Diatom ribosomal DNA sequence accession numbers from samples collected from the Eastern and Western Pacific and from the Western Atlantic between 2007 and 2009 (Diatom Gene Flow project)

Website: https://www.bco-dmo.org/dataset/514202
Version: 28 April 2014
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Project
» Connecting local, regional and global scales of gene flow in planktonic marine diatoms (Diatom Gene Flow)

Contributors	Affiliation	Role
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Dataset Description

GenBank accession numbers for ribosomal DNA sequences from the diatoms *Ditylum brightwellii*, *Thalassiosira rotula*, and *Thalassiosira gravida*.

Methods & Sampling

Summary of methods: *Thalassiosira rotula* and *Thalassiosira gravida*
See Whittaker et al. (2012) for more information. Cells of the diatom *Thalassiosira rotula/gravida* were collected from the Eastern and Western Pacific and from the Western Atlantic between 2007 and 2009. Cultured isolates were also obtained (refer to Table 1 of Whittaker et al. (2012)). Three regions of the ribosomal DNA (rDNA) were sequenced: the small subunit (18S), the D1 hypervariable region of the large subunit (28S), and the internal transcribed spacer region I (ITS1). ITS1 was amplified from 106 isolates by polymerase chain reaction (PCR) using a newly-designed primer specific to *T. rotula* and *T. gravida* and primer 1645F. The 18S was amplified from 16 isolates using universal 18SA and 18SB primers. The D1 region of the 28S was also amplified from those 16 isolates using the forward primer 28SF and a reverse primer. Sequencing was performed on an ABI 3130xl (Applied Biosystems). SeqMan II 3.61 (DNASTAR, Inc.) was used to assemble sequences and they were aligned using Clustal W in Mega4. Boundaries of the ITS1 were determined through alignment with Genbank accession EF208798.

Refer to Rynearson et al. (2009) for the *Ditylum brightwellii* methodology.

References:
Rynearson, T.A., E.O. Lin and E.V. Armbrust. 2009. Metapopulation structure in the planktonic diatom *Ditylum brightwellii* (Bacillariophyceae). *Protist*, 160(1):111-121. doi:10.1016/j.protis.2008.10.003

Whittaker, K., Rignanese, D., Olson, R., Rynearson, T., 2012. Molecular subdivision of the marine diatom *Thalassiosira rotula* in relation to geographic distribution, genome size, and physiology. *BMC Evolutionary*

Biology, 12:209. doi:10.1186/1471-2148-12-209

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Data Files

File
sequence_accessions.csv (Comma Separated Values (.csv), 20.40 KB) MD5:96db880e01107c3e696304394a03e3aa Primary data file for dataset ID 514202

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Parameters

Parameter	Description	Units
species	Name of the species.	text
description	Brief description of the type of sequence.	text
accession_number	GenBank accession number.	alphanumeric
accession_number_link	Link to GenBank (opens in new window) for the specific accession number.	alphanumeric hyperlink

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Instruments

Dataset-specific Instrument Name	ABI 3130xL (Applied Biosystems)
Generic Instrument Name	Automated DNA Sequencer
Dataset-specific Description	Sequencing was done on an ABI ABI 3130xL (Applied Biosystems) genetic analyzer.
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	Thermocycler
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

lab_Rynearson_diatoms

Website	https://www.bco-dmo.org/deployment/514257
Platform	URI-GSO
Start Date	2007-10-01
End Date	2013-09-01

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Project Information

Connecting local, regional and global scales of gene flow in planktonic marine diatoms (Diatom Gene Flow)

Coverage: global diatom samples; laboratory-based analyses

Description from NSF award abstract:
Diatoms are ubiquitous, unicellular, eukaryotes that generate about 40% of the organic carbon fixed annually in the sea. Interpretation of diatom species distributions and abundances in relation to environmental conditions has relied on two assumptions: (1) cells with identical morphologies represent the same species and (2) high potentials for dispersal and gene flow in passively drifting diatoms prevent local adaptation. Recent studies have challenged both assumptions, suggesting diatoms possess rich patterns of genetic and physiological variation both within and between species. Although there is emerging evidence of intra-specific population differentiation on local scales (~100km), it is commonly assumed that planktonic microbes are homogenously distributed on global scales (e.g. Fenchel and Finlay 2004). There is currently no data on diatoms to support this assumption. Aside from intriguing data on local scales, nothing is known about regional and global-scale population genetics and biogeography of diatoms.

The research proposed here will focus on the essential questions of if and how populations of planktonic diatoms are connected at local, regional and global scales. Connectivity among populations can influence a species" ecology, adaptive potential, evolutionary longevity and ultimately speciation potential. The proposed research will examine how local populations are connected to each other on regional scales and how regional dynamics connect to global-scale biogeographies using two model diatom species. rDNA sequence variation will be used to test whether broad species distributions observed in diatoms result from cryptic speciation. Within species, microsatellite markers will be used to identify genetically distinct populations, determine their

relatedness to each other and examine spatial patterns of differentiation. The degree of physiological variation that accompanies genetic differentiation between populations will also be examined. Samples will be collected in a framework of existing oceanography and biodiversity programs, permitting genetic data to be interpreted in the context of larger, often long-term, studies. Because little is known about diatom biogeography, this work will begin to shed light on the connections between local and global population dynamics. Because the proposed research will represent the first large-scale sampling of diatom population genetics, it will also serve to generate many new hypotheses about the mechanisms that regulate ecological processes such as bloom formation over space and time and evolutionary processes such as the development of reproductive isolation and eventual speciation in planktonic organisms.

Related publications:

Rynearson, T.A., E.O. Lin and E.V. Armbrust. 2009. Metapopulation structure in the planktonic diatom *Ditylum brightwellii* (Bacillariophyceae)*. Protist*, 160(1):111-121. doi:10.1016/j.protis.2008.10.003

Whittaker, K., Rignanese, D., Olson, R., Rynearson, T., 2012. Molecular subdivision of the marine diatom *Thalassiosira rotula* in relation to geographic distribution, genome size, and physiology. *BMC Evolutionary Biology,* 12:209. doi:10.1186/1471-2148-12-209

Boyd, P.W., Rynearson, T.A., Armstrong, E.A., Fu, F., Hayashi, K., Hu, Z., Hutchins, D.A., Kudela, R.M., Litchman, E., Mulholland, M.R., Passow, U., Strzepek, R.F., Whittaker, K.A., Yu, E., Thomas, M.K., 2013. Marine Phytoplankton Temperature versus Growth Responses from Polar to Tropical Waters - Outcome of a Scientific Community-Wide Study. *PLoS One*, 8(5), e63091. doi:10.1371/journal.pone.0063091

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Funding

Funding Source	Award
NSF Division of Ocean Sciences (NSF OCE)	OCE-0727227

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