Biochemical Systematics and Ecology 65 (2016) 66–71

Contents lists available at ScienceDirect

Biochemical Systematics and Ecology

journal homepage: www.elsevier.com/locate/biochemsyseco

Genetic homogeneity of the geoduck clam *Panopea generosa* in the northeast Pacific

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ARTICLE INFO

Article history:
Received 14 October 2015
Received in revised form 3 February 2016
Accepted 6 February 2016
Available online xxx

Keywords:
Panopea generosa
Mitochondrial genes
Microsatellite loci
Genetic homogeneity
Washington
Baja California

ABSTRACT

Geoduck clams are a valuable natural resource along the northeast Pacific, which makes the assessment of the biological and genetic status of their populations a key element to provide a basis for their proper management and conservation. In the present study, we assess the genetic variability and connectivity of *Panopea generosa* Gould, 1850 among four localities in the northeast Pacific using mitochondrial (DNA sequences from COI and COIII) and nuclear (five microsatellite loci) data. We found no evidence of genetic differentiation among localities encompassing scales of 100s to 1000s of kilometers along the northeast Pacific, which is consistent with a large effective population size and extensive gene flow in the absence of significant barriers acting on the larval stages. Our genetic findings and phenotypic evidence are consistent with the existence of a single management unit shared by Canada, the United States and Mexico, but further studies with increased geographic and genetic sampling are warranted to better estimate the extent and direction of gene flow to help in international management and conservation measures of this valuable resource.

1. Introduction

Many northeast Pacific coastal species have wide geographic ranges spanning from Canada to Mexico; of particular interest are those of commercial relevance that constitute shared fishery resources, for which trans-border patterns of connectivity impinge on the population dynamics of exploited stocks in a particular country (Selkoe et al., 2007). For demersal or sessile species, the predominant dispersal mechanism is through planktonic larval drift, which should produce genetic patterns strongly influenced by oceanographic circulation and physical barriers to dispersal (Rocha-Olivares and Vetter, 1999; Selkoe et al., 2010; Alberto et al., 2011).

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http://dx.doi.org/10.1016/j.bse.2016.02.003
0305-1978/

Geoduck clams are large sessile infaunal bivalves representing a valuable natural resource along the northeast Pacific. *Panopea generosa* Gould, 1850, formerly recognized as *Panopea abrupta* Conrad, 1849 (Vadopalas et al., 2010), is commercially exploited in British Columbia, Canada, Washington state in the U. S., and in Baja California, México; where it sustains multi-million dollar industries (Khan, 2006; SAGARPA, 2007). The commercial fishery in Mexico is the most recently established and catches are generally exported to Asian markets, hence it is a source of foreign currency for the region (Rocha-Olivares et al., 2010; Aragón-Noriega et al., 2012). Given its economic importance for the three countries sharing the resource, the assessment of connectivity levels among geoduck populations is of great value to inform resource managers about the potential demographic and evolutionary independence of exploited stocks, as they are a priori conceptualized as metapopulations in Mexican management plans (Diario Oficial de la Federación, 2012).

Genetic analyses of *P. generosa* from Canada and the U. S. began in the late 1990s and early 2000's and have continued to date (e.g., Vadopalas et al., 2012). In contrast, most genetic information on both geoduck species exploited in Mexico (*P. generosa* and *Panopea globosa* Dall, 1898) has only recently begun to be produced (Rocha-Olivares et al., 2010; Suárez-Moo et al., 2013); however, no study is available on the large scale connectivity patterns of *P. generosa* throughout most of its range in the northeast Pacific. Genetic data from northern populations in Alaska, British Columbia and Washington revealed complex scale-dependent patterns of genetic heterogeneity among samples of adult clams (Vadopalas et al., 2004; Miller et al., 2006). More recent efforts to test temporal genetic heterogeneity among year-classes found patterns inconsistent with sweepstakes recruitment (Vadopalas et al., 2012). Our goal is to provide a first order comparison of the level of genetic variation and differentiation of *P. generosa* samples from Mexico and distant clams sampled close to the northern end of its range (Washington, U. S.). Our results will help to establish the biological basis for the proper management and international conservation of this valuable commercial clam.

2. Materials and methods

2.1. Sampling and DNA extraction

Geoduck clams *P. generosa* were sampled from the local fishery catch harvested in four locations in the Northeast Pacific: Alden Bank, Washington, USA (PGAB, 48°49′43.2″N 122°49′50.6″W, n = 37, date 05/2000), Islas Coronado (PGIC, 32°25′00″N 117°15′00″W, n = 43, date 05/2008), San Quintín (PGSQ, 30°23′22.02″ 115°54′47.2″W, n = 40, date 04/2008) and Santa Rosaliíta (PGSR, 28°40′00″N 114°15′57″W, n = 32, date 01/2011), Baja California, Mexico (Fig. 1). Siphon muscle samples were

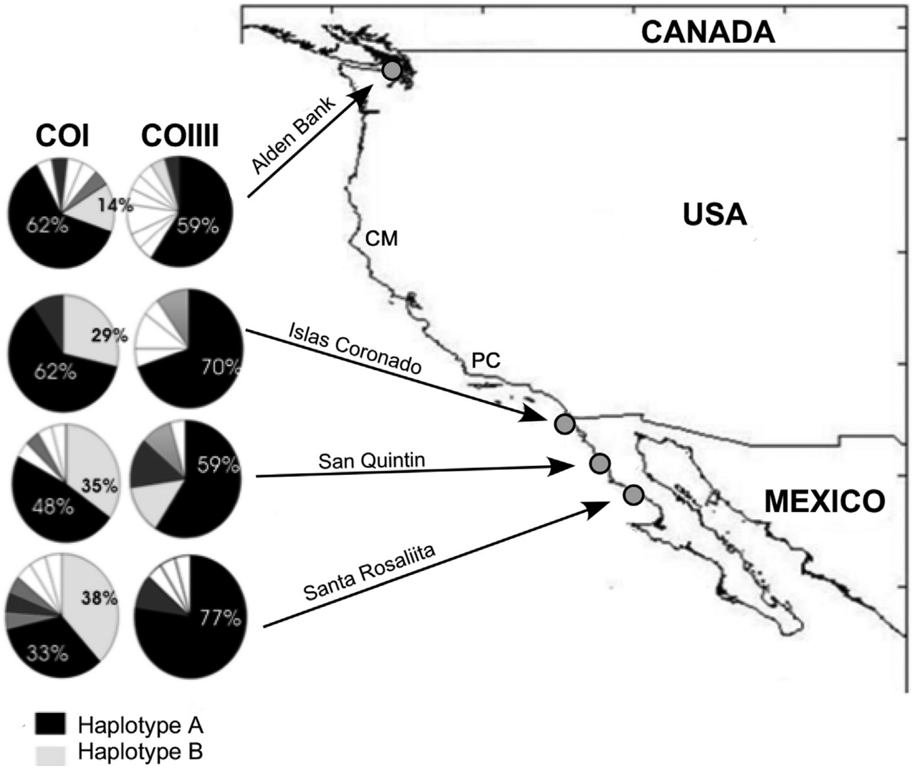

Fig. 1. Sampling localities of *P. generosa* in Washington, USA (Alden Bank) and Baja California, Mexico (Islas Coronado, San Quintin, and Santa Rosaliíta). Marine biogeographic breaks are Cape Mendocino (CM, 40°26′N, 124°24′W), Point Conception (PC, 34°26′N, 120°28′W). Also shown are pie diagrams of mitochondrial COI and COIII haplotypes.