



Potential and optimization of breeding programs in Pacific oyster in presence of mortalities

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Involvement of SYSAAF

- Simulation of within-group multi-traits mass selection breeding programs efficiency.
- Estimation of genetic parameters for production traits at commercial size measured in two environments differently affected by pathogens.

Japanese clam *Ruditapes phillipinarum*



Vibrio tapetis

Perkinsus olseni

Satmar...
Naturellement...

Pacific oyster *Crassostrea gigas*



Herpes virus OsHV-1

France
Naissain
naissains d'huîtres sélectionnés

Efficiency of within-group mass selection on threshold trait and successive mass or index selection on continuous trait

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Introduction

Mass selection: Low-cost selection method and efficient to improve traits measured on alive candidates (survival, production traits) when heritability is higher than 0.20.

Rotational crossings between groups: Simple method to limit efficiently inbreeding in preventing mating between sibs.

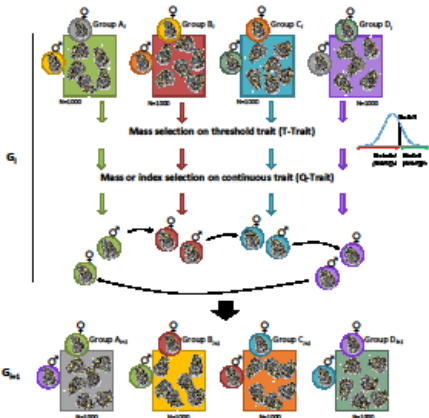
➔ What genetic gains and variability losses can be expected by successive within-group mass selection on a threshold trait "T-Trait" (2 modalities) and a continuous trait "Q-Trait" in rotational design?

➔ What increase in inbreeding can be fear by generation ?

➔ How access to pedigree (by parentage assignment) may limit inbreeding and increase genetic gain on both traits ?

Material & Methods

Within-group mass selection scheme:



Factors:

- Type of selection on Q-Trait: no selection, mass selection, index selection with inbreeding management
- Selection pressure on T-Trait $P_{T\text{-Trait}}$ (50% ; 25%) and on Q-Trait $P_{Q\text{-Trait}}$ (32% ; 10%)
- Heritability h^2 (0.25) and genetic correlation r_g (-0.8 ; 0)

Indicators:

- Phenotypic value and true breeding value (TBV)
- Inbreeding

...10 generations simulated

Conclusions

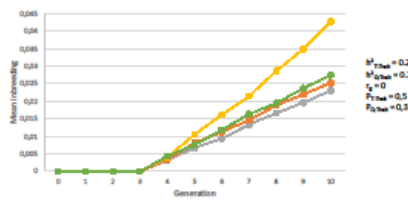
Multi-traits successive within-group selection is an efficient strategy for joint improvement of a threshold trait and a continuous trait, even when the genetic correlation between traits is negative.

Within-group selection allows effective inbreeding management. In case when traits are directly measurable on candidates and the number of parentage assignment is limited, benefits of parentage assignment are not obvious and mass selection is the most efficient selection method.

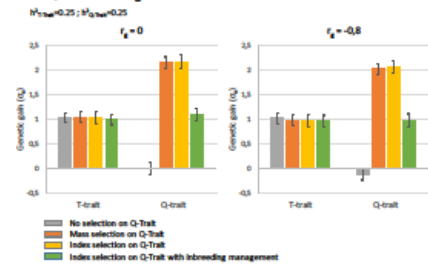
Expected gains depend directly on the genetic parameters of the traits and the selection pressures applied for both threshold and continuous trait.

Results

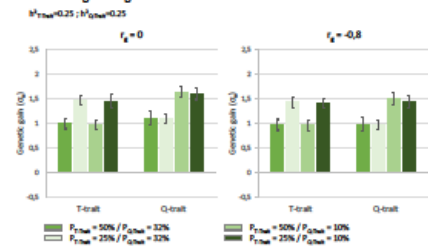
Evolution of inbreeding according to the type of selection on Q-Trait



Genetic gains after 10 generations according to the type of selection on Q-Trait and the genetic correlations



Genetic gains after 10 generations according to the selection pressure on T-Trait and Q-Trait in index selection with parentage assignment for inbreeding management



Simulations : Efficiency of a two traits within-group mass selection

Principles :

- 2 traits selected successively by generation :

- A threshold trait (survival, résistance as a category)
- A continuous trait (growth, morphology, meat, yield... with a mean and a standard déviation)

- Creation of many groups by generation.

- Management of inbreeding increase by rotational mating between groups.

Indicators of efficiency :

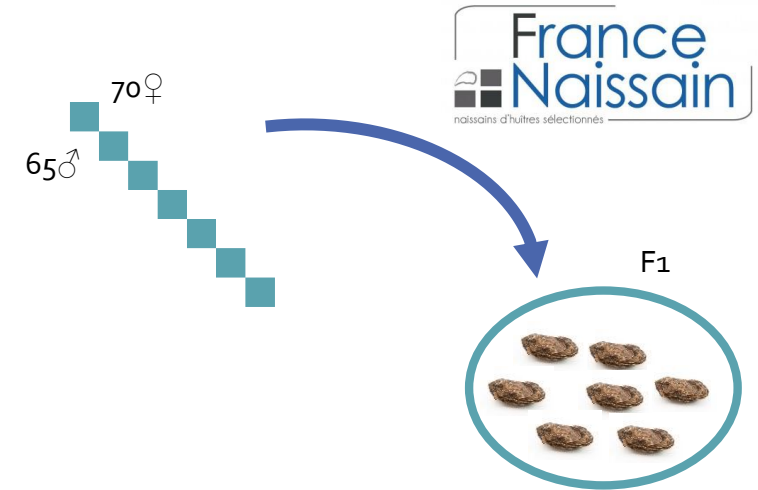
- Phenotypic values (performance measured)
- True Breeding Value (TBV, estimated under hypothesis of heritability and additive effect)
- Inbreeding level (estimated based on the pedigree relationship)

Main conclusions :

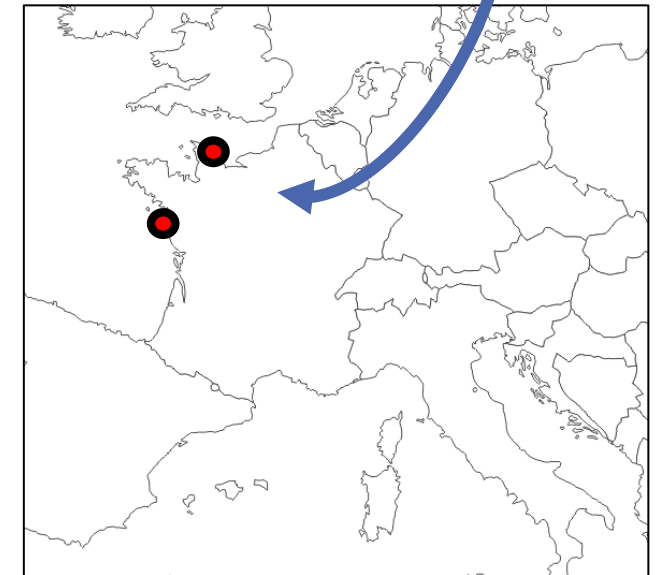
- Low-cost and efficient breeding programs, even in case of negative genetic correlations between traits.
- Benefits of parentage assignment not obvious when the number of assignments are limited and traits are measurable on candidates.

Estimation of genetic parameters of production traits in Pacific oyster : protocol

- Creation of > 650 families from 65 ♂ et 70 ♀ distributed by 7 complete factorial matings in April 2016
- Rearing in 2 sites, with individual counting and restocking during each winter :



| | Bougneuf Bay | Normandy |
|--|---------------|---------------|
| Transfer to sea | 01/07/2016 | 20/07/2016 |
| Mortality rate spring 2016 | 16.1% | - |
| Mortality rate spring 2017 (cumulated mortality rate) | 22.2% (34.7%) | 35% |
| Mortality rate spring 2018 (cumulated mortality rate) | 24% (50.4%) | 12.6% (43.2%) |



Phenotyping

| | Bougneuf Bay N=1502 | Normandy N=1388 |
|-------------------------|-------------------------------|---------------------------|
| Total weight (g) | 67.90 ± 21.96 | 52.70 ± 20.29 |
| Length (mm) | 88.31 ± 11.90 | 86.70 ± 13.86 |
| Width (mm) | 50.29 ± 6.78 | 46.21 ± 6.70 |
| Height (mm) | 29.04 ± 4.15 | 26.23 ± 4.84 |
| Meat weight (g) | 7.50 ± 2.67 | 4.90 ± 2.39 |
| Shell weight (g) | 45.33 ± 14.92 | 32.45 ± 0.02 |
| Yield | 0.11 ± 0.02 | 0.09 ± 0.02 |

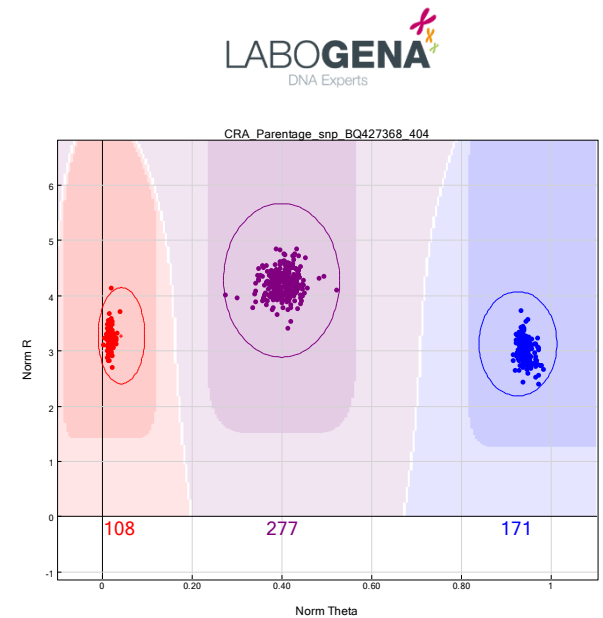
- Phenotyping in November 2018 for Bougneuf Bay and April 2019 for Normandy :
 - Production traits : weights, lengths, yield
 - Tissue sampling for DNA parentage assignment



Parentage assignment success

- Genotyping and parentage assignment with SNPs panel (Lapègue et al., 2014).

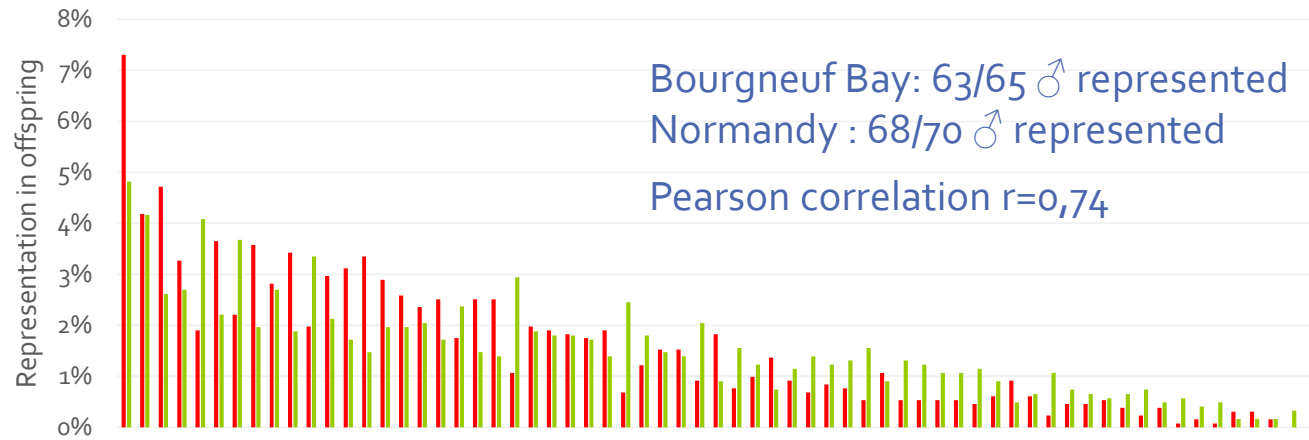
| | Bourgneuf Bay | Normandy |
|--|---------------|----------|
| Number of individuals phenotyped | 1367 | 1253 |
| Not genotyped (problem of quality) | 46 | 13 |
| Unassignable | 1 | 7 |
| Assigned out of the declared mating plan | 5 | 9 |
| Assigned within the declared mating plan | 1315 | 1224 |
| Usefull assignment rate | 87.5% | 88.2% |
| Theoretical assignment rate | 99.6% | 98.9% |



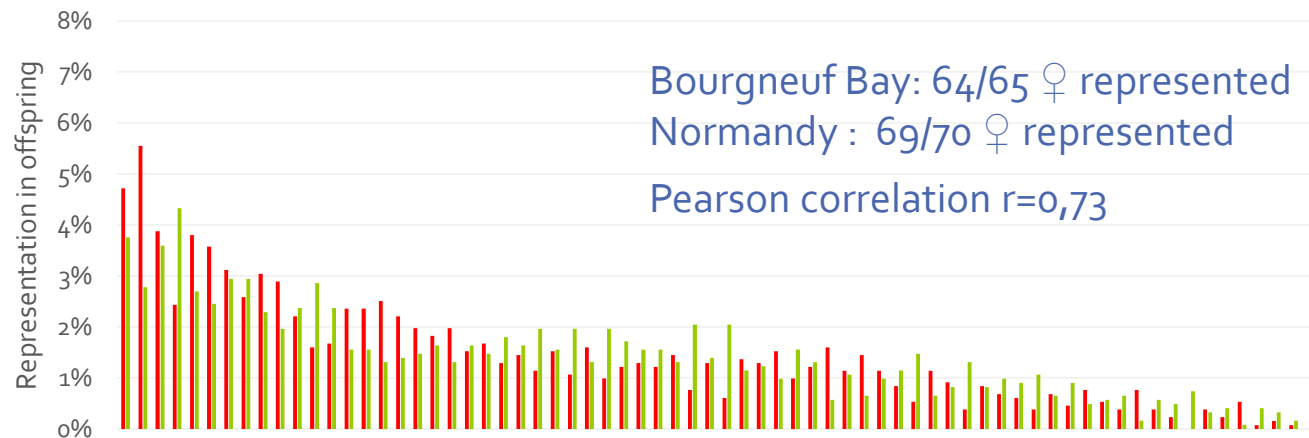
- High assignment rates → Good quality of SNPs panel

Representation of the parents

Offspring from sires



Offspring from dams



- Almost all parents are represented, without over-representation.
- Parents representation is close in the 2 sites.



Extendable to all sites ?

Limited effect of OsHV-1 in Normandy due to date of transfer to sea ?

■ Bourgneuf Bay
■ Normandy

Genetic parameters

| | Bourgneuf Bay h^2 | Normandy h^2 | Genetic correlation |
|-----------------|------------------------|-------------------|------------------------|
| Total weight | 0.15 [0.04] | 0.17 [0.04] | 0.86 [0.22] |
| Length | 0.24 [0.05] | 0.25 [0.05] | 0.80 [0.12] |
| Width | 0.09 [0.03] | 0.14 [0.04] | - |
| Height | 0.24 [0.05] | 0.18 [0.05] | 0.83 [0.14] |
| Height / Length | 0.28 [0.06] | 0.19 [0.05] | 0.64 [0.16] |
| Meat weight | 0.13 [0.04] | 0.19 [0.05] | 0.85 [0.17] |
| Shell weight | 0.15 [0.04] | 0.17 [0.05] | 0.79 [0.19] |
| Yield | 0.15 [0.05] | 0.16 [0.05] | 0.88 [0.21] |

- Low heritabilities for growth traits (but precise) and close in the 2 sites.
 - ⇒ Impact of environment ? Rearing practices ?
- High genetic correlations between sites.
 - ⇒ Genetic progress generated by selection in Bourgneuf Bay should be expressed in Normandy.

Genetic parameters

Genetic correlations between traits (Data Bourgneuf Bay + Normandy)

| | Length | Width | Height | Height / Length | Meat weight | Shell weight | Yield |
|-----------------|-------------|-------------|-------------|-----------------|-------------|--------------|--------------|
| Total weight | 0.86 [0.05] | 0.80 [0.07] | 0.88 [0.04] | 0.07 [0.16] | 0.91 [0.03] | 0.98 [0.01] | 0.25 [0.16] |
| Length | | 0.61 [0.11] | 0.57 [0.10] | -0.43 [0.12] | 0.82 [0.06] | 0.86 [0.05] | 0.32 [0.14] |
| Width | | | 0.60 [0.11] | 0.02 [0.17] | 0.71 [0.09] | 0.77 [0.08] | -0.12 [0.18] |
| Height | | | | 0.50 [0.12] | 0.79 [0.07] | 0.86 [0.05] | 0.19 [0.15] |
| Height / Length | | | | | 0.01 [0.16] | 0.03 [0.16] | -0.12 [0.16] |
| Meat weight | | | | | | 0.86 [0.05] | 0.62 [0.11] |
| Shell weight | | | | | | | 0.15 [0.17] |

- High genetic correlations between the different lengths and the weights (total, meat, shell).
- Low genetic correlations between the growth traits and yield.

⇒ Efficient protocol to measure the meat weight ?

Conclusions

- Limited GxE interaction (re-ranking of families between sites) on family representation at commercial size.
 - ➡ Genetic progress generated by a selection performed in one site should benefit to both sites. Extendable to all production sites ? To all production practices ?
 - ➡ Limited impact of mortalities between sites.
- Limited heritabilities on growth.
 - ➡ Are classical production practices optimal to estimate genetic differences ?
- High genetic correlations between growth traits.
No genetic correlations between growth traits and meat yield.
 - ➡ Selection on growth and yield could be combined to improve these two traits.



Thank you for your attention

