GenBank accession numbers used in phylogenetic analysis in Table S1, Halanych et al (2013) Nature Comm. (Antarctic Inverts project)

Website: https://www.bco-dmo.org/dataset/671551
Data Type: Cruise Results
Version:
Version Date: 2016-12-22

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 Supplementary Table 1 from Halanych et al (2013). It contains GenBank accession links of hemichordate and echinoderm specimens collected globally from 2001 to 2013.

Related Reference: Halanych, K.M., J.T. Cannon, A.R. Mahon, B.J. Swalla, C.R. Smith. 2013. Tubicolous acorn worms from Antarctica. Nature Communications DOI://10.1038/ncomms3738

Related Dataset: Halanych_2013: Video of acorn worm tubes

Methods & Sampling

Scientific research expeditions were aboard the RVIB Nathaniel B. Palmer in 2008 to the Antarctic Peninsula and 2013 to the Ross Sea. Benthic samples were obtained from the Ross Sea by a Blake trawl with a 2-m opening. Sampled were sorted and preserved on deck. Sequencing and phylogenetic protocols of 18S and 16S ribosomal DNA used the standard procedures3. PCR amplification used primers 16Sar 50-CGCCTGTTTATCAAAAA CAT-30 and 16Sbr 50-CCGGTCTGAACTCAGATCACGT-30 for 16S ribosomal DNA and 18e 50-CTGGTTGATCCTGCCAGT-30 and 18 P 50-TAATGATCCTTCCGCAGGTTCACCT-30 .

Maximum likelihood and Bayesian analyses (both used the best fitting model GTR+I+G) were conducted with RaxML version 7.3.9 (ref. 19) (5,000 bootstrap replicates) and MrBayes version 3.2.0 (ref. 20) (four independent runs for 5,000,000 generations sampled every 100 generations), respectively.

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 trailing blank spaces
- replaced cells with hyphen with nd (no data)
- added links to NCBI accession pages

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Data Files

File
Halanych_2013_T1.csv (Comma Separated Values (.csv), 12.43 KB) MD5:a568f54b8bbb02145f894536079187e5 Primary data file for dataset ID 671551

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Parameters

Parameter	Description	Units
taxon	more specific taxonomic group	unitless
species	taxonomic genus and species name	unitless
accession_rDNA_18S	18S NCBI GenBank accession number	unitless
accession_rDNA_16S	16S NCBI GenBank accession number	unitless
link_accession_rDNA_18S	link to 18S NCBI GenBank accession	unitless
link_accession_rDNA_16S	link to 16S NCBI GenBank accession	unitless

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Instruments

Dataset-specific Instrument Name	Illumina MiSeq (San Diego, CA) at Auburn University
Generic Instrument Name	Automated DNA Sequencer
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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