

SUMMARY

In this study, the genetic structure of species and populations of North Atlantic redfish (genus *Sebastes*; Cuvier 1829) was investigated, with special emphasis on the species complex occurring in the Irminger Sea and on the continental slopes of Greenland, Iceland and the Faroe Islands. For this purpose, DNA sequence analysis of the mitochondrial ND3 gene, microsatellite analysis and amplified fragment length polymorphism (AFLP) analysis were used to determine and assess inter- and intraspecific levels of genetic variation and genetic differentiation within and among samples of the four currently known North Atlantic *Sebastes* species *S. mentella* (Travin 1951), *S. marinus* (Linné 1758), *S. fasciatus* (Storer 1854) and *S. viviparus* (Krøyer 1845).

The results from these molecular methods provided evidence that the currently recognised species *S. mentella*, *S. fasciatus* and *S. viviparus* are genetically distinct and therefore represent valid species. Furthermore, the results of the genetic analyses revealed that samples of specimens pre-classified as *S. marinus* according to external morphological characters - collected on the continental slopes of Greenland, Iceland and the Faroe Islands - were genetically extremely heterogeneous. Findings from all methods indicated the existence of two genetically isolated groups of individuals within these samples. These two groups revealed genetic differences of the same order of magnitude as the genetic differences observed between all other North Atlantic *Sebastes* species. One of these genetically distinct groups was found in all areas studied, from Norway to the Flemish Cap, and most likely represents the species *S. marinus*. The occurrence of the second genetically distinct group of individuals suggested that another - apparently cryptic - species of *Sebastes* occurs on the continental slopes of Greenland, Iceland and the Faroe Islands. In particular, the results of the ND3 gene sequence analysis and the microsatellite analysis provided strong evidence of cryptic speciation due to (i) the prevalence of two distinct ND3 gene haplotype lineages with a relatively high level of intraspecific genetic divergence in the *S. marinus* samples from Iceland and Greenland and (ii) the occurrence of two genetically isolated groups of individuals within samples from Greenland, Iceland and the Faroe Islands, identified using microsatellite polymorphisms.

Even though the five groups - representing the four currently recognised species and the newly identified cryptic species - were genetically distinct, the results of the ND3 gene analysis revealed low levels of sequence divergence and a star-like phylogeny. In congruence with the prevalent perception about the phylogeny of this species complex, these results indicated that the North Atlantic *Sebastes* species are closely related and most likely derived from an explosive expansion after a population bottleneck or other demographic effects like founder events. Furthermore, the evolutionary scenario revealed by the phylogenetic analysis of the ND3 gene data provided support for the hypothesis that *S. mentella* is the representative of the most basal lineage of North Atlantic *Sebastes*, which gave rise to the other North

Atlantic *Sebastes* lineages - with *S. viviparus* representing the earliest split of the basal lineage.

Even though the results of the ND3 gene analysis indicated that the North Atlantic *Sebastes* species are closely related and evolved relatively recently, no evidence of recent broad-scale hybridisation between the species was found. The small number of admixed genotypes identified by microsatellite analysis indicated that there is only restricted, if any, hybridisation between *S. marinus*, *S. mentella* and the potential cryptic species in the areas off the Faroe Islands, Iceland and East and West Greenland, as well as between *S. fasciatus*, *S. marinus* and *S. mentella* on the Flemish Cap. Although no evidence of recent hybridisation between the North Atlantic *Sebastes* species was found, the observed incorporation of *S. fasciatus* specific ND3 gene haplotypes into individuals of *S. marinus* on the Flemish Cap - without any evidence of nuclear introgression - indicated that ancient introgressive hybridisation events occurred between *S. marinus* and *S. fasciatus*. Similarly, the observation of *S. mentella* specific ND3 gene haplotypes in several individuals of "giant" *S. marinus* without any evidence of nuclear introgression supports the hypothesis of ancient introgressive hybridisation events between *S. marinus* and *S. mentella*.

The results of the present study have also provided new insights into the intraspecific population structure of *S. mentella*, *S. marinus* and the newly identified potential cryptic species of North Atlantic *Sebastes*. The general patterns of population structure of these species - revealed by microsatellite polymorphism - were congruent with the weak genetic structuring usually reported for marine fish species.

Microsatellite analyses indicated population structure in *S. marinus* and *S. mentella*, but did not reveal such intraspecific structure within the newly identified cryptic species. The results indicated that there are at least three genetically distinct populations of *S. marinus* in the geographic area covered in this study, represented by the samples from (i) the Flemish Cap, (ii) Greenland and (iii) Norway, Iceland and the Faroe Islands. However, there appears to be some overlap in occurrence of the latter two populations in some areas, e.g. on the Dohrn Bank located between Iceland and Greenland and in some areas on the Icelandic shelf.

Similarly, microsatellite analysis indicated at least three separate populations of *S. mentella* in the area covered in the present study: One population occurring on the Flemish Cap, one in the central Irminger Sea and a third population distributed off East Greenland, West Greenland, the southern Irminger Sea and the NAFO areas 1F and 2J. Results from the other two analysis techniques particularly supported the genetic distinctness of *S. mentella* samples from the central Irminger Sea - consisting of relatively large and probably also old individuals - from samples from other regions throughout the North Atlantic. The observed genetic differences could either reflect differences between different cohorts (due to sweepstakes chance effects) or could be due to population separation caused by restricted adult dispersal and/or larval transport. Both hypotheses may be consistent with the findings of this study.

In this study, it was demonstrated that the combination of several molecular markers, in particular the combination of mtDNA sequences and microsatellite data, can provide new

insights into the species and population structure of North Atlantic *Sebastes*. However, given the relatively small number of temporal samples combined with the longevity and mobility of all *Sebastes* species, more temporal replicates are needed before definite conclusions about the population structure of the *Sebastes* species complex in the central North Atlantic can be drawn.