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

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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 1950ies 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 now first 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)

1989 G2 family (59% survival against 13% for control)

2000 F0
OE.L 2000 5th generation inbred line (no mortality in field testing)

2003 F1-L
OE.WL.03.21
OE.WL.03.23
OE.WL.03.27
OE.WL.03.30

2004 F2-L
OE.F2.04.63
OE.F2.04.45

Two F2-L families were selected based on microsatellite polymorphism

• 1989 G2 family
• 2000 F0
• 2003 F1-L
• 2004 F2-L

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)
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)a, and on the cupped oyster Crassostrea gigas by Launey & Hedgecock (2001)ab.

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

REFERENCES