SEAMOBB: SOLUTIONS FOR SEMI-AUTOMATED MONITORING OF BENTHIC HARD BOTTOMS

SEAMOBB project : **https://seamobb.osupytheas.fr/**

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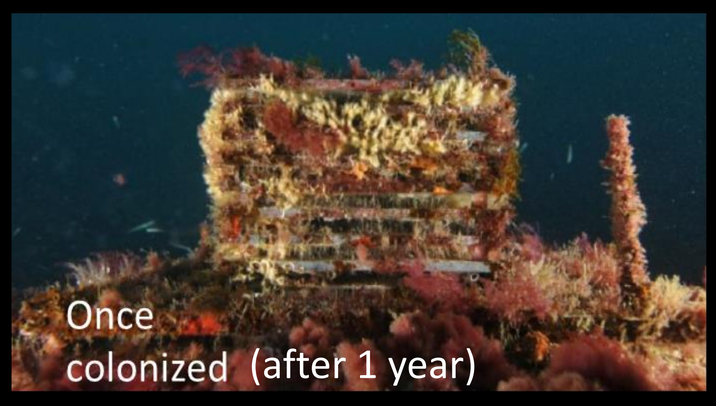
GOAL **Monitoring of the species composition of communities**

- Establish **connectivity networks** (physics & population genetics)
- **Standardize** marine community **sampling** (artificial & natural substrates)
- **Assess community composition**: Photo analysis & Metabarcoding



28 sites x (8 regions)
- 3 ARMS (1 year)
- 3 ASU
- 3 substrate scraping

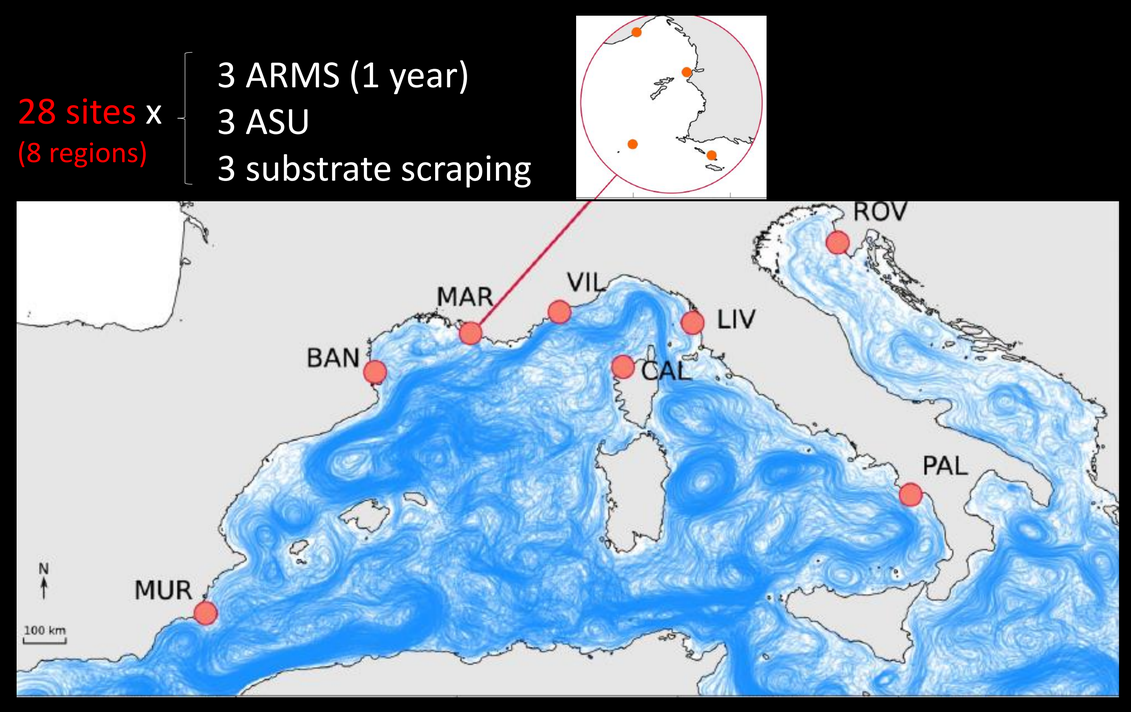


Photo-analyses

Computer vision algorithm (CORALNET, on the web)

-64 random points / photo → taxonomic identification

Different types of plate faces: ≠ niches → ≠ communities

The program learns rapidly: 3 weeks at the beginning, then only 4 days to analyse one region (200 photos)

Results of community composition analyses

- 600 photos (3 regions in France) →
  ca **80 taxa** identified (from species to phylum rank)
- Top Superior plate: more algae, stochasticity (grazing or not)…
- Level of diversity : varies among and within regions

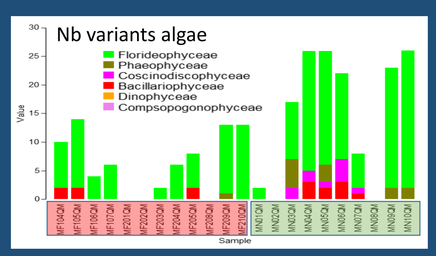
PERMANOVA (600 photos, France):
Community composition depends on:
Region ***(Site***) x Orientation*** x Compartmentalization*

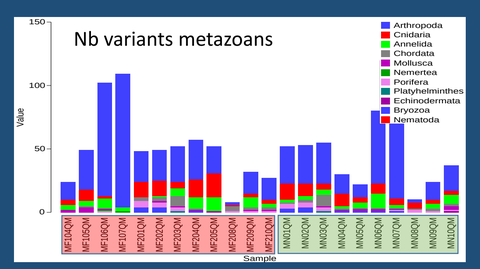
ARMS outperform simple colonization plates for monitoring marine communities: they provide a variety of niches (light, hydronynamism, predator exposure) even the 1st year of colonization.

Metabarcoding

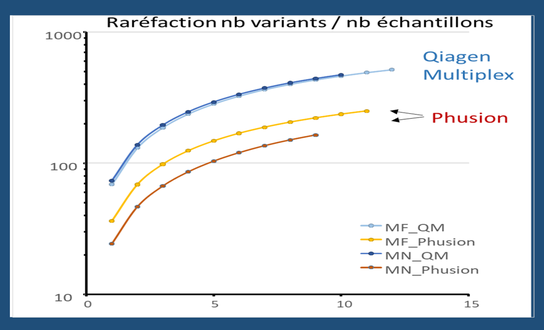
Laboratory protocol improvement

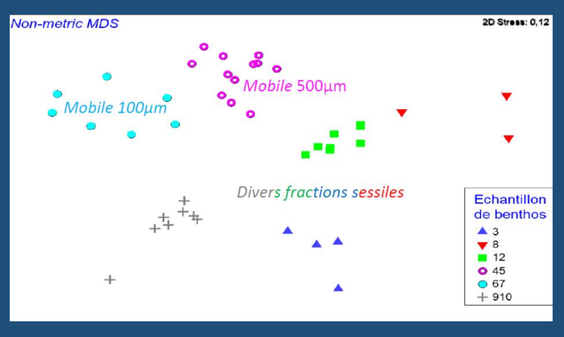
-DNA extraction method: kit MN-soil > kit MF (for diversity)





-Taq polymerase: Qiagen Multiples > Phusion (nb reads)





-Validation: biological replicates have similar mOTU communities

Results of community composition analyses

200 samples (3 regions in France) →
4000 mOTUS = **2000 « species »** (97% similarity clusters

Diversity: Small mobile fraction (100µm) > 500µm & sessile frac°s

Communities differ according to PERMANOVA :
- Fraction (sessile, mobile …)
- Site (within region) … more analyses ongoing

30 x more taxa identified by metabarcoding than by photo analysis

References

1 - Corse E, Meglécz E, Archambaud G, Ardisson M, Martin J-F, Tougard C, Chappaz R, Dubut V. **2017**. A from-benchtop-to-desktop workflow for validating HTS data and for taxonomic identification in diet metabarcoding studies. **Molecular Ecology Resources**, 10.1111/1755-0998.12703

2 - Cahill AE, Pearman JK, Borja A, Carugati L, Carvalho S, Danovaro R, Dashfield S, David R, Féral J-P, … & Chenuil A. **2018**. A comparative analysis of metabarcoding and morphology-based identification of benthic communities across different regional seas. **Ecology & Evolution** 8:8908-8920.

3 - David R, Uyarra M, Carvalho S, Anlauf H, Borja A, Cahill AE, Carugati L, Danovaro R, De Jode A, Féral J-P, Guillemain D, Lo Martire M, Thierry de Ville d'Avray L, Pearman JK & Chenuil A. **2019**. Lessons from photo analyses of Autonomous Reef Monitoring Structures as tools to detect (bio-) geographical, spatial, and environmental effects. **Mar Pol Bull** 141:420-429.

PARTNERS

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