NCBI Metagenomic metadata for Lau Basin (Tonga) mollusc gill tissue collected on R/V Thompson cruises TN235 and TN401 and R/V Falkor cruise FK160407 between May 2009 and Apr 2022

Website: https://www.bco-dmo.org/dataset/964236
Data Type: Cruise Results, Other Field Results
Version: 1
Version Date: 2025-08-06

Project
» RUI: Collaborative Research: The impact of symbiont-larval interactions on species distributions across southwestern Pacific hydrothermal vents (symbiont-larval interactions)

Contributors	Affiliation	Role
Beinart, Roxanne A.	University of Rhode Island (URI)	Principal Investigator
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Abstract
Metagenomic sequence data from Lau Basin hydrothermal vent mollusc gill tissues that contain chemosynthetic bacterial symbionts. Samples were collected between May 2009 to April 2022 using the ROV Jason aboard R/V Thompson cruises TN235 (May-June 2009) and TN401 (April 2016) and R/V Falkor cruise FK160407 (April 2022) for population and comparative genomics analysis of host animal and bacterial symbionts.

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Coverage

Location: Hydrothermal vents in the Lau back-arc basin.
Spatial Extent: **N**:-15 **E**:-173.79 **S**:-22.18 **W**:-176.6
Temporal Extent: 2009-05-22 - 2022-04-30

Methods & Sampling

Samples were collected between May 2009 to April 2022 aboard R/V Thompson cruises TN235 (May-June 2009) and TN401 (April 2016) and R/V Falkor cruise FK160407 (April 2022) using the ROV Jason.

Mollusc samples were collected with remotely operated vehicles from hydrothermal vent fields along the Eastern Lau Spreading Center-Valu Fa Ridge and Tonga Volcanic Arc. On board the ship, the symbiont-containing gill tissue of each animal was excised and either flash-frozen or stored in RNALater™ (Thermo Fisher Scientific, Inc., Waltham, MA, USA) at –80°C. DNA was extracted with the E.Z.N.A Mollusc DNA Kit (Omega Bio-tek, Norcross, GA) at the University of Rhode Island and sent to Psomagen, Inc. (Rockville, MD, USA) for metagenomic library preparation and sequencing. Libraries were prepared with the plexWell384 and Twist 96-Plex kits and 150 bp paired-end sequenced on Illumina NovaSeq 6000 and NovaSeq X Plus instruments.

BCO-DMO Processing Description

- Imported "TN401_Metagenomic_Sequencing_NCBI.xlsx" into the BCO-DMO system
- Split "Lat_lon" column into Latitude and Longitude in decimal degrees
- Converted date to ISO YYYY-MM-DD format
- Added accepted AphiaID and LSID for host species in "Host_AphiaID_accepted" and "Host_LSID"
- Exported file as "964236_v1_metagenomic_seq_ncbi.csv"

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Data Files

File
964236_v1_metagenomic_seq_ncbi.csv(Comma Separated Values (.csv), 147.08 KB) MD5:d33dcdce9ccd01002d664651b40cba23 Primary data file for dataset ID 964236, version 1

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Related Publications

Beinart, R., Arellano, S., & Young, C. (2025). Final Cruise Report: TN401. US National Science Foundation. https://doi.org/10.23860/tn401report https://doi.org/10.23860/TN401report
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,
Results

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Related Datasets

References

University of Rhode Island. Metagenomic analyses of Bathymodiolus septemdierum from the Mariner vent field, Lau Basin. 2024/09. In: BioProject [Internet]. Bethesda, MD: National Library of Medicine (US), National Center for Biotechnology Information; 2011-. Available from: https://www.ncbi.nlm.nih.gov/bioproject/PRJNA1159308. NCBI:BioProject: PRJNA1159308.

University of Rhode Island. Metagenomic analyses of hydrothermal vent symbioses from the Tonga Arc. 2024/09. In: BioProject [Internet]. Bethesda, MD: National Library of Medicine (US), National Center for Biotechnology Information; 2011-. Available from: https://www.ncbi.nlm.nih.gov/bioproject/PRJNA1159300. NCBI:BioProject: PRJNA1159300.

University of Rhode Island. Population bottlenecks in Lau Basin hydrothermal vent symbioses. 2024/09. In: BioProject [Internet]. Bethesda, MD: National Library of Medicine (US), National Center for Biotechnology Information; 2011-. Available from: https://www.ncbi.nlm.nih.gov/bioproject/PRJNA1159215. NCBI:BioProject: PRJNA1159215.

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Parameters

Parameter	Description	Units
Sample_ID	Sample ID is composed of the ROV Dive #_collection container ID - specimen #	unitless
Bioproject_accession	NCBI Bioproject accession number associated with this data	unitless
Biosample_accession	NCBI Specimen Biosample accession number associated with this data	unitless
Host_species	Molluscan host species	unitless
Tissue_type	Tissue type that sample originated from	unitless
Latitude	Latitude of sample collection, negative is South	decimal degrees
Longitude	Longitude of sample collection, negative is West	decimal degrees
Collection_date	Date of collection	unitless
Cruise	Cruise ID	unitless
Depth	Depth of collection in meters	meters (m)
MAG_biosample_accession	NCBI Biosample accession for metagenome-assembled genomes (MAGs)	unitless
Sequencing_technologies	Technology used for sequencing	unitless
SRA_Study	NCBI Short-Read Archive (SRA) study ID	unitless
SRA_accession	NCBI Short-Read Archive (SRA) sequence accession	unitless
Assembly_methods	Method used to assemble metagenome	unitless
Symbiont_MAG_ID	ID for the symbiont metagenome-assembled genome (MAG)	unitless
MAG_acc	NCBI Accession for metagenome-assembled genomes (MAGs)	unitless

MAG_organism	Taxonomic assignment for the symbiont metageome-assembled genome (MAG)	unitless
Host_AphiaID_accepted	AphiaID of Molluscan host species	unitless
Host_LSID	LSID of Molluscan host species	unitless

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Instruments

Dataset-specific Instrument Name	Illumina NovaSeq 6000
Generic Instrument Name	Automated DNA Sequencer
Dataset-specific Description	These samples were sequenced with Illumina NovaSeq 6000 and NovaSeq X Plus instruments.
Generic Instrument Description	A DNA sequencer is an instrument that determines the order of deoxynucleotides in deoxyribonucleic acid sequences.

Dataset-specific Instrument Name	NovaSeq X Plus
Generic Instrument Name	Automated DNA Sequencer
Dataset-specific Description	These samples were sequenced with Illumina NovaSeq 6000 and NovaSeq X Plus instruments.
Generic Instrument Description	A DNA sequencer is an instrument that determines the order of deoxynucleotides in deoxyribonucleic acid sequences.

Dataset-specific Instrument Name	ROV Jason
Generic Instrument Name	ROV Jason
Dataset-specific Description	Samples were collected between May 2009 to April 2022 aboard R/V Thompson cruises TN235 (May-June 2009) and TN401 (April 2016) and R/V Falkor cruise FK160407 (April 2022) using the ROV Jason.
Generic Instrument Description	The Remotely Operated Vehicle (ROV) Jason is operated by the Deep Submergence Laboratory (DSL) at Woods Hole Oceanographic Institution (WHOI). WHOI engineers and scientists designed and built the ROV Jason to give scientists access to the seafloor that didn't require them leaving the deck of the ship. Jason is a two-body ROV system. A 10-kilometer (6-mile) fiber-optic cable delivers electrical power and commands from the ship through Medea and down to Jason, which then returns data and live video imagery. Medea serves as a shock absorber, buffering Jason from the movements of the ship, while providing lighting and a bird’s eye view of the ROV during seafloor operations. During each dive (deployment of the ROV), Jason pilots and scientists work from a control room on the ship to monitor Jason’s instruments and video while maneuvering the vehicle and optionally performing a variety of sampling activities. Jason is equipped with sonar imagers, water samplers, video and still cameras, and lighting gear. Jason’s manipulator arms collect samples of rock, sediment, or marine life and place them in the vehicle’s basket or on "elevator" platforms that float heavier loads to the surface. More information is available from the operator site at URL. https://ndsf.whoi.edu/jason/

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Deployments

TN401

Website	https://www.bco-dmo.org/deployment/949221
Platform	R/V Thomas G. Thompson
Report	https://doi.org/10.23860/TN401report
Start Date	2022-03-23
End Date	2022-05-01

TN235

Website	https://www.bco-dmo.org/deployment/654455
Platform	R/V Thomas G. Thompson
Start Date	2009-05-16
End Date	2009-06-08
Description	More information is available from the Rolling Deck to Repository (R2R).

FK160407

Website	https://www.bco-dmo.org/deployment/740047
Platform	R/V Falkor
Start Date	2016-04-07
End Date	2016-05-05
Description	Chief Scientist: Leg 1 - Girguis, Peter, Harvard University Leg 2 - Fisher, Charles, Pennsylvania State University

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Project Information

RUI: Collaborative Research: The impact of symbiont-larval interactions on species distributions across southwestern Pacific hydrothermal vents (symbiont-larval interactions)

Coverage: Eastern Lau Spreading Center, Tonga

NSF Abstract:

Symbiosis with microbes is ubiquitous and critical to fundamental biological functions such as development and nutrition. Thus, the success of a host animal may depend on its ability to find and associate with its microbial partner(s). While some hosts directly transmit their symbionts from parent to offspring in order to guarantee this, acquisition of microbial symbionts from the environment is vital for the survival of many obligately-symbiotic animals. An understanding of the free-living symbiont population and how the host acquires those symbionts is fundamental to our comprehension of ecological processes in all ecosystems, yet almost nothing is known about either. Hydrothermal vent ecosystems provide important opportunities to investigate the role of microbial symbionts in host-, community-, and ecosystem-level ecology, since these ecosystems are dominated by animals whose survival is clearly linked to the acquisition of one or a few specific symbionts. This project begins to fill a gap in our understanding of the factors driving community structure at hydrothermal vents by addressing the potential for free-living symbiont populations to affect host animal establishment, while also expanding our general knowledge regarding the impact of host-associated microbes on fundamental ecological processes that apply across ecosystems. The results of this project will be shared via educational videos and live-broadcasts to the Smithsonian Institution's National Museum of Natural History and University-run museums. The investigators will also design and implement an educational program about symbiosis and hydrothermal vent biology suitable for middle and high school classes. Finally, the investigators will train a diverse group of undergraduate and graduate students in both research and the development of science educational programs.

This project will focus on two sister genera of snails, Alviniconcha and Ifremeria, which predominate at vents in the southwestern Pacific. At vents in the Lau Basin (Tonga), three species of Alviniconcha and one species of Ifremeria coexist. These four species all host distinct lineages of chemoautotrophic proteobacteria in their gill tissue as adults that provide the bulk of their nutrition. Previous work in this region showed a structured snail species distribution that corresponds to the concentrations of key chemical substrates for symbiont chemoautotrophic metabolism, suggesting that snail species are sorting into geochemical habitats based on symbiont physiology. It is not clear if this sorting is occurring among established snail-bacteria symbioses, or whether environmental effects on the availability of specific symbionts are influencing the recruitment of host species, since arriving and developing snail larvae must obtain their symbionts from the environment. This study aims to 1) assess the larval supply and population structure of symbiotic vent snails via collections of larval, juvenile, and adult snails, 2) investigate the developmental timing of symbiont acquisition through microscopy and marker gene sequencing of gametes, larvae, and juveniles, and 3) use metagenomic sequencing to quantify the availability of free-living symbionts in the environment to arriving larvae. Altogether, this series of interlinked efforts will allow for an improved understanding of free-living bacterial symbiont populations, the timing of symbiont acquisition, and host snail life history, as well as how these things interact to shape vent communities.

This award reflects NSF's statutory mission and has been deemed worthy of support through evaluation using the Foundation's intellectual merit and broader impacts review criteria.

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Funding

Funding Source	Award
NSF Division of Ocean Sciences (NSF OCE)	OCE-1736932
NSF Division of Ocean Sciences (NSF OCE)	OCE-1737145
NSF Division of Ocean Sciences (NSF OCE)	OCE-1737382

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