Physical meta associated with marine metagenome samples collected collected on the R/V Cape Hatteras (CH0112) cruise in the NW Atlantic Continental Shelf during 2015 (CiliateSequencing project)

Website: https://www.bco-dmo.org/dataset/626679
Version: 2015-11-23

Project
» Diversity and dynamics of planktonic ciliates - what can next-generation sequencing technologies tell us? (CiliateSequencing)

Contributors	Affiliation	Role
McManus, George	University of Connecticut (UConn - Avery Point)	Principal Investigator
Katz, Laura A.	Smith College	Co-Principal Investigator
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Dataset Description

Physical data associated with samples from NCBI BioProject SRA######, PRJNA297691 (not yet public, 2015-11-18)

References:

Santoferrara L.F., Grattepanche J-D., Katz L.A., McManus G.B. (submitted) Patterns and processes in microbial biogeography: do molecules and morphologies give the same answers?

Grattepanche J-D., Santoferrara L.F., McManus G.B., Katz L.A. (submitted) Unexpected biodiversity of ciliates in marine samples.

Methods & Sampling

Seawater samples were screened through a 80 um mesh, then sequentially filtered through 10 um and 2 um polycarbonate filters; DNA was extracted from half-filters.

Data Processing Description

Data were processed in SeaBird Seasave software, version 7.21a using instrument configuration files provided by RV Hatteras ship operations. Raw hexadecimal data files were converted to base 10. Processed data were imported into Excel.

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Data Files

File
SRA_Hatteras.csv (Comma Separated Values (.csv), 4.38 KB) MD5:318297aa0483702e322bebe6b530660d Primary data file for dataset ID 626679

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Parameters

Parameter	Description	Units
cruise_id	cruise identification	unitless
geo_loc_name	The geolocation of the collection: Atlantic Ocean	unitless
isolation_source	Source of the sample: seawater	unitless
organism	In this case the organism is a sample of marine seawater	unitless
samp_collect_device	sample collection device	unitless
depth_w	depth of water at sampling site	meters
date_collected	date sample was collected	dd-Mon-yyyy
lat	latitude; north is positive	decimal degrees
lon	longitude; east is positive	decimal degrees
sample_name	sample identification	unitless
layer_sampled	layer of water sampled	unitless
depth	depth of sample	meters
temp	temperature	degrees Celsius
sal	salinity	PSU
O2	dissolved oxygen	mg L-1
fluor	chlorophyll fluorescence	arbitrary units

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Instruments

Dataset-specific Instrument Name	
Generic Instrument Name	CTD Sea-Bird 9
Generic Instrument Description	The Sea-Bird SBE 9 is a type of CTD instrument package. The SBE 9 is the Underwater Unit and is most often combined with the SBE 11 Deck Unit (for real-time readout using conductive wire) when deployed from a research vessel. The combination of the SBE 9 and SBE 11 is called a SBE 911. The SBE 9 uses Sea-Bird's standard modular temperature and conductivity sensors (SBE 3 and SBE 4). The SBE 9 CTD can be configured with auxiliary sensors to measure other parameters including dissolved oxygen, pH, turbidity, fluorometer, altimeter, etc.). Note that in most cases, it is more accurate to specify SBE 911 than SBE 9 since it is likely a SBE 11 deck unit was used. more information from Sea-Bird Electronics

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Deployments

CH0112

Website	https://www.bco-dmo.org/deployment/59041
Platform	R/V Cape Hatteras
Start Date	2012-07-06
End Date	2012-07-09
Description	Cruise departed from and returned to Narragansett, RI. 39 stations were completed in 3 days. Each station included a CTD cast, water sampling, and a plankton net tow. Part of the project "Diversity and dynamics of planktonic ciliates - what can next-generation sequencing technologies tell us?" Sampling activity included: CTDFO Zooplankton (vertical tows 150 um mesh) Plankton DNA (3-5 depths); 2 L sample Preserved (lugols) for microzooplankton (3-5 depths) Cruise information and original data are available from NSF R2R data catalog.

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Project Information

Diversity and dynamics of planktonic ciliates - what can next-generation sequencing technologies tell us? (CiliateSequencing)

Website: http://microzooplankton.uconn.edu

Coverage: NW Atlantic Continental Shelf

The Ocean's biomass and diversity are predominantly microbial, yet this aspect of diversity remains underexplored. Efforts in recent years have begun to document microbial diversity in marine systems, and to elucidate the processes that structure assemblages across space and time. This project focuses on two important sister clades of microbial eukaryotes, the oligotrich and choreotrich ciliates. These organisms comprise a major component of planktonic food webs as they graze on phytoplankton, and are in turn eaten by zooplankton and larval fish.

Earlier molecular work on ciliate diversity relied on light microscopy, construction of clone libraries and Sanger sequencing. This revealed a high degree of cryptic diversity (similar species that are genetically distinct), which

is surprising, given the long-held idea that all microbes are globally distributed and that few species exist, at least as compared to animals and plants. This past work also showed that ciliate assemblages contain a few highly abundant forms and many rare ones, consistent with the concept of a "rare biosphere". However, these methods are limited by high costs of both labor and materials, so that efforts to sample any local assemblage comprehensively usually resulted in undersaturation (repeated sampling continued to uncover new species). Next generation approaches are needed to truly assess the depths of biodiversity in planktonic ciliates.

This project brings together investigators with strengths in ecology, taxonomy and oceanography (PI McManus) and in molecular evolution, systematics and bioinformatics (PI Katz). Pyrosequencing will be used to sample the oligotrich and choreotrich ciliates 'to exhaustion' in coastal environments. Denaturing gradient gel electrophoresis (DGGE), a technique that generates a fingerprint of the diversity in a sample, will be used to pre-select samples for pyrosequencing based on where strong gradients are observed in the composition of assemblages in relation to environmental factors (density fronts, thermolclines, etc.). Using these approaches, combined with the informatics pipeline already in place, this project will address three specific objectives:

Objective 1. Determine the spatial scale of variability in ciliate diversity by measuring how ciliate assemblages change over meter, kilometer, 100 km, and basin scales.

Objective 2. Assess the contributions of different size classes of ciliates to overall assemblage diversity.

Objective 3. Experimentally evaluate factors that control the temporal shift of individual species from rarity to commonness in a natural assemblage, and vice versa.

Note: See the related collaborative project, "Patterns of diversity in planktonic ciliates: spatio-temporal scales and community assembly in the coastal ocean", funded by awards OCE-1435515 and OCE-1436003.

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Funding

Funding Source	Award
NSF Division of Ocean Sciences (NSF OCE)	OCE-1130033

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