# Characterization, classification and localization of repetitive DNA sequences constituting the genome of the Pacific oyster (Crassostrea gigas)

P-01.1-10

**M. Tunjić Cvitanić**[I], T. Vojvoda Zeljko[I], J.J. Pasantes Ludeña[II], D. García-Souto[II,III,IV], M. Plohl[I], E. Šatović[I]

[I]Ruder Boskovic Institute, Zagreb, Croatia, [II]University of Vigo, Vigo, Spain, [III]University of Santiago de Compostela, Santiago de Compostela (A Coruña), Spain, [IV]Wellcome Sanger Institute, Hinxton, United Kingdom

Bivalve molluscs are a large group of economically and ecologically important invertebrates, which made them particularly interesting as model organisms for genomic research. So far, 31 bivalve genomes have been sequenced, the first one corresponding to the Pacific oyster (*Crassostrea gigas*). Segments of the genome enriched in repetitive sequences still present a challenge in the genome assemblies, leaving the composition of DNA sequences underlying the heterochromatic regions and the centromeres still unexplored in many organisms. The typical landmark of centromere chromatin is a variant of the H3 histone, CenH3, while DNA sequences building constitutive heterochromatin are associated with H3K9me3-histone modification. In order to investigate the DNA composition of genomic regions enriched in repetitive sequences, we employed chromatin immunoprecipitation followed by next-generation sequencing of the whole genome and CenH3- and H3K9me3-associated sequences. The obtained sequences were analysed using RepeatExplorer pipeline. Fifty-two satellite DNAs constitute the satellitome. CenH3-associated sequences resulted in diverse repetitive DNA content and were assigned to six different groups of repetitive sequences. Several sequences enriched in CenH3-ChIP were localized on metaphase chromosomes using fluorescence *in situ* hybridization, each encompassing centromeres of only a few chromosomes of *C. gigas*. The same sequences were also colocalized with CenH3 on male gonadal cells in different stages of spermatogenesis, revealing stage-specific distribution of the CenH3. The heterochromatin of *C. gigas* exhibited low abundance and localization limited on two chromosomal pairs, with H3K9me3-associated sequences being dominantly composed of DNA transposons. To conclude, we identified, characterized and localized the most abundant repetitive sequences present in the genome of the Pacific oyster.