Primers used for Pleurochrysis carterae virus dPCR assays from laboratory experiments at the Bigelow Laboratory for Ocean Sciences, Maine from 2015-2016

Website: https://www.bco-dmo.org/dataset/670450
Data Type: experimental
Version:
Version Date: 2016-12-15

Project
» Persistent Virus Infections in Marine Phytoplankton (Marine Chronic Viruses)

Contributors	Affiliation	Role
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Dataset Description

This dataset includes information for the five primers used in the Pleurochrysis carterae virus production dataset. It contains the primer ID, forward primer, reverse primer, amplicon length, annealing temperature, and probe amplicon sequence.

Related datasets:
* Pleurochrysis carterae growth
* Pleurochrysis carterae virus production
* Accession numbers (P. carterae viruses and field samples)
* TEM Pleurochrysis carterae thin section images
* TEM Pleurochrysis carterae virion images

Methods & Sampling

Probes and primers were designed to target genotypes: *Pleurochrysis carterae* endemic virus genotypes 2 and 1b (PsEV2 and PsEV1b, respectively; dsDNA viruses); *P. carterae* Polinton-like viruses (PleuroPLV; dsDNA viruses); and *P. carterae* CRESS viruses (PcCV1, ssDNA viruses). For the latter, we designed probes for both the REP and the CAP genes to discriminate viral particles with partial (i.e., amplification for only the REP or the CAP markers from a single dPCR intact drop) or complete genomes (i.e., amplification with both molecular markers from a single dPCR intact drop).

Data Processing Description

BCO-DMO Data Manager Processing Notes:

* made primer PcCV-1_Rep sequence uppercase (AGGAGGAG...)to match all other sequence formatting.
* added a conventional header with dataset name, PI name, version date
* modified parameter names to conform with BCO-DMO naming conventions
* blank values replaced with no data value 'nd'

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Data Files

File
VirusAssays.csv (Comma Separated Values (.csv), 1.15 KB) MD5:19b1fff7d82f8147dbb60155d0ecae09 Primary data file for dataset ID 670450

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Parameters

Parameter	Description	Units
primer_id	Primer identifier (see dataset acquisition section for details)	unitless
forward_primer	Forward primer sequence	unitless
reverse_primer	Reverse primer sequence	unitless
aplicon_length	Number of nucleobases in amplicon	unitless
annealing_temp	Annealing temperature	degrees Celsius
probe	Probe sequence	unitless
amplicon_sequence	Amplicon sequence	unitless

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Deployments

Bigelow_Martinez_2015-2016

Website	https://www.bco-dmo.org/deployment/670437
Platform	lab Bigelow
Start Date	2015-01-01
End Date	2016-12-30
Description	Bigelow Laboratory for Ocean Sciences **Methods & Sampling** laboratory experiment

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Project Information

Persistent Virus Infections in Marine Phytoplankton (Marine Chronic Viruses)

Description from NSF award abstract:

Description from NSF award abstract:
Viruses are prevalent in every part of the environment of our living planet, and yet our understanding of type, distribution, and function is the least well-known aspect of biodiversity. In recent years we have developed an increased appreciation for the role viruses play in driving host evolution in the environment, but fundamental knowledge about the mechanisms involved remain lacking. Additionally, viruses may influence diversity indirectly through "kill the winner" scenarios, as well as through cell lysis and subsequent release of dissolved nutrients, which facilitate restructuring of microbial communities. The majority of research on marine viruses to date has focused on combinations of acutely susceptible host strains with highly virulent virus isolates. However, it is likely that marine viruses also employ a persistent infection life strategy, arguably preferring it to the more widely recognized lytic cycle. The objective of this project is to demonstrate that persistent virus infections occur in marine phytoplankton, and that these are a crucial component of ocean ecosystem function and a key evolutionary driver in primary producers. Using a range of persistent virus:host systems, this project will investigate:
1) how pervasive persistent virus infections are in marine systems; and
2) the role of non-coding RNAs in maintaining host:virus symbiosis.

This is a high risk-high pay research as it involves a radically different approach to the analysis of viruses in marine systems. The investigators plan to apply a suite of molecular (transcriptomics, genomics and development of novel diagnostic markers) techniques to include the analysis of microRNAs to determine the functional importance of persistent viruses in the ocean. The results of this project will be potentially transformative for our understanding of virus-driven phytoplankton evolution and its potential impact on biodiversity in marine phytoplankton, a vital component of the global carbon cycle.

Note: William Wilson (Bigelow Laboratory) was the Former Principal Investigator on this project award.

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Funding

Funding Source	Award
NSF Division of Ocean Sciences (NSF OCE)	OCE-1346272

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