DOI 10.1007/s10577-009-9043-0

Chromosomal localization of histone H3 gene in the Pacific oyster, Crassostrea gigas

K. Bouilly [(1)], M. Fernandes [(1)], R. Chaves [(1)], H. Guedes-Pinto [(1)]

[(1)] Institute for Biotechnology and Bioengineering, Centre of Genetics and Biotechnology, University of Trás-os-Montes and Alto Douro (IBB/CGB–UTAD)

The Pacific oyster, Crassostrea gigas (2n=20) is an economically important mollusk species cultured throughout the world. The most frequently used technique for molecular cytogenetic studies is fluorescence *in situ* hybridization (FISH) which offers new opportunities for the identification of oyster chromosomes. It has been used to locate simple sequence repeats, satellite DNAs, telomeres or ribosomal DNA sequences. However, regarding chromosome identification, no study has been done with histone H3 gene. Histone H3 is among the most conserved eukaryotic proteins. Most histone H3 genes are repeatedly organized into clusters, which make them an ideal chromosomal marker. In bivalves, little knowledge is available concerning sequence DNA information or the physical mapping of histone genes. The histone H3 gene was mapped on two different pairs of chromosomes, one at an interstitial site on the long arm of chromosome pair 4, and the other on the telomeres of the smaller chromosome pair (pair 10). Polymorphism was detected on the telomeres of pair 10, once it was possible to observe single or double signals. Major ribosomal RNA genes, NORs (nucleolus organizer regions) and C-bands are also localized on the telomeres of pair 10 in C. gigas. In scallops, histone H3 gene was also clustered at two different loci or a single locus depending on the species. Comparative chromosomal mapping should improve our understanding of bivalve genome organization.