

Sea star specimen voucher data from the LA County Museum of Natural History (Sea Star Microbiology project)

Website: <https://www.bco-dmo.org/dataset/719924>

Version:

Version Date: 2017-10-13

Project

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

| Contributors | Affiliation | Role |
|--------------------------------|---|---------------------------------|
| Hewson, Ian | Cornell University (Cornell) | Principal Investigator, Contact |
| York, Amber D. | Woods Hole Oceanographic Institution (WHOI BCO-DMO) | BCO-DMO Data Manager |

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Dataset Description

This dataset includes sea star specimen information from the LA County Museum of Natural History.

Specimens described in this dataset were used in a survey of historical sea star-associated densovirus (SSaDV) presence and genome variation.

Methods & Sampling

Methodology: A survey of historical SSaDV presence and genome variation was performed on specimens donated by the LA County Museum of Natural History and the California Academy of Sciences.

Sampling and analytical procedures: SSaDV was detected using primers/probes targeting two genes on its genome in historical samples from 1947 to present (Hewson et al., 2014). We sought to extend this survey with additional specimens donated from the California Academy of Sciences (SF) and the LA County of Natural History, and to study genome variation in SSaDV by full-length genome sequencing. Donated samples were sampled at the museums by clipping 5 tube feet from each ethanol-preserved sample and placing these into sterile 1.5 ml cryovials. The samples were then returned to the lab at Cornell University for processing.

SSaDV abundance/load will be determined by qPCR following the approach of Hewson et al., 2014 (PNAS). Genome variation will be studied by applying PCR to qPCR positive samples to amplify overlapping parts of the SSaDV genome and then studying their direct sequence-sequence variation.

Note that species identifications in this dataset with a question mark indicate a questionable identification.

References:

Hewson, I., Button, J. B., Gudenkauf, B. M., Miner, B., Newton, A. L., Gaydos, J. K., ... & Fradkin, S. (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)

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
- * added data column "year" since the date had mixed formats (date ranges, partial dates)
- * commas changed to semicolons in text fields of data to support csv versions of the data.
- * split collection/location in collection into two separate columns "collection" and "location_in_collection."

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Data Files

| File |
|---|
| LACM.csv (Comma Separated Values (.csv), 5.85 KB) MD5:9dfeb301199f98b321af1cd4d30b7aa6 Primary data file for dataset ID 719924 |

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Parameters

| Parameter | Description | Units |
|------------------------|---|----------|
| date_sampled | Date a sample was taken from the specimen in format dd-mmm-yy | unitless |
| HEWSON_Z_num | Sample identifier used internally in the Hewson lab | unitless |
| LACM_num | The specimen identifier used in the collection | unitless |
| id | Taxonomic identification of the specimen to the Genus or Genus species level. A question mark at the end indicates the identification was questionable. | unitless |
| count | unknown | unknown |
| Field_num | Field location identifier | unitless |
| locality | Field location descriptive name | unitless |
| date_descriptive | Date the specimen was collected in various formats and time resolutions. | unitless |
| year | Year specimen was collected in format yyyy | unitless |
| collection | Collection the specimen was part of | unitless |
| location_in_collection | Location of specimen within the collection | unitless |
| Comments | Comments | unitless |

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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.

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Funding

| Funding Source | Award |
|--|-----------------------------|
| NSF Division of Ocean Sciences (NSF OCE) | OCE-1537111 |

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