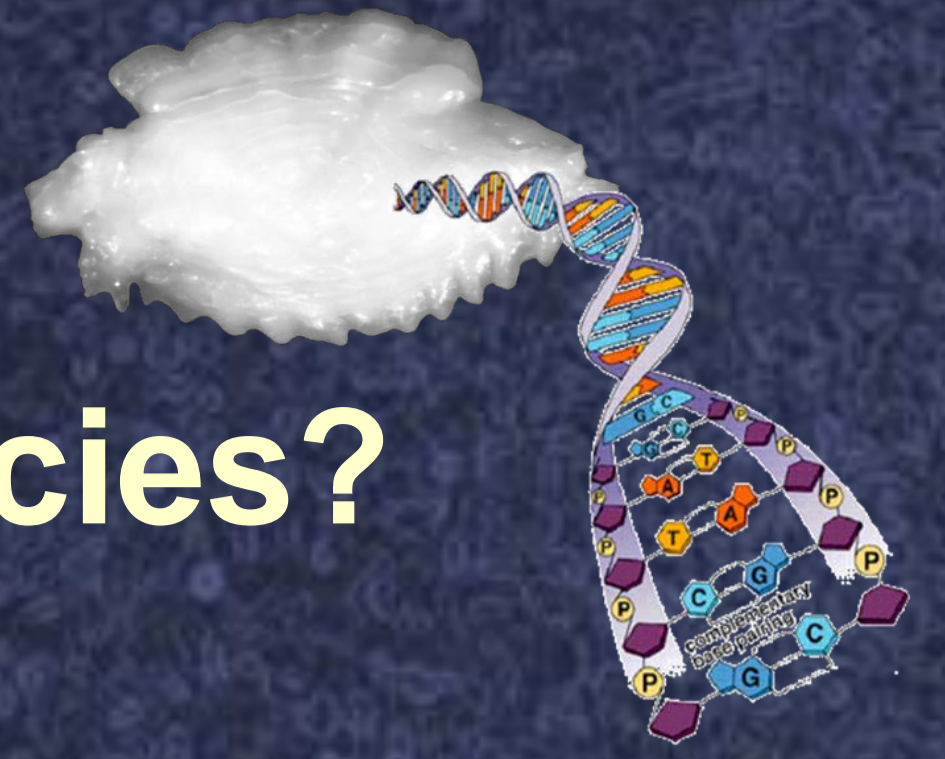




# Depth-associated genetic structure within redfish (*Sebastes mentella*) across the North Atlantic: one broad region, two depth strata, two incipient species?



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## INTRODUCTION

- The shallow-pelagic (above 500 m) and deep-pelagic (below 500 m) populations of *S. mentella* in the Irminger Sea are increasingly acknowledged as incipient species, whereby the divergence was driven by historical glaciation-related events (Shum *et al.* 2015 and ref. therein).
- The shallow-pelagic population is considered to belong to a panmictic population distributed across the North Atlantic (Roques *et al.* 2002), while 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 colonised other deep habitats across the North Atlantic.

## OBJECTIVES

- Investigating the genetic population structure of *S. mentella* across the North Atlantic, at depth above and below 500 m.
- Complementing the genetic analyses with otolith shape analyses.

## MATERIAL AND METHODS

- Selection of 853 archived otoliths representing the dominant individual length classes (for years 2009-2011) in:
  - six geographic areas (Fig. 1),
  - at depth above and below 500m
- DNA extraction from the otoliths and genetic analyses at 13 microsatellite loci (methods in Valentin *et al.* 2015)
- Detection of genetic groups — Bayesian clustering method (software STRUCTURE ver. 2.3.4)
- Test for spatial structure among *ad hoc* defined genetic groups — analysis of molecular variance (AMOVA, software Arlequin ver. 3.5.1.2)
- Otolith shape comparisons between the genetic groups and among regions — discriminant function analysis (DFA) on elliptical Fourier shape descriptors (Stransky and MacLellan, 2005)

## CONCLUSIONS

- The deep-pelagic and shallow-pelagic populations recognised in the Irminger Sea might well be incipient species distributed across the North Atlantic.
- The recent origin of these species might explain the overall absence of geographic structure observed at neutral microsatellite loci. BUT a different kind of genetic markers might reveal spatial structure within these recently diverged “species” (e.g. Shum *et al.* 2015).

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## RESULTS and DISCUSSION

### Genetic analyses based on microsatellites

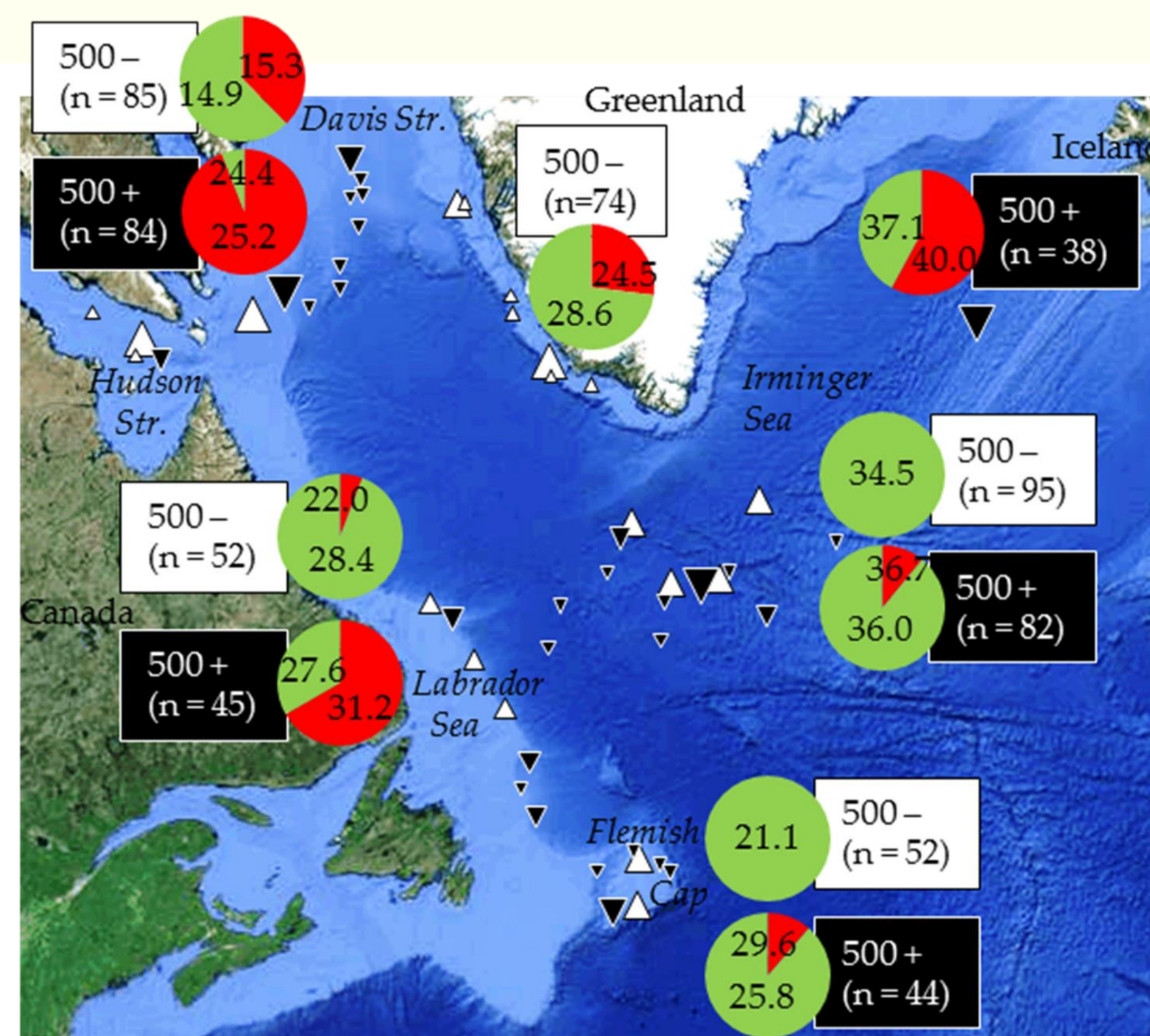


Figure 1. Map of the North Atlantic Ocean showing sampling locations shallower than 500 m (△) and deeper than 500 m (▼); symbol size reflects sample size. Pie charts represent the proportion of redfish belonging to genetic group I and genetic group II, by region and depth stratum (500- for shallower than 500 m and 500+ for deeper than 500 m; n = sample size). Numbers superimposed on the pie charts give the mean individual size (fork length in cm)

### AMOVA

Source of variation	Percentage of variation	F value	P value
Among genetic groups I and II	8.81	0.02900 (F <sub>CT</sub> )	< 0.00001
Among regions within genetic groups	-0.03	0.00033 (F <sub>SC</sub> )	0.61681
Within populations	91.21	0.02957 (F <sub>ST</sub> )	< 0.00001

- confirms a highly significant genetic differentiation between *S. mentella* groups I and II
- suggests an absence of spatial differentiation within each genetic group (but: pairwise F<sub>ST</sub> and estimates of genetic admixture with *S. fasciatus* suggest differentiation of the Flemish Cap population for *S. mentella* group II; not shown)

### Clustering analysis

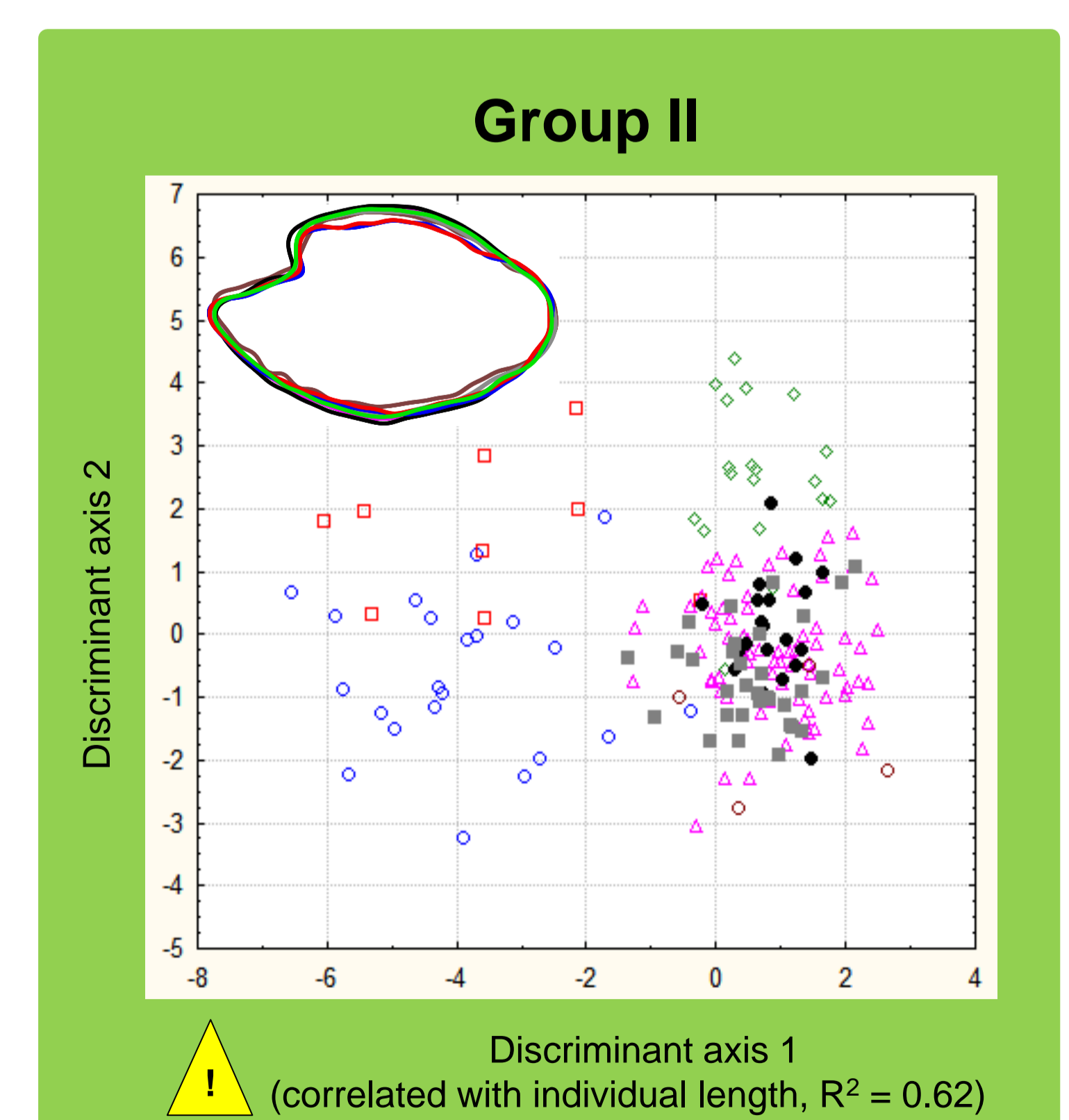
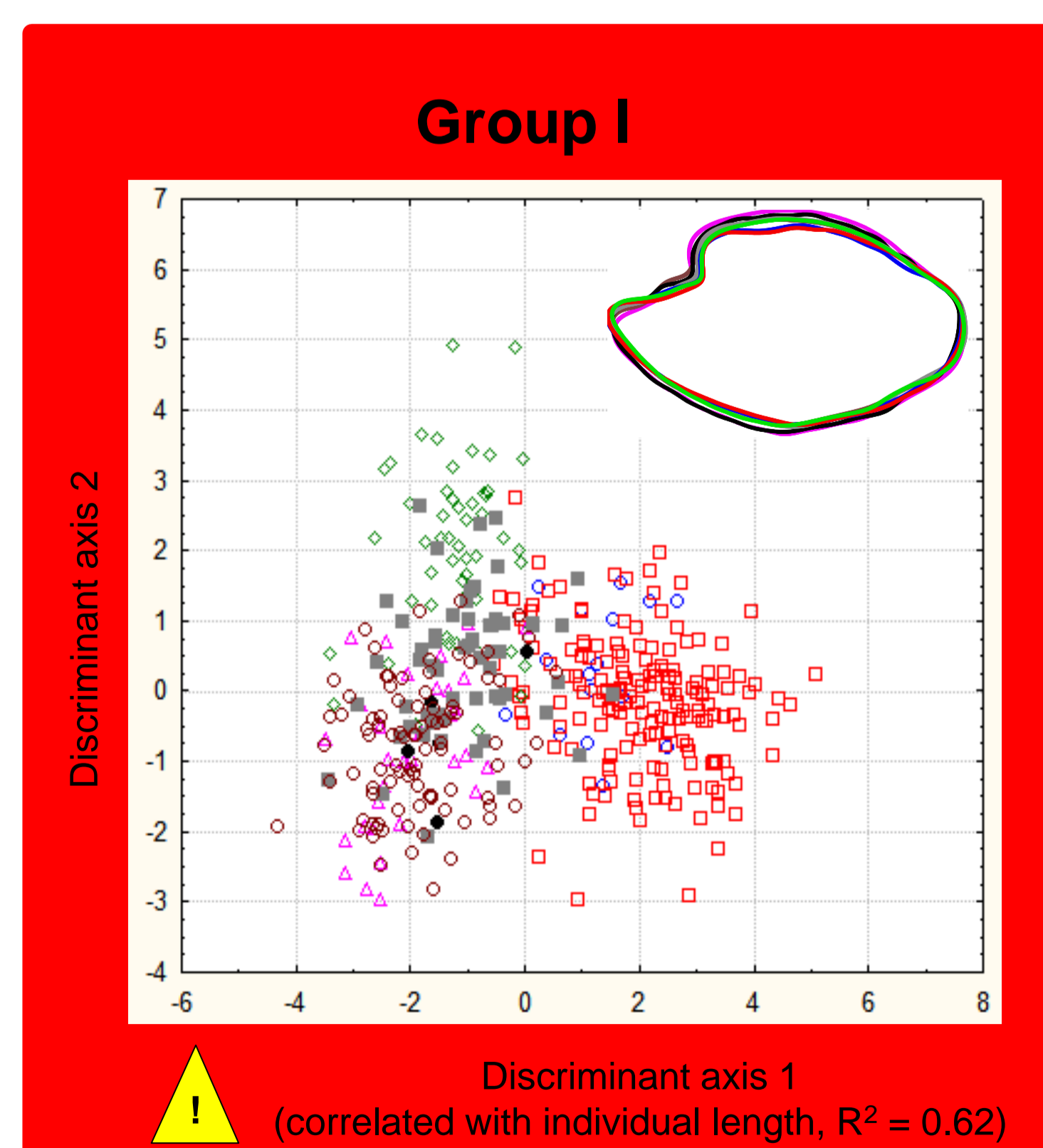
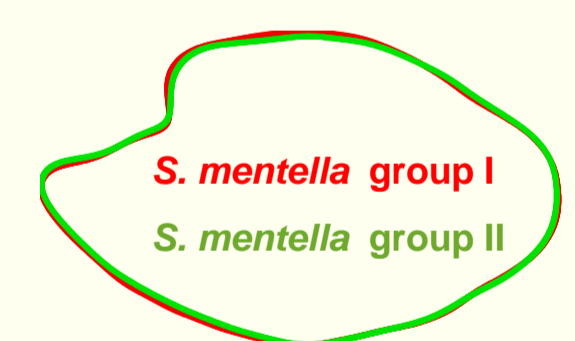
- Detection of two groups of *S. mentella* in all geographic regions (Fig. 1):
  - "group I" dominates the stratum deeper than 500 m (500+), but is rare in the SW Irminger Sea and on the Flemish Cap
  - "group II" dominates the stratum shallower than 500 m (500-), as well as the 500+ stratum in the SW Irminger Sea and on the Flemish Cap
- Juveniles of group I prefer the stratum shallower than 500 m.

### MESSAGE

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.

### Otolith shape comparisons

- The average otolith shape is very similar between the two identified genetic groups.
- Otolith shape differences are observed between regions within each genetic group. BUT the mean specimen size also varies between regions (Fig. 1). THEREFORE the observed shape differences between regions likely reflects allometry rather than population structure.



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