

## Molecular Markers as a Tool to Study Genetic Resources in Oysters

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Despite the world economic importance of oyster farming, genetic improvement has not yet had a great impact on these species. Oyster farming is traditionally based on wild stocks, whose natural populations are often overexploited, and frequently does not fulfil market demand (Goulletquer and Héral, 1997). Up to now, the most effective answer to disease problems or for the improvement of productivity has been the introduction of new species. However, these introductions are constrained by their potential ecological impact and also limited by the availability of suitable species. Proper management of genetic resources is still to be established, but could be of great importance for the long-term sustainability of the shellfish industry. For this reason, molecular markers have been developed and are of great use for the study of these resources, both at the between and the within species levels.

The taxonomy of oysters is not straightforward. Their shell morphology is highly plastic and species determination is often unclear. Furthermore, inter-specific hybridisation can occur (Gaffney and Allen, 1993) and cases of introductions of non-native species are numerous. Consequently, the development of species specific genetic markers has been initiated to ease their identification. These markers are used to trace the origin of non-native stocks (e.g. *Crassostrea angulata* and *C. gigas* in Europe, Boudry *et al.*, 1998), or to discriminate morphologically plastic species in the field (e.g. *C. gigas*, *C. ariakensis* and *C. sikamea* in Japan, Hedgecock *et al.*, 1999).

In areas where natural recruitment of oysters is limited (due to climatic constraints or to decreasing populations), the production of spat can be based in hatcheries. This makes the development of selective breeding programs possible, but such programs have not yet reached a scale enabling proper genetic diversity management, multi-site testing or effective improvement of the commercial stocks. Most of them have remained at an experimental scale, aiming to evaluate the possibility of selection for traits such as growth or disease resistance (e.g. Naciri-Graven *et al.*, 1998). Only with the support of the shellfish-farming community will selection programs be able to get past the experimental stage and reach an economic scale, such as the "Molluscan Broodstock Program" initiated in the USA (Hedgecock *et al.*, 1997).

Since oysters have a very high fecundity, it is common practice for hatcheries to produce large amounts of offspring from a limited number of parents. The genetic consequences of such practices are of concern, especially if some of these offspring are to be used as parents for the next generation. Inbreeding is likely to occur, leading to a decrease in performance (Bierne *et al.*, 1998). Furthermore, a reduced genetic variability limits the possibilities of genetic improvement by selective breeding. Highly polymorphic genetic markers such as microsatellites can be useful tools for the analysis genetic of variability and parental contributions in hatchery-produced stocks. Such analyses have been performed in the progeny of several *in vitro* factorial crosses of the cupped oyster *Crassostrea gigas*. Parentage analysis was eased by the large polymorphism observed at the 3 loci studied. Despite the balanced gametic contribution of each parent before fertilisation, unbalanced parental contributions are frequently observed in the progeny, both at larval and juvenile stages, due to gametic and zygotic competition.

In the European flat oyster, *Ostrea edulis*, *in vitro* fertilisation is not possible, as this is a larviparous (or brooding) species. Genetic variability of 3 strains selected for a resistance to the protozoan parasite *Bonamia ostreae* (Naciri-Graven *et al.*, 1998) was analysed using 5 microsatellite loci. The estimation of the effective number of breeders demonstrated the occurrence of bottlenecks and potential inbreeding (Launey, 1998).

We can conclude that, despite the limited impact of genetics in oyster farming, the recent development of molecular markers is likely to have a significant impact on the management of genetic resources in oysters in the near future. Most of these resources are still unexplored and genetics should bring new perspectives to oyster production.

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