Sea spider Pallenopsis sampling sites and COI NCBI accessions from Table 1, Harder et al (2016) Polar Biology (Antarctic Inverts project)

Website: https://www.bco-dmo.org/dataset/671927
Data Type: Cruise Results
Version:
Version Date: 2016-12-02

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

Contributors	Affiliation	Role
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Dataset Description

This dataset was published as Table 1 from Harder et al (2016). It contains collection information and GenBank COI accession links for sea spider of the genus specimens Pallenopsis from the Southern Ocean and around the southern tip of S. America.

Related Reference: Harder, A.M., K.M. Halanych and A.R. Mahon. Diversity and distribution within the sea spider genus Pallenopsis (Chelicerata: Pycnogonida) in the Western Antarctic as revealed by mitochondrial DNA. Polar Biol (2016) 39:677-688. DOI 10.1007/s00300-015-1823-8.

Methods & Sampling

From Harder et al (2016):

Sample collection
Samples were collected in 2006 and 2012-2013 aboard the RVIB Nathaniel B. Palmer and the ASRV Laurence M. Gould. Pycnogonids were obtained using a Blake trawl or epibenthic sled, and subsequently identified to genus level prior to preservation and shipment in ~95 % ethanol. Individuals were identified to species level according to standard pycnogonid taxonomic procedures (Child 1995; Weis and Melzer 2012b; Weis et al. 2014). In total, 64 specimens belonging to the genus Pallenopsis were collected and identified from 21 sampling sites, ranging from 53 16'S to 76 59'S and from 140 26'E to 37 26'W (Fig. 1). Sampling site locality information, including depth (when available), and GenBank accession numbers for all sequences generated for use in our analyses are provided in Table 1.

Molecular techniques

A tissue sample was taken from each individual as a 1-cm piece from the first tibial segment, and DNA was extracted from these using a Qiagen DNeasy Blood & Tissue Kit (Qiagen Inc., Valencia, CA) per manufacturer's instructions. A ~650 bp portion of the cytochrome c oxidase subunit I (COI) gene was amplified using LCO-1490 (Folmer et al. 1994) and HCOoutout (Prendini et al. 2005). Each PCR mixture consisted of 1x PCR buffer, 0.75 U Taq DNA polymerase (5 PRIME Inc., Gaithersburg, MD), 2.5 mM Mg^+2, 10 nmol of each dNTP, 1 ul of template DNA, 0.5 uM of each primer, and water to 25 ul. The PCR cycling program began with an incubation at 94C for 2 min, followed by 38 cycles of 94C for 20 s, 46C for 30 s, and 65 C for 80 s, and concluded with a final extension at 65C for 7 min. Successful amplification was confirmed by visualizing PCR products on a 1% agarose gel stained with ethidium bromide. Target DNA was gel extracted and purified using a Qiagen QIAquick Gel Extraction Kit (Qiagen Inc., Valencia, CA) according to the manufacturer's recommendations. Bidirectional Sanger sequencing of amplicons was performed atHigh Throughput Genomics Center (Seattle, WA). Obtained sequences were assembled and screened using Sequencher version 5.29 sequence analysis software (Gene Codes Corporation, Ann Arbor, MI), and aligned using Clustal W v1.8 (Thompson et al. 1994) in BioEdit v7.2.5 (Hall 1999). COI sequences were translated into amino acid sequences to further screen for sequencing error, including checking for frameshift mutations and stop codons.

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
- added links to NCBI accession pages
- converted lat and lon to decimal degrees
- replaced '-' with nd (no data)
- replaced special characters with ascii characters

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Data Files

File
Harder_2016_T1_sites.csv (Comma Separated Values (.csv), 16.93 KB) MD5:23eeb715975d2ea6c89e62611c98febd Primary data file for dataset ID 671927

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Parameters

Parameter	Description	Units
species	sea spider genus & species name	unitless
lat	latitude; north is positive	decimal degrees
lon	longitude; east is positive	decimal degrees
locality_source	lacation of collection or reference source	unitless
depth	depth collected	meters
GenBank_accession	NCBI GenBank accession number	unitless
accession_link	link NCBI GenBank accession page	unitless

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Instruments

Dataset-specific Instrument Name	
Generic Instrument Name	Automated DNA Sequencer
Dataset-specific Description	Sequencing performed at High Throughput Genomics Center (Seattle, WA)
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	Blake trawl
Generic Instrument Name	Beam Trawl
Generic Instrument Description	A beam trawl consists of a cone-shaped body ending in a bag or codend, which retains the catch. In these trawls the horizontal opening of the net is provided by a beam, made of wood or metal, which is up to 12 m long. The vertical opening is provided by two hoop-like trawl shoes mostly made from steel. No hydrodynamic forces are needed to keep a beam trawl open. The beam trawl is normally towed on outriggers, one trawl on each side. While fishing for flatfish the beam trawl is often equipped with tickler chains to disturb the fish from the seabed. For operations on very rough fishing grounds they can be equipped with chain matrices. Chain matrices are rigged between the beam and the groundrope and prevent boulders/stones from being caught by the trawl. Shrimp beam trawls are not so heavy and have smaller mesh sizes. A bobbin of groundrope with rubber bobbins keeps the shrimp beam trawl in contact with the bottom and gives flatfish the opportunity to escape. Close bottom contact is necessary for successful operation. To avoid bycatch of most juvenile fishes selectivity devices are assembled (sieve nets, sorting grids, escape holes). While targeting flatfish the beam trawls are towed up to seven knots, therefore the gear is very heavy; the largest gears weighs up to 10 ton. The towing speed for shrimp is between 2.5 and 3 knots. (from: http://www.fao.org/fishery/geartype/305/en)

Dataset-specific Instrument Name	
Generic Instrument Name	Epibenthic Sled
Generic Instrument Description	An epibenthic sled is a semi-quantitative bottom-sampling device designed to trawl just above the bottom at the sediment water interface (the epibenthic zone). The sled consists of a rectangular steel frame with a mesh net (often more than one) attached to it. Towed along the ocean floor, its weight scrapes into the benthos, collecting any organisms on the surface or in the first few centimeters of sediment. It also collects the organisms in the water column just above the benthos. Descriptions from WHOI and Census of Marine Life.

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

LMG1312

Website	https://www.bco-dmo.org/deployment/666516
Platform	ARSV Laurence M. Gould
Report	http://dmoserv3.bco-dmo.org/jg/serv/BCO-DMO/OA_Antarctic_organisms/727518.html0%7Bdir=dmoserv3.whoi.edu/jg/dir/BCO-DMO/OA_Antarctic_organisms/,info=dmoserv3.bco-dmo.org/jg/info/BCO-DMO/OA_Antarctic_organisms/mg_ca_ratios%7D
Start Date	2013-11-22
End Date	2013-12-20
Description	Benthic invertebrate studies

NBP1210

Website	https://www.bco-dmo.org/deployment/568987
Platform	RVIB Nathaniel B. Palmer
Report	http://dmoserv3.bco-dmo.org/jg/serv/BCO-DMO/OA_Antarctic_organisms/727518.html0%7Bdir=dmoserv3.whoi.edu/jg/dir/BCO-DMO/OA_Antarctic_organisms/,info=dmoserv3.bco-dmo.org/jg/info/BCO-DMO/OA_Antarctic_organisms/mg_ca_ratios%7D
Start Date	2013-01-06
End Date	2013-02-09
Description	Seaglider AUV-SG-503-2012 was recovered on this cruise.

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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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