Chromosome Evolution in Bivalvia (Mollusca): Ostrea edulis and O. stentina, and the clam Chamelea gallina. Inferences by ribosomal and telomeric sequences

J. Pereira (1), A. Leitão (2), R. Chaves (1), F. Batista (3), H. Guedes-Pinto (1)

(1) Institute for Biotechnology and Bioengineering, Centre of Genetics and Biotechnology, University of Trás-os-Montes and Alto Douro (CGB–UTAD/IBB)
(2) INRB/L-IPIMAR. (3) School of Ocean Sciences, Bangor University

Bivalves constitute a group of marine invertebrates of great economic and ecological significance, and therefore, genetic information concerning their genome is particularly important. Cytogenetic analysis may provide useful information for phylogenetic comparisons and insight on major genomic changes at chromosome level in this group. The genome of three commercially important bivalves species: the oysters Ostrea edulis and Ostrea stentina, and the clam Chamelea gallina, was characterized using molecular cytogenetic approaches such as Giemsa staining, DAPI staining and fluorescence in situ hybridization (FISH) with repetitive DNA probes [ribosomal (18S–28S rDNA, 5S rDNA) and telomeric (TTAGGG)n]. The results obtained, particularly the study of the repetitive sequences at the molecular level and their physical mapping, revealed to be a valuable tool in the illumination of the phylogenetic relationships among bivalves and their chromosome evolutionary processes. These studies are extremely useful for the implementation of bivalve species preservation or aquaculture interspecific hybridization programs.