GenBank accession numbers for sequences from deep-sea protobranch bivalves collected on R/V Endeavor cruise EN447 in the Western North Atlantic (34-39N, 68-70W) in 2008 (Ev Deep Sea Molluscs II project)

Website: https://www.bco-dmo.org/dataset/542665
Data Type: Other Field Results
Version: 2
Version Date: 2016-09-23

Project
» Evolution of Deep Sea Molluscs II (Ev Deep Sea Molluscs II)

Contributors	Affiliation	Role
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Rauch, Shannon	Woods Hole Oceanographic Institution (WHOI BCO-DMO)	BCO-DMO Data Manager

Abstract

This dataset is comprised of GenBank accession numbers for sequences from deep-sea protobranch bivalves collected on R/V Endeavor cruise EN447 in the Western North Atlantic (34-39N, 68-70W) in 2008.

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Dataset Description

Sequence data from this research are available on Genbank with metadata (sample location, depth, date, etc.) and accession numbers listed in the publications given below. Details of molecular work are also described in the various publications listed below.

Refer to publications:
Glazier, A.E., and Etter, R.J. 2014. Cryptic speciation along a bathymetric gradient. Biological Journal of the Linnean Society, 113:897-913. doi:10.1111/bij.12389
Sequences were deposited in GenBank under accession numbers KM102340-KM102448.

Jennings R.M., and Etter, R.J. 2014. Phylogeographic estimates of colonization of the deep Atlantic by the protobranch bivalve *Nucula atacellana.* Polish Polar Research, 35: 261-278. Invited Paper. doi:10.2478/popore-2014-0017
New sequences generated in this work were deposited in GenBank under Accessions KJ950184–KJ950282 (Table 1).

Boyle, E.E. and Etter, R.J. 2013. Heteroplasmy in a deep-sea protobranch bivalve suggests an ancient origin of doubly uniparental inheritance of mitochondria in Bivalvia. Marine Biology, 160:413-422. doi:10.1007/s00227-012-2099-y
Sequences from this study are available from GenBank (Accession numbers 16S HQ907887–HQ907914; cytb JX435273–JX435297).

Jennings R.M., Etter, R.J. and Ficarra,L. 2013. Population differentiation and species formation in the deep sea: the potential role of environmental gradients and depth. PLoS ONE, 8(10): e77594.

doi:10.1371/journal.pone.0077594
All sequences were deposited in GenBank (Accessions KC563091-KC563901, Table 2).

Sharma, P.P., Zardus, J.D., Boyle, E.E., González, V.L., Jennings, R.M., McIntyre, E., Bouchet, P., Wheeler, W.C., Etter, R.J., and Giribet, G. 2013. Into the deep: A phylogenetic approach to the bivalve subclass Protobranchia. Molecular Phylogenetics and Evolution, 69:188-204. doi:10.1016/j.ympev.2013.05.018
Sequences from this study are available from GenBank (Accession numbers given in Table 2).

Etter, R.J., Boyle, E.E., Glazier, A., Jennings, R.M., Dutra, E., and Chase, M.R. 2011. Phylogeography of a pan-Atlantic abyssal protobranch bivalve: Implications for evolution in the deep Atlantic. Molecular Ecology, 20:829-843. doi:10.1111/j.1365-294X.2010.04978.x
Sequences from this study are available from GenBank - accession numbers are HQ452629–HQ452677.

Jennings, R.M., and Etter, R.J. 2011. Exon-Primed, Intron-Crossing (EPIC) loci for five nuclear genes in deep-sea protobranch bivalves: primer design, PCR protocols, and locus utility. Molecular Ecology Resources, 11:1102-1112. doi:10.1111/j.1755-0998.2011.03038.x
DNA Sequences from this study are available from GenBank - Accessions JF410881– JF411003.

Data Processing Description

Version History:
2019-09-23 (v2) - added links to GenBank for the Jennings 2014 accession numbers (current version)
2014-12-17 (v1) - original version

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Data Files

File
accession_numbers.csv (Comma Separated Values (.csv), 221.50 KB) MD5:6cda85f7a90f94ad66176b4ae33d960b Primary data file for dataset ID 542665

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Supplemental Files

File
Reference List filename: reference_list_v2.csv (Comma Separated Values (.csv), 1.46 KB) MD5:e703b27ef65e319c3686ce29c02c4ea6 Full citation information for entries in the "reference" column of dataset 542655 (PI: Ron Etter). The "abbreviation" column contains the shortened reference name that appears in dataset 542655. The "full_reference" column contains the full citation of the paper.

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Related Publications

Boyle, E. E., & Etter, R. J. (2012). Heteroplasmy in a deep-sea protobranch bivalve suggests an ancient origin of doubly uniparental inheritance of mitochondria in Bivalvia. Marine Biology, 160(2), 413–422.

https://doi.org/10.1007/s00227-012-2099-y
Results

ETTER, R. J., BOYLE, E. E., GLAZIER, A., JENNINGS, R. M., DUTRA, E., & CHASE, M. R. (2011). Phylogeography of a pan-Atlantic abyssal protobranch bivalve: implications for evolution in the Deep Atlantic. Molecular Ecology, 20(4), 829–843. https://doi.org/10.1111/j.1365-294x.2010.04978.x
Results

Glazier, A. E., & Etter, R. J. (2014). Cryptic speciation along a bathymetric gradient. Biological Journal of the Linnean Society, 113(4), 897–913. https://doi.org/10.1111/bij.12389
Results

JENNINGS, R. M., & ETTER, R. J. (2011). Exon-primed, intron-crossing (EPIC) loci for five nuclear genes in deep-sea protobranch bivalves: primer design, PCR protocols and locus utility. Molecular Ecology Resources, 11(6), 1102–1112. Portico. https://doi.org/10.1111/j.1755-0998.2011.03038.x
Results

Jennings, R. M., & Etter, R. J. (2014). Phylogeographic Estimates of Colonization of The Deep Atlantic by The Protobranch Bivalve Nucula Atacellana. Polish Polar Research, 35(2), 261–278. https://doi.org/10.2478/popore-2014-0017
Results

Jennings, R. M., Etter, R. J., & Ficarra, L. (2013). Population Differentiation and Species Formation in the Deep Sea: The Potential Role of Environmental Gradients and Depth. PLoS ONE, 8(10), e77594. https://doi.org/10.1371/journal.pone.0077594
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Sharma, P. P., Zardus, J. D., Boyle, E. E., González, V. L., Jennings, R. M., McIntyre, E., Wheeler, W. C., Etter, R. J., & Giribet, G. (2013). Into the deep: A phylogenetic approach to the bivalve subclass Protobranchia. Molecular Phylogenetics and Evolution, 69(1), 188–204. https://doi.org/10.1016/j.ympev.2013.05.018
Results

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Parameters

Parameter	Description	Units
reference	Name of the reference paper in which the accession numbers were published. Full citation information is provided in the Supplemental File "reference_list_v2.csv"	text
Genbank_accession_number	GenBank accession number for the sequence.	unitless
popset_id	NCBI PopSet ID number (if applicable). (A PopSet is a set of DNA sequences that have been collected to analyse the evolutionary relatedness of a population.)	unitless
organism	Name of the organism.	text
description	Description of the type of sequence.	text
accession_link	Hyperlink to GenBank for the accession number.	unitless

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Deployments

EN447

Website	https://www.bco-dmo.org/deployment/542217
Platform	R/V Endeavor
Start Date	2008-06-04
End Date	2008-06-21

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Project Information

Evolution of Deep Sea Molluscs II (Ev Deep Sea Molluscs II)

Website: http://www.etterlab.umb.edu/Evolution.html

Coverage: Western North Atlantic (34 to 39N, 68 to 70W), Depths 1000-5200m

Description from NSF award abstract:
The first explicit model of population differentiation and speciation in the deep-sea fauna, the depth-differentiation hypothesis, was formulated in the early 1990s. According to this theory, the potential for population differentiation decreases with depth because the bathyal zone (200- 4000 m) has stronger selective gradients and more opportunity for geographic isolation to impede gene flow than does the more extensive and environmentally uniform abyssal plain (>4000 m). To determine whether depth-related variation is genetic, and therefore a consequence of evolutionary change, the PI has developed new methods to extract and sequence mitochondrial DNA from archived deep-sea molluscan species collected in earlier expeditions that had been fixed in formalin and preserved in alcohol. These preliminary studies supported the depth-differentiation hypothesis. They also revealed the limitations of using preserved material. For this project, the PI describes 2 hypotheses about evolution in the deep sea that emerged from the previous work: 1) The depth differentiation hypothesis suggests population divergence decreases with depth; and 2) A strong break in population structure at 3300 m might represent an unrecognized phylogeographic barrier.

The PI will test each of these hypotheses with multiple independent loci using deep-sea protobranch bivalves and recently developed statistical phylogeographic and phylogenetic models. The aforementioned work relied on formalin-fixed tissues, restricting analyses to a single locus (mtDNA). Nuclear loci are essential as independent measures of population structure, gene flow and historical influences, but are also critical to establish whether some of the remarkable divergences the PI documented represent cryptic species. The new material collected during the previous round of funding allowed the PI to develop the necessary nuclear loci and assess their utility for this work. The primary focus of this proposal is to use these new markers to test each of these hypotheses and distinguish intra- versus inter-specific variation.

The deep-sea supports one of the most diverse and unique marine communities, the evolutionary and historical development of which is virtually unknown. The proposed research will contribute very significantly to answering the two most basic questions about evolutionary diversification in this vast and remote environment: Where does it occur, and how? Analysis of the strong bathymetric divergence in Deminucula atacellana will provide the first detailed investigation of potential incipient speciation in a deep-sea organism (apart from reducing environments) and possibly identify the scales and mechanisms involved. It will also create a solid conceptual and methodological context for future evolutionary studies in the deep sea and lay the groundwork for understanding bathymetric and geographic variation at much larger scales (e.g., among ocean basins or pan-Atlantic).

Related Publications:

Baco, AR, RJ Etter, PA Ribeiro, S von der Heyden, P Beerli, BP Kinlan. 2016. A synthesis of genetic connectivity in deep-sea fauna and implications for connectivity and marine reserve design. Molecular Ecology 25:3276-3298. doi:10.1111/mec.13689

Etter, R.J., and A.S. Bower. 2015. Dispersal and population connectivity in the deep North Atlantic estimated from physical transport processes. Deep Sea Research I 104:159-172. doi:10.1016/j.dsr.2015.06.009

Glazier, AE, and RJ Etter. 2017. Genetic divergence across an oxygen minimum zone. Marine Ecology Progress Series 577: 79–91. doi:10.3354/meps12239

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Funding

Funding Source	Award
NSF Division of Ocean Sciences (NSF OCE)	OCE-1130541

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