

# Sea star sample information from Dutch Harbor, AK from September 12-14th, 2015 (Sea Star Microbiology project)

**Website:** <https://www.bco-dmo.org/dataset/719906>

**Data Type:** Other Field Results

**Version:**

**Version Date:** 2017-10-13

## Project

» [Microbial ecology of sea star wasting disease](#) (Sea Star Microbiology)

Contributors	Affiliation	Role
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## Coverage

**Spatial Extent:** N:53.902823 E:-166.465081 S:53.856984 W:-166.5631

**Temporal Extent:** 2015-09-12 - 2015-09-14

## Dataset Description

This dataset includes sea star sampling information collected for a survey of sea star-associated densovirus (SSaDV) prevalence and load in asymptomatic animals from near Dutch Harbor, Unalaska, AK from September 12-14th, 2015. The data include sample number, species, size, collection time, latitude, and longitude.

## Methods & Sampling

**Methodology:** A previous survey (March 2015, before currently funded work) established that among 66 asteroids collected from Dutch Harbor, AK, none were positive for SSaDV. We again surveyed this population during aquarium specimen collection in September 2015 to determine the presence/load of SSaDV.

**Sampling and analytical procedures:** Animals were collected by hand or by SCUBA diver at 3 locations near Dutch Harbor, AK in September 2015. Body wall tissues were biopsied on site to determine the presence/load of SSaDV. Biopsy punches were immediately placed in 100% EtOH before transport back to the lab at Cornell University. At the same time, 68 live asteroids (n = 8 *Pycnopodia helianthoides*, n = 20 *Solaster stimpsonii*, n = 20 *Evasterias troscheli*, n = 20 *Crossaster papposus*) were collected by SCUBA diver at Dead Man's Bend, placed into shipping containers, and then sent back to the lab at Cornell University. Unfortunately, all except 6 *Evasterias troscheli* and 3 *Solaster stimpsonii* died in transit due to Alaska Airlines and Fedex delays. Size was measured by measuring the diameter of the individual (longest arm to longest arm) visually using a ruler.

SSaDV abundance/load will be determined by qPCR following the approach of Hewson et al., 2014 (PNAS).

## Data Processing Description

BCO-DMO Data Manager Processing Notes:

- \* added a conventional header with dataset name, PI name, version date
- \* modified parameter names to conform with BCO-DMO naming conventions

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## Data Files

File
<b>DutchHarbor.csv</b> (Comma Separated Values (.csv), 1.92 KB) MD5:ce5e0f0d37727c8beedcfb2b7307b40d
Primary data file for dataset ID 719906

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## Related Publications

Hewson, I., Button, J. B., Gudenkauf, B. M., Miner, B., Newton, A. L., Gaydos, J. K., ... Harvell, C. D. (2014). Densovirus associated with sea-star wasting disease and mass mortality. *Proceedings of the National Academy of Sciences*, 111(48), 17278–17283. doi:[10.1073/pnas.1416625111](https://doi.org/10.1073/pnas.1416625111)  
*Methods*

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## Parameters

Parameter	Description	Units
Sample_No	Sample identifier	unitless
Location	Location name	unitless
Site	Site name at location	unitless
Species	Species name	unitless
Size	Diameter of the individual (longest arm to longest arm) visually using a ruler.	centimeters (cm)
Depth	Collection depth	meters (m)
Date_Collected	Collection date in format yyyy-mm-dd	unitless
Lat	Collection latitude	decimal degrees
Long	Collection longitude	decimal degrees

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## Deployments

### SeaStarMicrobiology\_Hewson

<b>Website</b>	<a href="https://www.bco-dmo.org/deployment/720080">https://www.bco-dmo.org/deployment/720080</a>
<b>Platform</b>	shoreside Alaska

## Project Information

### Microbial ecology of sea star wasting disease (Sea Star Microbiology)

**Website:** <http://seastarwastingdisease.wordpress.com>

**Coverage:** Salish Sea and Alaskan Waters

Beginning in June 2013 and continuing to present (May 2015), over 20 species of sea stars (Asteroidea, Echinodermata) have been affected by sea star wasting disease (SSWD), affecting populations from central Alaska to Baja California. The disease has led to greatly reduced abundance or disappearance of these keystone predators, which may result in profound alteration to benthic community structure. Recent work has identified the sea star associated densovirus (SSaDV) as the most likely causative agent of the disease. SSaDV is related to densoviruses inhabiting other echinoderms worldwide, and has been present in West Coast asteroid populations for at least 72 years. Hence, there remain significant knowledge gaps in our understanding of how SSaDV actually elicits SSWD symptoms, especially how the echinoderm host, densovirus and microbiome constituents interact. This project will address three major questions: 1) does viral infection change the composition of the sea star microbiome?, 2) what is the variation of viral genomes and their associated virulence?, and 3) does larval dispersal spread the disease between habitats? This project will address these hypotheses through time-course measurements of host, pathogen and associated microorganisms, genome-genome comparisons between historical and contemporary viral strains, and through experiments targeting larvae and juvenile asteroids in aquaria and in nature.

This project will address three fundamental questions relating to Sea Star Wasting Disease (SSWD): 1) How does SSaDV causes SSWD symptoms and how does the disease progress from primary infection through animal mortality; 2) How do current genotypes of SSaDV vary from those present historically, and is virulence related to genome polymorphisms; and 3) Are larvae and juvenile asteroids differentially affected by SSaDV, and are broadcast-spawned bipinnaria a viable mechanism for SSaDV dispersal between distant habitats. The first question will be addressed by experimental inoculation of naïve sea stars with SSaDV, then time-course monitoring of host transcription (i.e. transcriptomics via RNAseq), microbiome composition via 16S rRNA sequencing and quantitative PCR, and viral load and prevalence using quantitative PCR. The second question will be addressed by amplifying the entire genome of SSaDV and related densoviruses, then perform genome-genome comparisons to identify polymorphic DNA in key protein-encoding regions. The third question will be addressed by collecting bipinnaria from plankton at field locations adjacent to spawning asteroid populations, and by performing time-course observations of captive juvenile sea stars and monitoring their bacterial and viral loads using quantitative PCR. This work will be performed primarily in the Salish Sea region, with SSaDV - naïve asteroids collected from Alaskan waters.

## Funding

Funding Source	Award
<a href="#">NSF Division of Ocean Sciences (NSF OCE)</a>	<a href="#">OCE-1537111</a>