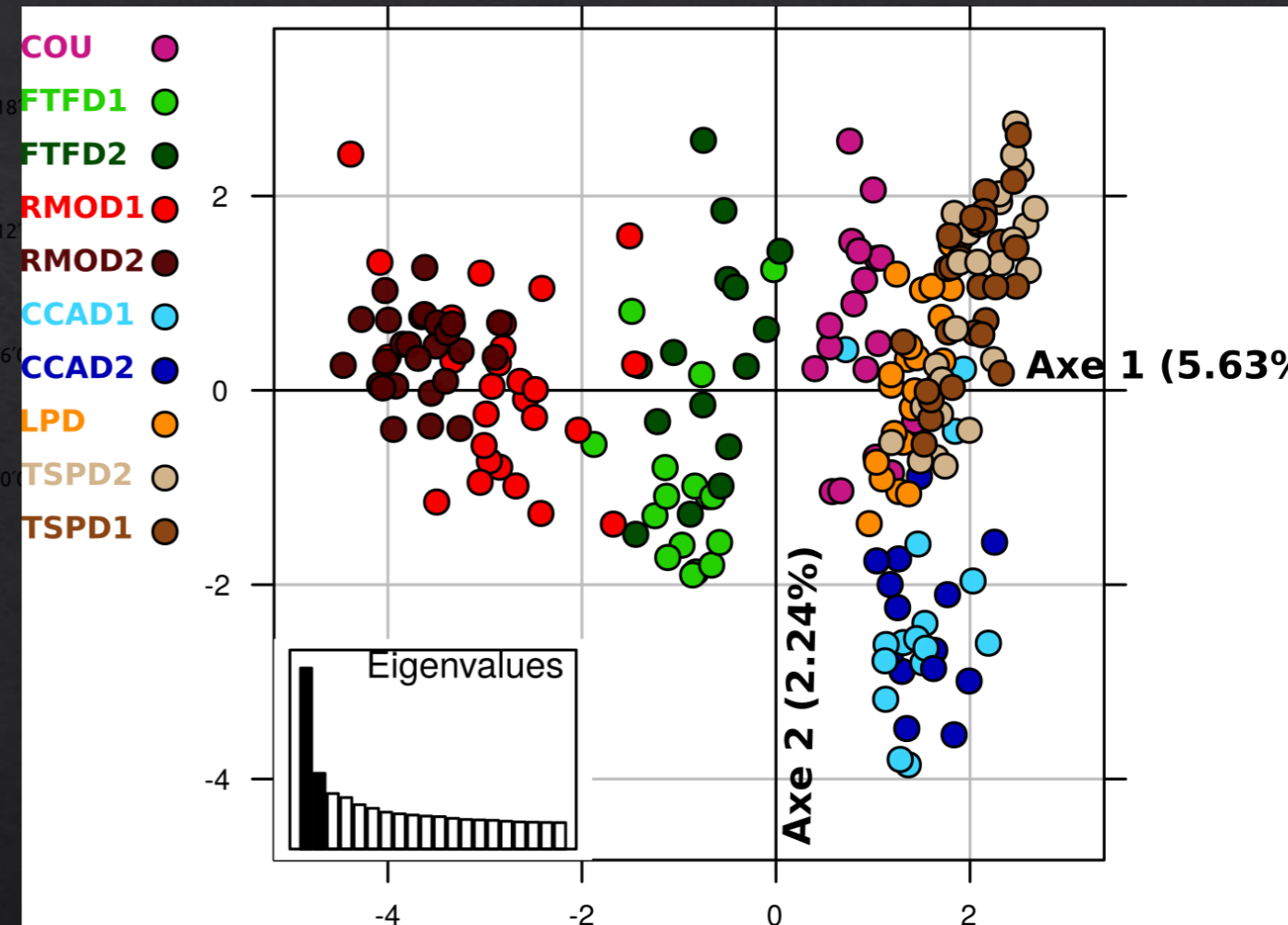
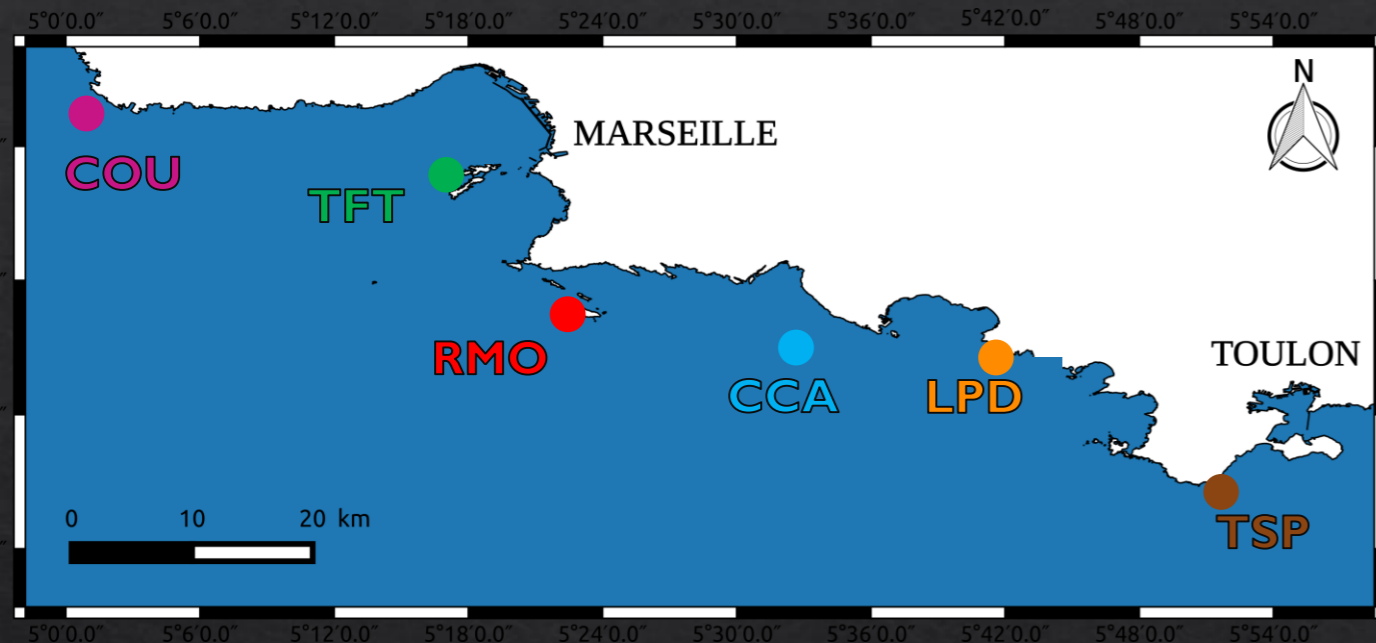


Genetic structure in the most abundant species



- Strong genetic structure even at small spatial scale
- Current in Marseille
- No differentiation between depth

Genetic structure in the most abundant species



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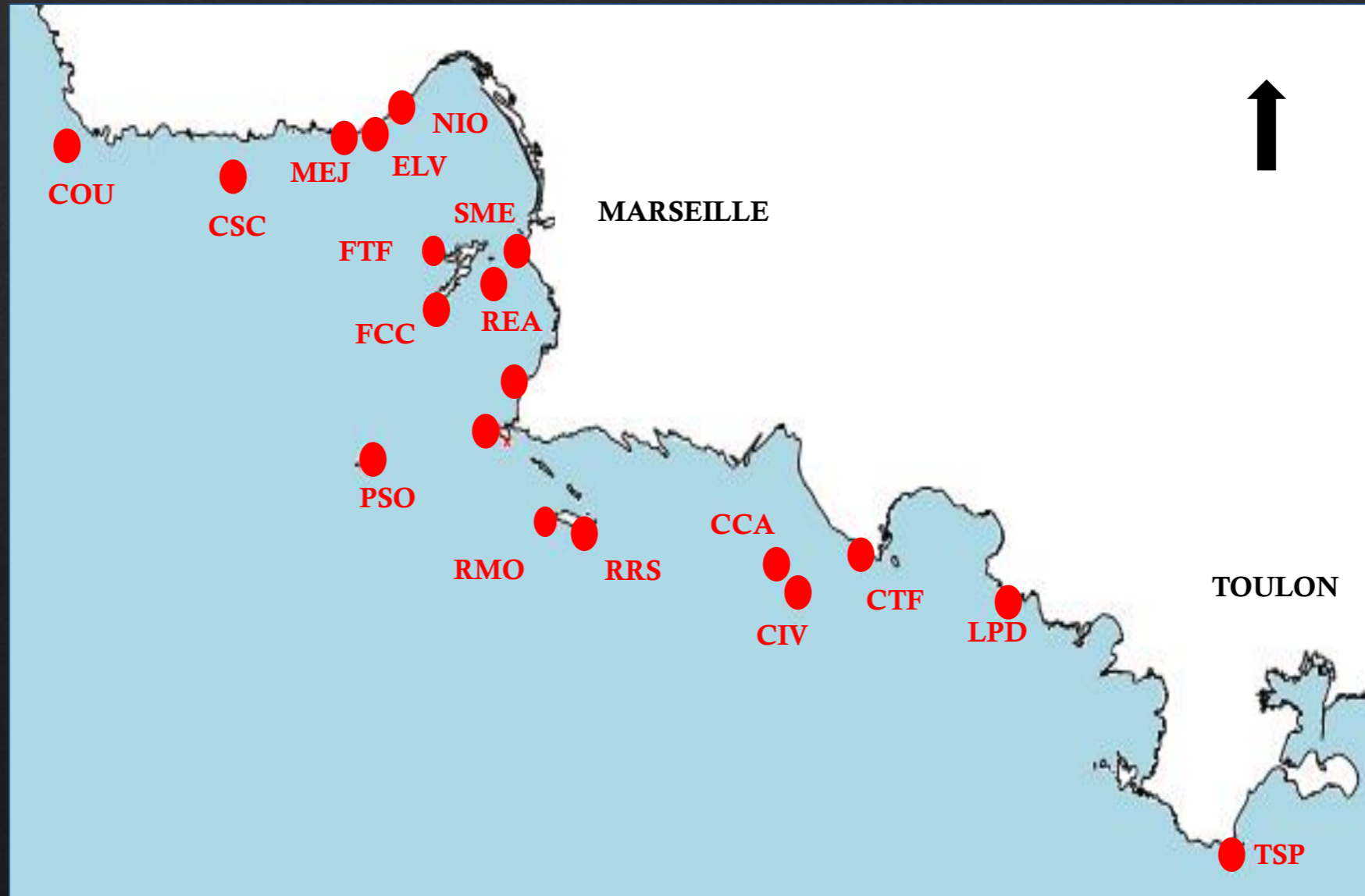
BUT

We found several loci « outliers » or correlated with depth indicating a potential local adaptation of these population to depth

What about coralligenous species communities ?

Coralligenous communities using a metabarcoding approach

- 240 samples from 20 sites



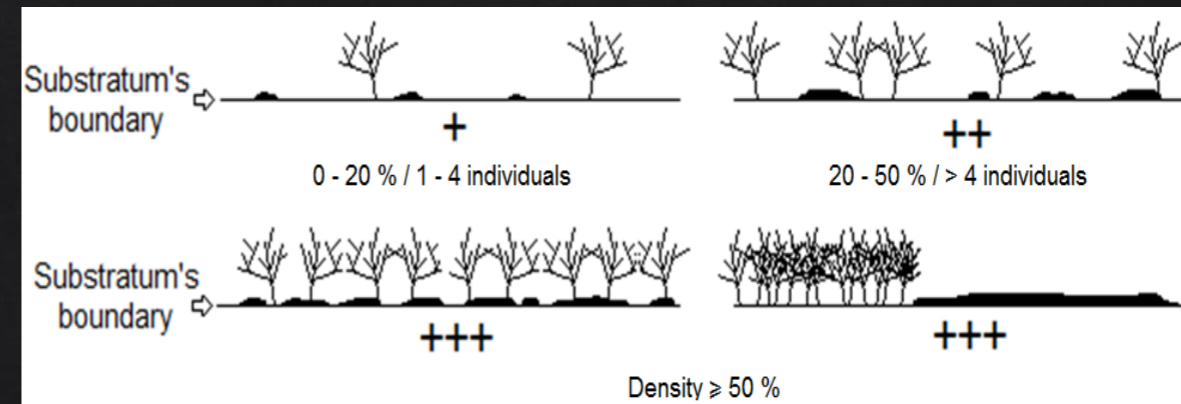
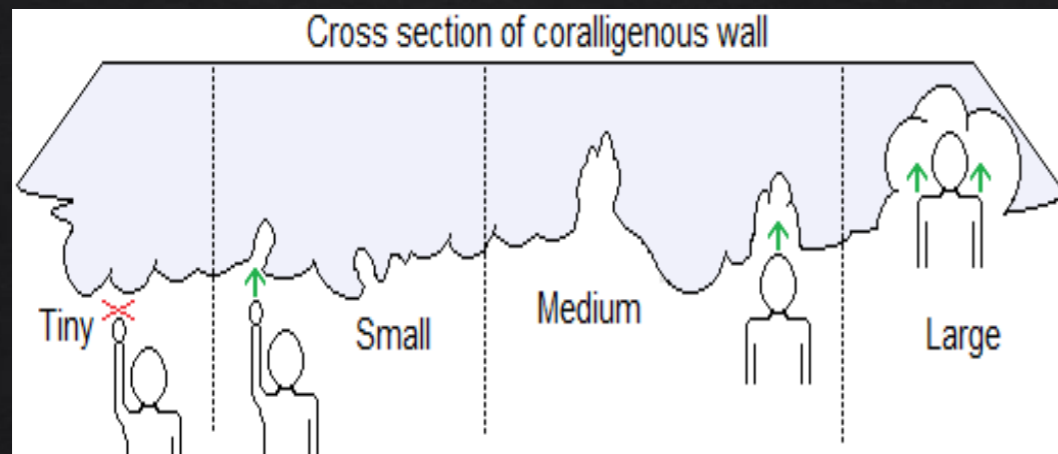
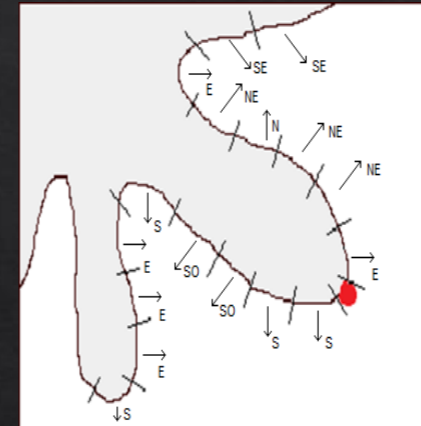
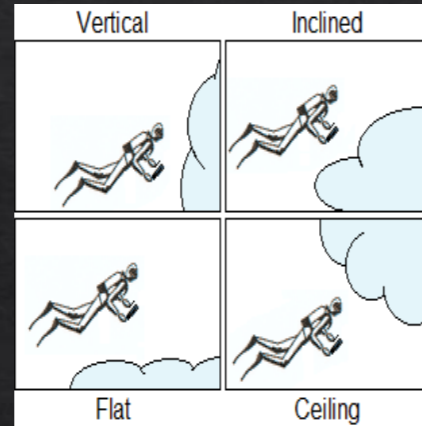
Sampling protocol

- **Suction sampler**
- **Surface square of 10cm**



Sampling protocol

- **Suction sampler**
- **Surface square of 10cm**
- **Depth and topological** data were recorded on each segment
 - **Inclination**
 - **Orientation**
 - **Rugosity**
 - **Most abundant species**



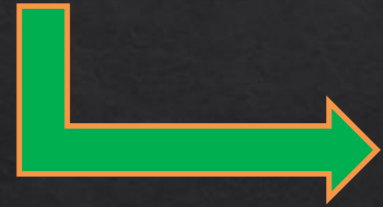
Molecular biology and bioninformatics

**DNA
Extraction**



Molecular biology and bioinformatics

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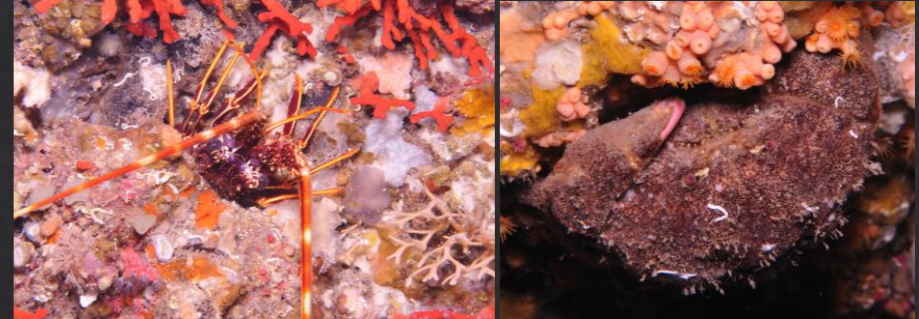
**PCR COI
fragment**

**Primers
targeting
metazoans**

Bryozoa



Crustacea



Mollusca



Cnidaria



Annelida



Porifera



Echinodermata



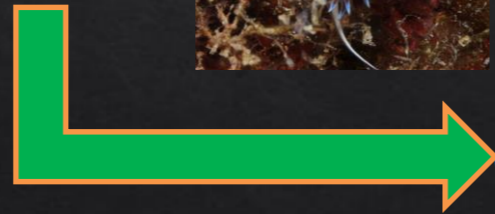
Molecular biology and bioinformatics

DNA
Extraction



PCR COI
fragment

Primers
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Illumina MiSeq
Sequencing



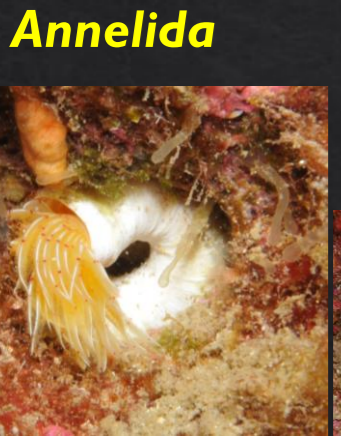
Molecular biology and bioinformatics

DNA
Extraction



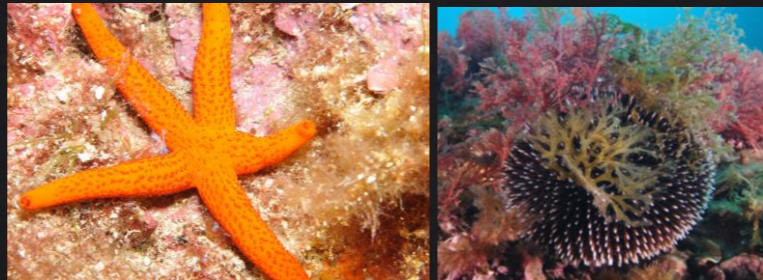
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Primers
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metazoans



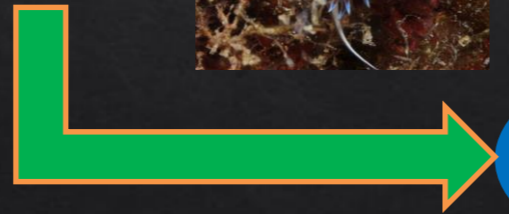
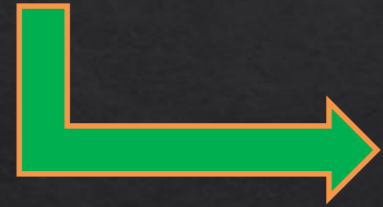
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Primers
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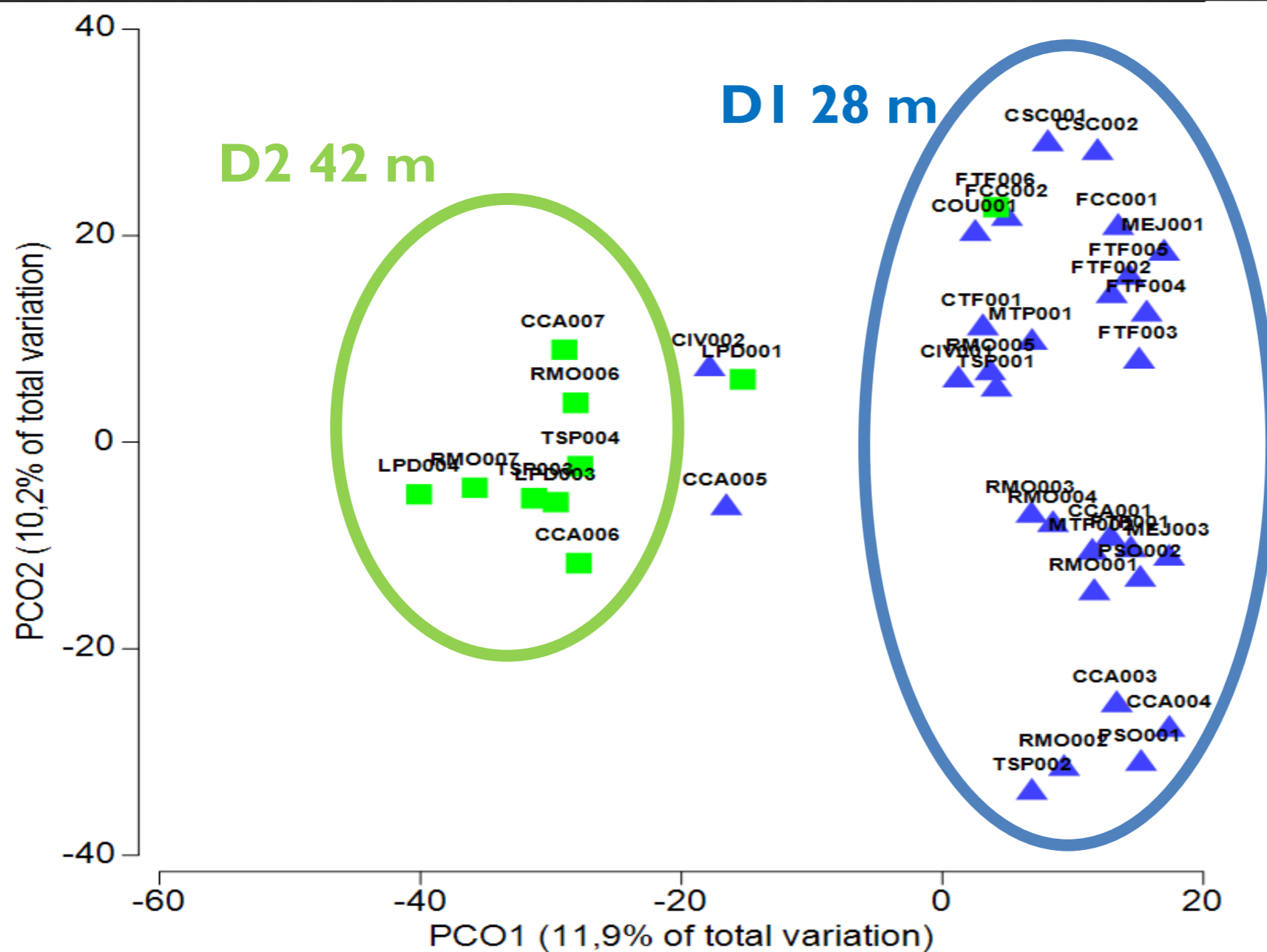


Illumina MiSeq
Sequencing

Bioinformatic
Analyses



Communities in coralligenous habitats



▪ **3029 mOTUs**

- Differences between sites
- No clear correlation with geographical position in the bay
- Correlations with environmental variables such as depth

Conclusions & Perspectives

- **Eight cryptic engineering species with varying abundances among sites and depth**
 - **Adaptative capacities of these different species in the context of climate change ?**
 - **Phenotypical differences between these cryptic species (photosynthesis, carbonate precipitation ...) ?**

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- **Species communities structured by depth :**
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 - **Maybe temperature (but no clear temperature regimes between 30 and 40 meters depth)**
- **The study of diversity structure at the species level and genetic level provides critical information to protect efficiently coralligenous habitats.**

Thank you for your attention

Looking for postdoctoral position

