Antarctic salp genome and RNAseq transcriptome from ARSV Laurence M. Gould, Umitaka-Maru, R/V Polarstern LMG1110, UM-08-09, ANT-XXVII-2 in the Southern Ocean from 2009-2011 (Salp_Antarctic project)

Website: https://www.bco-dmo.org/dataset/675040
Data Type: Cruise Results
Version:
Version Date: 2017-01-27

Project
» Population ecology of Salpa thompsoni based on molecular indicators (Salp_Antarctic)

Contributors	Affiliation	Role
Bucklin, Ann	University of Connecticut (UConn - Avery Point)	Principal Investigator
O'Neill, Rachel J.	University of Connecticut (UConn)	Co-Principal Investigator
Payne, Diana	Connecticut Sea Grant (CTSG)	Co-Principal Investigator
Copley, Nancy	Woods Hole Oceanographic Institution (WHOI BCO-DMO)	BCO-DMO Data Manager

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Coverage

Spatial Extent: **N**:-60.901 **E**:42.002 **S**:-66.183 **W**:-74.567
Temporal Extent: 2009-01-12 - 2011-12-02

Dataset Description

This dataset reports Salpa thompsoni specimens used for genomics/transcriptomics with their GenBank accession links.

Related Dataset: Salp sample log: www.bco-dmo.org/dataset/672600

Methods & Sampling

1) Cruise R/V LM GOULD (LMG1110): Samples collected using Multiple Opening/Closing Net and Environmental Sensing System (MOCNESS) with a mouth opening of 1-m2 and nine 335µm mesh nets; upper 200 m were sampled with a 2.3 m2 Isaacs-Kidd Midwater Trawl (IKMT) with a 505 µm mesh net. Western Antarctic Peninsula region, Southern Ocean (November-December 2011)

2) Cruise R/V Polarstern (PS-ANT-XVII/2): Samples collected using a Rectangular Midwater Trawl (RMT 1+8) from the upper 200 m. Western Antarctic Peninsula region, Southern Ocean (January 2011)

3) Cruise R/V Umitaka Maru (UM-08-09): Samples collected using a RMT 1+8 from 2,000 m to surface. Indian Sector, Southern Ocean (January 2009)

Data Processing Description

Molecular genetic (genomic and transcriptomic) data resulting from this project have been submitted to appropriate sections of the NCBI GenBank database, as follows:

The Salpa thompsoni Whole Genome Shotgun project (see Jue et al., 2016) has been deposited at DDBJ/ENA/GenBank Genome section under the Accession No. MKHR00000000. The version described in this paper is version MKHR01000000. The genomic data include the final assembly and annotations, as well as all of the raw data files (genomic and small RNAs). Accession Nos. are assigned to the genomic data submission, as follows: SUBID, SUB1479239; BioProject, PRJNA318929; BioSample, SAMN04870323. The Salp Genome Bioproject information and data are available at https://www.ncbi.nlm.nih.gov/genome/?term=MKHR00000000.

The Salpa thompsoni Transcriptome Shotgun Assembly project (see Batta-Lona et al., 2016) has been deposited at DDBJ/ENA/GenBank under the Accession No. GFCC00000000. The version described in this paper is version GFCC01000000. The transcriptomic data includes raw sequencing data and alignment information. The Bioproject Accession No. is PRJNA279245, which includes RNA-seq data from 48 field-collected specimens, which are assigned Biosample Accession Nos. SAMN05604989 - SAMN05605036. The Salp Transcriptome Bioproject information and data are available at https://www.ncbi.nlm.nih.gov/nuccore/GFCC00000000.

BCO-DMO Processing notes:
- added conventional header with dataset name, PI name, version date
- modified parameter names to conform with BCO-DMO naming conventions
- added cruise deployment identifiers
- removed SRA accessions from data display

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Data Files

File
salp_accessions.csv (Comma Separated Values (.csv), 11.83 KB) MD5:0ad3f2c8164b89f8ea80fe78eeb013b0
Primary data file for dataset ID 675040

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Related Publications

Batta-Lona, P.G., A. Maas, R. O'Neill, P.H. Wiebe, and A. Bucklin (2016). Transcriptomic profiles of spring and summer populations of the Southern Ocean salp, Salpa thompsoni, in the Western Antarctic Peninsula region. Polar Biology, 40(6), 1261–1276. doi:10.1007/s00300-016-2051-6
Methods

Jue, N. K., Batta-Lona, P. G., Trusiak, S., Obergfell, C., Bucklin, A., O'Neill, M. J., & O'Neill, R. J. (2016). Rapid Evolutionary Rates and Unique Genomic Signatures Discovered in the First Reference Genome for the Southern Ocean Salp,Salpa thompsoni(Urochordata, Thaliacea). Genome Biology and Evolution, 8(10), 3171–3186. doi:10.1093/gbe/evw215
Methods

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Related Datasets

References

University of Connecticut (2015). Salpa thompsoni Transcriptome or Gene expression. 2015/03. In: BioProject [Internet]. Bethesda, MD: National Library of Medicine (US), National Center for Biotechnology Information; 2011-. Available from: http://www.ncbi.nlm.nih.gov/bioproject/PRJNA279245. NCBI:BioProject: PRJNA279245.

University of Connecticut. (2016). Salpa thompsoni, First reference genome for the Southern Ocean salp, Salpa thompsoni (Urochordata, Thaliacea). 2016/09. In: BioProject [Internet]. Bethesda, MD: National Library of Medicine (US), National Center for Biotechnology Information; 2011-. Available from: http://www.ncbi.nlm.nih.gov/bioproject/PRJNA318929. NCBI:BioProject: PRJNA318929.

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Parameters

Parameter	Description	Units
specimen	salp specimen identifier	unitless
cruise_id	cruise identifier	unitless
station	station number	unitless
length	salp length	millimeters
BioSample_accession	GenBank BioSample accession number	unitless
BioSample_accession_link	GenBank BioSample accession number with link to GenBank page	unitless
SRA_accession	GenBank SRA accession number	unitless
SRA_accession_link	GenBank SRA accession number with link to GenBank page	unitless

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Instruments

Dataset-specific Instrument Name	Multiple sequencing platforms: Ion Torrent Proton (Life Technologies, Grand Island, NY), a 454 FLX WGS (Roche Applied Science, Branford, CT), and an Illumina HiSeq 200 (Illumina, San Diego, CA)
Generic Instrument Name	Automated DNA Sequencer
Dataset-specific Description	For genome sequencing
Generic Instrument Description	A DNA sequencer is an instrument that determines the order of deoxynucleotides in deoxyribonucleic acid sequences.

Dataset-specific Instrument Name	Agilent 2100 Bioanalyzer
Generic Instrument Name	Bioanalyzer
Dataset-specific Description	For RNA quality control, and to assess the size distribution of library fragments.
Generic Instrument Description	A Bioanalyzer is a laboratory instrument that provides the sizing and quantification of DNA, RNA, and proteins. One example is the Agilent Bioanalyzer 2100.

Dataset-specific Instrument Name	2.3 m2 Isaacs-Kidd Midwater Trawl (IKMT) with a 505 µm mesh net
Generic Instrument Name	Isaacs-Kidd Midwater Trawl
Generic Instrument Description	A trawl with a pentagonal mouth opening and a dihedral depressor vane as part of the mouth opening. IKMTs come in various dimensions (refer to individual dataset documentation). The original IKMTs were 10 foot (304 cm) and 15 foot (457 cm) at the mouth. The 10 foot IKMT net was 31 feet (9.45 m) in length (Wiebe and Benfield 2003).

Dataset-specific Instrument Name	Rectangular Midwater Trawl (RMT 1+8)
Generic Instrument Name	Midwater Trawl
Generic Instrument Description	A mid-water or pelagic trawl is a net towed at a chosen depth in the water column to catch schooling fish such as herring and mackerel. Midwater trawl nets have very large front openings to herd schooling fish toward the back end where they become trapped in the narrow "broiler". The sides of the deployed net are spread horizontally with two large metal foils, called "doors," positioned in front of the net. As the trawler moves forward, the doors, and therefore the net, are forced outward, keeping the net open. This instrument designation is used when specific make and model are not known.

Dataset-specific Instrument Name	Multiple Opening/Closing Net and Environmental Sensing System (MOCNESS) with a mouth opening of 1-m2 and nine 335µm mesh nets
Generic Instrument Name	MOCNESS1
Generic Instrument Description	The Multiple Opening/Closing Net and Environmental Sensing System or MOCNESS is a family of net systems based on the Tucker Trawl principle. The MOCNESS-1 carries nine 1-m2 nets usually of 335 micrometer mesh and is intended for use with the macrozooplankton. All nets are black to reduce contrast with the background. A motor/toggle release assembly is mounted on the top portion of the frame and stainless steel cables with swaged fittings are used to attach the net bar to the toggle release. A stepping motor in a pressure compensated case filled with oil turns the escapement crankshaft of the toggle release which sequentially releases the nets to an open then closed position on command from the surface. -- from the MOCNESS Operations Manual (1999 + 2003).

Dataset-specific Instrument Name	
Generic Instrument Name	Thermal Cycler
Dataset-specific Description	A PCR product ~500 bp was generated, followed by development of internal primers to produce a smaller PCR product amenable to qPCR.
Generic Instrument Description	A thermal cycler or "thermocycler" is a general term for a type of laboratory apparatus, commonly used for performing polymerase chain reaction (PCR), that is capable of repeatedly altering and maintaining specific temperatures for defined periods of time. The device has a thermal block with holes where tubes with the PCR reaction mixtures can be inserted. The cycler then raises and lowers the temperature of the block in discrete, pre-programmed steps. They can also be used to facilitate other temperature-sensitive reactions, including restriction enzyme digestion or rapid diagnostics. (adapted from http://serc.carleton.edu/microbelife/research_methods/genomics/pcr.html)

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Deployments

LMG1110

Website	https://www.bco-dmo.org/deployment/58728
Platform	ARSV Laurence M. Gould
Report	http://data.bcodmo.org/LMG11-10/LMG11-10_Cruise_Report_06dec11.pdf
Start Date	2011-11-02
End Date	2011-12-01
Description	UNOLS STRS record: http://strs.unols.org/Public/diu_cruise_view.aspx?cruise_id=127242 The primary science objectives of the cruise are to examine genome-wide patterns of gene expression, target gene expression levels, and patterns of population genetic diversity and structure of the Antarctic salp, Salpa thompsoni in relation to biological and physical environmental parameters in the Western Antarctic Peninsula region. High-frequency acoustics data will be used to provide information about the distribution of salps, krill, and other zooplankton. Sampling from shelf and oceanic waters between 0 and 2,000 meters will take place at selected stations using a 1-meter^2 MOCNESS to characterize the planktonic assemblage, and a Reeve net to collect live material for molecular and biochemical analysis. Environmental parameters to be measured include standard hydrographic variables (temperature, salinity, and depth), as well as fluorescence and turbidity. Water samples will be collected using a CTD rosette to determine chlorophyll concentration. An additional science objective is to develop a method of using acoustics to assess the abundance and distribution of salps in the Southern Ocean. Cruise Data Report

UM-08-09

Website	https://www.bco-dmo.org/deployment/672610
Platform	Umitaka-Maru
Start Date	2009-01-12
End Date	2009-01-30
Description	A cruise of the Japanese Research Vessel Umitaka-Maru in the Indian sector of the Southern Ocean, from Cape Town, South Africa to Fremantle, Australia.

ANT-XXVII-2

Website	https://www.bco-dmo.org/deployment/672615
Platform	R/V Polarstern
Report	http://dmoserv3.bco-dmo.org/data_docs/Salp_Antarctic/cruise-rpt_ANT-27-2_Fah2011b.pdf
Start Date	2010-11-28
End Date	2011-02-05

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Project Information

Population ecology of Salpa thompsoni based on molecular indicators (Salp_Antarctic)

Coverage: Southern Ocean

The Antarctic salp, *Salpa thompsoni*, is an increasingly important player in the vulnerable Antarctic Peninsula pelagic ecosystem. Observations of high abundance of Salpa thompsoni during the summer in the Southern Ocean suggest that this species is capable of rapid somatic and population growth, and frequently forms dense blooms under favorable environmental conditions. The proposed research will examine genome-wide

patterns of gene expression, target gene expression levels, and patterns of population genetic diversity and structure of the target salp species. Our preliminary results and data analysis have provided a promising basis for transcriptomic studies of *S. thompsoni* in the Southern Ocean. The proposed next steps in our genomic/transcriptomic analysis of *Salpa thompsoni* are: 1) completion of a reference transcriptome as a basis for genome-wide analysis of gene expression; 2) whole transcriptome shotgun sequencing (RNA-Seq) analysis to characterize gene expression in relation to individual characteristics and environmental conditions; 3) quantitative real-time PCR (qRT-PCR) characterization and validation of gene expression for 10-20 top differentially-expressed genes; and 4) detection of strand-specific allelic variation at SNP (Single Nucleotide Polymorphic) sites to analyze clonal diversity and population genetic diversity and structure. We hypothesize that: 1) deep analysis of the Salpa thompsoni transcriptome will reveal significant associations among selected set of differentially-expressed genes and critical life history stages and events (e.g., ontogenetic maturation, sexual reproduction, senescence) of the salp; and 2) the species will show variable levels of clonal diversity and significant genetic differentiation among salp populations in different regions of the Southern Ocean. Samples will be obtained from research cruises during 2011-2013 in diverse regions of the Southern Ocean; dedicated sample and data collection will be carried out during a cruise of the R/V LM GOULD (LMG11-10) to the Western Antarctic Peninsula region in November, 2011. The significance of this effort lies in new understanding of the molecular processes underlying the complex life history and population dynamics of *S. thompsoni* in relation to the Antarctic pelagic ecosystem and extreme and variable environmental conditions of the Southern Ocean.

Most of the data from this project are available from the Marine Geoscience Data System (MGDS), part of IEDA and is available at http://www.marine-geo.org/tools/search/Files.php?data_set_uid=18148.

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Funding

Funding Source	Award
NSF Antarctic Sciences (NSF ANT)	ANT-1044982

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