

the origin of this transition zone. The aim of this study is to determine if the 30-33 °S zone coincides with genetic changes in the kelp *Lessonia nigrescens* continuously distributed along the coast. We used a phylogeographic approach based on a comparison of three different DNA markers: mitochondrial (ATP8S), nuclear (ITS) and chloroplastic (Rubisco spacer). The markers agreed to show the existence of two highly divergent clades, occurring on each side of the 30 °S biogeographic transition zone. These possible cryptic species never co-occur in populations (even in the contact zone between the two clades), suggesting a complete reproductive isolation. In this contact zone characterized by a mosaic of populations of the two clades, transplantation experiments have been performed in order to discuss the existence of an ecological barrier.

12:45 – 13:00      ORIGIN OF SOUTHERN HEMISPHERE MYTILUS (MOLLUSCA, BIVALVIA) POPULATIONS: CONTRASTING PATTERNS INFERRED FROM MITOCHONDRIAL AND NUCLEAR DNA.

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Smooth-shelled mussels (*Mytilus* spp.) are antitropically distributed. In the Northern Hemisphere, the *M. edulis* species complex includes *M. edulis*, *M. galloprovincialis* and *M. trossulus*, which are genetically well differentiated. In the Southern Hemisphere, morphological characters, allozymes and intron length polymorphisms, suggested that *Mytilus* spp. populations from South America and Kerguelen Islands were related to *M. edulis* and those from Australasia to *M. galloprovincialis*. On the other hand, a phylogeny of the 16S rDNA mitochondrial locus (16S) demonstrated a clear distinctiveness of southern mussels and suggested their relationships with Mediterranean *M. galloprovincialis*. Here, we analysed the faster evolving locus cytochrome oxidase subunit I (COI). The divergence between haplotypes of southern and northern populations, was confirmed with more support. A strong genetic structure was detected among southern samples. This southern differentiation was partly explained by recent introduction of northern mussels. However, three genetic entities were also revealed among southern endemics populations: 1) South America and Kerguelen Island, 2) Tasmania, 3) New Zealand. The apparent cyto-nuclear discordance suggests two alternative biogeographic scenarios that imply either one or two trans-equatorial migrations.

13:00 – 13:15      DISTRIBUTIONAL AND DEMOGRAPHIC CONSEQUENCES OF PLEISTOCENE GLACIATIONS FOR A MARINE DEMERSAL FISH.

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The Pleistocene glaciations were the most significant historical event during the evolutionary lifespan of most extant species. However, little is known about the consequences of the ice ages on the distribution and demography of marine animals of the Northeastern Atlantic. Because of reduced levels of contemporary gene flow, a marine demersal fish, the sand goby (*Pomatoschistus minutus*; Gobiidae, Teleostei) has been chosen for a phylogeographic study using cytochrome b sequences and eight microsatellites. Because of the absence of a fossil record, only ecological and taxonomical information could be used to calibrate the for gobies typically high evolutionary clock. Reciprocal monophyly occurred between the Mediterranean and Atlantic populations with a divergence dated in the Middle-Pleistocene. The Atlantic Clade contains an Iberian and North Atlantic (NA) Group, from which only the latter did contribute to the most recent postglacial distribution expansion. The historical demography of the Mediterranean Clade was mainly influenced by Middle Pleistocene glaciations in contrast to the two Atlantic ESUs who show for the first time evidence for a recent, most likely post-LGM, expansion.

13:15 -13:30      RECONSTRUCTING THE EVOLUTIONARY AND DEMOGRAPHIC HISTORY OF TWO KELP SPECIES.