

Genetic population structure in a commercial marine invertebrate with long-lived lecithotrophic larvae: *Cucumaria frondosa* (Echinodermata: Holothuroidea)

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Abstract The patterns of genetic diversity and connectivity were investigated in *Cucumaria frondosa*, the most abundant sea cucumber in the North Atlantic, to assist in the management and conservation of this ecologically important marine invertebrate, which is the target of an emerging fishery. Mitochondrial DNA COI sequences of 334 *C. frondosa* were obtained and analyzed, mainly from its western North Atlantic range, where the commercial fishery is being developed, with complementary sampling in the mid- and eastern North Atlantic. Analysis of molecular variance showed no significant ($P > 0.05$) differences among subpopulations in the western region suggesting that it constitutes one panmictic population. The same analysis showed low, but significant differences between eastern and western Atlantic populations. Coalescent analyses using isolation with migration models and a Bayesian skyline plot indicated historical divergence and a general increase in population size prior to the last glacial maximum and highly asymmetric gene flow (nearly 100 times lower from west to east) between sea cucumbers from North America and Norway. Results suggest that

subpopulations of *C. frondosa* within the western North Atlantic have been highly connected. We propose that aided by the high-connectivity local subpopulations can recover rapidly from natural (i.e., ice ages) or anthropogenic (i.e., overfishing) population declines through recruitment from deep refugia.

Introduction

Cucumaria frondosa is the most common sea cucumber in the North Atlantic and one of the most abundant worldwide (Hamel and Mercier 1996a; Singh et al. 2001). It is therefore a prominent member of cold-temperate and polar benthic communities. While the species has recently become the target of commercial fisheries in eastern North America (Hamel and Mercier 2008), data on its population connectivity and genetic patterns are lacking.

An understanding of genetic patterns and population connectivity with respect to the biology of a species is crucial to fisheries management. Commercially harvested marine invertebrates with low mobility are particularly susceptible to Allee effects whereby decreasing densities of sexually mature adults cause a proportionate decline in the number of juveniles produced (Stephens and Sutherland 1999; Uthicke et al. 2009) thus reducing their ability to recover from exploitation. Sea cucumber fisheries provide striking evidence of this. Since all commercial species are broadcast spawners, lowering adult densities increases the distance between individuals and reduces fertilization rates and subsequent recruitment (Leviton and Petersen 1995). It has been shown that relatively low annual catches of 5% of virgin biomasses of *Holothuria whitmaei* on the Great Barrier Reef resulted in severely reduced stocks with very slow recovery rates (Uthicke 2004). It is therefore of

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