

Viral metagenome sequence data acquired in a study of the applicability of a new DNA sequencing technology for research problems in marine microbial ecology

Website: <https://www.bco-dmo.org/dataset/541197>

Version: 01 Dec 2014

Version Date: 2014-12-01

Project

» [Exploratory application of single-molecule real time \(SMRT\) DNA sequencing in microbial ecology research](#)
(PacBio sequencing in microbial ecology)

Contributors	Affiliation	Role
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Dataset Description

This project focused on testing the applicability of a new DNA sequencing technology for research problems in marine microbial ecology. The data resulting from the project have been DNA sequence data that will ultimately be deposited in GenBank.

Dataset Status (as of 01 December 2014): The investigators are currently analyzing the sequence data and expect that data will be deposited in GenBank by Q2 of 2015.

Methods & Sampling

The genetic sequence data collected in this study will be deposited in GenBank.

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Parameters

Parameters for this dataset have not yet been identified

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Project Information

Exploratory application of single-molecule real time (SMRT) DNA sequencing in microbial ecology research (PacBio sequencing in microbial ecology)

Website: <http://virome.dbi.udel.edu>

Coverage: Gulf of Maine and Chesapeake Bay

Description from NSF award abstract:

Microbial communities are the primary drivers of the global biogeochemical cycles that maintain the nutrient balance of ecosystems and ultimately shape overall ecosystem function. Today, we appreciate the critical role microbes play in the biochemical processing of nutrient elements; yet our understanding of how the structure of microbial communities influences the suite of biogeochemical processes within a given nutrient cycle is somewhat rudimentary. Limited understanding of structure-function relationships between microbial communities and biogeochemical cycles is due in large part to technological limitations in characterizing the ecology of microbial communities. Until recently, microbial ecologists simply had no means of unambiguously characterizing the richness and evenness of species within a microbial community and the prevailing biochemical capabilities of constituent microbial populations. Using high-throughput DNA sequencing and three methodological approaches, shotgun metagenomics, PCR amplicon sequencing, and genomics microbial ecologists are beginning to unveil the inner workings of microbial communities and connect genetic details with biogeochemical processes. While this work holds great promise for the advancement of microbial ecology, currently-available high-throughput sequencing technologies are not ideally suited to the high-sample throughput demands of ecosystem science, the small genome size of bacteria and viruses, and their genetic novelty. Moreover, in some cases the failure to adequately ground-truth application of next-generation DNA sequencers to environmental DNA samples has resulted in biased data and erroneous scientific conclusions.

This "high-risk; high-reward" research seeks to explore and test the use of a new, next-generation DNA sequencer, the PacBio RS, which has several attributes that may make it better suited to the specific needs of microbial ecology research and has the potential to be highly transformative to this geoscience discipline. A series of controlled and carefully replicated experiments will be conducted that will test the use of PacBio sequencing for shotgun metagenomics, 16S PCR amplicon sequencing, and single cell genome sequencing. This project will leverage existing datasets from other high-throughput sequencing platforms (e.g., Illumina and 454) to directly compare the performance of PacBio in each of these application areas. Through a NSF Major Research Instrumentation award to the University of Delaware, the PIs will have access to one of the few PacBio RS instruments available at an academic institution. Ultimately, these investigations will constrain the experimental error within PacBio sequencing and serve as an initial demonstration of the utility of the instrument for microbial ecology research.

Note: This is a collaborative research project, funded by NSF's EAGER mechanism.

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Funding

Funding Source	Award
NSF Division of Ocean Sciences (NSF OCE)	OCE-1148118

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