First steps toward selection in the Manila clam, *Ruditapes philippinarum*.

Work Package 3: Genetic solutions for disease resistance / tolerance

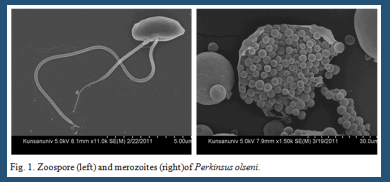
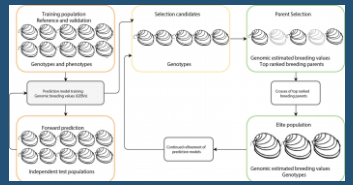


Fig. 1. Zoospore (left) and merozoites (right)of *Perkinsus olseni*.



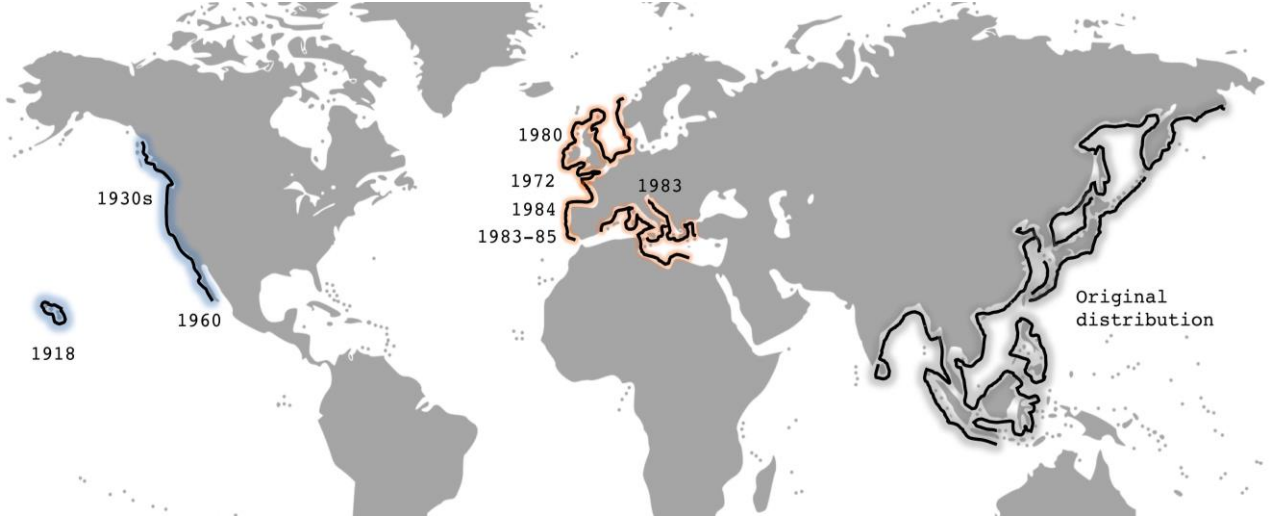
- Manila clam aquaculture and diseases
- Objectives and experimental design
- First estimations of genetic parameters for growth and disease resistance
- Conclusions and perspectives

The Manila clam as a cultured species

- Venerid clam, wide salinity and temperature ranges, high growth and fecundity
- 1970s introduction to France for aquaculture, then the rest of Europe
- 25% of cultured mollusk production worldwide (23% of market value)

The Manila clam,
Ruditapes philippinarum

Global distribution of Manila clam populations



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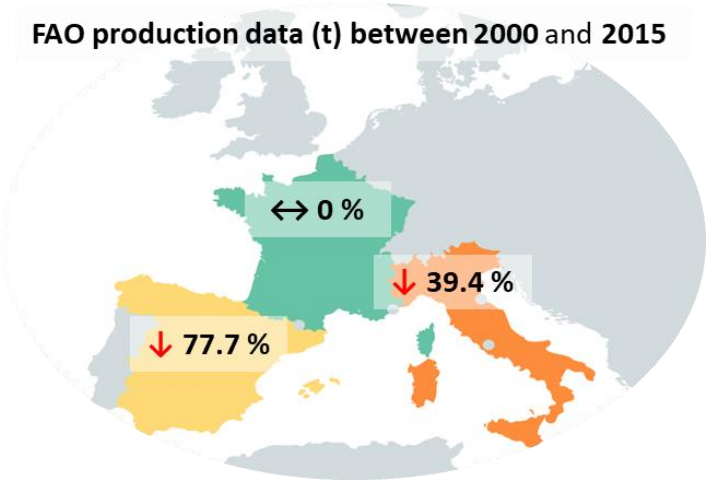


- EU production limited and precarious
- Impact of pathogens on **mortality, seed availability, growth**…

Infections with *Perkinsus olseni*

Protozoan parasite *Perkinsus olseni*

- Chronic infection, reduced respiration, growth, fecundity
- Impact on natural seed availability

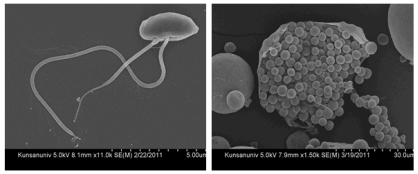


Fig. 1. Zoospore (left) and merozoites (right)of *Perkinsus olseni*.

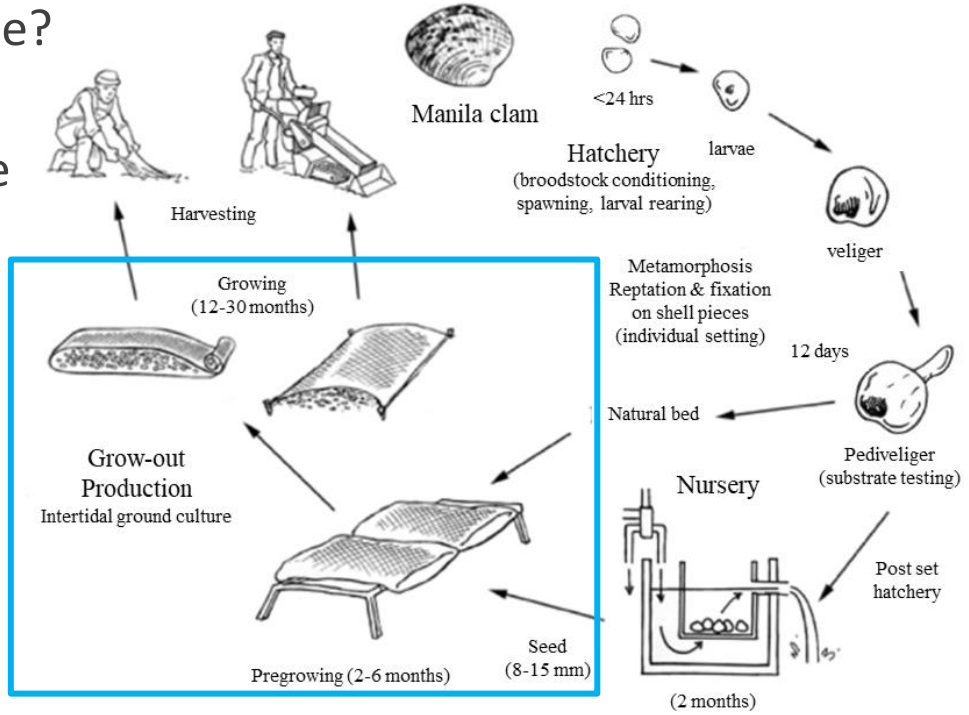
Difficulties in disease management:

- Open water farming → no treatment options through antibiotics or cleaning
- Dependency on innate immunity → vaccination is not viable

High variability in host response → potential for selection

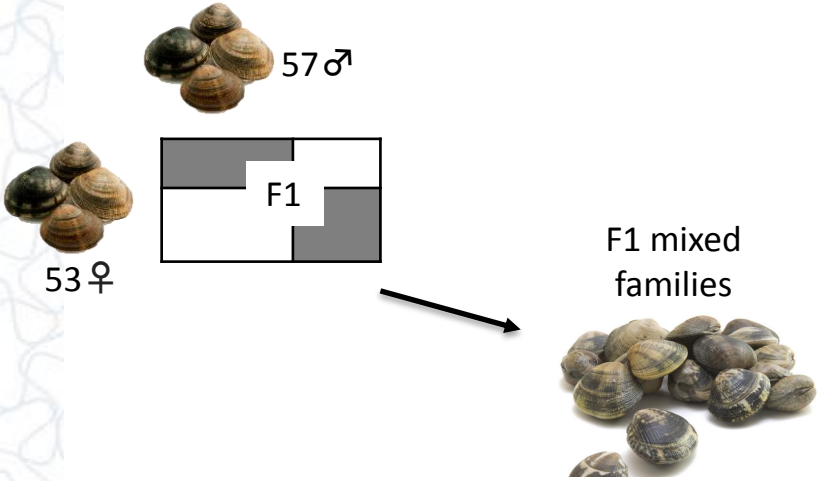
Objective

- Is there a genetic basis for resistance?
- Can selection for disease resistance and other production traits improve clam aquaculture?



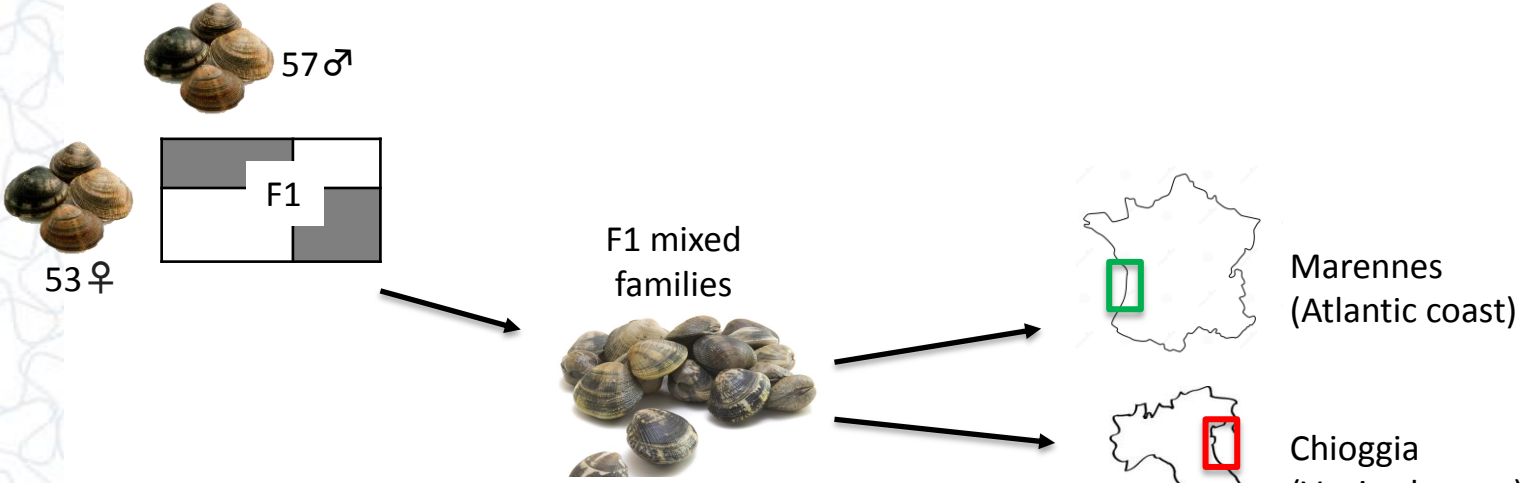
Experimental design

- SATMAR hatchery cohort produced in May 2016 (mass spawning), potential of 1479 crosses
- Families raised together as a single mixed group



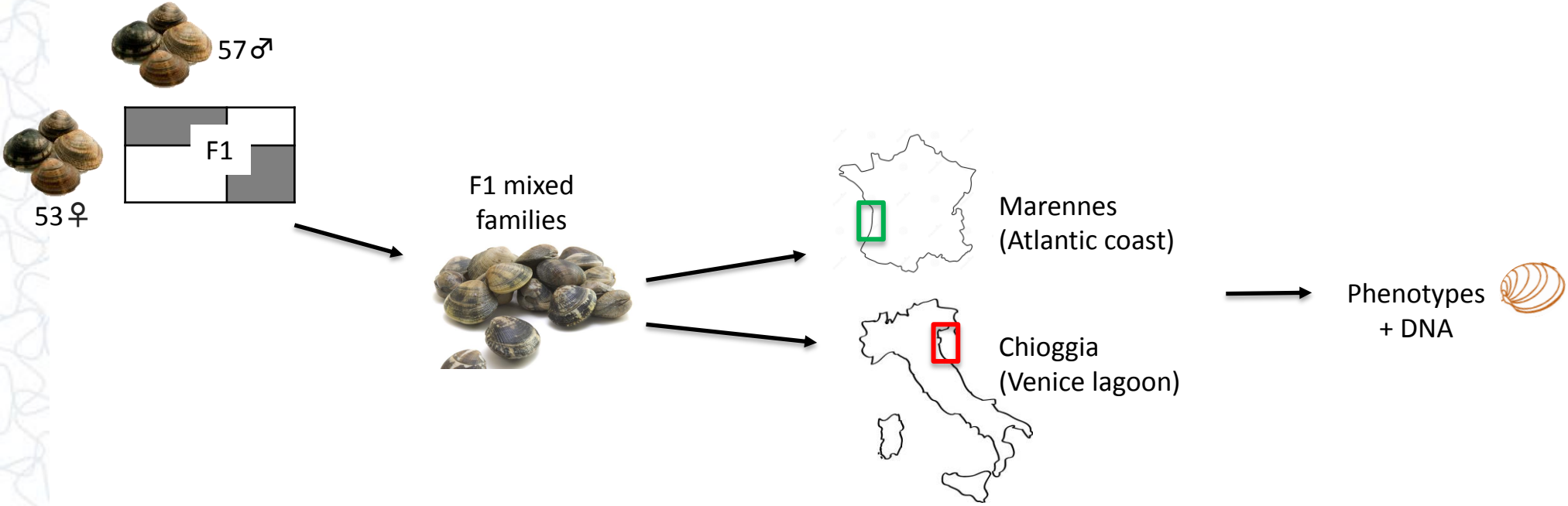
Experimental design

- At 1.5 yrs, batches of >10 000 F1 seeded in two grow-out zones
- Marennes: protected ponds with no recorded instances of disease
- Chioggia: lagoon grow-out zone with a historic prevalence 80-100% of *P. olseni*



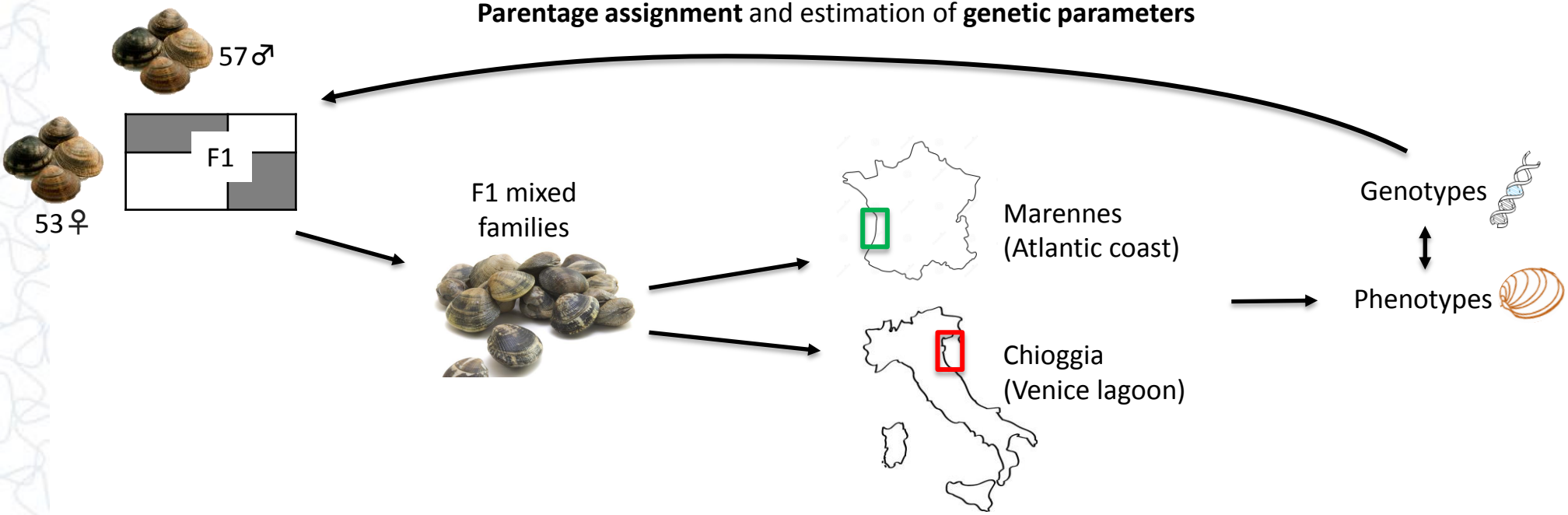
Experimental design

- Phenotype recording and DNA sampling for ca. 1 000 individuals per site
- Traits of interest to production: weight, length, yield, color, sex, and parasite load (Chioggia)



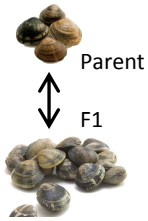
Experimental design

- Use of 245-SNP array developed within VIVALDI for genotyping and parentage assignment
- Evaluate family representation and estimate genetic parameters of recorded traits



Parentage assignment

245 SNP array

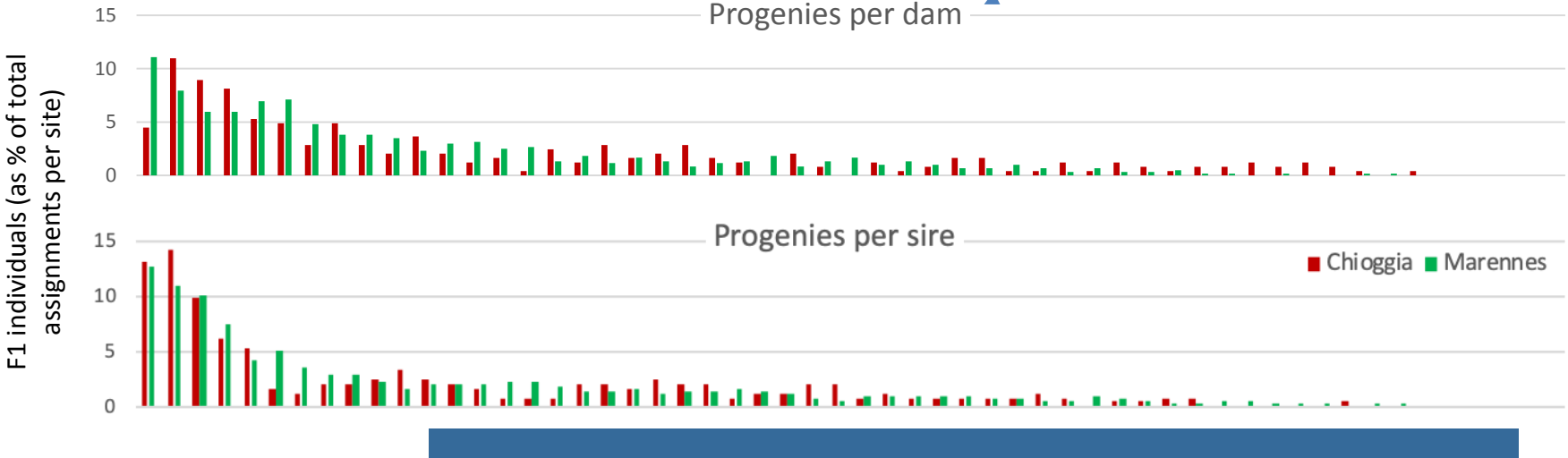


	Marennes	Chioggia
Individuals **recorded**	1016	992
Individuals **genotyped**	946	601
Assigned to parent-pair	604 (59.4%)	246 (24.8%)
Sire representation	49 (88%)	42 (75%)
Dam representation	44 (83%)	45 (85%)

Low genotyping and assignment rates

High parent representation

Balanced representation between sites



Estimations of genetic parameters

	Marennes h^2	Chioggia h^2
Total weight	0.46 [0.11]	0.23 [0.11]
Shell length	0.42 [0.10]	0.29 [0.13]
Shell height	0.41 [0.11]	0.25 [0.13]
Shell width	0.39 [0.10]	0.30 [0.12]
Tissue weight	0.33 [0.10]	0.19 [0.10]
Yield	0.29 [0.10]	0.18 [0.08]
Sex	-	0.42 [0.19]
Parasite load *Perkinsus olseni*	-	0.52 [0.22]

- Medium heritability estimates across all traits
- Higher heritability in Marennes
- Parasite load appears heritable and a potential candidate for selection

Seemingly a genetic component associated with sex

- Maternal or paternal effect on sex determinism?

Estimations of genetic parameters

	Marennes h^2	Chioggia h^2	Genetic correlation
Total weight	0.46 [0.11]	0.23 [0.11]	0.54 [0.26]
Shell length	0.42 [0.10]	0.29 [0.13]	0.67 [0.21]
Shell height	0.41 [0.11]	0.25 [0.13]	0.62 [0.67]
Shell width	0.39 [0.10]	0.30 [0.12]	0.51 [0.43]
Tissue weight	0.33 [0.10]	0.19 [0.10]	0.04 [0.36]
Yield	0.29 [0.10]	0.18 [0.08]	0.30 [1.87]
Sex	-	0.42 [0.19]	
Parasite load *Perkinsus olseni*	-	0.52 [0.22]	

No significant correlations between the two sites

- GxE effect?
- Does the presence of the pathogen affect parameters for other traits?

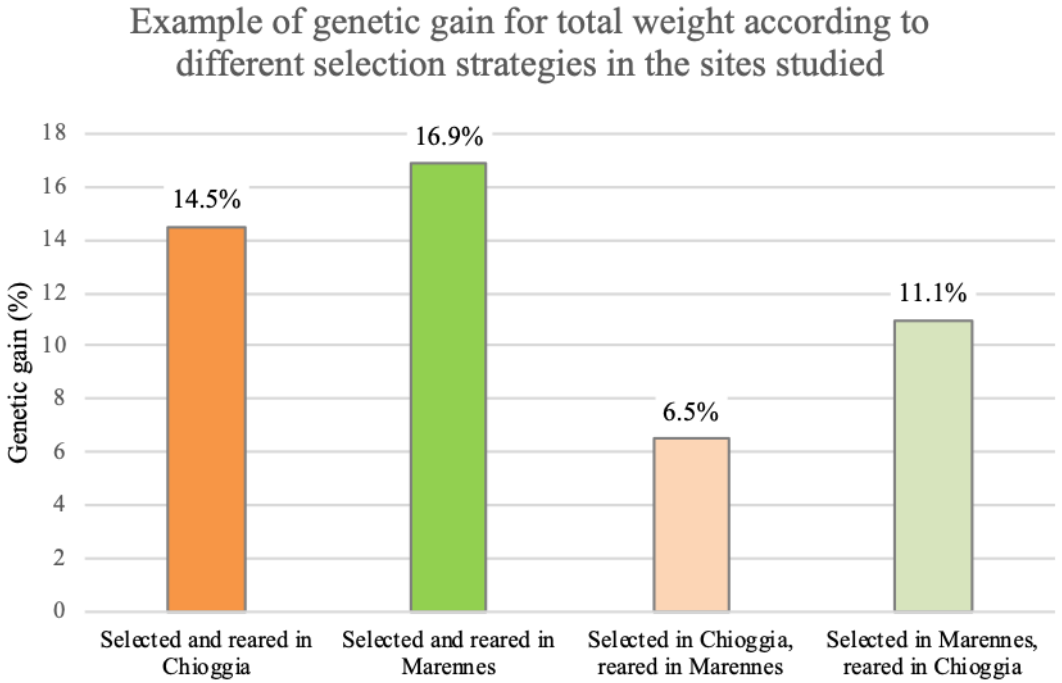
Low number of assignments affect precision of the estimates

Genetic gain: a simulation for total body weight

Lack of genetic correlation between sites: does selection have to be site-specific?

Different selection strategies compared

=> Clams selected in Marennes and reared in Chioggia show 11.1% gain in total weight



Estimations of genetic parameters

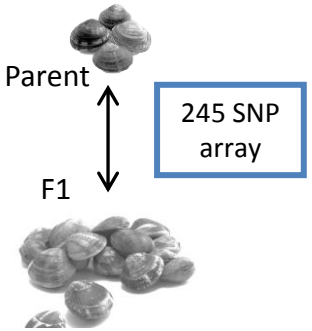
Genetic correlations for traits measured in Chioggia, Italy.

	Length	Height	Width	Tissue weight	Yield	Sex	*Perkinsus olseni* load
Total weight	0.90 [0.07]	0.76 [0.28]	0.97 [0.03]	0.84 [0.14]	-0.19 [0.39]	0.06 [0.65]	-0.26 [0.40]
Length		0.81 [0.24]	0.80 [0.12]	0.79 [0.16]	-0.10 [0.38]	0.11 [0.72]	0.16 [0.41]
Height			0.87 [0.11]	0.90 [0.11]	0.06 [0.37]	0.07 [0.62]	-0.15 [0.40]
Width				0.86 [0.12]	-0.08 [0.37]	0.08 [0.56]	-0.35 [0.31]
Tissue weight					0.46 [0.32]	0.11 [0.18]	-0.14 [0.19]
Yield						0.00 [0.09]	-0.02 [0.58]
Sex							0.22 [0.26]

- Strong correlations between growth traits
- Yield, parasite load and sex appear show no correlation with growth traits

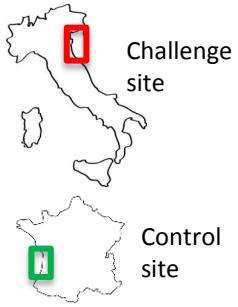
=> Selection objectives can include multiple traits without negatively affecting resistance/growth

Conclusions and perspectives



Parentage assignment

- High parent representation despite low assignment
- ✓ Maintain genetic variability through mass spawning



Estimations of genetic parameters for resistance and growth

- Moderate heritability estimates across traits
- ✓ Selection has potential to increase genetic gain, even across sites

- No correlations between growth traits and resistance
- ✓ Dual selection growth/resistance

! Estimations need to be validated with higher assignment capacity

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