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The introduction of new species constitutes a serious threat to native aquatic biodiversity. *Xenostrobus securis* is a bivalve native of Australia and New Zealand which has been described at many locations outside its native range of distribution. This species is present now at the inner part of Ría de Vigo (NW Spain) so presenting a potential threat to its biodiversity. Despite its danger, little is known about the genome organization of this species so we decided to cytogentically characterize it.

Chromosome preparations were obtained from gill and gonadic tissues of juvenile *X. securis* after hypotonic treatment and fixation with ethanol/acetic. Chromosome counts were carried out and karyotypes were constructed. The presence of CG- and/or AT-rich chromosome regions was analyzed by chromomycin A3 (CMA) / 4',6-diamidino-2-phenylindole (DAPI) and propidium iodide (PI / DAPI) staining. Besides, ribosomal and histone gene families were mapped to the chromosomes of these species by fluorescent *in situ* hybridization (FISH) using species specific H3, H1, 28S rRNA and 5S rRNA gene probes generated by PCR. Telomeric sequences were also mapped by FISH using human telomeric probes.

The karyotype of *X. securis* is composed by 15 chromosome pairs, 8 of them metacentric and 7 submetacentric. DAPI/PI and CMA/DAPI staining revealed DAPI negative/CMA bright regions close to the centromeres on two metacentric chromosome pairs. As demonstrated by FISH, these DAPI negative regions are the chromosomal positions occupied by the major ribosomal genes (18+28S rDNA). FISH experiments also demonstrated the presence of 5 *loci*, located on 4 chromosome pairs, for the minor rRNA genes (5S rDNA), 4 *loci* for the core histone genes and 2 *loci* for the linker histone genes (H1 genes). Double- and triple-FISH experiments allow concluding that most of the loci for these gene family clusters are situated on different chromosome pairs. Only one metacentric chromosome pair bears clusters of both histone H3 and 5S rRNA gene families. The chromosomal distribution of these 4 gene family clusters allow to distinguish 11 of the 15 chromosome pairs of this species.

POSTER

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DESCRIPTION OF INTERTIDAL ALGAL-BASED BIOTOPES OF PICO ISLAND, AZORES, PORTUGAL

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The present study aimed at identifying, describing and classifying algae-based biotopes of Pico Island, Azores (Portugal), while assessing the effectiveness of the methods proposed by the Phycology Group of Universidade dos Açores (PGUA) by the PGUA proved to be effective in defining algae-based biotopes on the Azorean islands of São Miguel, Santa Maria and Graciosa. It was hypothesized that the proposed methodologies would also be effective if implemented by non-skilled surveyors, and could therefore be widely used for algal community characterisation surveys. Eighteen littoral sites of Pico Island were surveyed, covering three rocky substrate types: cobbles, boulders and bedrock. The point intersection method with 0.25 x 0.25 m quadrats and 36 intersection points was used in order to register the frequency of occurrence of taxa/ecological categories. Multivariate analysis was used to identify association of abiotic (substrate and shore height) and biotic (algae species) information, that were then classified as biotopes. Four algae-based biotopes were identified for Pico Island, based on substrata and shore-height differences ($R \geq 0.3$). Community structure was influenced by substrata stability and shore level; bedrock and boulders presented equal biotopes (associated with lower- and upper-littoral) and cobble were characterised by different ones (associated with lower- and mid-/upper-littoral). The methodologies used proved to be effective when implemented by the nonskilled surveyor in Pico Island. The biotope methodology is a useful tool in understanding and identifying species distribution, thus providing information that can be used in conservation policies for the marine environment

POSTER

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GENE FLOW, INDIVIDUAL ASSIGNMENT AND GENETIC STRUCTURING OF SW EUROPEAN HAKE *(MERLUCCIUS MERLUCCIUS)* STOCKS

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The European hake *Merluccius merluccius* is the demersal species of major commercial importance in Western Europe. Since its populations are threatened by overexploitation, fishery assessment incorporating population genetic data would provide useful data for fisheries management. Previous genetic studies on the European hake performed with allozymes and nuclear DNA markers have established the existence of a genetic split between Atlantic and Mediterranean populations of hake, a partition not detected with mitochondrial DNA. Such incongruence is probably caused, among other factors, by the distinct evolutionary pace of markers and by strong inter-annual fluctuations in broodstock biomass that determine the migration rate of larvae and juveniles between fisheries and consequently its structuring scenario. In this study we have analysed the molecular variation of five polymorphic microsatellites and a 465 bp fragment from the cytochrome *b* gene on SW European hake populations to determine the genetic status of this species across European fisheries. While weak genetic differences ($F_{CT} = 0.0092$, $P < 0.01$) exist between the seven major oceanographic regions considered (North Sea, Celtic Sea, Cantabrian Sea, Iberian Atlantic, Iberian Mediterranean, Tyrrhenian Sea and Canarian Sea), the deepest