Accession numbers for Labyrinthulomycetes detected in sea fans collected in the Florida Keys and Puerto Rico from 2006-2010 (Climate_CoralDisease project)

Website: https://www.bco-dmo.org/dataset/3718
Version: 12 Sept 2012
Version Date: 2012-09-12

Project
» Influence of Temperature and Acidification on the Dynamics of Coral Co-Infection and Resistance (Climate_CoralDisease)

Contributors	Affiliation	Role
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Mydlarz, Laura	University of Texas at Arlington (UT Arlington)	Co-Principal Investigator
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Dataset Description

Accession numbers to NCBI's GenBank are provided for *Labyrinthulomycetes* detected in sea fans collected in Florida and Puerto Rico.

References:

Burge CA, Douglas N, Conti-Jerpe I, Weil E, Roberts S, Friedman CS & CD Harvell. In press (May 2012) Friend or foe: the association of Labyrinthulomycetes with the Caribbean sea fan, *Gorgonia ventalina*. Dis Aquat Org.

Methods & Sampling

Sampling and Analytical Methodology:
Healthy and diseased sea fans were collected from Florida and Puerto Rico. *Labyrinthulomycetes* cells were isolated from a diseased sea fan from Florida; DNA extracted, amplified, cloned, sequenced, and deposited with accession # JQ248602. Fragments of healthy and diseased sea fans were extracted, amplified, cloned and sequenced under accession numbers JQ248603 (Florida), JQ248604 (Florida), JQ248605 (Puerto Rico), and JQ248606 (Puerto Rico).

Labyrinthulomycota small-subunit ribosomal DNA (SSU rRNA) specific primers, Laby-A and Laby-Y, were used (Stokes et al., 2002). Those containing bands of the expected (~ 430 bp) size were purified using the QIAquick PCR kit (Qiagen,) and sent to the Cornell University Life Sciences Core Laboratories for direct sequencing on an Applied Biosystems Automated 3730 DNA Analyzer. Although direct sequencing of all of the PCR products showed unambiguous DNA chromatographs throughout, the homogeneity of samples was additionally confirmed by cloning the PCR products into the TOPO-TA vector, using the TOPO TA cloning kit (Invitrogen) for

sequencing of 2 to 5 clones of each isolate.

Data Processing Description

The BLAST algorithm (Altschul et al.1990) was used to compare resulting sequences (overlapping 398 nt from Florida samples and 292 nt from Puerto Rico samples) with those deposited in the National Center for Biotechnology Information (NCBI) GenBank database, and alignments were made using the EMBL-EBI Clustal W tool (Larkin et al. 2007, Goujan et al. 2010). Representative sequences from the cultured microorganism and sea fan isolates were submitted to GenBank.

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Data Files

File
sea_fan_parasite_seq.csv (Comma Separated Values (.csv), 844 bytes) MD5:0efb013350beecb6ace3838174d929aa Primary data file for dataset ID 3718

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Parameters

Parameter	Description	Units
site	Name of the reef where the sample was collected.	text
lat	Latitude of the collection site. North = positive.	decimal degrees
lon	Longitude of the collection site. West = negative.	decimal degrees
sequence_name	Name of the sequence/sample.	text
accession_number	Assigned accession number and link to GenBank.	unitless

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Instruments

Dataset-specific Instrument Name	Automated DNA Sequencer
Generic Instrument Name	Automated DNA Sequencer
Dataset-specific Description	Direct sequencing was performed at the Cornell University Life Sciences Core Laboratories on an Applied Biosystems Automated 3730 DNA Analyzer
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.

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Deployments

Coral_Dive_HM

Website	https://www.bco-dmo.org/deployment/58855
Platform	shoreside PR_Keys_Reef
Start Date	2006-09-01
End Date	2010-09-01
Description	Four dive sites for the Harvell/Mydlarz project 'Influence of Temperature and Acidification on the Dynamics of Coral Co-Infection and Resistance': Big Pine Ledges, Florida Keys: 24° 33.207 N, 81° 22.731 W Laurel patch reef, La Parguera, Puerto Rico: 17° 56.608 N, 67° 03.208 W Media Luna, La Parguera, Puerto Rico: 17°56.093 N, 67°02.931 W (3 to 18 m depths) Buoy, La Parguera, Puerto Rico: 17° 53.38 N, 66° 59.09 W (18 to 25 m depths)

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Project Information

Influence of Temperature and Acidification on the Dynamics of Coral Co-Infection and Resistance (Climate_CoralDisease)

Coverage: Florida Keys & Puerto Rico

This award is funded under the American Recovery and Reinvestment Act of 2009 (Public Law 111-5).

Coral reef ecosystems are highly endangered by recent increases in temperature and by projected increases in ocean acidification. Although temperature has been identified as a driver of some coral disease outbreaks, nothing is known about direct effects of acidification on host immunity and pathogen virulence, or the potential for synergism with temperature. Natural coral populations often suffer from simultaneous infection by multiple pathogens that can also influence host immune responses, but co-infection dynamics have not been investigated in invertebrate systems lacking classical adaptive immunity. Changing climate will very likely influence the outcome of single and co-infection.

This project will investigate the influence of environmental stress on co-infection dynamics of the sea fan coral,

Gorgonia ventalina, with a fungal pathogen, *Aspergillus sydowii* and a protist parasite, SPX. The goal is to identify the mechanisms through which multiple infections, temperature and acidification modify host resistance, leading to changes in within- and among-colony rates of disease spread.

The objectives of this project are to:
(1) Identify incidence and co-infection frequency of *Aspergillus sydowii* and SPX. Detailed field surveys of the two diseases will test the hypothesis that co-infection is significant, provide valuable information about drivers of aspergillosis, and will help to characterize an emerging new sea fan disease.
(2) Investigate how co-infection influences sea fan susceptibility, resistance, and within host disease dynamics. Through manipulative lab inoculation experiments we will test the hypothesis that single infections increase susceptibility to a second pathogen.
(3) Examine the effects of temperature increase and ocean acidification on pathogen virulence, on underlying host resistance, and on the dynamics of single and co-infections.

The hypotheses that acidification will increase pathogen virulence and host susceptibility will be tested in a temperature and pH controlled experimental system. This system will also allow the potential synergistic effects of temperature and acidification on host immunity and co-infection dynamics to be explored. The primary intellectual merit of the proposed work will be a greater understanding of how changing climate mediates co-infection and immunity in a non-model invertebrate. While fungal pathogens are primarily opportunistic, labyrinthulid protozoans are recognized as primary pathogens in shellfish. Even in shellfish, little is known about co-infections involving labyrinthulids, and these protists are entirely unstudied in corals.

Publications associated with this project:
Burge CA, Douglas N, Conti-Jerpe I, Weil E, Roberts S, Friedman CS & CD Harvell. (May 2012) Friend or foe: the association of *Labyrinthulomycetes* with the Caribbean sea fan, *Gorgonia ventalina*. Dis Aquat Org. 101:1-12. doi: 10.3354/dao02487

Burge CA, Mouchka, ME, Harvell, CD & S Roberts. (In review) Immune response of the Caribbean sea fan, *Gorgonia ventalina* exposed to an *Aplanochytrium* parasite as revealed by transcriptome sequencing.

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Funding

Funding Source	Award
NSF Division of Ocean Sciences (NSF OCE)	OCE-0849776

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