Depth-associated genetic structure within redfish (*Sebastes mentella*) across the North Atlantic: one broad region, two depth strata, two incipient species?

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Summary

Genetic and shape analyses of archived otoliths were used for investigating redfish (*Sebastes mentella*) population structure at depths above and below 500 m, at the scale of the North Atlantic (i.e., Canadian waters, West Greenland shelf, and Irminger Sea). DNA was extracted from 853 archived otoliths sampled in 2009-2011 and was genotyped at 13 microsatellite loci. An individual-based clustering method detected two genetic groups; both groups were observed within each region. Overall, these groups segregated by depth, but juveniles from the genetic “deep group” were usually found at depth shallower than 500 m, in regions close to the continental shelf/slope and (ii) large adult specimens from the genetic “shallow group” strongly dominated all sampling depths in the southwest Irminger Sea and Flemish Cap. No consistent spatial structure was observed within each group, but introgression with *Sebastes fasciatus* was observed on the Flemish Cap within the genetic “shallow-group”. Specimen size disparity between regions resulted in a dominant effect of allometry which confounded otolith shape comparisons between regions. The present study supports the hypothesis of incipient speciation and calls for a better integration of genetic identity, depth, and life-history information into redfish management practices.

Introduction

A shallow-pelagic (above 500 m) and a deep-pelagic (below 500 m) population of *S. mentella* are now recognized in the Irminger Sea and managed separately (Cadri *et al.* 2010). These two depth-segregated populations are increasingly acknowledged as incipient species, whereby the divergence was driven by historical glaciation-related events (Shum *et al.* 2015 and reference therein). Available genetic information suggests that the shallow-pelagic population belongs to a panmictic population distributed from the Irminger Sea to waters off eastern Canada (Roques *et al.* 2002). The deep-pelagic population is still considered to be circumscribed to the Northeast Irminger Sea (Shum *et al.* 2015). Recently, Valentin *et al.* (2014) detected a signal of depth-associated genetic difference in the Labrador Sea, suggesting that the deep-pelagic incipient species might have colonized other deep habitats across the North Atlantic. For the first time, the present study investigates the genetic population structure of *S. mentella* at depths above and below 500 m across a large area of its geographic range. The genetic analyses are complemented with otolith shape analyses.

Materials and Methods

Otoliths were selected from collections sampled during scientific surveys and a commercial sampling trip (2009-2011). The otoliths represented dominant individual length classes in six different geographic areas (Northeast Irminger Sea, Southwest Irminger Sea, West Greenland, Davis & Hudson Straits, Labrador Sea, and Flemish Cap) from two depth strata (i.e. above and below 500 m), noting that samples were only available from one depth stratum in the NE Irminger Sea and in West Greenland. DNA from 853 otoliths was analysed at 13 microsatellite loci (see methods in Valentin *et al.* 2015). A Bayesian clustering method was used to infer population structure (software Structure ver. 2.3.4). An analysis of molecular variance (AMOVA) was carried out (software Arlequin ver. 3.5.1.2) to test for spatial structure among ad hoc defined genetic clusters. The genetic clusters were also compared for differences in otolith shape, using elliptical Fourier shape descriptors for group comparisons in discriminant function analysis (Stransky and MacLellan, 2005).

Results and Discussion

The clustering analysis detected three distinct genetic groups. The first group corresponded to *Sebastes fasciatus* and was only observed in the Labrador Sea and on the Flemish Cap. The two other groups belonged to *S. mentella* (hereafter “group I” and “group II”). Both *S. mentella* groups were observed in every region. Overall, group I dominated the stratum deeper than 500 m, but was rare in the SW-Irminger Sea and on the Flemish Cap, where group II dominated at all depths (Figure 1). Group II
dominated the stratum shallower than 500 m in every region. When observed at depth shallower than 500 m, group I mostly comprised small individuals, which suggests that juveniles of group I prefer shallower depths than their adults. The dominant length classes varied more between regions than between groups; the smallest modes were associated with Davis & Hudson Straits (15.3 - 25.3 cm), while the largest modes were observed in the Irminger Sea (34.5 - 40 cm). Specimen size disparity between regions resulted in a dominant effect of allometry, which confounded otolith shape comparisons between regions (not shown).

The clustering analysis detected genetic admixture with *S. fasciatus* within individuals from *S. mentella* group II. Admixture was higher on the Flemish Cap (q-value = 0.059) than in the five other regions (q-value = 0.009 - 0.019). These observations are consistent with introgressive hybridization between the two species on the Flemish Cap and suggest that *S. mentella* group II is further differentiated as a local population. Otherwise, the AMOVA revealed no significant spatial differentiation within each of the *S. mentella* groups (F_sc < 0), but confirmed a highly significant genetic differentiation between *S. mentella* groups I and II (F_C = 0.029).

Altogether, these observations suggest that the deep-pelagic and shallow-pelagic groups from the Irminger Sea are incipient species which distribution extends across the North Atlantic. The apparent absence of spatial structure within each group does not necessarily mean than there is a single panmictic population; different kind of genetic markers might be necessary for detecting structure within these recently diverged "species" (e.g. Shum et al. 2015). Nevertheless, the present study calls for a better integration of genetic identity, depth, and life-history information into *S. mentella* management practices in the North Atlantic.

**References**


