

Physical mapping of BAC clones in the pacific oyster, *Crassostrea gigas*

Karine Bouilly, Sandra Louzada, Dulce Santos, Sara Teixeira, Henrique Guedes-Pinto, Raquel Chaves

IBB-CGB UTAD, Vila Real, Portugal

The Pacific oyster, *Crassostrea gigas*, is an economically important mollusk species cultured throughout the world. This species has a haploid complement of ten metacentric chromosomes. Chromosomal identification is essential in genomic research. The most frequently used technique for molecular cytogenetic studies is fluorescent in situ hybridization (FISH) which offers new opportunities for the identification of oyster chromosomes. Bacterial artificial chromosome (BAC) clones are composed of specific regions of the genome. The Pacific oyster BAC library contains 73,728 *C. gigas* clones with an average insert size of 152 kb representing an 11.8-fold genome coverage. Some of these clones were tested for chromosomal identification in *C. gigas*. A few BAC clones were mapped by FISH experiments on the chromosomes of *C. gigas*. The BAC clones studied are chromosome-specific and allowed the identification of several chromosome pairs of *C. gigas*. Some of these clones are already sequenced, so we could assign some genes and sequences to specific *C. gigas* chromosomes. This preliminary physical map of *C. gigas* will provide a foundation for comparative genomics and chromosome evolution in oysters. S194 Chromosome Res (2011) 19 (Suppl 1):S37–S231.

Keywords: BAC clones, *Crassostrea gigas*, FISH, Oyster, Physical map