



APPLICATION OF GENOMIC TOOLS AND PERSPECTIVES

Vivaldi Final Conference

Romain Morvezen, Florian Enez, Pierrick Haffray

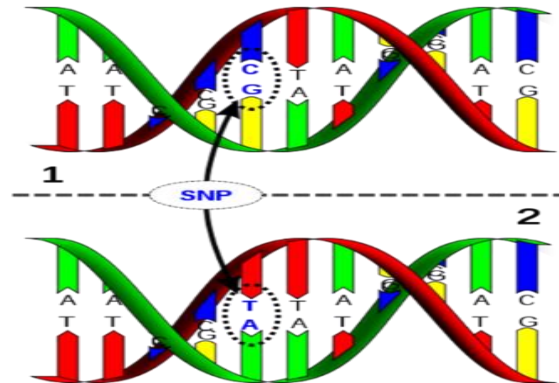
26/11/2010



Genomic tools for disease resistance

What is a genomic tool ?

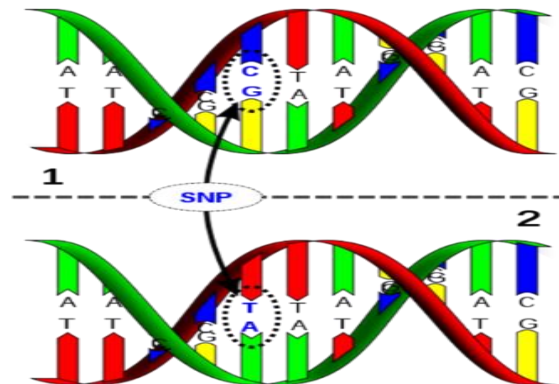
- Position on the genome that exhibits variation (for example, a SNP) between individuals, population



Genomic tools for disease resistance

What is a genomic tool ?

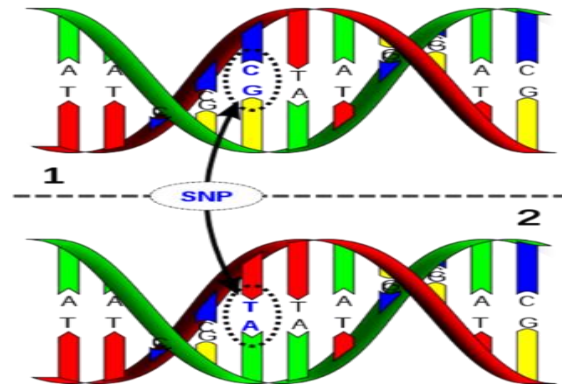
- Position on the genome that exhibits variation (for example, a SNP) between individuals, population
- Can be used for different purposes : genetic variability estimation, parentage assignment, genomic selection, marker assisted selection



Genomic tools for disease resistance

What is a genomic tool ?

- Position on the genome that exhibits variation (for example, a SNP) between individuals, population
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- For marker assisted selection, you need to find an association between your markers and the phenotype of interest -> QTL (quantitative trait loci)

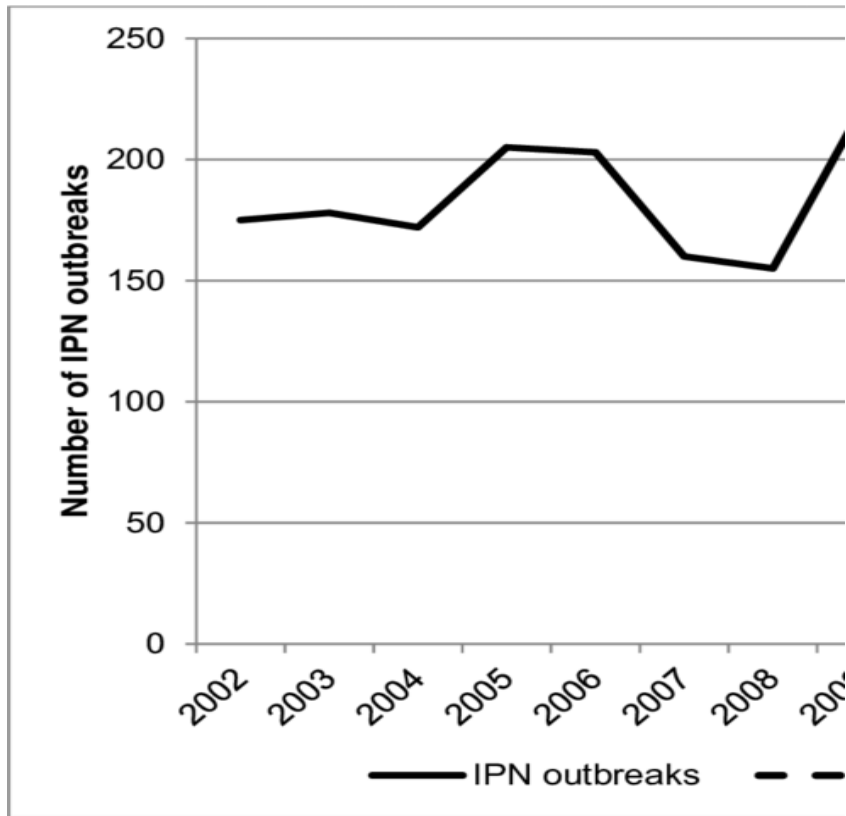
A case-study from the salmon industry



>2.2 millions tons/year



A case-study from the salmon industry



Number of outbreaks per year in Norwegian farmed salmon

IPN disease

- Viral disease
- Up to 70% mortality in salmon fry
- Up to 40% mortality post-smolt (transfer to seawater)



Infected fish

A case-study from the salmon industry

Houston et al. 2008 - QTL identification

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DOI: 10.1534/genetics.107.082974

Major Quantitative Trait Loci Affect Resistance to Infectious Pancreatic Necrosis in Atlantic Salmon (*Salmo salar*)

**Ross D. Houston,^{*,1} Chris S. Haley,^{*} Alastair Hamilton,[†] Derrick R. Guy,[†] Alan E. Tinch,[†]
John B. Taggart,[‡] Brendan J. McAndrew[‡] and Stephen C. Bishop^{*}**

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Manuscript received October 5, 2007
Accepted for publication December 14, 2007

A case-study from the salmon industry

Houston et al. 2008 - QTL identification

One region of the genome (on LG21) strongly associated with resistance or susceptibility

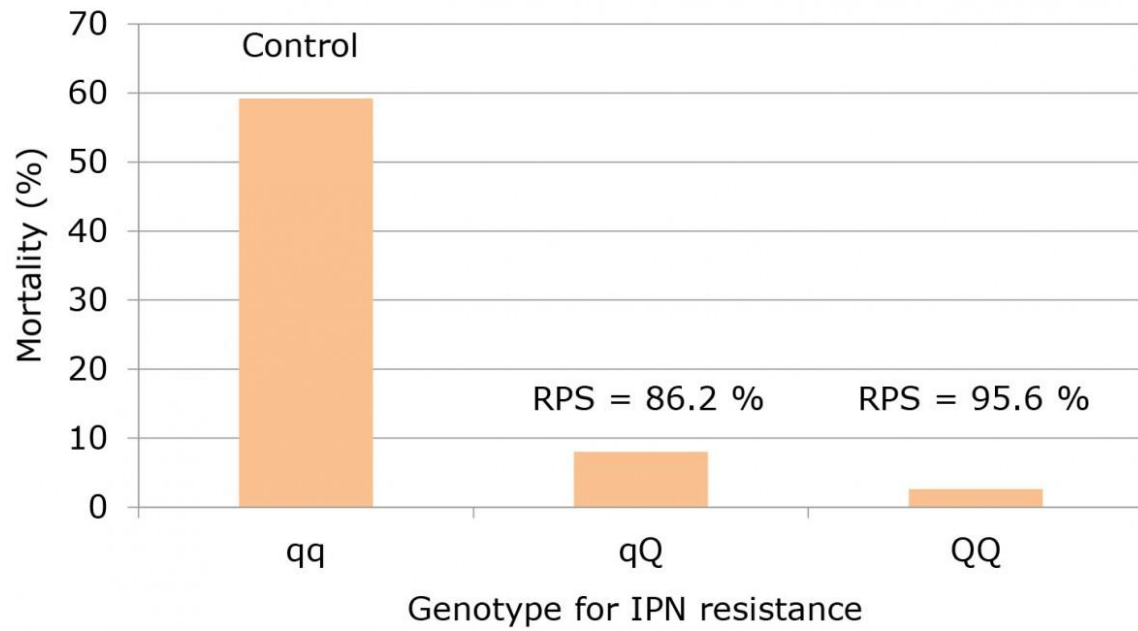
		Dam genotype	
		R	S
Sire genotype	R	0 / 73 (0 %)	1 / 74 (1 %)
	S	2 / 85 (2 %)	69 / 109 (63 %)

R = Resistant ; S = Susceptible

Is it applicable/ reproducible ?

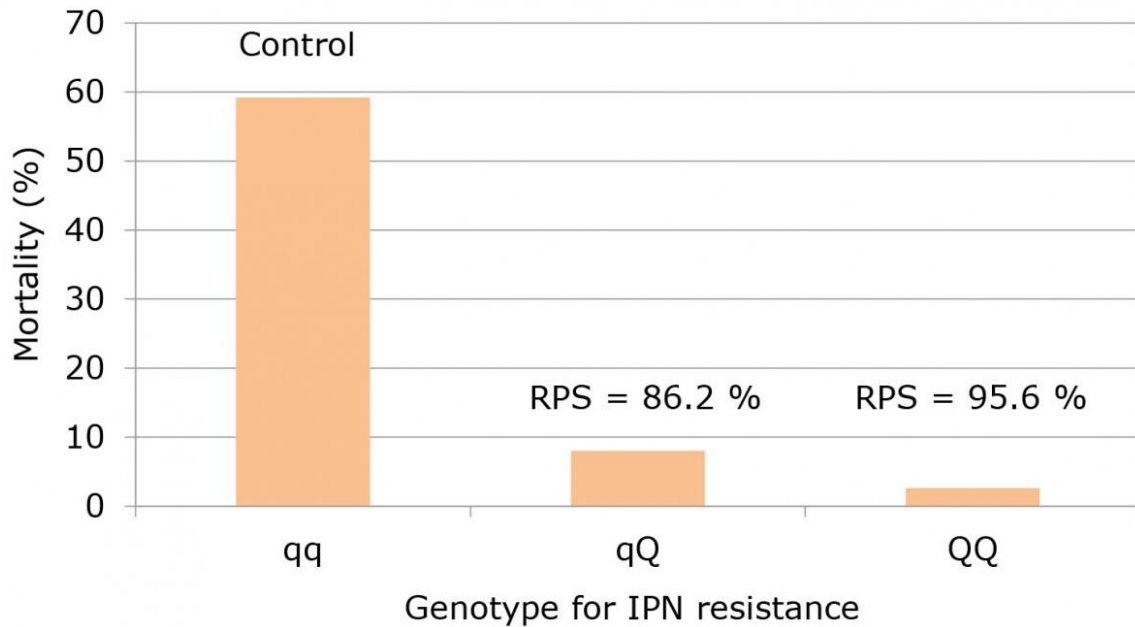
A case-study from the salmon industry

QTL used in a farming context



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Product name

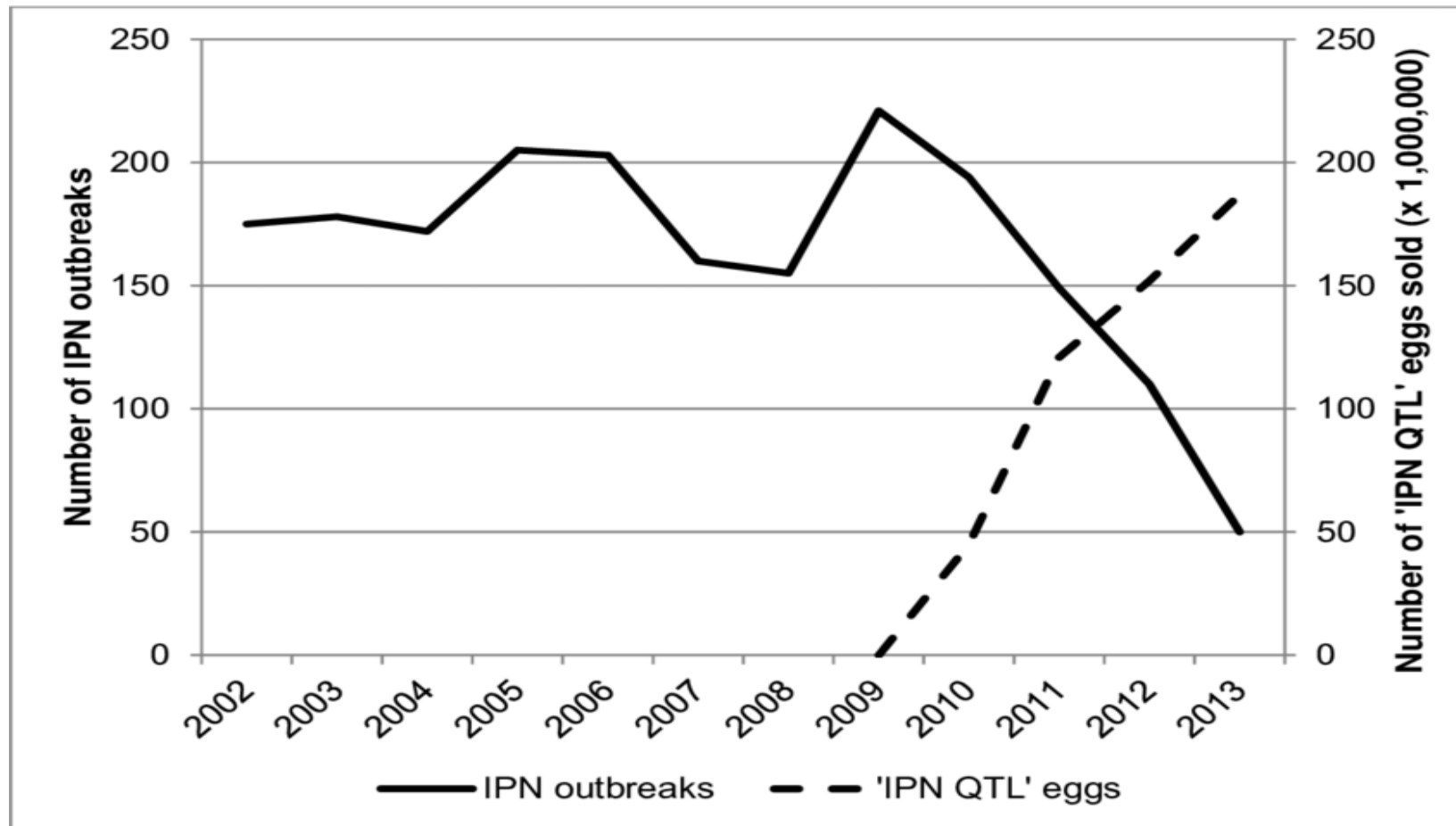
- AquaGen® Atlantic
- QTL-innova® PRIME
- QTL-innova® SHIELD
- GEN-innova® GAIN
- TERRA-nova®

----- QTL-selection

	IPN	LICE	PD	CMS
AquaGen® Atlantic				
QTL-innova® PRIME	●	●		
QTL-innova® SHIELD	●	●	●	●
GEN-innova® GAIN	●	●	●	●
TERRA-nova®	●			

A case-study from the salmon industry

QTL used in a farming context



What about mollusks ?

What about mollusks ?



INVESTIGATION

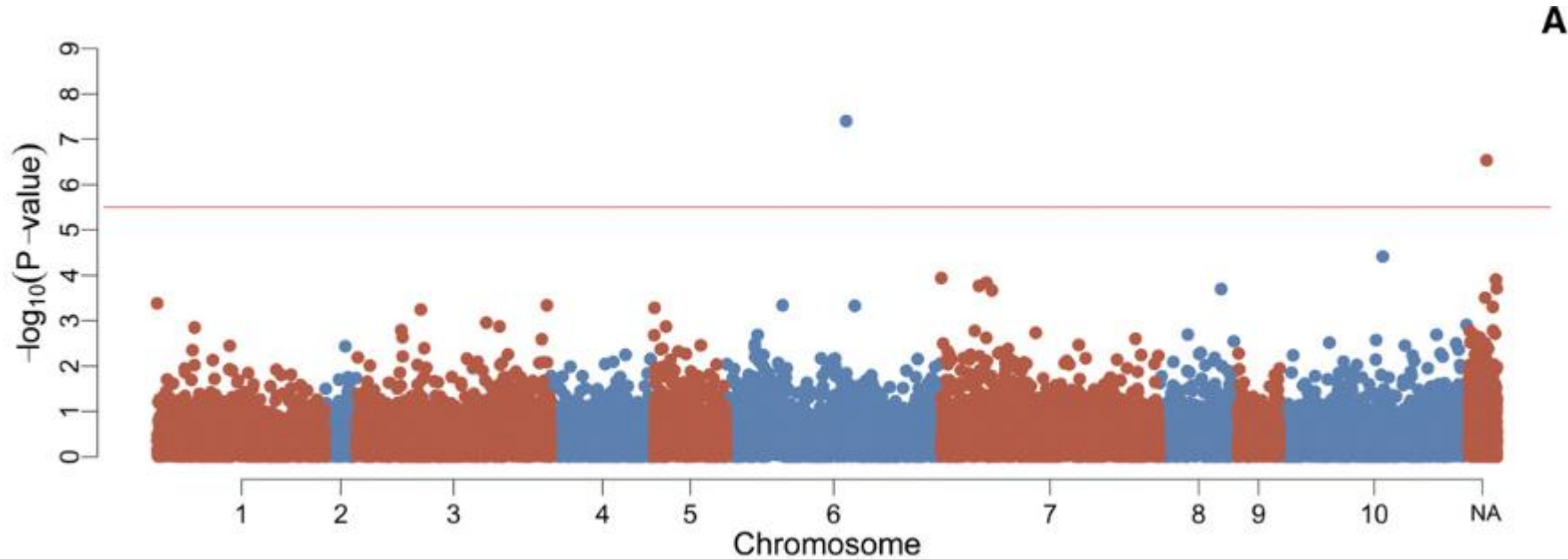
A Genome-Wide Association Study for Host Resistance to Ostreid Herpesvirus in Pacific Oysters (*Crassostrea gigas*)

Alejandro P. Gutierrez,* Tim P. Bean,[†] Chantelle Hooper,[†] Craig A. Stenton,[†] Matthew B. Sanders,[†] Richard K. Paley,[†] Pasi Rastas,[‡] Michaela Bryrom,[§] Oswald Matika,* and Ross D. Houston*

* The Roslin Institute and Royal (Dick) School of Veterinary Studies, University of Edinburgh, Midlothian EH25 9RG, United Kingdom, [†]Centre for Environment Fisheries and Aquaculture Science (Cefas) Weymouth Laboratory, Dorset DT4 8UB, United Kingdom, [‡]Department of Biosciences, Ecological Genetics Research Unit, University of Helsinki, Helsinki, Finland, and [§]Guernsey Sea Farms Ltd. Parc Lane, Vale, Guernsey GY3 5EQ.

ORCID ID: 0000-0003-1805-0762 (R.D.H.)

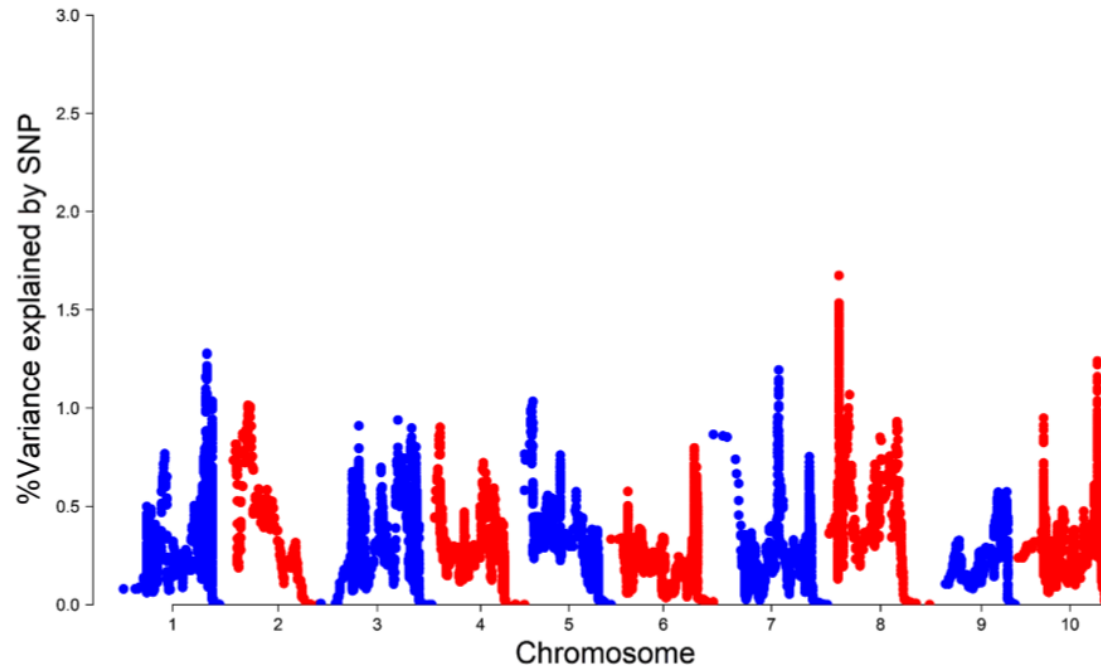
What about mollusks ?



Gutierrez et al 2018, *C. gigas* and OsHV-1

Association with few markers, poorly mapped, no big QTL with substantial effect
Herpes resistance in oyster seems to be polygenic

What about mollusks ?



Gutierrez et al 2019, on *C. gigas* and OsHV-1

-> same results : polygenic trait

What about mollusks ?

With a polygenic trait :

using whole genome information to select the best breeders :

-> *Genomic selection*

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For genomic selection on disease resistance you need :

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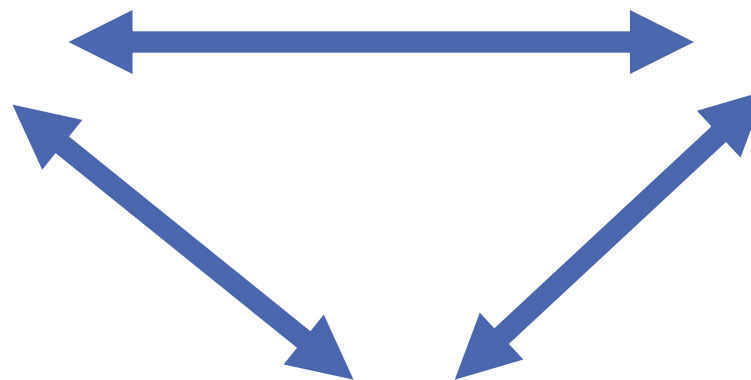
For genomic selection on disease resistance you need :

Robust, repeatable phenotyping methods

- Test sites
- Experimental challenges

Robust, reliable genomic tool

- SNPs arrays



A breeding program

What about mollusks ?

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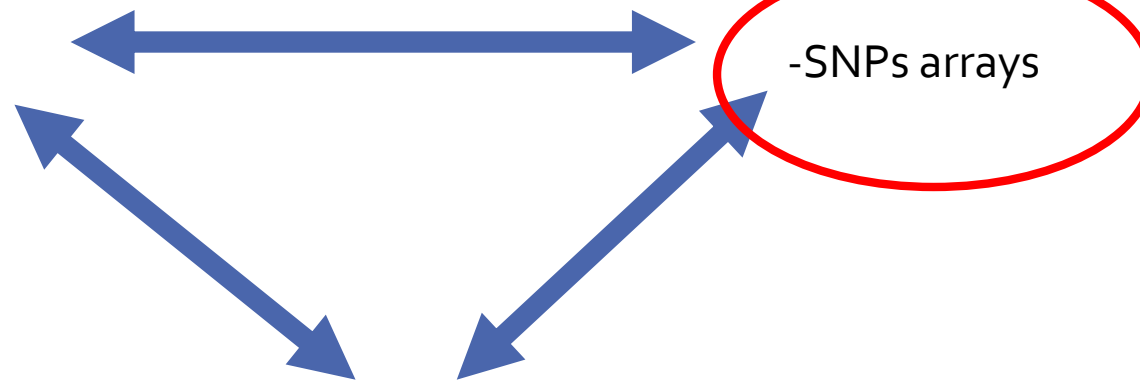
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- Test sites (?)
- Experimental challenges

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A breeding program

Available tools for genomic selection

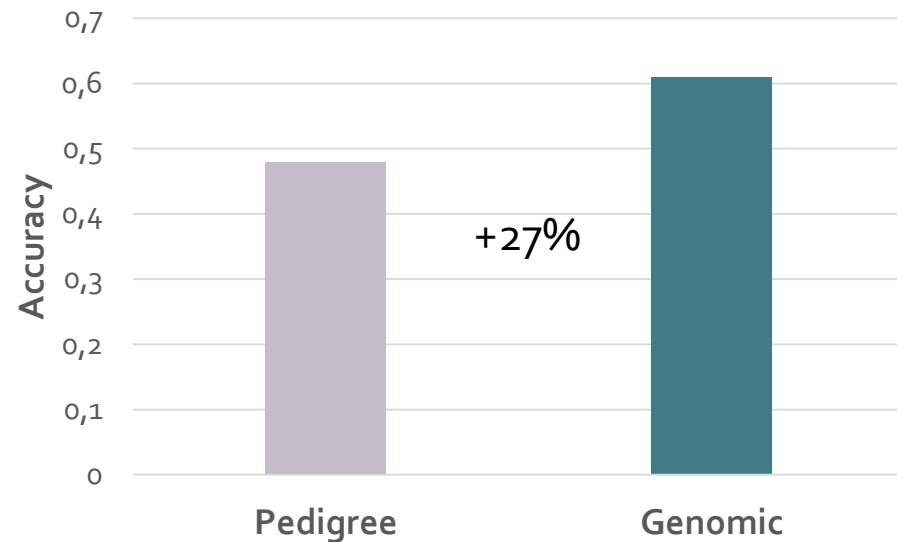
High density public SNP arrays available in aquaculture species

Species	Number SNPs	Assay Type	Reference
Atlantic salmon (<i>Salmo salar</i>)	132K	Affymetrix Axiom	Houston et al., 2014
Nile tilapia (<i>Oreochromis niloticus</i>)	50K	Illumina	Yanez, ISGA 2018
Channel catfish (<i>Ictalurus punctatus</i>) & blue catfish (<i>Ictalurus furcatus</i>)	250K	Affymetrix Axiom	Liu et al., 2014
Channel catfish (<i>Ictalurus punctatus</i>) & blue catfish (<i>Ictalurus furcatus</i>)	690K	Affymetrix Axiom	Zeng et al., 2017
Rainbow trout (<i>Oncorhynchus mykiss</i>)	57K	Affymetrix Axiom	Palti et al., 2015
European sea bass (<i>Dicentrarchus labrax</i>)	57k	Affymetrix Axiom	Allal et al. ISGA 2018
Pacific oyster (<i>Crassostrea gigas</i>)	190K	Affymetrix Axiom	Qi et al., 2017
Pacific oyster (<i>Crassostrea gigas</i>) & European flat oyster (<i>Ostrea edulis</i>)	41K / 15K	Affymetrix Axiom	Gutierrez et al., 2017

Genomic selection

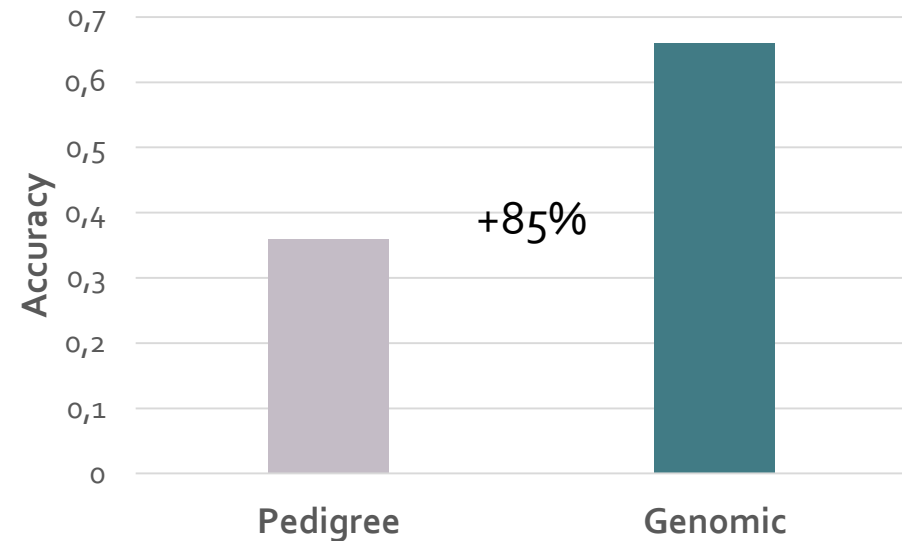
Examples in aquaculture :

Farmed Atlantic salmon resistance to sea lice
(Tsai et al., 2016)



$h^2 = 0,22-0,33$
Array: 35K (subset of the 132K array)
1119 individuals with phenotype and genotype

BCWD resistance in rainbow trout
(Vallejo et al. 2017)







$h^2 = 0,33-0,37$
Array: 35K
1473 individuals with phenotype and genotype
+ 6420 individuals with phenotype

Regarding mollusks

Regarding mollusks

Application of DNA markers : parentage assignement

GenOyster 

				
Total assignment rate	89,4%	86,2%	94,3%	72,1%
Total effective assignment rate	95,1%	91,6%	96,2%	98,5%

-> Effective tool for parentage assignement in oyster commercial hatcheries

Regarding mollusks



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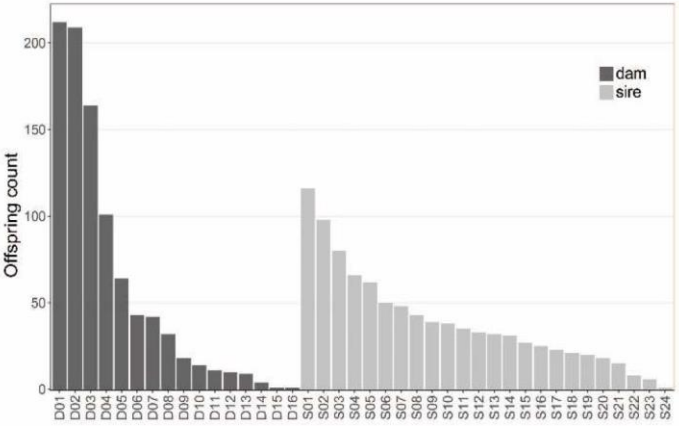


94,3%
96,2%



72,1%
98,5%

-> Effective tool for parentage assignement in oyster commercial hatcheries



GENORMEAU



Haliotis tuberculata Total effective assignment rate : 98.9%

-> Effective tool for parentage assignement in abalone commercial hatcheries

Regarding mollusks

Application of DNA markers : genomic selection

Oysters genomic array

40K SNP (~15K good quality)



Gutierrez et al 2017

	Sample N	MAF > 0	
		# SNPs	Average MAF
UK (combined) ^a	56	27,313	0.186
GSF + parents	38	26,549	0.19
Maldon	9	22,079	0.216
Sea Salter	9	22,821	0.214
Average within UK populations ^b		23,816	0.207
France (combined) ^a	52	26,891	0.182
Ifremer	13	23,010	0.203
Hatchery 1	10	21,479	0.217
Hatchery 2	10	20,141	0.221
Hatchery 3	10	21,730	0.215
Hatchery 4	9	22,052	0.214
Average within French populations ^b		21,682	0.214
All populations (combined) ^a	108	27,697	0.182

MAF, minor allele frequency; #, number; SNPs, single nucleotide polymorphisms; Ho, level of genetic variability in terms of observed variability in terms of expected heterozygosity; GSF, Guemsey Sea Farm.

^aValues were obtained by the analysis of the combined dataset, not the average of the individual populations.

^bValues represent the within-population average.

Regarding mollusks

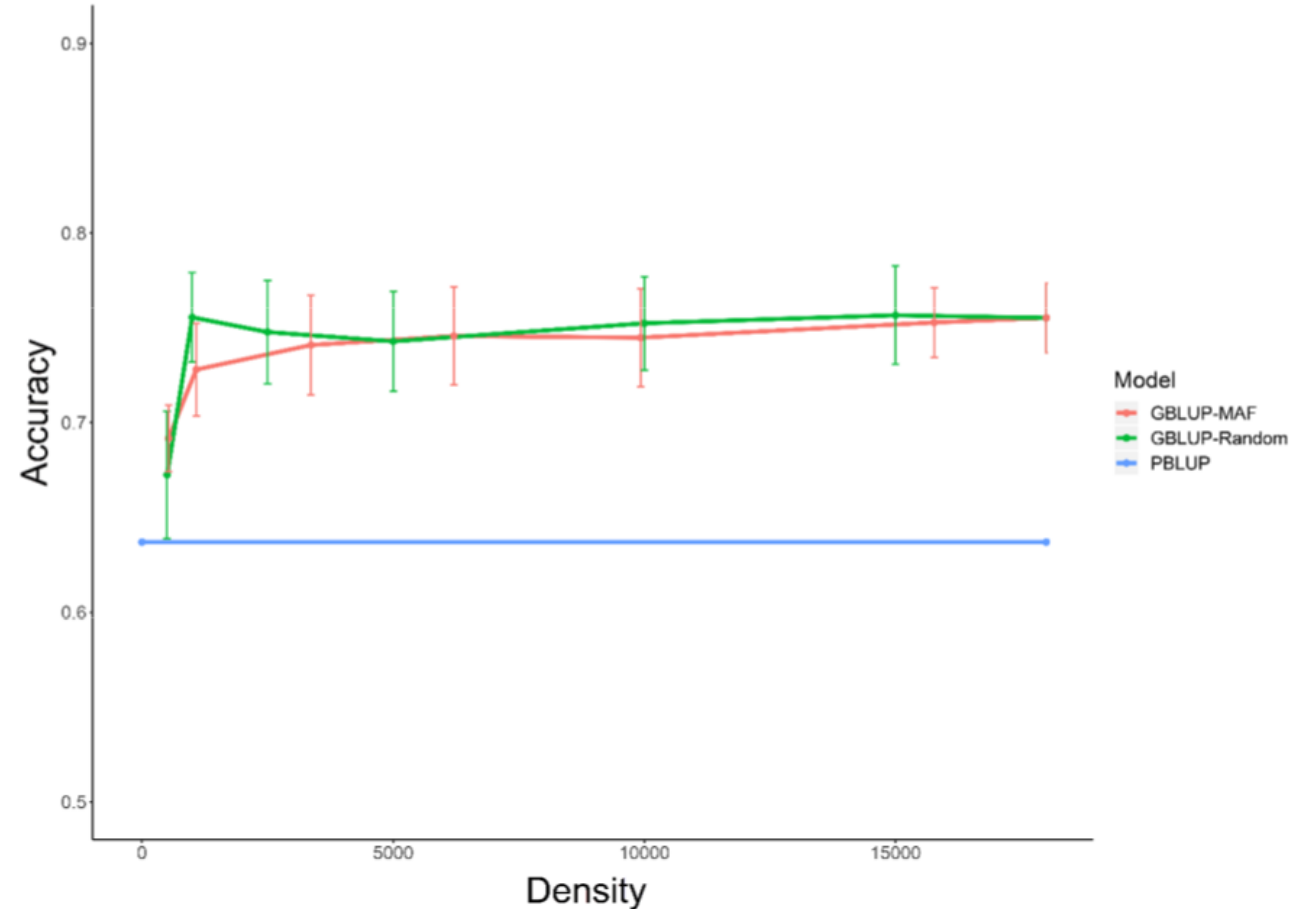
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Gutierrez et al 2019



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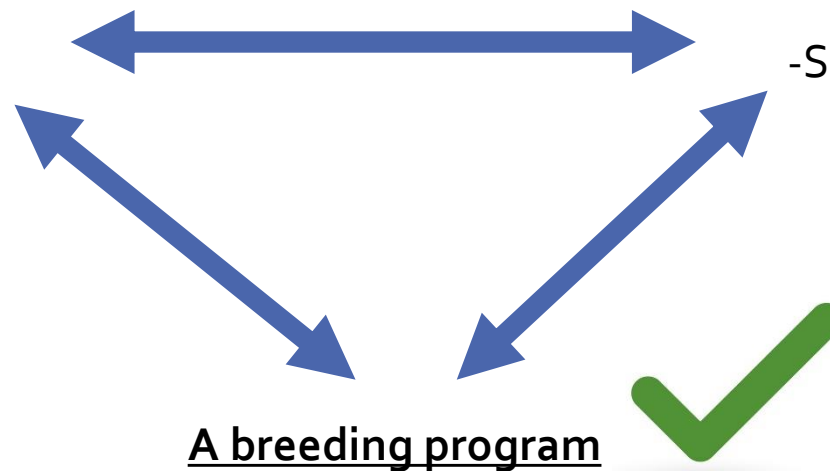
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Repeatability/reliability ?

-Experimental challenges



Protocol exist in research labs and the litterature

-How robust/representative are they ?

-Are they accessible to breeders ?

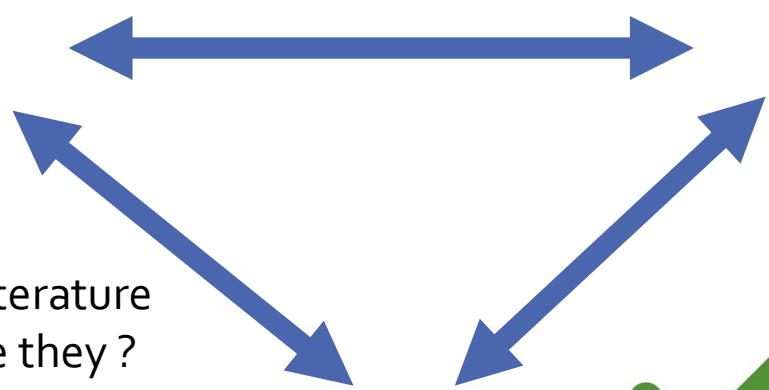
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Could be improved

A breeding program



Next challenges for shellfish breeding

- Estimation of heritabilities and identification of QTLs for interest traits : production traits, disease resistance...
- Confirm genetic gains by testing offspring of selected broodstock
- Development of methods to phenotype shellfish (for ex. controlled challenges for breeding programs)
- Adaptation of breeding programs to new tools – implementing genomic selection
- Genomic resources for other commercially important shellfish species



Thank you for your attention

