Accession numbers for planktonic ciliate haplotypes collected on R/V Lowell Weicker in the Long Island Sound in 2008

Website: https://www.bco-dmo.org/dataset/3652
Version: 11 May 2012
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Project
» Testing hypotheses about diversity, gene flow, and effective population size in marine planktonic ciliates (CiliateDivGenePop)

Contributors	Affiliation	Role
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Dataset Description

Accession numbers are given for planktonic ciliate haplotypes found in Long Island Sound.

Methods & Sampling

Six stations were sampled in Long Island Sound on 13 August 2008. DNA was extracted and amplified. Two rDNA primers were used (OCSP-A and OCSP-B), resulting in the generation of two separate clone libraries.

More information on sample locations, methodology, and results can be found in the following publication and its supplement:
Tamura, M, LA Katz, and GB McManus. 2011. Distribution and diversity of Oligotrich and Choreotrich ciliates in a large temperate estuary. Aquat. Microb. Ecol. 64:51-67. doi:10.3354/ame01509 (PDF)

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Data Files

File
accession_numbers.csv (Comma Separated Values (.csv), 8.68 KB) MD5:50f5efa2f18d976305c70809a353532a Primary data file for dataset ID 3652

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Parameters

Parameter	Description	Units
primer_set	Name of the primer and resulting clone library.	dimensionless
sequence_name	Haplotype name.	dimensionless
accession_number	Accession number and link to GenBank.	dimensionless

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Instruments

Dataset-specific Instrument Name	Automated Sequencer
Generic Instrument Name	Automated DNA Sequencer
Dataset-specific Description	Samples were sequenced in either an ABI 3000 automated sequencer or in an ABI 377 automated 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	Niskin bottle
Generic Instrument Name	Niskin bottle
Dataset-specific Description	Suface samples were taken with a bucket; Niskin bottles were used to take samples below the pycnocline.
Generic Instrument Description	A Niskin bottle (a next generation water sampler based on the Nansen bottle) is a cylindrical, non-metallic water collection device with stoppers at both ends. The bottles can be attached individually on a hydrowire or deployed in 12, 24, or 36 bottle Rosette systems mounted on a frame and combined with a CTD. Niskin bottles are used to collect discrete water samples for a range of measurements including pigments, nutrients, plankton, etc.

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Deployments

LW_LIS08

Website	https://www.bco-dmo.org/deployment/58823
Platform	R/V Lowell Weicker
Start Date	2008-08-13
End Date	2008-08-13
Description	Samples were collected at 6 stations in Long Island Sound on 13 August 2008 as part of the project titled "Collaborative Research: Testing hypotheses about diversity, gene flow, and effective population size in marine planktonic ciliates".

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Project Information

Testing hypotheses about diversity, gene flow, and effective population size in marine planktonic ciliates (CiliateDivGenePop)

Website: http://microzooplankton.uconn.edu

Coverage: Coastal Northwest Atlantic, from Long Island Sound to Maine

The microbial ecologist Tom Fenchel recently said, “The decoupling of molecular and classical (including experimental) approaches to environmental microbiology has not been fruitful and it represents one of the most important challenges for the field in the coming years.” (Fenchel 2005). Classical approaches center on the centuries-old tradition of describing individual species via meticulous observation and analysis to generate monographs, such as is done for plants and animals. Unfortunately, the rush to new molecular techniques has sometimes ignored this tradition, with claims about new lineages never seen before and reports of staggering diversity of microbial eukaryotes based on environmental DNA samples not backed up by even the most elementary microscopic observations.

In the face of this disconnect between the traditional and the molecular, we propose a marriage of the two approaches in the study of marine ciliate diversity and gene flow. Our own data show that in some clades of planktonic ciliates (Strombidiidae) there is indeed a high level of molecular diversity underlying a relatively small number of morphospecies. In other clades (some choreotrichs), the opposite appears to be true, with morphological heterogeneity underlain by apparently clonal lines, based on molecular data. Currently, we do not understand what sustains diversity in some clades; nor do we know why other clades show low diversity. But this problem is amenable to both experimental and observational approaches.

This proposal uses a two-pronged approach, combining molecular (clone libraries, DGGE,FISH) and traditional (light microscopy) techniques to address three broad questions:
i. What are the most important physical and biological factors that affect distribution and diversity of planktonic marine ciliates?
ii. What is the effective population size for marine ciliate populations, and how does this compare to census population sizes?
iii. How well do traditional morphological descriptions of ciliate species fare when compared with molecular characterizations?

Using a combination of molecular and microscopy methods, we will address these questions in coastal planktonic ciliates. Analyses of the resulting data will yield insights into the nature of ciliate species and patterns of gene flow within the North Atlantic.

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Funding

Funding Source	Award
NSF Division of Ocean Sciences (NSF OCE)	OCE-0648711

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