Genetic homogeneity in the deep-sea grenadier *Macrourus berglax* across the North Atlantic Ocean

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ABSTRACT

Paucity of data on population structure and connectivity in deep sea species remains a major obstacle to their sustainable management and conservation in the face of ever increasing fisheries pressure and other forms of impacts on deep sea ecosystems. The roughhead grenadier *Macrourus berglax* presents all the classical characteristics of a deep sea species, such as slow growth and low fecundity, which make them particularly vulnerable to anthropogenic impact, due to their low resilience to change. In this study, the population structure of the roughhead grenadier is investigated throughout its geographic distribution using two sets of molecular markers: a partial sequence of the Control Region of mitochondrial DNA and species-specific microsatellites. No evidence of significant structure was found throughout the North Atlantic, with both sets of molecular markers yielding the same results of overall homogeneity. We posit two non-mutually exclusive scenarios that can explain such outcome: i) substantial high gene flow among locations, possibly maintained by larval stages, ii) very large effective size of post-glacially expanded populations. The results can inform management strategies in this by-caught species, and contribute to the broader issue of biological connectivity in the deep ocean.

1. Introduction

Over the last few decades, it has become routine to use genetic techniques to investigate population structure in marine fishes (Carvalho et al., 2016). The results have led to the widespread rejection of the commonly held view that marine species are mostly panmictic, due to the lack of visible barriers to larval and adult movements (Hauser and Carvalho, 2008). The action of ocean circulation can in fact be two-fold: superficial or deep-water currents can increase gene flow by aiding individual dispersal, especially at the larval stages, but they can also act as a barrier to it, hence favouring divergence between groups.

The vast majority of published studies on marine fish have dealt with coastal pelagic species, given their commercial value and/or the convenient sampling. Yet, the fishing pressure on deep-sea stocks has been steadily increasing since the 1970s (Roberts, 2002), and the depth at which fisheries operate has also been increasing at an average pace of

65.2 m per decade (Morato et al., 2006; Watson and Morato, 2013). Despite being increasingly exploited, deep-sea fish species still suffer from a paucity of data, compared to their coastal and shallow counterparts, which can have deleterious effects on their management (see Clarke et al., 2015 for a quantitative discussion). The assessment of the level and range of spatial structure of exploited species is pivotal for the sustainable harvest and management of species, and failure to identify population structure may result in population collapse (Reiss et al., 2009; Lowe and Allendorf, 2010). Given the typical life history traits of deep-sea species (discrete spawning aggregations, slow growth, late maturity), any fishing pressure might have serious consequences for the persistence of stocks (Baker et al., 2009). Thus, it is important to gather data in order to better understand the population structure and dynamics of these fish stocks, whether they are directly exploited or caught as by-catch. The most recent studies on the dynamics of deep sea fish species have reported lack or very low genetic structuring across wide geographical scales (*Centroscymnus crepidater* in Cunha et al.,