

Establishment of a genetic map in the European flat oyster *Ostrea edulis* L.

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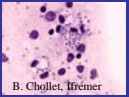
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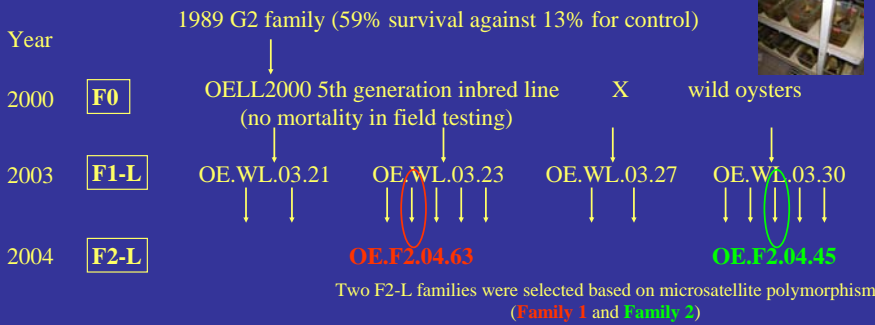
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CONTEXT OF THE STUDY

The flat oyster *Ostrea edulis* is the species endemic from European coasts, Atlantic and Mediterranean. It has been exploited since Roman times in Europe. But its production decreased from around 20000 tons in the 1950^{ies} to 1500 tons nowadays because of two successive diseases due to the intracellular parasites *Marteilia refringens* and *Bonamia ostreae*. Since 1985, Ifremer initiated a program of selection to produce families of oysters tolerant to *Bonamia*. In this context, a further step is to identify QTLs of resistance to this parasite. Therefore, a genetic map is first now being built. The establishment of a genetic linkage map will represent the basement for the mapping of QTLs, with the ultimate objective to implement marker-assisted selection in *O. edulis*.

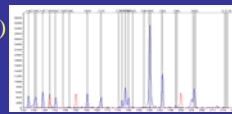


PRODUCTION OF SEGREGATING FAMILIES (biparental crosses)



MOLECULAR TOOLS

- 20 microsatellites (1, 2, 3, 4, 5) (ABI 3100-Avant sequencing machine) (GeneMapper® Software 3.7.) Determination of fully, semi and non informative loci in each cross
- 60 AFLPs primer pairs (6) (ABI 3100-Avant sequencing machine) (GeneMapper® Software 3.7.) Three dyes: FAM, HEX and NED Positioning of bins manually to select good-quality peaks

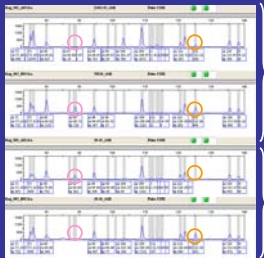


FIRST RESULTS

• Genotyping of 48 adult flat oysters per F2-L family

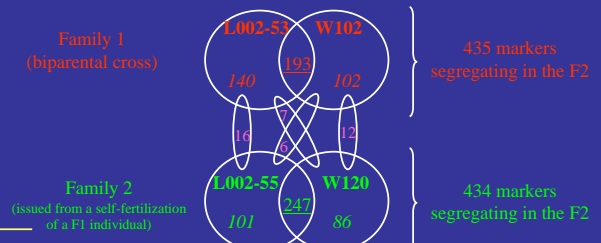
Microsatellite genotyping of Family 2 revealed that it is issued from the self-fertilization of one F1 individual, and not from the expected biparental cross. This is the first time that such phenomenon is recorded in *O. edulis*.

• Determination of the number of potential AFLPs to be mapped (i.e. segregating in the F2s)



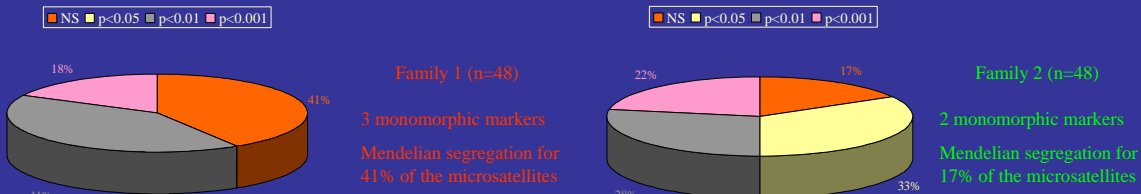
- 2 cases of segregating AFLP markers:
 - Type 1:1 (allele specific of one of the 2 F0 parents)
 - Type 3:1 (allele common to the 2F0 parents)

- In italics* : Number of Type 1:1 markers
- Underlined : Number of Type 3:1 markers
- In pink* : Markers common to both families, allowing the establishment of a consensus map



A minimum of 200 AFLP markers are expected to be mapped in each mapping family, taking into consideration the Type 1:1 markers. The use of Type 3:1 markers (thanks to a F2 design) should increase the number of mapped markers.

• High segregation distortions of microsatellites assessed by Chi-square goodness of fit



Segregation distortions are higher in the mapping family issued from a self-fertilization (Family 2). These results support the observation of a high genetic load made on the same species by Bierne *et al.* (1998)⁽⁷⁾, and on the cupped oyster *Crassostrea gigas* by Launey & Hedgecock (2001)⁽⁸⁾.

➡ According to these results, some of the markers will not be mapped due to their high segregation distortions

PERSPECTIVES

- Construction of a genetic map (in collaboration with Chris Haley, Roslin Institute, UK)
 - ↳ Based on AFLP and microsatellite data obtained on the two families
 - ↳ CRIMAP software
- QTL mapping of traits of economical importance
 - ↳ growth (follow-up of total length and weight monthly for 550 F2-L oysters Family 2)
 - 6-month data are already available
 - ↳ *Bonamia* "resistance"
 - 150 oysters Family 1 and 550 oysters Family 2 (F2-L)- 2 year-old
 - ↳ Challenge by cohabitation with over-infected oysters
 - ↳ Mortality will be recorded daily

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