

# Sea star specimen voucher data from the California Academy of Sciences (Sea Star Microbiology project)

**Website:** <https://www.bco-dmo.org/dataset/719932>

**Version:**

## Project

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

Contributors	Affiliation	Role
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## Dataset Description

Note: This dataset was submitted to BCO-DMO and is in the process of being served.

This dataset includes sea star specimen information from the California Academy of Sciences. The 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 1942 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.

## 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

- \* removed quotation marks around ship names due to character restrictions
- \* commas changed to semicolons in text fields of data to support csv versions of the data.
- \* version 2018-02-21 replaces version 2017-10-06 with the only change being that a blank column with parameter "Coord" was removed.

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## Data Files

File
<b>CAS.csv</b> (Comma Separated Values (.csv), 14.46 KB) MD5:51b50e08c02cc7149a242a7535bc86ec
Primary data file for dataset ID 719932

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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
CatNum	Identifier for the specimen in the catalog	unitless
Hewson_Lab_Z_Num	Identifier for the sample taken from the specimen used in the Hewson lab	unitless
Size	Size of the specimen (both numeric and descriptive). Numeric values are in cm.	various
AccNum	California Academy of Sciences Accession Number	unitless
AccAcro	California Academy of Sciences Accession Acronym	unitless
Phylum	Specimen phylum	unitless
Family	Specimen family	unitless
HigherClassif	Specimen taxonomic information	unitless
Genus	Specimen genus	unitless
Species	Specimen species	unitless
Author	Author of the species description	unitless
Locality	Specimen collection location	unitless
BegDepth	Start of specimen collection depth range	various
EndDepth	End of specimen collection depth range	various
DepthUnits	Units of beginning and end depth	various
Intertidal	Location description indicating whether the collection site was intertidal (TRUE or FALSE)	unitless
Substratum	Description of sample location substratum	unitless

CollName	Collection the specimen belongs to	unitless
CollDate	Date of organism accession to collection	date
Identifier	Person who made the identification	unitless
IdDate	Date of the identification	date
OrigFix	Original preservative used to fix the specimen	unitless
Preservative	Preservative used for long-term preservation	unitless
Photos	Denotes whether photos are available	unitless
FieldNum	Specimen number designated by field collector	unitless
NumSpecimens	Number of specimens in collection	unitless
ExpeditionName	Expedition name that collected the specimen	unitless
GenBankNum	Genbank accession number for genetic work	unitless
CollectMethod	Method of collection	unitless
Collector	Name of collector or vessel	unitless
CollDateText	Date of collection	date
IdDateText	Date of identification	date
BegDepthMeters	Beginning depth of collection	meters
EndDepthMeters	Ending depth of collection	meters
BLatDeg	Beginning latitude degrees	degrees
BLatMin	Beginning latitude minutes	minutes
BLatSec	Beginning latitude seconds	seconds
LatHemi	Latitude hemisphere (N = north or S = south)	unitless
ELatDeg	Ending latitude degrees	degrees
ELatMin	Ending latitude minutes	minutes
ELatSec	Ending latitude seconds	seconds
BLongDeg	Beginning longitude degrees	degrees
BLongMin	Beginning longitude minutes	minutes
BLongSec	Beginning longitude seconds	seconds
LongHemi	Longitude hemisphere (W = west or E = east)	unitless
ELongDeg	Ending longitude degrees	degrees
ELongMin	Ending longitude minutes	minutes
ELongSec	Ending longitude seconds	seconds
BegLat	Start of specimen collection latitude range	decimal degrees
EndLat	End of specimen collection latitude range	decimal degrees
BegLong	Start of specimen collection longitude range	decimal degrees
EndLong	End of specimen collection longitude range	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

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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

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

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