

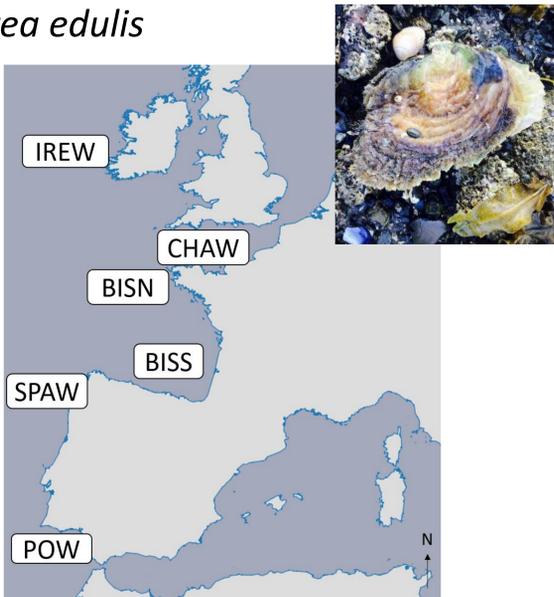
# Phylogeography of three oyster species: *Ostrea edulis*, *Crassostrea gigas* and *Crassostrea angulata*

Solène AVIGNON<sup>1</sup>, Françoise DENIS<sup>1,2</sup>

<sup>1</sup> UMR Biologie des Organismes et Ecosystèmes Aquatiques (BOREA), MNHN/CNRS/SU/IRD, Museum national d'histoire naturelle, Station Marine de Concarneau, 29900 Concarneau, France  
<sup>2</sup> Laboratoire Mer Molécules Santé (EA 2160), Université du Maine, Institut Universitaire Mer et Littoral FR3473 CNRS, 72085 Le Mans cedex 9, France

The flat oyster *Ostrea edulis*, the Pacific oyster *Crassostrea gigas* and the Portuguese oyster *Crassostrea angulata* are three species of strong economic interest distributed all over the Atlantic coast. While the morphological distinction between the two *Crassostrea* species is not necessarily clear, the aim of this study was to use genetic markers to discriminate these species and to identify the genetic structuration. Mitochondrial (COI) and nuclear (microsatellites) markers were used to study traceability and phylogeography of these three oyster species.

## *Ostrea edulis*



- POPULATION DIFFERENTIATION (excepted for SPAW and CHAW)
- POPULATION EXPANSION (excepted for BISN and BISS)

F <sub>ST</sub>	BISN	POW	CHAW	BISS	SPAW	IREW
BISN						
POW						
CHAW						
BISS						
SPAW						
IREW						

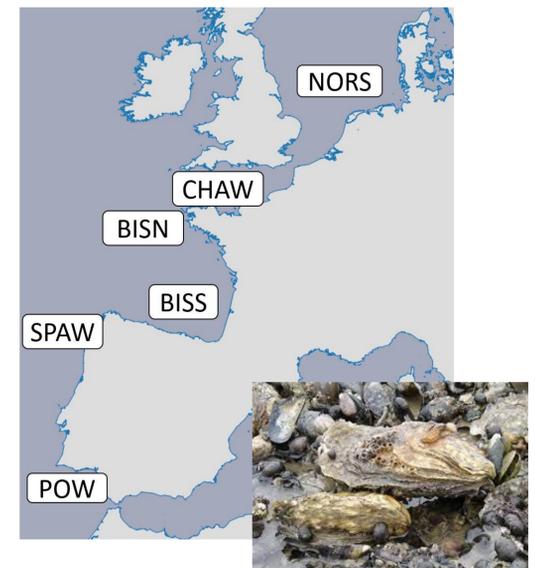
Significant F<sub>ST</sub> values

- NORS, CHAW and BISS are DIFFERENTIATED
- BISN: Population EXPANSION (excess of rare alleles, high diversity)

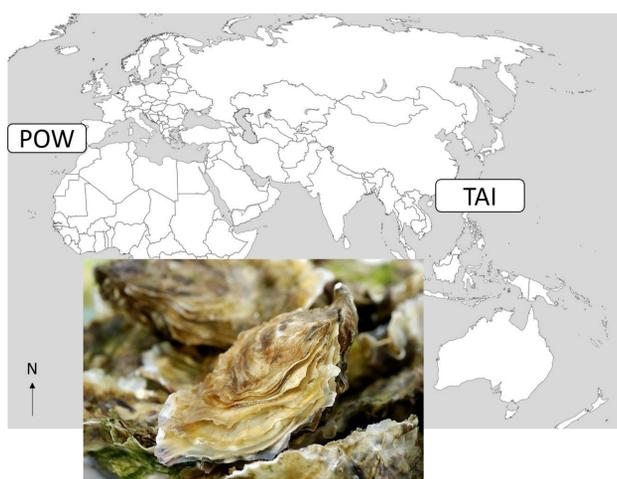
F <sub>ST</sub>	BISN	CHAW	POW	SPAW	NORS	BISS
BISN						
CHAW						
POW						
SPAW						
NORS						
BISS						

Significant F<sub>ST</sub> values

## *Crassostrea gigas*



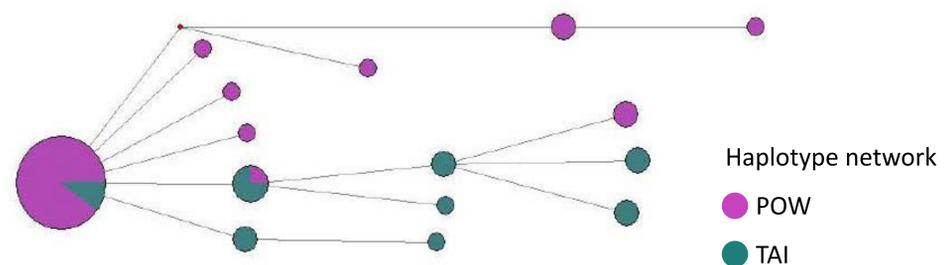
## *Crassostrea angulata*



- POPULATION DIFFERENTIATION
- High GENETIC DIVERSITY for TAI

F <sub>ST</sub>	POW	TAI
POW		
TAI		

Significant F<sub>ST</sub> values



This work allowed the discrimination of the two *Crassostrea* species with the mitochondrial marker. The combination of molecular and nuclear markers highlighted the phylogeography of the three oyster species. Oyster populations are genetically differentiated allowing the population discrimination according to the geographic location. This study made it possible to develop reliable genetic tools to identify species and geographic origins, data which are necessary and obligatory for the good traceability of seafood.