Restriction enzyme digestion chromosome banding in *Crassostrea* and *Ostrea* species: Comparative karyological analysis within Ostreidae

A. Leitao¹, R. Chaves², S. Santos², H. Guedes-Pinto² and P. Boudry³

¹Institut National des Sciences et Technologies de la Mer, Tunisia;
²Department of Genetics and Biotechnology, ICETA-UTAD, Portugal;
³IFREMER, Station de La Tremblade, France

Reliable banding techniques are one of the major needs to develop the genetic research in oysters. In this study, we have carried out the cytogenetical characterization of four oyster species (family Ostreidae) using restriction endonucleases treatments. Chromosomes were treated with three different restriction enzymes (REs), stained with Giemsa, and examined for banding patterns: *Crassostrea gigas* (2n=20, total number of bands with ApaI: 74, HaeIII: 61, PstI: 76), *Crassostrea angulata* (2n=20, total number of bands with ApaI:62, HaeIII:61, PstI: 55 ) (sub-family Crassostreinae) and *Ostrea edulis* (2n=20, total number of bands with ApaI: 82, HaeIII: 59, PstI: 66), *Ostrea conchaphila* (2n=20, total number of bands with ApaI: 68, HaeIII: 62, PstI: 69) (subfamily Ostreinae). The treatment of samples with ApaI, HaeIII and PstI REs produced specific banding patterns, which demonstrate the potential of these enzymes for chromosome banding in oysters. This is of special interest since it has been recently shown in mammal chromosomes that restriction enzyme banding is compatible with fluorescent *in situ* hybridisation. This study therefore provides a fundamental step in genome mapping of oysters, since the chromosome banding with restriction enzymes will facilitate physical gene mapping in these important aquacultured species. The analysis of the banded karyotypes revealed a greater similarity within the genera of *Crassostrea* and *Ostrea* than between them.