Microbial culture collection, strain IDs, locations and depths R/V F.G. Walton Smith (WS1209) cruise in the Yucatan Carribean and Mexico during 2012 (CEMSB project)

Website: https://www.bco-dmo.org/dataset/632875
Version: 2016-01-19

Project
» The Chemical Ecology of Marine Sediment Bacteria (CEMSB)

Contributors	Affiliation	Role
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Dataset Description

This dataset includes microbial Salinispora strains and co-occurring bacteria found in samples from WS1209, their associated collection information, and links to GenBank accession pages. The collections were made from sediments off of Yucatan in the Mexican Caribbean Sea. Bacteria were cultured from marine sediments and identified based on 16S sequence analysis.

Coordinates (this study) or year of isolation are given for each strain, as well as sample depth if known. BC stands for Banco Chinchorro, which divided into North (N), Middle (M), and South (S) locations.
The following are also flagged in the data:
* Genome sequence available.
+ Strains used in secondary assays to determine the temporal onset of antagonism.

Related Reference:

Patin,NV; Duncan,KR; Dorrestein,PC; Jensen,PR. (2012) Competitive strategies differentiate closely related species of marine actinobacteria. ISME J 10:478-490. doi:10.1038/ismej.2015.128

Methods & Sampling

Methodolody (pdf)

Data Processing Description

BCO-DMO Processing:

- added conventional header with dataset name, PI name, version date
- renamed parameters to BCO-DMO standard
- added hyperlinks to GenBank accessions
- changed '<1' to 'lt_1'
- split collection year and location into 2 columns, adding 'nd' in empty cells
- replaced empty cells with 'nd' (no data)
- replaced blanks with underscores

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Data Files

File
WS1209_strains_16S.csv (Comma Separated Values (.csv), 24.89 KB) MD5:e992f2169232ffca0acdeaae861b37cf Primary data file for dataset ID 632875

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Parameters

Parameter	Description	Units
sample	sample identification	unitless
species_strain	species and strain	unitless
GenBank_accession	GenBank accession number	unitless
BLAST_pcent	BLAST result	percent
seq_avail_flag	genome sequence available	unitless
study_2_flag	flag denoting strains used in secondary assays to determine the temporal onset of antagonism	unitless
site	collection site	unitless
lat	latitude; north is positive	decimal degrees
lon	lonitude; east is positive	decimal degrees
year	year of Isolation	yyyy
depth	collection depth	meters

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Instruments

Dataset-specific Instrument Name	
Generic Instrument Name	Automated DNA 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	
Generic Instrument Name	Thermal Cycler
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)

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Deployments

WS1209

Website	https://www.bco-dmo.org/deployment/632899
Platform	R/V F.G. Walton Smith
Start Date	2012-06-28
End Date	2012-07-11
Description	Cruise for project Chemical Ecology of Sponges on Caribbean Reefs

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Project Information

The Chemical Ecology of Marine Sediment Bacteria (CEMSB)

Coverage: The Mexican Yucatan, Fiji (South coast of Viti Levu), Belize (Smithsonian Field station, Carrie Bow Cay)

This project explores the ecological functions of bacterial secondary metabolites as agents of chemical defense. It targets marine sediments, a major and poorly explored marine biome. The aims are to test three hypotheses related to the effects of bacterial secondary metabolites on co-occurring microorganisms and protistan grazers. The focus is on the bacterial genus Salinispora, which is well defined in terms of its diversity and distributions in marine sediments, and well characterized at the genomic level and in terms of secondary metabolite production. A genetic system recently developed for these bacteria will be employed to establish links between biological activities and specific secondary metabolites. By employing a variety of innovative methodologies including imaging mass spectrometry, it will be possible for the first time to gain insight into the potential roles of Salinispora secondary metabolites in structuring marine sediment microbial communities. The results will have broad implications for our understanding of the factors that regulate the diversity and distributions of bacteria in the marine environment. They will additionally address the supplemental hypothesis that secondary metabolites represent ecotype-defining traits that delineate Salinispora species.

The hypotheses to be tested are:
H1: Secondary metabolites inhibit microbial competitors,
H2: Secondary metabolites affect bacterial community composition, and
H3: Secondary metabolites function as invertebrate feeding deterrents.

A large collection of diverse, co-occurring microbes will be tested for sensitivity to Salinispora secondary metabolites using a direct challenge assay. These types of assays are highly informative in that they can detect behavioral and morphological responses in addition to toxicity. A recently developed imaging mass spectrometry technique will be used to visualize secondary metabolites associated with any observed biological activities. The results will be linked to existing genome sequences and used to aide in compound identification. The associated pathways will be knocked out to provide experimental support for the biological activities of specific compounds.

Given that most marine bacteria are not readily cultured, these experiments will additionally address the effects of secondary metabolites on the sediment bacterial community by employing culture independent techniques. In situ growth chambers and next generation sequencing technologies will be used to test extracts and pure compounds against a natural assemblages of sediment bacteria. The results will inform future cultivation efforts and provide a more comprehensive assessment of the organisms targeted by native chemical defenses. Finally, a robust feeding assay using two model protists will be developed and used to test the roles of bacterial secondary metabolites as invertebrate feeding deterrents. In situ experiments will provide insight into the natural assemblage of invertebrates affected by these defenses. The overall results of these studies have the potential to profoundly impact our understanding of the ecological functions of microbial secondary metabolites and the extent to which these compounds affect community composition.

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Funding

Funding Source	Award
NSF Division of Ocean Sciences (NSF OCE)	OCE-1235142

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