Scanning the genome of the Pacific cupped oyster, *Crassostrea gigas*, for adaptive differentiation during geographic range expansion

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Context of the introduction of *Crassostrea gigas*

Native oyster in Europe : *Ostrea edulis*

Bonamia ostreae

Marteilia refrengens
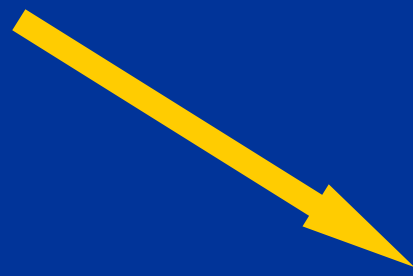
Crash of *O. edulis* **production**

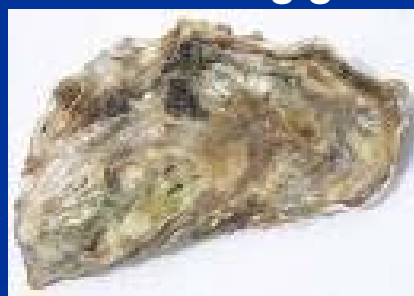**Cultivated oyster in Europe :** *Crassostrea angulata*

Iridovirus

Crash of *C. angulata* **production**

Introduction of *Crassostrea gigas* **originated from Japan**

Ifremer

Crassostrea gigas way of life

- Habitat -

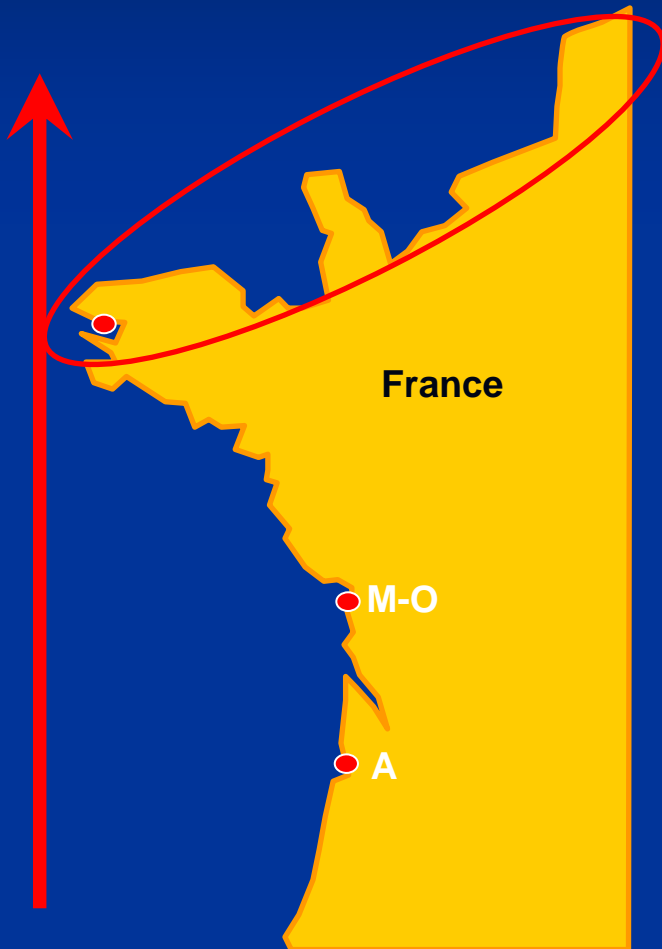| Native range	Europe
Estuarine and coastal marine waters of Japan and south-east Asia	Estuarine and coastal intertidal marine waters
Usually attach to rocks	When hard surfaces are scarce : -artificial hard substrate -dead shell -blue mussel beds …

Invasion history

- France – ProGig program -

1970s introduced massively on Atlantic coast

1970-1980 : Natural populations in Marennes-Oleron and Arcachon basins

1976 : Warm summer ➔ reproduction in Brittany

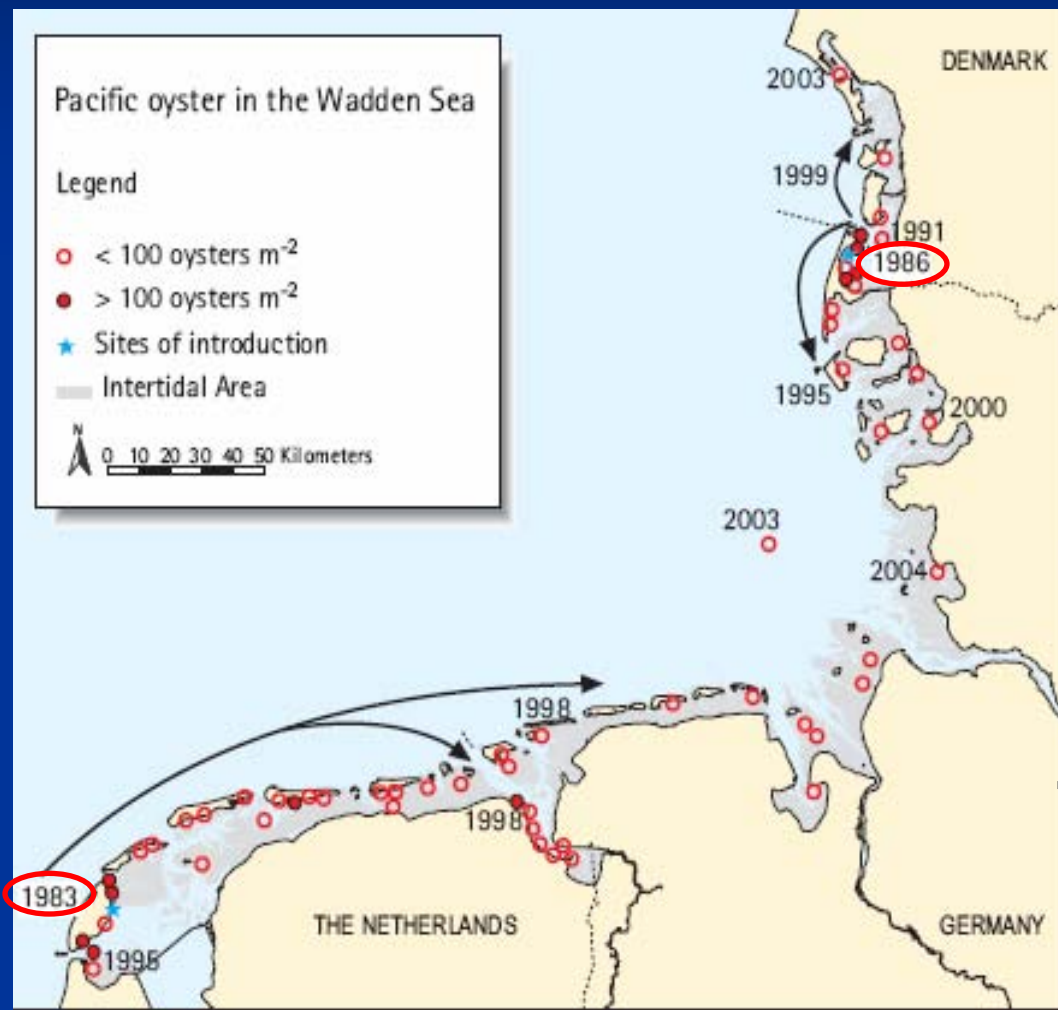**1990-2006 : Natural populations in English Channel**

France

M-O

A

Ifremer

Invasion history

First introduction : 1964 in Oosterschelde

1975-1976 : first natural settlement

1980 : colonization of other estuaries

1983 : found in Texel in the Wadden sea

Wadden sea

**1983
Texel**

The Netherlands

1980

Dutch Delta region

Oosterschelde

1964
1975
1976

Invasion history

- Wadden Sea -

Pacific oyster in the Wadden Sea

Legend

- ○ < 100 oysters m^{-2}
- ● > 100 oysters m^{-2}
- ★ Sites of introduction
- ▨ Intertidal Area

N 0 10 20 30 40 50 Kilometers

1983 found in Texel

1986 commercial oyster farming in Sylt

1990s natural spread of larvae

Reise et al 2005. Wadden Sea Ecosystem 19:155-61

Ifremer
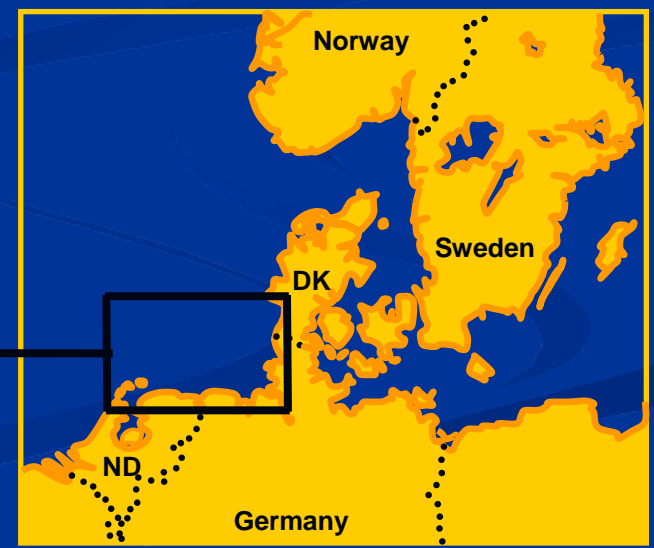
Invasion history

Denmark

Several attempts of oyster farming 🟢

Since 1999 natural populations 🔴

Oyster reefs in the Wadden sea + western part of Limfjorden

Sweden

Dense populations of recently settled oysters

Norway

No aquaculture up to now

**Hyp : larval dispersal ?
Imported as food and released in the sea ?**

Norway

Sweden

DK

Germany

1999
1986

Only opportunity or adaptation ?

Objective : Quantifying adaptative part implied in *C. gigas* success

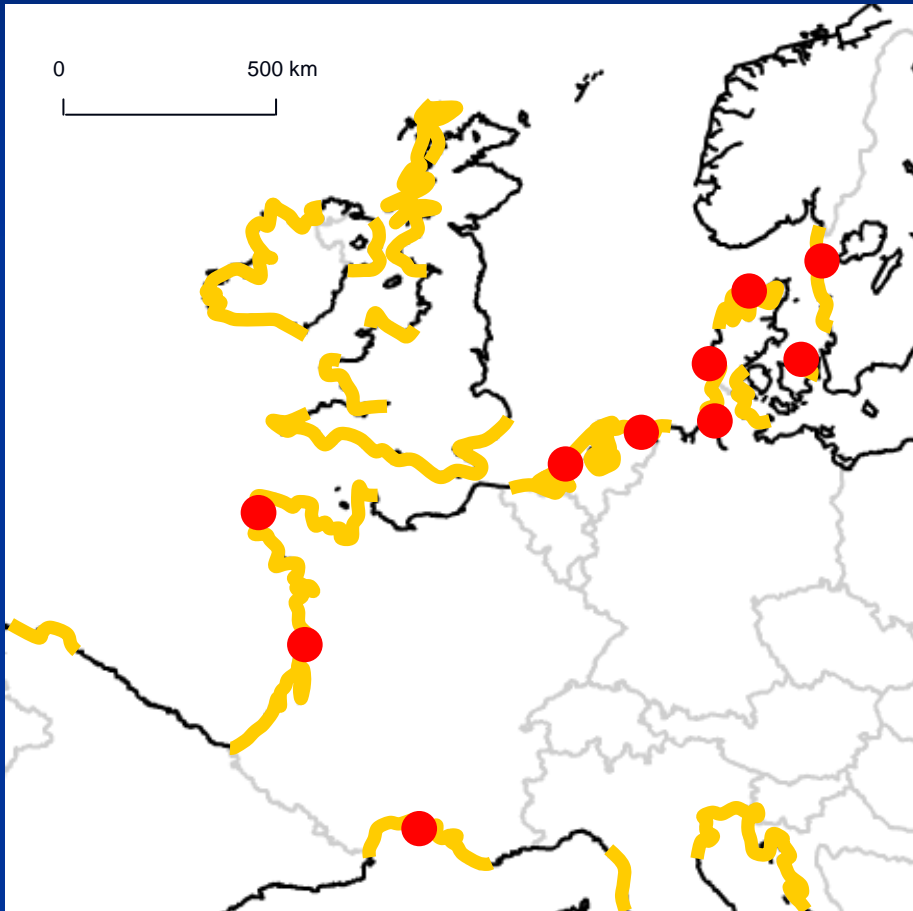**Tools : population genomics («genome scan») / AFLP**

= "scan" of several loci trough the whole genome

⇩

SELECTION ?

Ifremer

Sampling of natural populations

3 populations from France

2 populations from the Netherlands

1 population from Germany

3 populations from Denmark

1 population from Sweden

1 population from Japan

11 populations ⟷ 528 samples

Data from D Minchin, S Gollasch, B. Galil, 2007

AFLP (amplified fragment length polymorphism)

principle
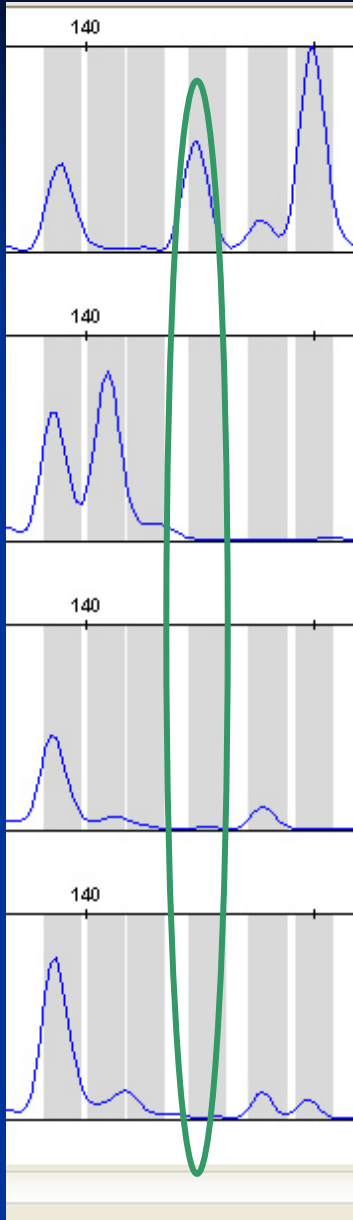
Enzyme digestion followed by successive PCR
Polymorphism of "presence/absence"

assets

Multilocus (>100 loci/primer pair)
No prior knowledge on the genome
Repeatability
High genome cover

disadvantages

Dominant marker
Require high DNA quality and quantity

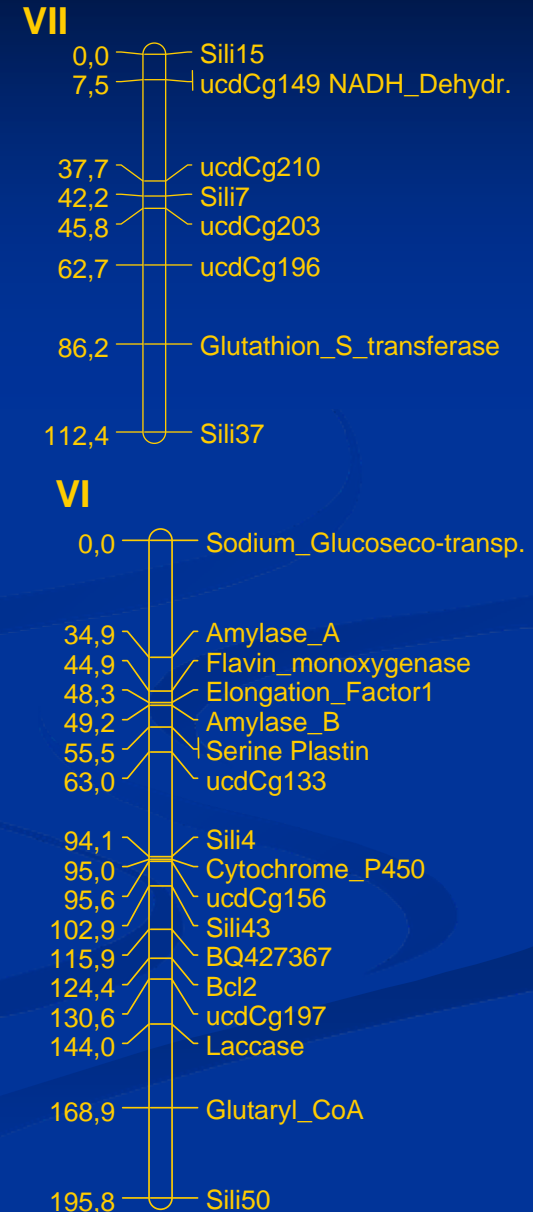**Ifremer**

The different markers

AFLP

Test with AFLP : almost 30 primer pairs selected

528 samples genotyped with one primer pair
➔ almost 10 workable loci

Other kind of markers available in the lab

SNP : all populations genotyped with 29 SNP
and mapped on a linkage map

53 microsatellites already mapped on a linkage map

VII

0,0	Sili15
7,5	ucdCg149 NADH_Dehydr.
37,7	ucdCg210
42,2	Sili7
45,8	ucdCg203
62,7	ucdCg196
86,2	Glutathion_S_transferase
112,4	Sili37

VI

0,0	Sodium_Glucoseco-transp.
34,9	Amylase_A
44,9	Flavin_monoxygenase
48,3	Elongation_Factor1
49,2	Amylase_B
55,5	Serine Plastin
63,0	ucdCg133
94,1	Sili4
95,0	Cytochrome_P450
95,6	ucdCg156
102,9	Sili43
115,9	BQ427367
124,4	Bcl2
130,6	ucdCg197
144,0	Laccase
168,9	Glutaryl_CoA
195,8	Sili50

Fst outlier

- Beaumont and Nichols approach -

Based on simulated distributions of genetic differentiation estimators between population pairs

Real data

F_{ST} **outlier**

Expected Fst under neutral equilibrium

F_{ST}

0.3
0.25
0.2
0.15
0.1
0.05
0
-0.05

0   0.2   0.4   0.6   0.8   1

Heterozygocity

95 % confidence interval under neutral equilibrium

Beaumont and Nichols 1996 Proc. R. Soc. Lond. B 263, 1916-26

Ifremer
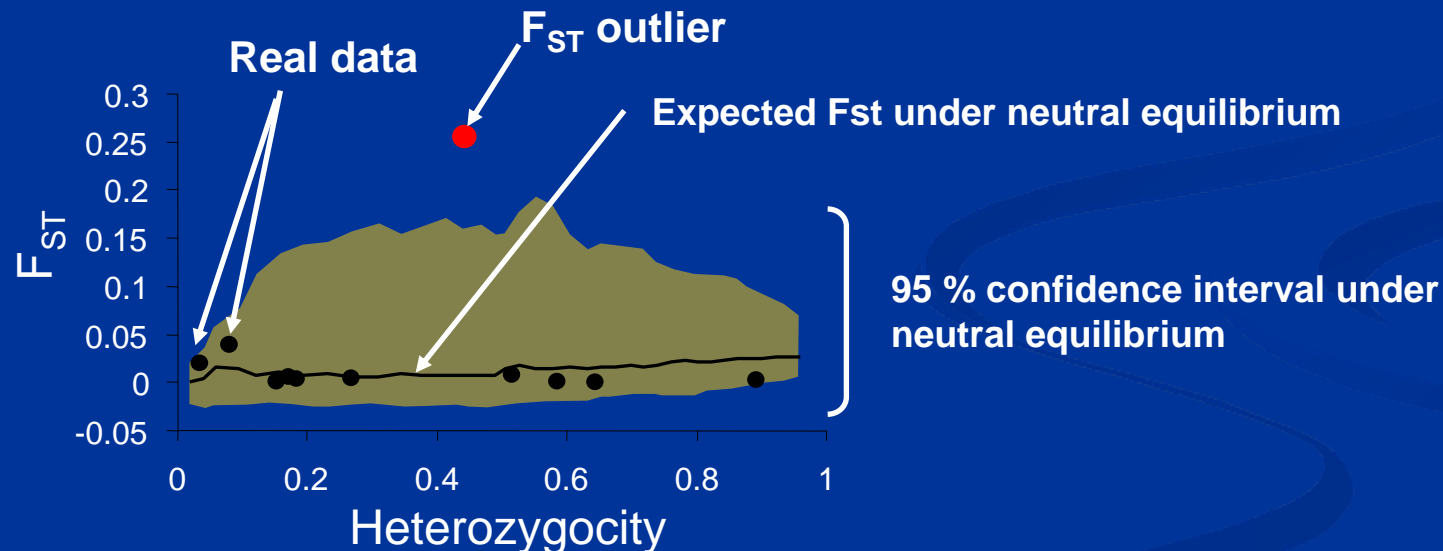
Genome scan

- Valley of diversity -

**Drop in diversity by hitch-hicking
in the neighbor of the mutation
under selection**

Diversity

genes

Distance (kb)

Selection

Advantageous mutation ➜ fixation = selective sweep

Ifremer
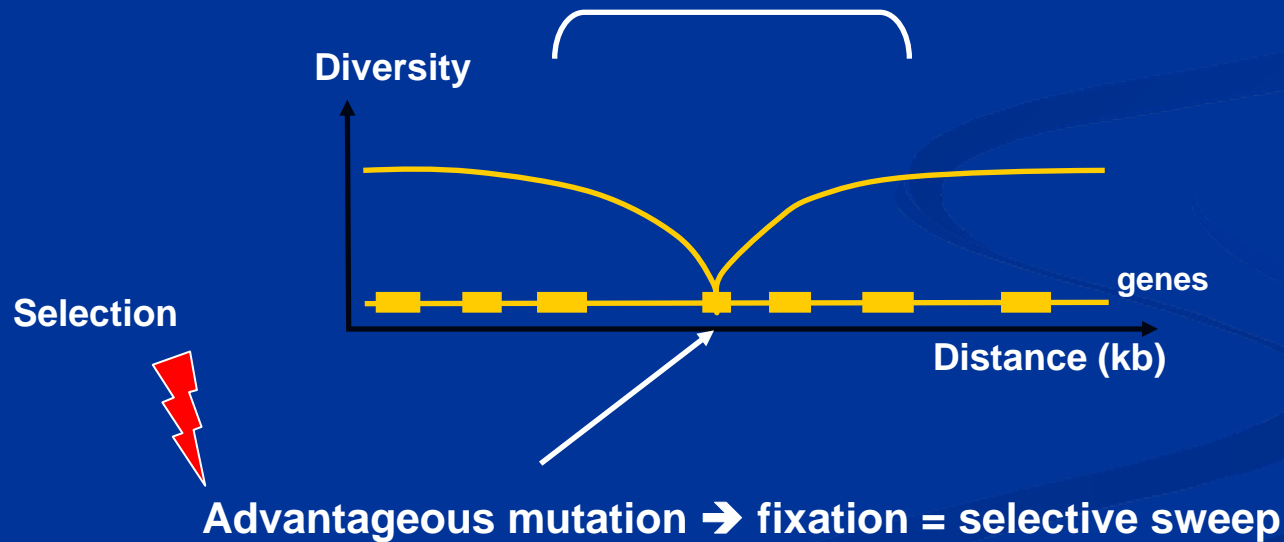
Two scenarios

🙁 **Selection not found**

No trace of selection in *C. gigas* genome ?

The tools we used were not enough powerful ?

🙂 **Selection found, yes but…**

Genome scan = blind anonymous scan

⬇

It would be interesting to get more information about the region
under potential selection (gene, function, sequence…)

To be continued…

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