THE USE OF SNPs IN CHARACTERIZING OYSTERS GENOMES AND THEIR RESISTANCE TO PATHOGENS

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Species

The Pacific cupped oyster

Crassostrea gigas

Native from Japan, introduced in many countries

Highest annual production of any aquacultured organism (4.5 million metric tons/year mainly in Asia)

The European flat oyster

Ostrea edulis

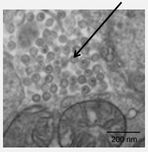
Native from Europe, introduced in a few countries

Produced mainly in Europe (Spain, Netherland, Ireland, France)

Genetic improvement by selective breeding still limited but in development for the Pacific oyster

Resistance to pathogens

herpesvirus OsHV-1

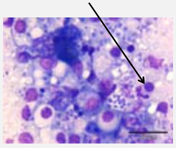


The virus is involved in spat summer mortality (Renault et al.,1994)

The heritability for the survival to summer mortality is high (Degremont et al., 2007)

Zone of the genomes involved in the survival and virus load (QTLs) can be detected (Sauvage et al., 2010)

Bonamia ostreae

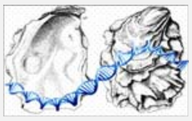


The parasite is involved in two-three years old oyster mortality (Pichot et al., 1979)

Mass and family selection improve survival

Zone of the genomes involved in the survival (QTLs) can be detected (Lallias et al., 2009)

Genomic resources



2n = 20 chromosomes

For *C. gigas*:

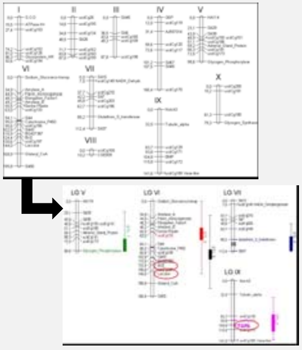
- Genome size ~824 Mb : among the smallest known mollusk genomes
- GigasDatabase (Fleury et al., 2009) :
  23,356,508 base pairs,
  29,745 unigenes
  27% annotated (GO)
- More than 200 microsatellite markers
- AFLPs

http://public-contigbrowser.sigenae.org:9090/Crassostrea_gigas/index.html

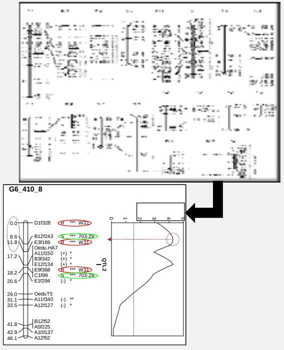
For *O. edulis*:

- Tens of microsatellites and AFLP
- EST resources from SSH libraries (Morga et al., 2010)

QTLs detection in low density maps



Five QTLs detected in four linkage groups explaining 50% of the variance of the trait

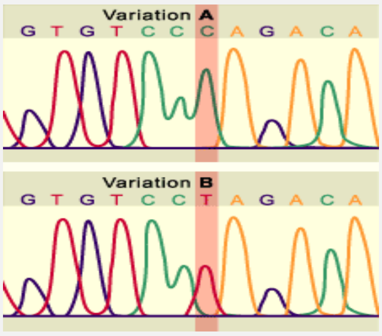


Five QTLs detected in the two parental maps

SNPs potential

- High polymorphism and heterozygocity
  C. gigas : 1 SNP every 60/40 bp in coding/non-coding regions (Sauvage et al., 2007)
  O. edulis : 1 SNP every 39 bp
- 500 contigs with SNPs in GigasBase
- GIGASNP' (Hedgecock et al., USDA funded project under development)
- Whole *C. gigas* genome sequence released (http://buzzg.com/science/chinese-experts-release-worlds-first-oyster-genome-map.html)

SNP = **S**ingle **N**ucleotide **P**olymorphism



Conclusion

- SNps are numerous in the oysters' genomes
- SNPs can be genotyped with high through-put technologies but genotyping SNPs in a such polymorphic species remains a challenge
- SNPs can increase the density of the maps
- SNPs can make the link between quantitative genomics and candidate genes approaches
- SNPs can help understanding the physiology of the traits
- SNPs could become markers assisting selection

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