Phylogeography of the Ocean Quahog (Arctica islandica)

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Introduction

Arctica islandica (Lamy, 1787), commonly called the ocean quahog, is a northern Atlantic clam that is commercially harvested in the USA, Canada, and Iceland. Larger specimens (80-90 mm in length) are often 40-100 years old and have a reported growth rate of 1 mm/year (Foster 1981; Murawski et al. 1992). Kraus et al. 1992, Whiinhud 1999). It takes an individ-ual 5-10 years to reach maturity (Thompson et al. 1980; Rosen et al. 1992) and recruitment rates can be low and unpredictable (NEFSC 1998). This disjunctive bivalve produces planktonic larvae that are present in waters off New England U.S.A. throughout much of the year (Lonnouff 1952), Maine 1953). Geographical differences in growth rates (compare Murawski et al. 1992, Kraus et al. 1992, Whiinhud 1999) and population size-structure (NEFSC 1995) have been reported, however little is known about the population genetic structure of this species.

Materials and Methods

Material was obtained during the 1999 National Marine Fisheries Service (NMFS) clam survey or mailed to us by colleagues and was subsequently freeze-stored with a vented reactor. Us-ing standard PCR and sequencing techniques, we obtained 385 nucleotides of the mitochondrial common haplotype among western Atlantic samples (64.4% of individuals sampled excluding specimens and the Faroe Islands show mixed affinities. Figure 2 shows a parsimony network (sensu Arctoa et al. 1997) illustrating the differences between the observed haplotypes. For the most common haplotype among western Atlantic samples (84.4% of individuals sampled excluding Iceland) and occurs in a central position in the parsimony network, suggesting that it is the ancestral most widespread. In addition to the parsimony network, we also employed likelihood analysis to determine the evolutionary history of observed haplotypes (Figure 3).

Results

The cyt b data delimited 11 haplotypes (Table 1) with 0.26% - 8.1% nucleotide difference (calculated by MEGA software package). Among them, only 3 haplotypes were detected in 30 specimens collected along the USA coastline, compared to five haplotypes from nine Icelandic individuals. Baseline characteristics among western and eastern populations are significantly different (p < 0.001). Also Icelandic populations appear to be more genetically similar to western Atlantic populations and the Faroe Islands show mixed affinities. Figure 2 shows a parsimony network (sensu Arctoa et al. 1997) illustrating the differences between the observed haplotypes. For the most common haplotype among western Atlantic samples (84.4% of individuals sampled excluding Iceland) and occurs in a central position in the parsimony network, suggesting that it is the ancestral most widespread. In addition to the parsimony network, we also employed likelihood analysis to determine the evolutionary history of observed haplotypes (Figure 3).

Discussion

Whereas present-day distributions of intertidal species have been shaped by glacial events (e.g., Johannesen 1988; Fommin and Kessing 1993, Cunningham et al. 1992; Caldeux et al. 1996; Bond 1996). Qrav and Weidick 1997). Observations in nearshore to coastal ecosystems in the Barents Sea (Bergen, Norway) and Kattegat Sea (inland near Copenhagen, Denmark) confirm the presence of A. islandica in the Barents Sea (Galkin and Weykamp 1998). The cyt b data delimited 11 haplotypes (Table 1) with 0.26% - 8.1% nucleotide difference (Newport b 2002; Wyeckamp 1998). The tree was rooted with haplotype X. Branch lengths are drawn proportional to 26 changes to the inferred amount of nucleotide change. (GeRT model with estimated parameters). The tree was rooted with haplotype X. Branch lengths are drawn proportional to the inferred amount of nucleotide change.

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Fig. 1. Artica islandica. The present day and past distribution. We are not certain of the range or age of fossil shelf clams along the eastern coast of Greenland although Pleistocene deposits are reported from ice-free fjords. (Based on Weidick and Weliksi in press). The moving and range in southern Greenland. Note the shell remains on the Taymyr peninsula date back to the Pleistocene, but shells west of the Obsk peninsula may be considerably younger (<10,000 YBP; Table 2). Where present-day distributions of intertidal species have been shaped by glacial events (e.g., Johannesen 1988; Fommin and Kessing 1993, Cunningham et al. 1992; Caldeux et al. 1996; Bond 1996). Qrav and Weidick 1997). Observations in nearshore to coastal ecosystems in the Barents Sea (Bergen, Norway) and Kattegat Sea (inland near Copenhagen, Denmark) confirm the presence of A. islandica in the Barents Sea (Galkin and Weykamp 1998).

Fig. 2. Arctica islandica. Parsimony network of cytochrome b haplotypes. Line crossing branches represent the estimated number of nucleotide differences between haplotypes. Haplotype distributions are shown in Table 1.

Fig. 3. Phylogeographic analysis of Arctica islandica haplotypes. Zatsepin and Filatova (1961). Information on occurrences in high latitude archipelagoes (e.g., Franz Josef Land and Novaya Zemlya) is lacking. This figure is a compilation of several references (Nicol 1951; Zatsepin and Filatova 1961; Ref Doc 98-15, pp 171-244). The cyt b data delimited 11 haplotypes (Table 1) with 0.26% - 8.1% nucleotide difference (calculated by MEGA software package). Among them, only 3 haplotypes were detected in 30 specimens collected along the USA coastline, compared to five haplotypes from nine Icelandic individuals. Baseline characteristics among western and eastern populations are significantly different (p < 0.001). Also Icelandic populations appear to be more genetically similar to western Atlantic populations and the Faroe Islands show mixed affinities. Figure 2 shows a parsimony network (sensu Arctoa et al. 1997) illustrating the differences between the observed haplotypes. For the most common haplotype among western Atlantic samples (84.4% of individuals sampled excluding Iceland) and occurs in a central position in the parsimony network, suggesting that it is the ancestral most widespread. In addition to the parsimony network, we also employed likelihood analysis to determine the evolutionary history of observed haplotypes (Figure 3).

Fig. 4. Distribution of A. islandica in the Barents Sea (Bergen, Norway) and Kattegat Sea (inland near Copenhagen, Denmark) confirm the presence of A. islandica in the Barents Sea (Galkin and Weykamp 1998). The cyt b data delimited 11 haplotypes (Table 1) with 0.26% - 8.1% nucleotide difference (Newport b 2002; Wyeckamp 1998). The tree was rooted with haplotype X. Branch lengths are drawn proportional to 26 changes to the inferred amount of nucleotide change. (GeRT model with estimated parameters). The tree was rooted with haplotype X. Branch lengths are drawn proportional to the inferred amount of nucleotide change.