

Hemichordata and Echinodermata NCBI accessions, Table 2, Cannon et al (2013) Biol. Bull. (Antarctic Inverts project)

Website: <https://www.bco-dmo.org/dataset/671459>

Data Type: Cruise Results

Version: 1

Version Date: 2016-12-22

Project

» [Genetic connectivity and biogeographic patterns of Antarctic benthic invertebrates](#) (Antarctic Inverts)

Contributors	Affiliation	Role
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Abstract

This dataset was published as Table 2 from Cannon et al (2013). It contains GenBank accession links of hemichordate and echinoderm specimens collected globally from 2001 to 2013.

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Coverage

Temporal Extent: 2001 - 2013

Methods & Sampling

from Cannon et al (2013) Biol Bull:

Collection:

Eleven specimens sequenced in this study were collected in September 2011 during Senckenberg's German Center for Marine Biodiversity Research (DZMB) IceAGE expedition led by Dr. Saskia Brix aboard the R/V Meteor, which circled Iceland, crossing the Mid-Atlantic and Greenland-Scotland ridges. Cephalodiscus specimens were collected during two research expeditions to the Antarctic Peninsula aboard the R/V Lawrence M. Gould in 2001 and 2004. Antarctic enteropneusts were collected in January-February 2013 in the Amundsen and Ross Seas by the R/V Nathaniel B. Palmer. Enteropneusts from Norway were collected on the R/V Håkon Mosby or R/V Aurelia with the aid of Dr. Christiane Todt and the late Dr. Christoffer Schander. Balanoglossus sp. specimens from Mississippi were collected with the assistance of Dr. Richard Heard. Dr. Jon Norenburg and Dr. Darryl Felder provided material from Rhabdopleura sp. collected in the Gulf of Mexico on the R/V Pelican. Specimens were collected at depths ranging from the intertidal to over 2500 m, using diverse sampling methods (Table 1). Enteropneusts from Iceland were collected by decanting sediment through a 1-1.5-mm sieve, and were retained on either a 500- or 300-um sieve; enteropneusts from Antarctica and off Oregon

were decanted from sediment directly onto a 250-um sieve. Freshly collected worms were preserved in 95%-100% ethanol, and when multiple specimens were available, voucher specimens were relaxed in 7.5% magnesium chloride and fixed in 4%-10% formalin for morphological studies.

Molecular methods

Molecular laboratory methods followed Cannon et al. (2009). In addition to in-house sequencing on a CEQ8000 (Beckman-Coulter, Inc., Brea, CA), some PCR products were sent to Genewiz (South Plainfield, NJ). In the case of *Rhabdopleura* cf. *normani* from Bermuda, we were able to generate a full-length 18S rDNA sequence using publically available partial sequences (Genbank Accession numbers: U15664, JF900483, and JF900484) and 454 transcriptome data (Cannon and Halanych, unpubl.) prepared following the methods of Kocot et al. (2011). Assembled 454 contigs were formatted into a BLAST (Altschul et al., 1997) database, which was searched with a query composed of diverse hemichordate 18S sequences. Fragments with E-values below 1×10^{-30} were aligned to the partial 18S sequences as a backbone, and then assembled into a full-length 18S rDNA contig using the software package CLC Genomics Workbench ver. 5 (Aarhus, Denmark). As reported previously (Cannon et al. 2009), *Stereobalanus canadensis* (Enteropneusta, Harrimaniidae) has a highly divergent 18S rDNA sequence. Previously we had sequenced this acorn worm multiple times, but to further verify this sequence, genomic DNA was extracted from *S. canadensis* and sequenced via an Illumina MiSeq (San Diego, CA) at Auburn University. This work employed a 2x150-bp paired end run and the Nextera DNA sample kit. Scaffolds generated using the genome assembler Ray (Boisvert et al., 2010) were formatted into a BLAST database, and queried as above. A single 18S rDNA sequence was recovered, with 99.6% identity to our previously reported sequence; thus we have retained *Stereobalanus canadensis* in our analyses.

Taxon sampling and NCBI accession numbers for sequences used in phylogenetic analyses are given in Table 2. Representatives of each echinoderm class were used as outgroup taxa (Table 2). Sequences were aligned with MAFFT ver. 6.09b (Katoh et al., 2005) using the L-INS-i method, and uninformative sites were trimmed using the perl scripts Aliscore and Alicut (Misof and Misof, 2009). Models of evolution were selected under the Akaike Information Criterion (AIC) implemented by MrModelTest (Nylander, 2004). The best fitting model for both 16S and 18S rDNA, GTR+I+G, was used in maximum likelihood (ML) and Bayesian inference analyses (BI) of concatenated alignments. ML analyses were performed with RaxML version 7.3.9 (Stamatakis, 2006) using 5000 bootstrap replicates. Bayesian analyses were conducted using MrBayes ver. 3.2.0 (Ronquist and Huelsenbeck, 2003). Four independent BI analyses were run for each dataset for 5,000,000 generations with trees sampled every 100 generations using three heated and one cold chain. Plotting likelihood values versus generation number revealed that stationarity was reached after approximately 1,000,000 generations, and thus the first 25% of sampled trees was discarded as burn-in. Competing hypotheses of hemichordate phylogeny were evaluated using the SH-test (Shimodaira, 2002) as implemented in RAXML ver. 7.3.8 with the GTR+I+G model.

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 phylum column
- replaced cells with hyphen with nd (no data)
- added links to NCBI accession pages

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Data Files

File
Cannon_2013_T2.csv (Comma Separated Values (.csv), 21.85 KB) MD5:dbd32e63a739b0ab24a17a3cc54431ed
Primary data file for dataset ID 671459

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Related Publications

Boisvert, S., Laviolette, F., & Corbeil, J. (2010). Ray: Simultaneous Assembly of Reads from a Mix of High-Throughput Sequencing Technologies. *Journal of Computational Biology*, 17(11), 1519–1533.

doi:[10.1089/cmb.2009.0238](https://doi.org/10.1089/cmb.2009.0238)

Methods

Cannon, J. T., Rychel, A. L., Eccleston, H., Halanych, K. M., & Swalla, B. J. (2009). Molecular phylogeny of hemichordata, with updated status of deep-sea enteropneusts. *Molecular Phylogenetics and Evolution*, 52(1), 17–24. doi:[10.1016/j.ympev.2009.03.027](https://doi.org/10.1016/j.ympev.2009.03.027)

Methods

Cannon, J. T., Swalla, B. J., & Halanych, K. M. (2013). Hemichordate Molecular Phylogeny Reveals a Novel Cold-Water Clade of Harrimaniid Acorn Worms. *The Biological Bulletin*, 225(3), 194–204.

doi:10.1086/bblv225n3p194 <https://doi.org/10.1086/BBLv225n3p194>

Results

Katoh, K. (2005). MAFFT version 5: improvement in accuracy of multiple sequence alignment. *Nucleic Acids Research*, 33(2), 511–518. doi:[10.1093/nar/gki198](https://doi.org/10.1093/nar/gki198)

Methods

Kocot, K. M., Cannon, J. T., Todt, C., Citarella, M. R., Kohn, A. B., Meyer, A., ... Halanych, K. M. (2011).

Phylogenomics reveals deep molluscan relationships. *Nature*, 477(7365), 452–456. doi:[10.1038/nature10382](https://doi.org/10.1038/nature10382)

Methods

Misof, B., & Misof, K. (2009). A Monte Carlo Approach Successfully Identifies Randomness in Multiple Sequence Alignments : A More Objective Means of Data Exclusion. *Systematic Biology*, 58(1), 21–34.

doi:[10.1093/sysbio/syp006](https://doi.org/10.1093/sysbio/syp006)

Methods

Nylander, J. A. A.. (2004). MrModeltest v2. Program distributed by the author. Evolutionary Biology Centre, Uppsala University.

Methods

Shimodaira, H. (2002). An Approximately Unbiased Test of Phylogenetic Tree Selection. *Systematic Biology*, 51(3), 492–508. doi:[10.1080/10635150290069913](https://doi.org/10.1080/10635150290069913)

Methods

Stamatakis, A. (2006). RAxML-VI-HPC: maximum likelihood-based phylogenetic analyses with thousands of taxa and mixed models. *Bioinformatics*, 22(21), 2688–2690. doi:[10.1093/bioinformatics/btl446](https://doi.org/10.1093/bioinformatics/btl446)

Methods

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Related Datasets

IsSupplementedBy

Halanych, K. M., Mahon, A. (2016) **Collection and locality information by taxon of Hemichordata from global sites, Table 1, Cannon et al (2013) Biol. Bull. (Antarctic Inverts project)**. Biological and Chemical Oceanography Data Management Office (BCO-DMO). (Version 1) Version Date 2016-12-29 <http://lod.bco-dmo.org/id/dataset/671215> [[view at BCO-DMO](#)]

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Parameters

Parameter	Description	Units
phylum	taxonomic phylum	unitless
family	taxonomic family	unitless
taxon	more specific taxonomic group	unitless
new_seq	whether these are new sequences for this study	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	A DNA sequencer is an instrument that determines the order of deoxynucleotides in deoxyribonucleic acid sequences.

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

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.who.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.

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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