



**ECRS 2024**  
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## TEMPORAL CHANGES IN POPULATION CONNECTIVITY OF THE GORGONIAN PARAMURICEA CLAVATA IN THE NORTH-WESTERN MEDITERRANEAN SEA

**Camille Sant**, Didier Forcioli, Katell Guizien, Lorenzo Bramanti, Federica Costantini,  
Jessica Dos Santos, Jean-Olivier Irisson, Cecile Fauvelot





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### POPULATION CONNECTIVITY

Exchange of individuals between geographically separated populations.

→ In coral reefs, primarily due to the **transport of larvae**

population  
recovery and  
persistence

genetic  
differentiation  
among  
populations

local adaptation



## Oceanic circulation

Water mass balance and density anomalies ?

Stratification ↗

Wind forcing ?

## Species life history

spawning time ↘

larval swimming behaviour ↗

larval stage duration ↘

larval daily mortality rate ↗

## POPULATION CONNECTIVITY

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genetic differentiation among populations

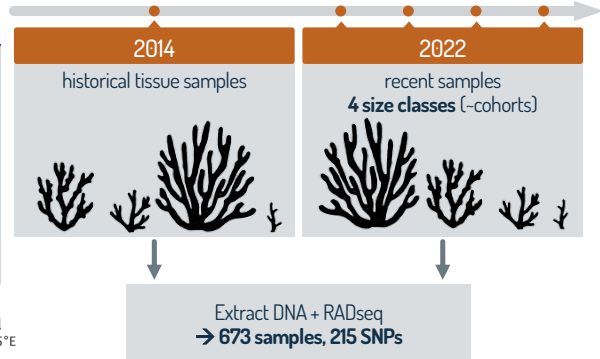
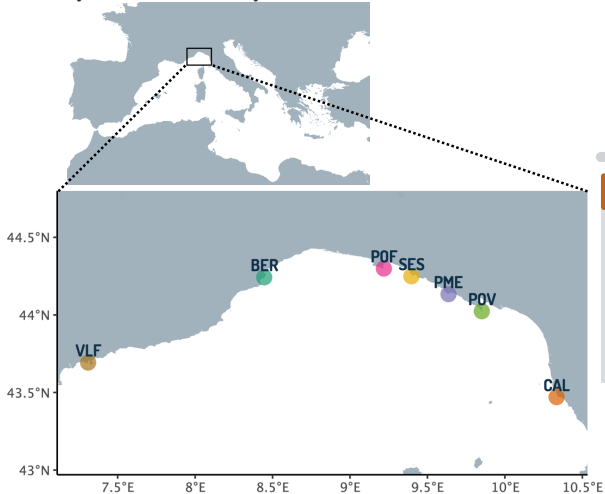
local adaptation



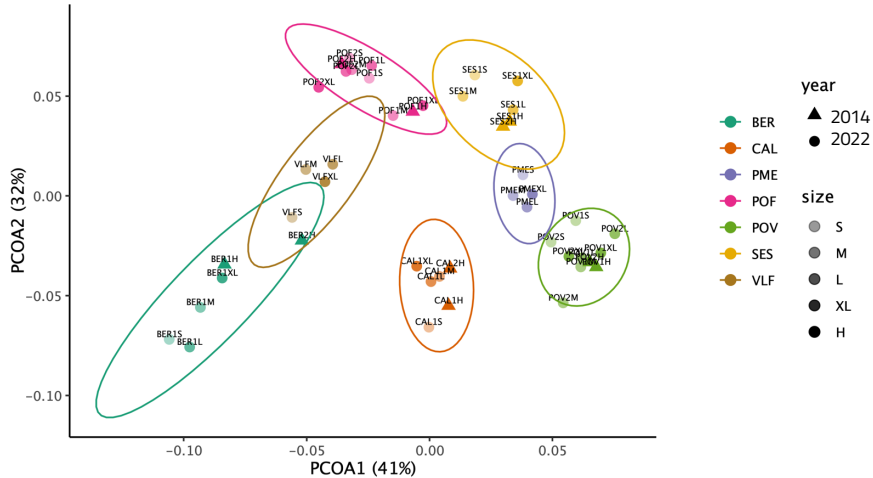
Future climate-driven changes → changes in marine connectivity (local oceanographic and taxon-specific biological factors)

*How much does connectivity change over time?*

# Spatial and temporal structure of *Paramuricea clavata* sampling

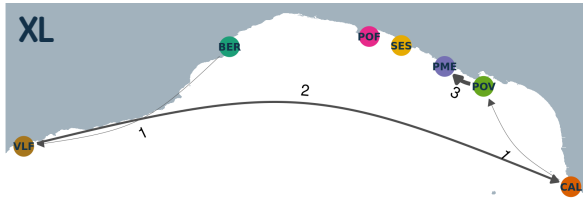


## PCOA on genetic differences between each size class at each site



→ Genetic variability is more driven by geography than time

## Connectivity networks of each 2022 size class

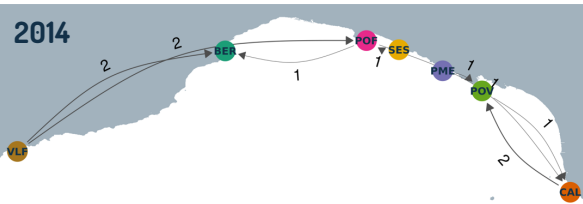


Clustering by network community detection

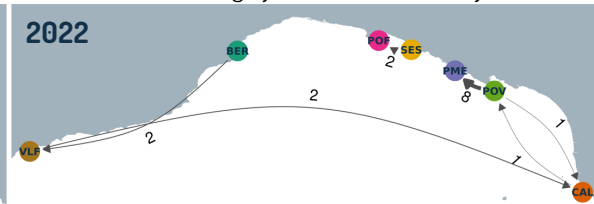
→ Some connections appear stable over time (POV→PME), most are not

## Connectivity networks of 2014 and 2022 samples

2014



2022



Clustering by network community detection

→ Strong variation in connectivity estimates over large time scales

### POPULATION CONNECTIVITY

Large variations over time

### USUAL CONNECTIVITY STUDY

One-shot study = snapshot of the connectivity at a given time

Not representative of the connectivity over a longer period of time

But : other methods → large inter method variance in connectivity estimates  
Although the spatial structure is well found, the data are not sufficient to reliably estimate connectivity.

#### **Hypothesis to explain discrepancies**

degraded DNA for some samples + difficulty with RADseq libraries  
→ much reduced amount of data (individuals and SNPs) and a lot of missing data

Benchmark of the methods on simulated datasets → shows that connectivity networks estimates are very impacted by the lack of data, especially by the lack of individuals represented.

**Assessing uncertainty in population connectivity estimates from genetic data: a benchmark of commonly used methods and tools on simulated datasets (Sant et al., in prep)**

#### **Planned solution**

repeat sequencing using ddRAD :  
less sensitive to DNA degradation, promising results on another species





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# THANK YOU FOR YOUR ATTENTION

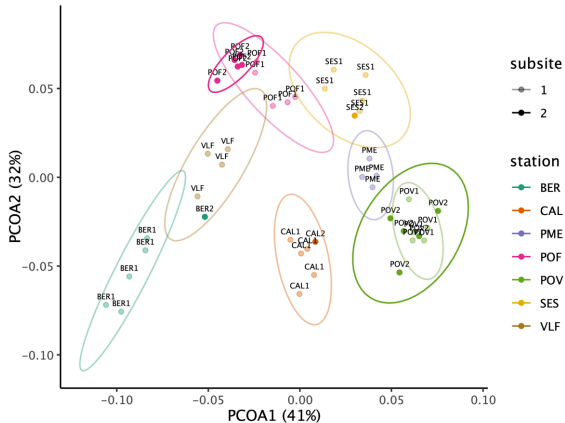


[camille.sant@imev-mer.fr](mailto:camille.sant@imev-mer.fr)



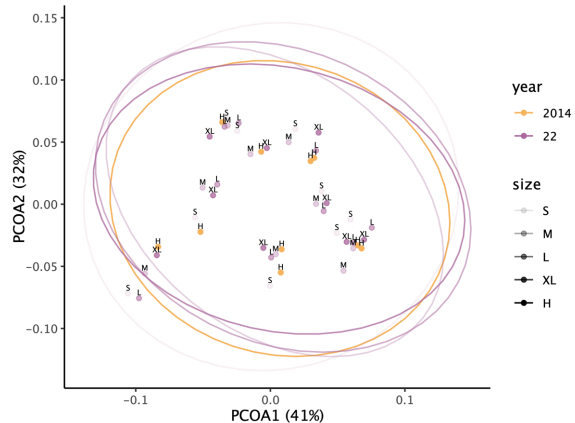
## Données RADseq

### Sites et sous-sites



→ Structure spatiale forte

### Année et classes de tailles



→ Pas de structure temporelle globale

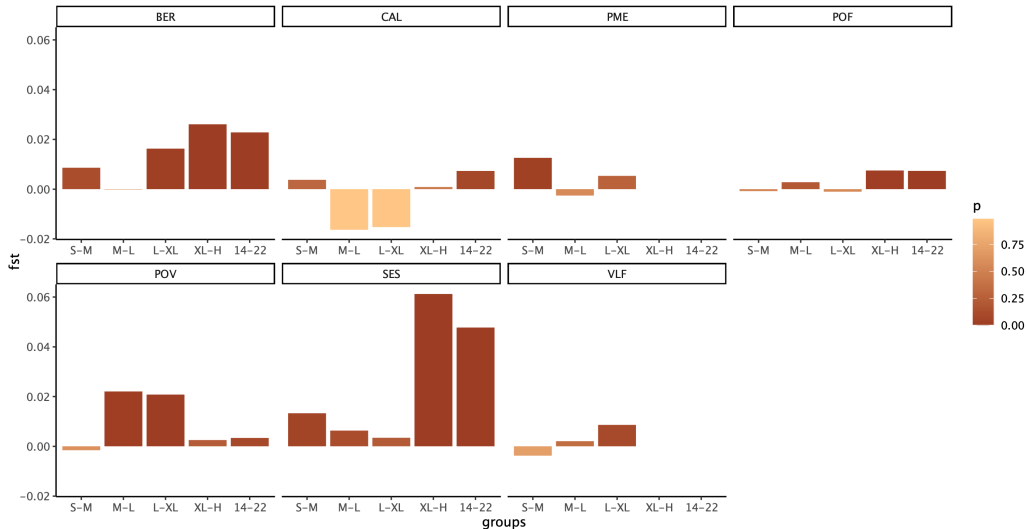
## Temporal changes in population connectivity of the gorgonian *Paramuricea Clavata* in the northwestern Mediterranean Sea

Connectivity (the exchange of individuals between fragmented populations) has a major impact on metapopulation regeneration and persistence. It is therefore increasingly taken into account in biodiversity conservation programs. In coral ecosystems, connectivity is mainly ensured by larval transport, and therefore depends on species life history characteristics (spawning time, duration of larval stage, larval behavior...) and ocean currents. These two factors are strongly influenced by the environmental context, which varies not only on an inter-annual scale, but also on a much longer timescale due to climate change. The extent of these variations on different time scales is largely unknown. However, connectivity is usually assessed as a one-shot study, resulting in a screenshot of the connectivity at a given time and not always representative of the connectivity over a longer period of time.

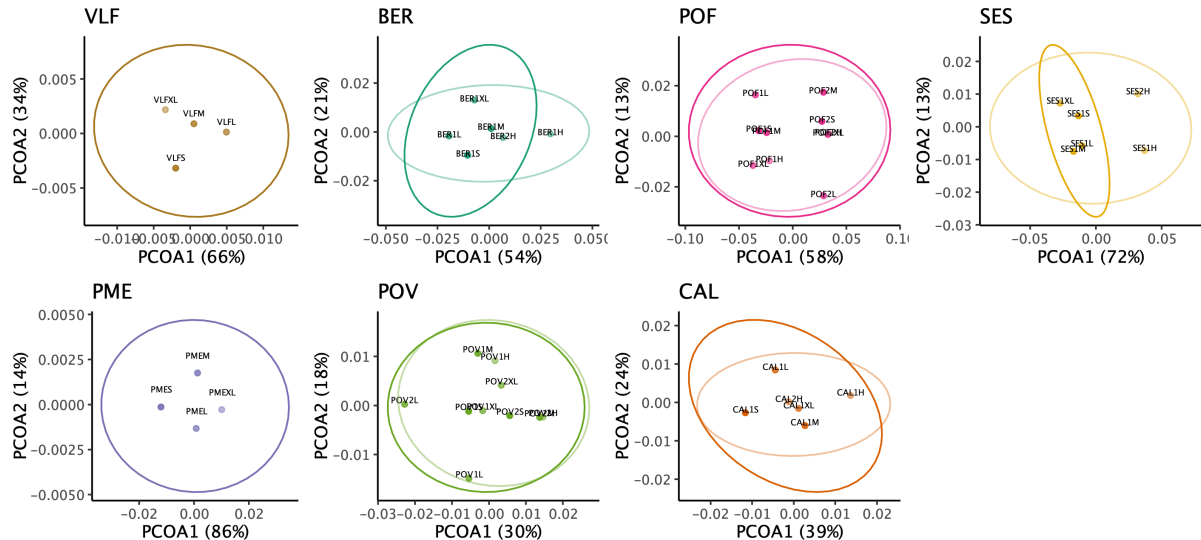
Here, we used a time-structured sampling scheme of *P.clavata* in the northwestern Mediterranean Sea : each population was sampled in 2014 and resampled in 2022 in 4 size classes (cohort representatives). This allows us to estimate the connectivity of *P.clavata* populations at different times and on different timescales. As a first result, we show that while population genetic structure is stable across time, the proportion of exchanged individuals shows large variations across the sampled years. This highlights the need to study the extend of connectivity variation at different timescales in order to evaluate the long-term effectiveness of current management actions and anticipate necessary updates of connectivity assessment.

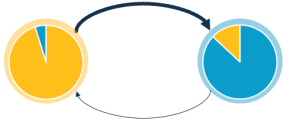
→ Genetic variability is more driven by geography than time

# Fst entre classes de taille ou années dans chaque site (test de permutation nrep=200)



## PCOA dans chaque site

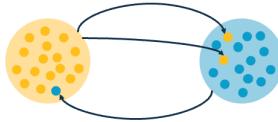




## Gene flow :

allele frequency → connectivity that best explains the **structure of genetic divergence between populations**

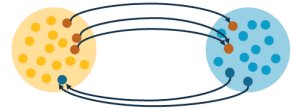
⊖ Can not estimate interannual variability



## Population assignment :

**clustering** of individuals according to their genotype → detection of **first generation migrants**

⊖ Highly connected populations will cluster together.



## Parentage assignment :

assignment of juvenile to potential parents → detection of **first generation migrants**

⊖ Need a high coverage sampling and two age classes.



Select the appropriate tool to estimate connectivity from genotype data.