

# GenBank accession numbers for pathogens identified as causing Montipora White Syndrome in corals sampled from Kaneohe bay, Oahu, Hawaii during 2014

Website: <https://www.bco-dmo.org/dataset/545991>

Data Type: experimental

Version: 2014-08-28

## Project

» [Host-environment-pathogen interactions in a model coral disease system](#) (coral-pathogen interaction)

Contributors	Affiliation	Role
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## Dataset Description

### Related datasets:

[Montipora antibacterial-aqueous](#)  
[Montipora antibacterial-mucus](#)  
[Montipora antibacterial-organic](#)  
[Montipora chemical fingerprints](#)  
[MWS lesion progression](#)

### Related references:

Ushijima et al. 2012: *Vibrio owensii* Induces the Tissue Loss Disease *Montipora* White Syndrome in the Hawaiian Reef Coral *Montipora capitata*. *PLoS ONE* 7: e46717.

Ushijima et al. 2013: Draft Genome Sequence of *Vibrio coralliilyticus* Strain OCN008, Isolated from Kāne'ohe Bay, Hawai'i. *Genome Announcements*. 1:e00786-13-e00786-13.

Ushijima et al. 2014: *Vibrio coralliilyticus* Strain OCN008 Is an Etiological Agent of Acute *Montipora* White Syndrome. *Applied and Environmental Microbiology* 80:2102-2109.

## Methods & Sampling

See the publications above for detailed methodology.

For accession numbers JX127210 to JX127222 from Ushijima et al. 2012, *PLoS ONE*

For accession number AV0000000000 from Ushijima et al. 2013, *Genome announcements*.

For accession numbers KF042020 to KF042038 from Ushijima et al. 2014, *Applied and Environmental Microbiology*.

### Brief summary of methods:

Samples were collected from Kaneohe Bay, Oahu, Hawaii in 2011, 2012, and 2013.

Bacteria were isolated using standard microbiology techniques. DNA was extracted using a phenol-chloroform technique. PCR amplification was performed using DNA oligos. Refer to publications mentioned above for detailed methodology, statistical analyses, and results.

### Data Processing Description

DNA sequences were trimmed using Gene Construction Kit software.

#### BCO-DMO Processing:

- added conventional header with dataset name, PI name, version date
- renamed parameters to BCO-DMO standard or to match other datasets in project
- replaced blanks with underscores

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### Data Files

File
<b>accession_nums.csv</b> (Comma Separated Values (.csv), 5.25 KB) MD5:6c11c15d4e52fe23e46edb594d39c1e6
Primary data file for dataset ID 545991

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### Parameters

Parameter	Description	Units
Genbank_accession_num	GenBank accession number	unitless
organism	organism taxonomic name and strain	unitless
description	description of sequenced genetic material	unitless
accession_link	link to GenBank accession number page	unitless

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### Deployments

#### Aeby\_2014

<b>Website</b>	<a href="https://www.bco-dmo.org/deployment/544868">https://www.bco-dmo.org/deployment/544868</a>
<b>Platform</b>	Hawaii_reef
<b>Start Date</b>	2010-06-01
<b>End Date</b>	2014-05-31
<b>Description</b>	Coral reef pathogen studies.

## Project Information

### Host-environment-pathogen interactions in a model coral disease system (coral-pathogen interaction)

**Coverage:** Kaneohe Bay, Oahu, Hawaii (21 26' N, 157 47' W)

*Extracted from the NSF award abstract:*

Diseases of marine organisms have emerged as a serious problem contributing to the decline of coral reef resources worldwide. Loss of coral reef habitats carry social and economic implications especially in island states, such as Hawaii, which depend on reefs for food, shoreline protection and tourism. Our ability to manage coral diseases is hampered by a lack of knowledge of which environmental variables affect disease, mechanisms of host defense, and the etiology of most of the numerous described coral diseases. The PIs of this project discovered a coral disease system that can be used as a model to explore many components of the host-environment-pathogen triangle of disease causation. Montipora white syndrome (MWS) is an infectious disease that results in progressive tissue loss on colonies of *Montipora capitata*, and has been found on reefs throughout the Hawaiian archipelago. It is particularly prevalent in Kaneohe Bay, Oahu, which has a long history of reduced water quality, and this suboptimal environment sets the stage where host-pathogen interactions occur. In Kaneohe Bay, *M. capitata* is a major reef-building species, and is found in two color morphs (red and orange) that harbor different clades of zooxanthellae. During preliminary surveys, the PIs discovered intraspecific variability in response to MWS between color morphs. Although the red morph was dominant within survey transects (80% of the colonies), the orange morph was disproportionately affected by MWS (70% of the affected colonies). Microbial studies found a shift in bacterial communities on MWS-affected and healthy *M. capitata* and allowed identification of potential pathogens. Numerous bacterial strains were cultured and screened for pathogenicity and three strains, which produced lesions, were identified as potential pathogens. Two of the putative pathogens (*Vibrio* spp.) produced diffuse tissue whereas the other bacterial strain (*Pseudoalteromonas* sp.) produced acute tissue loss.

In the field, the PIs also observed two patterns of tissue loss on *M. capitata*; a slow, chronic pattern of tissue loss, which they followed through time with tagged colonies (chronic MWS), but also a rapid onset of acute tissue loss (acute MWS). Thus they discovered an infectious coral disease that results in significant coral mortality that has the unique component of differences in disease susceptibility among color morphs. The PIs identified three potential bacterial pathogens that will be used to investigate underlying factors affecting the coral-environment-pathogen triad of disease causation. The Hawaii Institute of Marine Biology (HIMB) is located within Kaneohe Bay allowing year-round access to reefs for research on Montipora white syndrome. The goal of this project is to investigate the host- environment-pathogen triangle of disease causation for Montipora white syndrome. The objectives of this research will be to: 1) investigate mechanisms contributing to differential disease resistance in red (less susceptible) vs. orange (more susceptible) morphs of *M. capitata*. The PIs will compare antimicrobial activity in the holobiont, mucus and mucus-associated bacteria of the two color morphs of *M. capitata*, and will compare the natural coral-associated microbial flora between the two color morphs; 2) use manipulative aquarium studies to determine whether environmental stressors (elevated temperature, nutrient stress) differentially affect the progression or transmission efficiency of MWS in red vs. orange morphs of *M. capitata*; 3) use challenge experiments to confirm the role of bacterial pathogens as causative agents of MWS, and to determine the response of red vs. orange morphs of *M. capitata* to three putative pathogens. This project will involve a multidisciplinary team to provide a broader perspective of coral disease processes. This will be the first comprehensive study conducted on a coral disease in Hawaii.

*Related Publications:*

Ushijima, B, Videau, P, Burger, A, Shore-Maggio, A, Runyon, C, Sudek, M, Aeby, G and S. Callahan. 2014. *Vibrio coralliilyticus* strain OCN008 is an etiological agent of acute Montipora white syndrome. *Applied & Environ Microbiology* doi:10.1128/AEM.03463-13.

Ushijima B, Videau P, Aeby GS, Callahan SM. 2013. Draft Genome Sequence of *Vibrio coralliilyticus* Strain OCN008, Isolated from Kane'ohe Bay, Hawai'i. *Genome Announc.* 2013 Oct 3;1(5). doi:pil: e00786-13. 10.1128/genomeA.00786-13. PMID: 24092784

Ushijima B, Smith A, Aeby GS, Callahan SM (2012) *Vibrio owensii* Induces the Tissue Loss Disease Montipora

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## Funding

Funding Source	Award
<a href="#">NSF Division of Ocean Sciences (NSF OCE)</a>	<a href="#">OCE-0961814</a>

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