

North-Eastern Atlantic since the 1970s. Introduction history in these two areas remained unresolved because introduced populations were found to be genetically monomorphic. For instance, a previous study showed that all 1200 individuals, from 46 introduced American and European populations, shared the exact same multi-locus genotype at 14 microsatellites. To understand this pattern, and elucidate the invasion history of *S. muticum*, we developed a genotyping-by-sequencing method (ddRadseq), for the first time in an invasive seaweed. Large scale libraries were successfully sequenced for 303 individuals from 21 populations (Europe: 9, North-West America: 7 and Japan: 5). Conversely to previous studies, genetic polymorphism was detected in the introduced populations with 2026 SNPs ( $H_e = 0.15$  and  $0.12$  in American and European areas respectively). Nevertheless, much larger diversity was found in the native range and, as expected, severe founder events were evidenced in the introduction ranges. A decreasing number of polymorphic loci was observed between the native range, NW America and Europe (1259, 455 and 232 respectively) as well as strong genetic similarities between America and Europe; both supporting predictions of a secondary introduction in Europe from America where *S. muticum* was introduced earlier. Genetic structure was observed within each introduction range. In Europe, the Mediterranean and Portuguese populations differed significantly and in America, populations from the Puget Sound were highly differentiated from those of southern California. While the link between genetic diversity and invasion success has often been highlighted in marine systems, our results document a success story of a global invasion with limited genetic polymorphism. More generally, they confirm the relevance of genome-wide strategies to investigate the genetic diversity of weakly polymorphic algal species.

## 1OR.5

### EVOLUTIONARY ORIGIN OF CORALLINE RED ALGAE (CORALLINOPHYCIDAE, RHODOPHYTA) INFERRED FROM MULTILOCUS TIME-CALIBRATED PHYLOGENY

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The subclass Corallinophycidae encompasses four orders of benthic red algae unique by the presence of calcite. While the order Rhodogorgonales is a species-poor and mainly a tropical group of gelatinous algae with calcification limited to calcite husks, the orders Sporolithales, Hapalidiales and Corallinales are diverse and widely distributed, characterized by having calcified walls and highly variable morphology. Despite recent clarification of phylogenetic relationships, the origin and evolution of this group is still controversial. Based on the presence of distinctive anatomical features, the literature dated back the first fossil records in the early Cretaceous (140 Mya); however, the presence of ancient extinct taxa resembling coralline red algae could suggest an earlier origin back to the Neoproterozoic (*ca.* 600 Mya). In this study we will apply a molecular evolution approach integrating comprehensive molecular data and fossil records toward estimating the degree of genetic divergence among lineages and their time of evolutionary divergence as well as the age of their most recent common ancestor. This approach will involve phylogenetic analyses of molecular data obtained for seven genes (*cox1*, *psbA*, *rbcL*, 23S rRNA, SSU rRNA, LSU rRNA and EF2), and the revision of available literature on taxonomy, phylogeny and systematics for all the genera currently accepted taxonomically. An exhaustive list of fossil records encompassing different genera will be compiled in order to obtain the most accurate timeline for calibrating the Corallinophycidae phylogeny. Diagnostic characters employed for the distinction at the suprageneric level pertaining to the three phases of their life cycle will be also analysed in order to select characters, which have relevant signal in light of the evolution of coralline algae inferred from our phylogeny.

## 1OR.6

### THE PATHOGENS OF BROWN ALGAE *ANISOLPIDIUM ECTOCARPII* AND *ANISOLPIDIUM ROSENGEII* DEFINE A NEW CLASS OF MARINE ANTERIORLY UNICILIATE OOMYCETES

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