

CoralMicrobes.org: An Interactive, Public **Database Designed to Facilitate Research** Focused on Coral Microbial Diversity

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Abstract

Bacterial communities associated with corals vary among coral species and along environmental gradients and are further influenced by ecological stressors, including increased ocean temperature and disease. A global perspective of the temporal and spatial variability of these communities can best be achieved by the joint efforts of researchers sharing data that allow for the examination of broader ecological questions over larger spatial scales. For this purpose, we have developed a publicly-accessible website, CoralMicrobes.Org, which will serve as a repository for culture-independent and culture-dependent data of bacteria associated with corals. For culture-dependent data, information on isolates obtained will include a suite of phenotypic as well as phylogenetic parameters, while the culture-independent data will focus on 16S rRNA gene clone libraries with future inclusion of metagenomic libraries. In conjunction with a suite database query tools, these data will allow for comprehensive investigations of the ecology of coral-associated bacteria from a wide range of locations, coral species, environmental states, and health conditions. This archival system is supported jointly by the National Science Foundation's Biodiversity Survey's and Inventories program, the Hollings Marine Laboratory, and Clemson University's Cyberinfrastructure Technology Integration group and Genomics Institute. The site will facilitate new scientific objectives, provide the capacity for long-term data storage and data dissemination, as well as provide new opportunities for discovery and foster new collaborations. Together, participants in this virtual organization can freely exchange data and ideas that will expand our understanding of the complex biological components

Introduction

The CoralMicrobes.org Project is based at the Hollings Marine Laboratory (Charleston, SC, USA) and reflects a cooperative effort between research groups at the Medical University of South Carolina, the Clemson University Genomics Institute and the Cyberinfrastructure Technology Integration.

The development of this project has been supported by the National Science Foundation Biodiversity Surveys and Inventories program, the Marine Biomedicine and Environmental Sciences Center of the Medical University of South Carolina, and by the NOAA Center of Excelle Oceans and Human Health at the Hollings Marine Laboratory

Objectives

To develop an interactive, public database to facilitate the global study of coral-associated microbial communit

The database will incorporate information related to both culture-dependent and culture-independent microbial communities, and include key metadata for each isolate or sequence contributed. As such users will be able to search the database using a number of different key parameters.

To provide a suite of tools to query and analyze uploaded

Integrated Tools

The match tool will use a web service, SEQMATCH, associated with the Ribosomal Database Project (RDP). Users will select sequences within their sandbox and view the closest matching sequences from RDP. Then the user can select the match sequences they want to add to their sandbox for further analysis.

> Taxonomy Classifier

The taxonomy information will be updated through a web service, CLASSIFIER, associated with RDP. Taxonomy hierarchies will be stored locally to allow additional analysis by other tools.

≻Phylogenetic Tree Building

A user will be able to build an interactive phylogenetic tree with sequences in their sandbox.

≻Maps

A global map will be available when a user wants to analyze and compare libraries. A graphical map with push-pins representing sample locations will give users an easy way to see where all sequences in the database were collected. Clicking on a sample will pop-up a pie chart describing its taxonomic distribution.

>Multiple Library Comparisons

A user can select multiple samples from the map and view them in an interactive table. The table will be normalized for comparing libraries of different size and can be sorted and manipulated to display custom views.

Data Input and Analysis

After evaluating current off-the-shelf database schemas and discussing our requirements with other sequence repositories we decided to develop a custom relational database schema for coralmicrobes.org. This allows us to relate all the data suggested in the Minimum Information about a Genome Sequence (MIGS) perspective to all the 16S and metagenomic sequences submitted.

The website will be hosted by Clemson University and employs Web2.0 approach. Coralmicrobes.org is integrating services developed at HML with others provided by RDP and Google. For the website content we are using Drupal to create an environment that users can comment, share and discuss their ideas and concerns.

Example coral colony

- 16S rDNA clone libraries FASTA format Aligned to RDP's alignment

454 Metagenomic libraries (to be developed)

- Assembled contigs Annotated ORFs
- Metabolic pathway maps

Phenotypic characterization

- Colony morphology Cell morphology
- Antimicrobial activity Antibiotic resistance

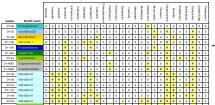
Genotypic characterization

16S rDNA sequence
Organism identification

Metadata

Authors	Williams, Weil, and Morris
Collection date	3/13/2006
Latitude	17.97
Longitude	-67.05
Water depth (m)	2.0
Coral species	Pseudopterogorgia americana
Health Status	Diseased
Habitat (mucus, tissue, skeleton)	Mucus
Habitat comment (how collected)	Syringe aspirated
Are isolates	True
Incubation temp (*C)	24.0
Media	Glycerol-amended artificial seawater
Volume (mL)	5.0
Shaking	True
Light	False
Has been accepted	False

Table of antibiotic resistance profiles of culturable isolates from P. americana mucus











Map Tool

Below is a screen shot of the interactive Map tool. Users will be able to access metadata, isolate data, and community composition from locations by



Significance

- >The coralmicrobes.org database will be provide a single repository for coral-associated microbial data from multiple
- The site is intended to facilitate investigations of coral-microbe interactions on a global scale and to foster collaboration among
- ➤ Compliance with proposed MIGS/MIMS data standards will allow rigorous examination of potential methodological biases.
- >Inclusion of both culture-dependent and culture-independent data will enable researchers to investigate both genotypic and phenotypic characteristics of coral-associated microbiota
- >The success and utility of coralmicrobes.org is entirely dependent on the participation and feedback of users. WE WANT YOUR DATA AND YOUR INPUT!

Contact us at: info@coralmicrobes.org

