Outgroup species, description reference, and GenBank accession numbers from Table 2, from Janosik & Halanych (2013) (Antarctic Inverts project)

Website: https://www.bco-dmo.org/dataset/671822
Data Type: Cruise Results
Version:
Version Date: 2016-12-27

Project
» Genetic connectivity and biogeographic patterns of Antarctic benthic invertebrates (Antarctic Inverts)

Contributors	Affiliation	Role
Halanych, Kenneth M.	Auburn University	Principal Investigator
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Dataset Description

This dataset was published as Table 2 from Janosik et al (2013). It contains a list of outgroup species with their description reference and NCBI GenBank accession numbers.

Related Reference: Janosik, A.M., and K.M. Halanych,. 2013. Seeing stars: a molecular and morphological investigation of the evolutionary history of Odontasteridae (Asteroidea) with description of a new species from the Galapagos Islands. Marine Biology.160:821-841. DOI 10.1007/s00227-012-2136-x

Related Datasets:
Janosik_2013_T1: Odontasteridae species collection information
Janosik_2013_T3: matrix of Odontasteridea morphological characters

>

Methods & Sampling

From Janosik et al (2013):

Specimen collection
Specimens were obtained from the Division of Echinoderms, Smithsonian Institution National Museum of Natural History (USNM) in Washington, DC, the Department of Invertebrate Zoology, California Academy of Sciences (CASIZ), San Francisco, California, and the National Institute of Water and Atmospheric Research (NIWA), New Zealand (Table 1). Most specimens were dried. Antarctic species were collected during two five-week research cruises aboard the R/V Laurence M. Gould in November/December of 2004 and May/June of

2006. Images of D. clarki were provided by NIWA.

Molecular data
Molecular methods follow Janosik et al. (2011). DNA extraction of specimens was performed by using DNeasy Tissue Kit (Qiagen). Two mitochondrial DNA markers (16S and COI) were utilized to estimate the evolutionary history of Odontasteridae. Specifically, a 508-bp region of the mitochondrial 16S gene was amplified using the 16SarL and 16SbrH primers and protocols of Palumbi et al. (1991). For the same individuals, a 627-bp region of the COI gene was amplified using primers designed to work with Odontaster COI-Ast 22F (5'-TTYTCNACNAAACA YAAGGA-3') and COI-Ast722R (5'-GGRTGNCCRAAR AAYCARAA-3') (Janosik et al. 2011). Amplified products were purified with either a Qiagen QIAquick Gel Extraction Kit (Qiagen Inc.) or a Montage PCR Filter Units (Millipore) according to the manufacturer's directions. Purified products were then sequenced bidirectionally on a Beckman CEQ 8000 Genetic Analysis System (Beckman Coulter). Sequences were edited and aligned using Sequencher 4.6 (Gene CodesCorporation) andBioedit v.7.0.8 (Hall 1999). COI sequences were translated according to the echinoderm mitochondrial DNA code to aid in proofreading. Genbank accession number is listed in Table 2.

Based on current understandings of sea star relationships (Blake 1987; Mah and Foltz 2011), Bathybiaster loripes, Chaetaster moorei, Crossaster papposus, Luidia foliolata, Mediaster aequalis, and Solaster stimpsoni were selected for the outgroup, and these sequences were downloaded from GenBank (www.ncbi.nlm.nih.gov/genbank/) (Table 2).

Data Processing Description

BCO-DMO Processing notes:
- added conventional header with dataset name, PI name, version date
- modified parameter names to conform with BCO-DMO naming conventions
- removed special characters (')

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Data Files

File
Janosik_2013_T2.csv (Comma Separated Values (.csv), 1.30 KB) MD5:704268aac45b43da57e48b08c3c02938 Primary data file for dataset ID 671822

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Parameters

Parameter	Description	Units
taxon	taxonomic genus and species name	unitless
reference	published taxonomic description of the species	unitless
NCBI_accession	NCBI GenBank accession number	unitless
link_NCBI_accession	link to GenBank accession page	unitless

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Instruments

Dataset-specific Instrument Name	Beckman CEQ 8000 Genetic Analysis System (Beckman Coulter)
Generic Instrument Name	Automated DNA Sequencer
Dataset-specific Description	Purified products were then sequenced bidirectionally
Generic Instrument Description	General term for a laboratory instrument used for deciphering the order of bases in a strand of DNA. Sanger sequencers detect fluorescence from different dyes that are used to identify the A, C, G, and T extension reactions. Contemporary or Pyrosequencer methods are based on detecting the activity of DNA polymerase (a DNA synthesizing enzyme) with another chemoluminescent enzyme. Essentially, the method allows sequencing of a single strand of DNA by synthesizing the complementary strand along it, one base pair at a time, and detecting which base was actually added at each step.

Dataset-specific Instrument Name	
Generic Instrument Name	Thermal Cycler
Generic Instrument Description	A thermal cycler or "thermocycler" is a general term for a type of laboratory apparatus, commonly used for performing polymerase chain reaction (PCR), that is capable of repeatedly altering and maintaining specific temperatures for defined periods of time. The device has a thermal block with holes where tubes with the PCR reaction mixtures can be inserted. The cycler then raises and lowers the temperature of the block in discrete, pre-programmed steps. They can also be used to facilitate other temperature-sensitive reactions, including restriction enzyme digestion or rapid diagnostics. (adapted from http://serc.carleton.edu/microbelife/research_methods/genomics/pcr.html)

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Deployments

Halanych_lab_2011-16

Website	https://www.bco-dmo.org/deployment/671488
Platform	Auburn University lab
Start Date	2011-08-01
End Date	2016-07-31
Description	Invertebrate genomics

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Project Information

Genetic connectivity and biogeographic patterns of Antarctic benthic invertebrates (Antarctic Inverts)

Coverage: Antarctica

Extracted from the NSF award abstract:

The research will explore the genetics, diversity, and biogeography of Antarctic marine benthic invertebrates, seeking to overturn the widely accepted suggestion that benthic fauna do not constitute a large, panmictic population. The investigators will sample adults and larvae from undersampled regions of West Antarctica that, combined with existing samples, will provide significant coverage of the western hemisphere of the Southern Ocean. The objectives are: 1) To assess the degree of genetic connectivity (or isolation) of benthic invertebrate species in the Western Antarctic using high-resolution genetic markers. 2) To begin exploring planktonic larvae spatial and bathymetric distributions for benthic shelf invertebrates in the Bellinghausen, Amundsen and Ross Seas. 3) To continue to develop a Marine Antarctic Genetic Inventory (MAGI) that relates larval and adult forms via DNA barcoding.

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Funding

Funding Source	Award
NSF Office of Polar Programs (formerly NSF PLR) (NSF OPP)	PLR-1043745
NSF Office of Polar Programs (formerly NSF PLR) (NSF OPP)	PLR-1043670

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