Pseudo-nitzschia species microbiome identification collected from the Santa Cruz Warf in 2011 (bacteria, virus, diatom interactions project)

Website: https://www.bco-dmo.org/dataset/564378
Version: 2015-08-05

Project
» Interactions of bacteria, viruses and bloom-forming diatom genus Pseudo-nitzschia (bacteria, virus, diatom interactions)

Contributors	Affiliation	Role
Jiang, Sunny	University of California-Irvine (UC Irvine)	Principal Investigator
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Methods & Sampling

Bacterial total genome DNA was extracted from the single species Pseudo-nitzschia culture. 16S rDNA pyrosequencing were carried out using the bTEFAP method based on the Titanium reagents and protocol for Genome Sequencer FLX System.

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Data Files

File
diatom_microbiome.csv (Comma Separated Values (.csv), 176 bytes) MD5:262860733979b675a15baeb087ba1f47 Primary data file for dataset ID 564378

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Parameters

Parameter	Description	Units
project_type		dimensionless
attributes		dimensionless
NCBI_bioproject_id		dimensionless

Instruments

Dataset-specific Instrument Name	Genome Sequencer FLX System
Generic Instrument Name	Automated DNA Sequencer
Dataset-specific Description	Genome Sequencer FLX System was used for pyroseqencing of pseudo-nitzschia microbiome.
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	Seqman II
Generic Instrument Name	Automated DNA Sequencer
Dataset-specific Description	A Seqman II (version 9.0 DNASTAR Inc, Madison, WI, USA) was used for sequencing of bacterial 16s rDNA.
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	Light Microscope
Generic Instrument Name	Microscope - Optical
Generic Instrument Description	Instruments that generate enlarged images of samples using the phenomena of reflection and absorption of visible light. Includes conventional and inverted instruments. Also called a "light microscope".

Dataset-specific Instrument Name	Plankton Net
Generic Instrument Name	Plankton Net
Dataset-specific Description	20um mesh size plankton net was used for sampling.
Generic Instrument Description	A Plankton Net is a generic term for a sampling net that is used to collect plankton. It is used only when detailed instrument documentation is not available.

Dataset-specific Instrument Name	GeneAmp 2700 PCR system
Generic Instrument Name	Thermal Cycler
Dataset-specific Description	GeneAmp 2700 PCR system (Applied Biosystems, Foster City, CA) was used for PCR amplification.
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)

Deployments

SantaCruz_Plankton_Jiang

Website	https://www.bco-dmo.org/deployment/614791
Platform	Santa Cruz Warf
Start Date	2011-06-15
End Date	2011-06-15
Description	Sampling location for the project 'Diatom Microbiome' (PI: Sunny Jiang). A 20um mesh plankton net was used to collect sample.

Project Information

Interactions of bacteria, viruses and bloom-forming diatom genus Pseudo-nitzschia (bacteria, virus, diatom interactions)

Coverage: Santa Cruz Warf 36.96023 N, -122.01996 W

This project seeks to elucidate the interactions between viruses, bacteria and toxic bloom-forming marine

diatom genus Pseudo-nitzschia in the coastal marine environment. The cosmopolitan Pseudo-nitzschia sp. (Bacillariophyceae) causes harmful algal blooms in various parts of the world. Recent genome sequences of two marine diatoms revealed that bacterial genes contribute up to 5% of their genome make-up, highlighting the close association of marine diatoms with bacteria in evolutionary history. So far, few have looked at the interactions of diatoms with their epibiotic bacteria and none have studied the interactions of virus, bacteria and phytoplankton using direct experimental approach.

This project investigates the physiological, biochemical, genetic and ecological interactions of algae-microbe associations in order to decipher the influences of microbes on algal bloom dynamics and toxigenesis. By incorporating methods in phylogeny, physiology, biochemistry, comparative genomics and metagenomics, the research seeks answers to the following questions: 1) What are the epiphytic bacteria associating with different species of Pseudo-nitzschia and how do they change at different stages of the bloom? 2) How do these bacteria affect the physiology of the Pseudo- nitzschia hosts and how does the algal host regulate these microbial interactions? 3) Can viruses promote a bloom by selectively lysing algicidal bacteria, while creating opportunities for growth- promoting bacteria or vice versa? This project is guided by the preliminary research on microbe- algae interaction, where significantly different epibiotic bacterial communities were found to associate with two Pseudo-nitzschia species. Bacterial associates of one Pseudo-nitzschia sp. stimulated the growth of the algal-host but acted as a pathogen on another Pseudo-nitzschia sp. This project will expand the work on epibiotic bacterial community diversity and dynamics by sampling additional species of Pseudo-nitzschia and investigating the changes in epibiotic and planktonic bacterial community structure following the initiation, peak and decline phases of Pseudo-nitzschia blooms in coastal oceans. Algal host responses to epibionts association will be investigated using physiological experiments of binary and multi-culture experimental approaches. The chemical communication between algal host and epibiont bacteria will be addressed by looking at the algal exudate excretions and bacterial enzyme secretions using established LC-MS and enzyme assays. To illustrate the influences of viruses on bacterial-algal interaction, bacteriophages specific to epibiotic bacteria will be isolated and included in the physiological experiments.

Related Publications:

Sison-Mangus, M., Jiang, S., Tran, K. N., Kudela, R. M. Host-specific adaptation governs the interaction of the marine diatom, Pseudo-nitzschia and their microbiota. *ISME Journal* 8, 63-76 doi:10.1038/ismej.2013.138

Rowe, J.; Jiang, S. Interactions of bacterial microbiome with bloom forming marine diatom *pseudo-nitzchia*. Ocean Science Meeting. Honolulu, Hawaii. 2014. (http://www.sgmeet.com/osm2014/viewabstract.asp?AbstractID=17958)

Sison-Mangus, M.; Jiang, S.; Tran, K.; Kudela, R. Factors that influence the association between marine diatom *pseudo-nitzschia* and their bacterial associates. Ocean Science Meeting. Honolulu, Hawaii. 2014. (http://www.sgmeet.com/osm2014/viewabstract.asp?AbstractID=17910)

Sison-Mangus, M., S. C. Jiang. The microbiota of marine diatoms: is it influenced by algal host phylogeny? American Society for Liminology and Oceanography, Ocean Science Meeting, Salt Lake City, Utah, Feb. 20-24, 2012 (http://www.sgmeet.com/osm2012/viewabstract2.asp?AbstractID=12577)

Sison-Mangus, M. P., Tran, K., Jiang, S. Growth stimulation and killing of *pseudo-nitzschia* by non-native epibiotic bacteria. American Society for Liminology and Oceanography, Aquatic Science Meeting, San Juan, Pureto Rico, Feb. 13-18, 2011 (https://www.sgmeet.com/aslo/sanjuan2011/viewabstract2.asp?AbstractID=8790)

Tran, K., M., Sison-Mangus, S. C. Jiang. Bacterial diversity associated with toxic and non-toxic *pseudo-nitzschia* species. American Society for Liminology and Oceanography, Aquatic Science Meeting, San Juan, Pureto Rico, Feb. 13-18, 2011 (http://www.sgmeet.com/aslo/sanjuan2011/viewabstract2.asp?AbstractID=9063)

Funding