

Session 2 : Establishing effective breeding and farming programs against mollusc diseases

**Sylvie Lapègue (Ifremer, FR) and
Luca Bargelloni (UNIPD, IT)**



Establishing effective breeding and farming programs against mollusc diseases

Brief presentation of the main Objectives/results of VIVALDI

Examples

- *Genomic solutions for shellfish selective breeding* by Lucie Genestout (LABOGENA, FR) & Romain Morvezen (SYSAAF, FR)
- *Genomic approaches to understanding and improving disease resistance in Pacific oysters* by Ross Huston (The Roslin Institute, UK)
- *A Production calendar based on water temperature, spat size and husbandry practices reduces herpesvirus impact on cultured Pacific oyster *Crassostrea gigas*, in the Ebro Delta*, by Noelia Carrasco Querol (IRTA, ES)

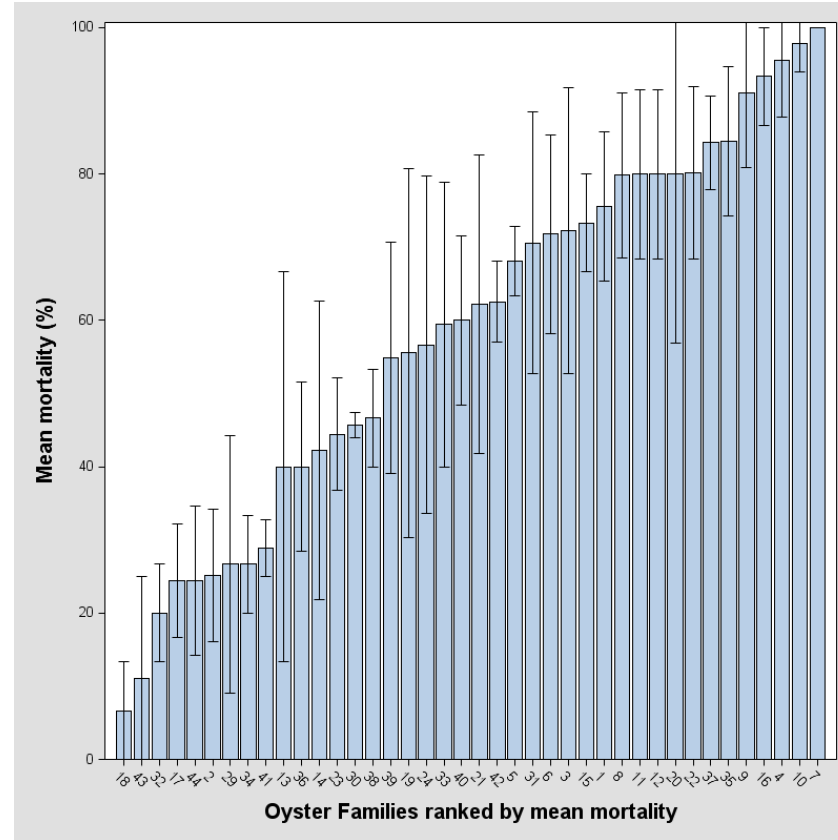
Round Table

Context

There is a high variability for survival in shellfish

High heritabilities are observed for survival at spat level
(Dégremont et al., 2015)

Sorting animals, that is to say selecting survivors, works !



(Azéma et al., 2016)

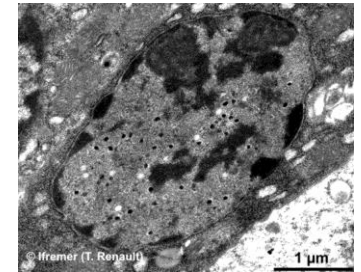
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Context



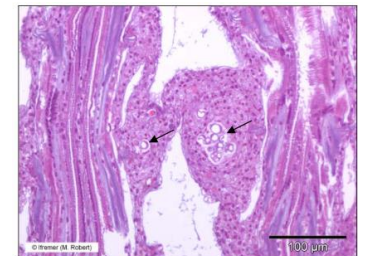
The Pacific cupped oyster *Crassostrea gigas*

OsHV1 and *Vibrio*



The Manila clam *Ruditapes philippinarum*

Vibrio tapetis and *Perkinsus olseni*



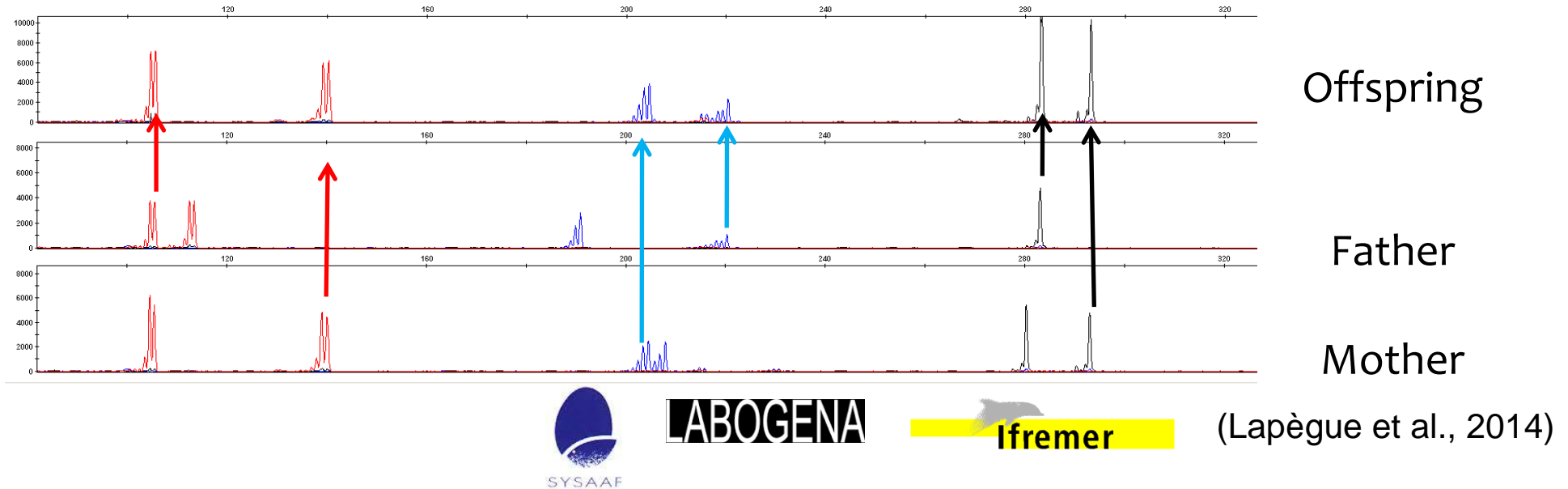
General objectives of WP3 in Vivaldi

- Developing genomic tools to perform pedigree assignment and breed animals together
- Developing marker assisted selection or genomic selection to improve selection for disease tolerance/resistance
- Estimating genetic parameters of parasite load in the Manila clam and pinpointing them for in the cupped oyster
- Characterizing the different types of breeding programs
- Obtaining more information on potential impact of selection for survival on selected animals and environment

General objectives of WP3 in Vivaldi



Panels of markers usable by farmers



This preliminary panel for cupped oysters has been improved and is available (see presentation by Florian Enez and Lucie Genestout)

Another one for clams is being developed

Developing marker assisted selection or genomic selection



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All the biological material has been produced for different experiments (selected lines or contrasted natural populations)

Most of the experiments are ongoing

One testing interaction between spat survival and diet at larval stage is being analysed with the previous panel



Another molecular tool is tested on an experiment on oysters (see presentation by Ross Houston)

Developing marker assisted selection or genomic selection

All the biological material has been produced for different experiments: Manila clams in the Venice Lagoon



Developing marker assisted selection or genomic selection



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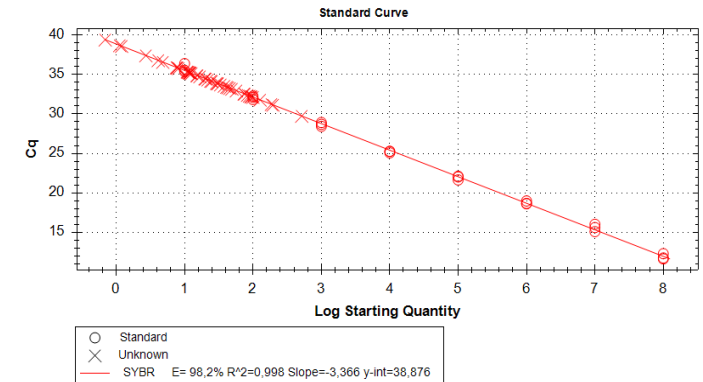
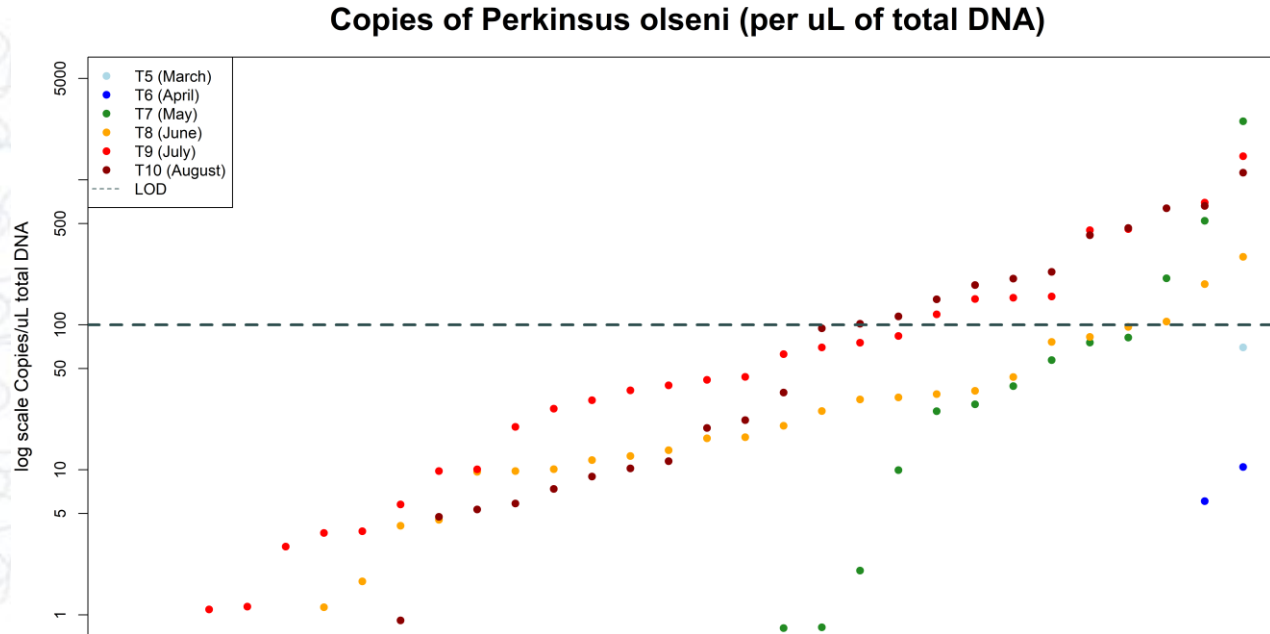
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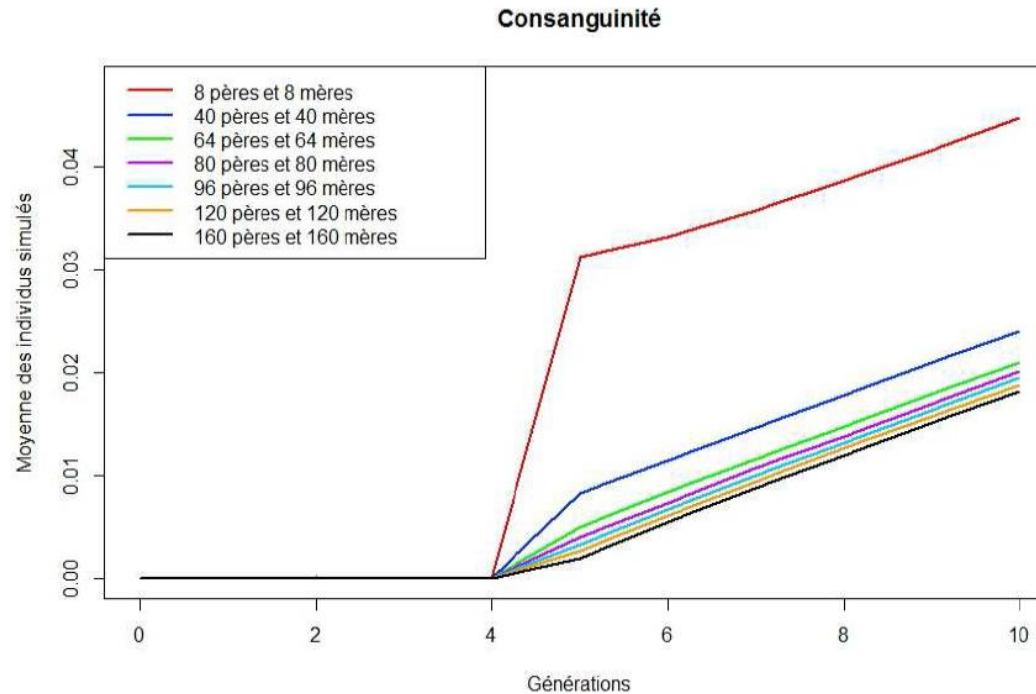
Development of a fast and specific diagnostic test for *Perkinsus olseni* and its implementation in large scale phenotyping



A new tool has been developed that allows rapid and large-scale phenotyping in the context of the experiments performed on Manila clams and *Perkinsus olseni*.

It has been already tested by Italian and Spanish reference laboratories

Optimizing the breeding programs



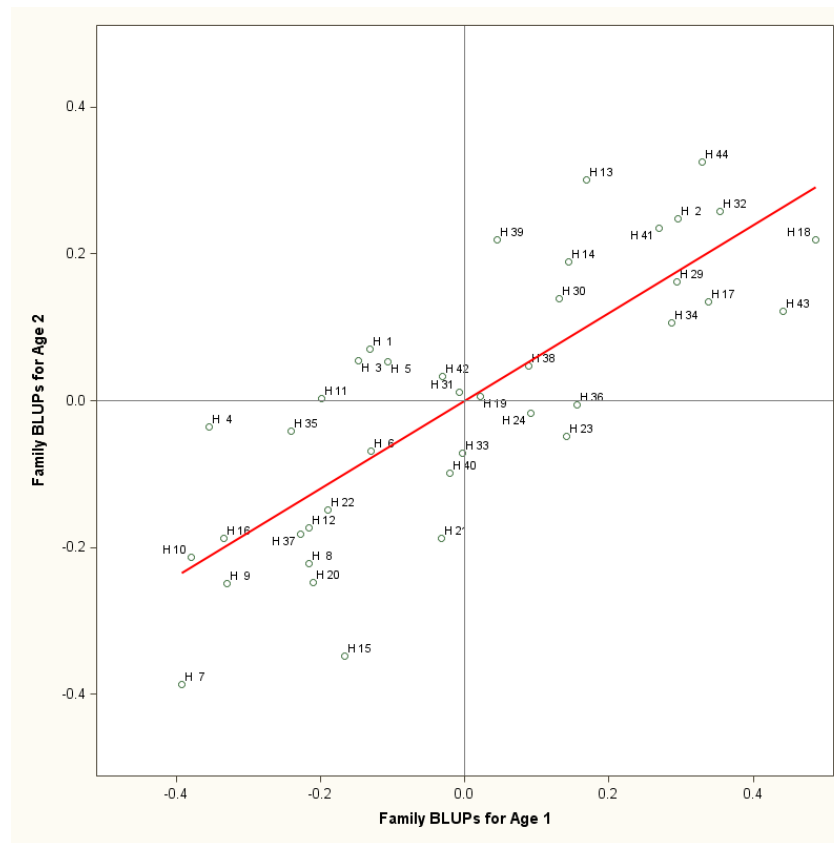
(Enez et al., 2016)



Example of impact of selection on inbreeding according to the number of progenitors

Optimizing the breeding programs

Studying correlations to
sort animals at early stage



(Azema et al., 2016)

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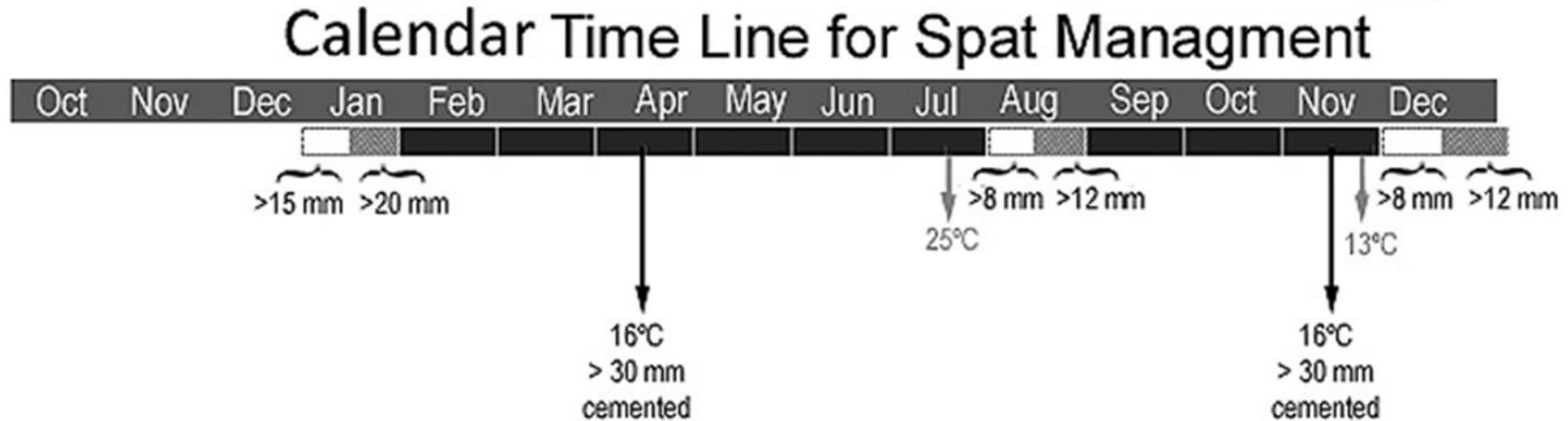
Optimising the breeding programs

Getting more information on the potential impact of selection on:

- Dynamics and diversity of naturalised populations (simulation for the cupped oyster)
- Physiology of selected animals
- Presence and concentration of other microbes in oysters

Improving farming practices

Production calendar designed and tested between the end of 2014 and 2015, showing optimal periods for spat immersion in the Ebro delta



(See presentation from Noelia Carrasco Querol)



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CONTACT for WP3 activities

Sylvie Lapègue
Jean-Baptiste Lamy

Ifremer La Tremblade
Avenue du Mus de Loup
17390 Ronce Les Bains

sylvie.lapegue@ifremer.fr
jean.baptiste.lamy@ifremer.fr

www.vivaldi-project.eu