Counts of meroplankton collected with McLane Pump, Sentry/SyPRID, or larval traps from vent field at the Eastern Lau Spreading Center-Valu Fa Ridge on cruise TN401 in Apr 2022

Website: https://www.bco-dmo.org/dataset/997940
Data Type: Cruise Results
Version: 1
Version Date: 2026-05-05

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

Contributors	Affiliation	Role
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Abstract
These data include counts, identifications, and sample volumes for meroplankton taken within vent fields, above vent fields, around (in the periphery) vents, and near the seafloor at seven vent fields in the Lau Basin on cruise TN401 (R/V Thompson) from April 4-30, 2022. Samples within vent fields were taken with a McLane large volume pump deployed with the ROV Jason. Samples from above vent field and around vent field were taken with the AUV Sentry using the SyPRID sampler. Near-seafloor samples were collected with larval tube traps. These samples provide baseline data for meroplankton presence shortly after the catastrophic Hunga submarine volcanic eruption on January 15, 2022, which impacted these sites. These data were collected by Dr. Shawn Arellano of Western Washington University.

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Coverage

Location: Six known vent sites along a ~ 240 km section of the Eastern Lau Spreading Center-Valu Fa Ridge
Spatial Extent: **N**:22.180667 **E**:-173.79425 **S**:15.003529 **W**:-176.60614
Temporal Extent: 2022-04-02 - 2022-04-30

Methods & Sampling

To estimate larval supply to the seafloor, two replicate larval tube traps were simultaneously deployed for approximately two weeks at the base of a vent chimney at each site (except Mariner or Mata Tolu) in an animal-free patches. These self-opening tube traps (described in Young et al. 2015) consisted of four tubes made of three 50-mL Falcon tubes conjoined with cyanoacrylate adhesive to form a single tube that was 23 cm high

with a 3-cm in diameter opening (7.6 aspect ratio) with two internal funnels in the middle preventing resuspension during recovery. The four tubes were fit in a PVC frame with a central weight. Two tubes on each trap were prefilled with RNA preservative for DNA preservation and the other two were filled with hypersaline 10% formalin buffered for morphological preservation. Tubes were deployed covered with plastic wrap held by rubber bands attached with A2 galvanic time releases that dissolve in 4 °C seawater within 24 hours. After recovery, the samples in RNA preservative were rinsed and stored in fresh RNA preservative, and formalin-fixed samples were rinsed then stored in 70% ethanol at -20 °C until processing. The sorting of larval trap samples was later conducted at Shannon Point Marine Center where samples were imaged and sorted into morphological groups using a dissecting microscope. All RNAlater-preserved gastropod samples in the traps were set aside for mtCO1 genotyping.

A Large Volume Water Transfer System WTS-LV50 (McLane Research Laboratories, Inc.) was used to collect and quantify larval abundances in the water column among vent chimneys. A mooring suspended the pump ~ 2 meters above the bottom (mab) for 7-18 hour deployments at each site. The pump gently drew water onto a 63-µm Nitex mesh filter, running for 7.3 -18.7 hours and filtering 11.9-30.5 m^3 into an insulated compartment upstream from the filter. Upon recovery, live specimens on the pump filter were immediately rinsed with 0.3-µm filtered seawater onto a 63-µm sieve, examined under dissecting microscopes, sorted into morphological groups, and imaged with an Olympus EP50 Camera mounted on an Olympus CX43 compound microscope at 40-100X magnification. Larval samples were then stored in 95% EtOH at -20 °C for CO1 genotyping.

AUV *Sentry* (National Deep Submergence Facility, Woods Hole Oceanographic Institution) equipped with SyPRID (Sentry Precision Robotic Impeller Driven Sampler) was used to collect larvae in the water column around the periphery of the vent fields and above the vent fields. This device uses an impeller pump to gently suction plankton from the water onto a 150-µm Nitex mesh filter in the cod end (Billings et al. 2016). At each vent field, AUV *Sentry* collected two SyPRID samples (~11-hour duration each): one sample around the periphery and one above the vent structures, filtering up to 3,619 m^3 of seawater per sample. The periphery sample was collected from 8-15 mab in a repeating back-and-forth pattern around the periphery of the target vent field. At Tahi Moana, periphery samples were collected at 30 mab rather than 8-15 mab due to tall vent features and strong currents. At ABE, due to the proximity of a ~20 m tall wall feature to the west, half of the periphery sample was acquired from the base of the wall and the other half was acquired from the top of the wall. Above vent field samples were taken in a series of parallel tracks back and forth over a standard area over each vent field at approximately 26-45 m above the tallest known hydrothermal chimney structures. The sampling pattern was planned such that spaces between tracks reduced over successive passes and were offset to avoid repeating tracks, encouraging wide sample coverage over the select area. Upon recovery, all SyPRID samples were immediately rinsed with 0.3-µm filtered seawater onto a 63-µm sieve, sorted into morphotypes using dissecting microscopes, imaged with an Olympus EP50 Camera mounted on an Olympus CX43 compound microscope at 40-100X magnification, and stored in 95% EtOH at -20°C for mtCO1 genotyping.

All larvae were sorted under a dissecting microscope, imaged, and identified to larval type by morphology. Gastropod, bivalve, and zooea larvae were identified to the lowest taxonomic level possible using a combination of morphology and sequencing. Sorting and sequencing was conducted between July 2022 and September 2025.

For sequencing, DNA from individual gastropod larvae was extracted using the Nucleospin Tissue XS DNA (Machery-Nagel, Inc.) and eluted into 30-µl volumes. PCR amplification and sequencing of the mtCO1 gene was conducted for each larva as described above. Morphological identifications were made using the hydrothermal vent larvae identification guide (Mills et al., 2009) and our own identification guides when possible.

Sequences and images have been submitted to the Barcode of Life Data System v4 (BOLD4) and NCBI.

Data Processing Description

Data are raw counts.

Identifications

Individual identities were assigned according to mtCOI sequences matches within the NCBI database with at least 97% pairwise identity. However, due to the novelty of many deep-–sea organisms, many successfully sequenced individuals did not match to known organisms with sequences in NCBI. For these individuals, a mixture of phylogenetic analysis and morphological characteristics were used to identify the lowest possible

taxonomic level. For phylogenetic analysis, sequences were aligned using the MUSCLE PPP algorithm alignment in Geneious and assembled into phylogenetic trees using PHYML with a GTR substitution model and aLRT statistics. Identities based on morphology or the combined method are listed as 'Taxonomic Group' in the data sheet.

BCO-DMO Processing Description

- Loaded data from "FINAL_Meroplankton_Counts_12.10.25.xlsx" (sheet 1, Excel format), treating "", "nd", and "NA" as missing values, using filename as resource name
- Renamed 15 fields, replacing dot notation with underscores and removing embedded units from field names: Sample.Volume.m3 to Sample_Volume, Time.Deployed.hrs. to Time_Deployed, Ash.depth.cm. to Ash_depth, Meters.Above.Bottom to Meters_Above_Bottom, Ash.Average to Ash_Average, Sample.ID to Sample_ID, Larval.Type to Larval_Type, Identification.Type to Identification_Type, Taxonomic.Level to Taxonomic_Level, Taxonomic.Group to Taxonomic_Group, Top.BLAST.Hit to Top_BLAST_Hit, Pairwise.Identity to Pairwise_Identity, Less.than.97 to Less_than_97, BOLD.Collection.Code to BOLD_Collection_Code, and Individuals.per.SampleID to Individuals_per_SampleID
- Output written to "997940_v1_eslc_vfr_meroplankton_counts.csv"

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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
Results

Billings, A., Kaiser, C., Young, C. M., Hiebert, L. S., Cole, E., Wagner, J. K. S., & Van Dover, C. L. (2017). SyPRID sampler: A large-volume, high-resolution, autonomous, deep-ocean precision plankton sampling system. Deep Sea Research Part II: Topical Studies in Oceanography, 137, 297–306. https://doi.org/10.1016/j.dsr2.2016.05.007
Methods

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Parameters

Parameter	Description	Units
SampleMethod	Sampling method including larval traps, McLane pump, SyPRID (above vents) and SyPRID (vent periphery)	unitless
RecoveryDive	Jason or Sentry dive # on which the samples were recovered. For Sentry dives P indicates the portside sampler and S indicates the startboard sampler	unitless
Sample_Volume	Sample volume in m3; larval traps are NA because trap size was standardized	m3
Meters_Above_Bottom	Height above bottom	m

SampleLocation	Categories of where the samples were taken: 'Within vents' samples were nestled between chimneys, 'above vents' were take above the tallest chimney, 'vent periphery' were taken around the vents	unitless
Time_Deployed	Time the sampler was deployed	hours
Ash_Average	Average ash thickness for the sites from Beinart et al. 2024	cm
Ash_depth	Ash depth range at the site in cm, from Beinart et al. 2024	cm
Site	Site names	unitless
Sample_ID	Sample ID as cruise_Dive_sampleTypeCode_number	unitless
Larval_Type	Larval type name	unitless
Stage	Larval, juvenile, or Adult	unitless
Identification_Type	How the sample was identified, 'morphology' or the primer set used	unitless
Taxonomic_Level	Lowest taxonomic level identified	unitless
Taxonomic_Group	Name of taxonomic level	unitless
Top_BLAST_Hit	Top hit in the Basic Local Alignment Search Tool, NCBI	unitless
Pairwise_Identity	Pairwise identity of the top BLAST hit	Percent (%)
Less_than_97	Flags sequences with < 97% similarity to the top BLAST hit, Y (<97%), N(>97%)	unitless
BOLD_Collection_Code	Identification code to cross reference with the BOLD database	unitless
Individuals_per_SampleID	Number of individuals per sample	unitless

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Instruments

Dataset-specific Instrument Name	AUV Sentry
Generic Instrument Name	AUV Sentry
Dataset-specific Description	AUV Sentry (National Deep Submergence Facility, Woods Hole Oceanographic Institution) equipped with SyPRID (Sentry Precision Robotic Impeller Driven Sampler) was used to collect larvae in the water column around the periphery of the vent fields and above the vent fields.
Generic Instrument Description	The autonomous underwater vehicle (AUV) Sentry is a fully autonomous underwater vehicle capable of exploring the ocean down to 6,000 meters (19,685 feet) depth. Sentry builds on the success of its predecessor the ABE, with improved speed, range, and maneuverability. Sentry's hydrodynamic shape also allows faster ascents and descents. Sentry carries a superior science sensor suite and an increased science payload enabling it to be used for both mid-water and near-seabed oceanographic investigations. Sentry produces bathymetric, sidescan, subbottom, and magnetic maps of the seafloor and is capable of taking digital bottom photographs in a variety of deep-sea terrains such as mid-ocean ridges, deep-sea vents, and cold seeps at ocean margins. Sentry is uniquely able to operate in extreme terrain, including volcano caldera and scarps. Sentry's navigation system uses a doppler velocity log and inertial navigation system, aided by acoustic navigation systems (USBL or LBL). The USBL system also provides acoustic communications, which can be used to obtain the vehicle state and sensor status as well as to retask the vehicle while on the bottom. In addition its standard sensors, Sentry has carried a variety of science-supplied sensors, including the Nakamura redox potential probe, ACFR 3-D imaging system, and the Tethys in-situ mass spectrometer. Sentry can be used to locate and quantify hydrothermal fluxes. Sentry is also capable of a much wider range of oceanographic applications due to its superior sensing suite, increased speed and endurance, improved navigation, and acoustic communications. Sentry can be used as a stand alone vehicle or in tandem with Alvin or an ROV to increase the efficiency of deep-submergence investigations. More information is available from the operator site at URL: https://ndsf.whoi.edu/sentry/

Dataset-specific Instrument Name	SyPRID
Generic Instrument Name	AUV Sentry Precision Robotic Impeller Driven Sampler
Dataset-specific Description	AUV Sentry (National Deep Submergence Facility, Woods Hole Oceanographic Institution) equipped with SyPRID (Sentry Precision Robotic Impeller Driven Sampler) was used to collect larvae in the water column around the periphery of the vent fields and above the vent fields.
Generic Instrument Description	The SyPRID (Sentry Precision Robotic Impeller Driven) sampler is an innovative deep-rated (6000 m) plankton sampler that partners with the Sentry Autonomous Underwater Vehicle (AUV) to obtain paired, large-volume plankton samples at specified depths and survey lines to within 1.5 m of the seabed and with simultaneous collection of sensor data. SyPRID uses a perforated Ultra-High-Molecular-Weight (UHMW) plastic tube to support a fine mesh net within an outer carbon composite tube (tube-within-a-tube design), with an axial flow pump located aft of the capture filter. The pump facilitates flow through the system and minimizes the bow wave at the mouth opening. The cod end, a hollow truncated cone, is also made of UHMW plastic and is designed to 'soften' the landing of zooplankton on the capture surface. SyPRID attaches as a saddle-pack to the Sentry vehicle. Sentry itself is configured with a flight control system that enables autonomous survey paths to altitudes as low as 1.5 m. In its inaugural deployment at the Blake Ridge Seep (2160 m) on the US Atlantic Margin, SyPRID was operated for 6 h at an altitude of 5 m. It recovered plankton samples from that stratum in excellent condition and with greater larval numbers than recovered in a typical 'near-bottom' MOCNESS sample from comparable habitats and depths. The prototype SyPRID and its next generations will enable studies of plankton or other particulate distributions associated with patchy habitats, localized physico-chemical strata (e.g., above and below the thermocline), or discrete water masses at an unprecedented spatial resolution for a large volume system [1]. More information is available by contacting: Carl Kaiser Program Manager Applied Ocean Physics & Engineering NDSF AUV Operations Manager Office Phone: +1 508 289 3269 ckaiser@whoi.edu [1] Billings, A., Kaiser, C., Young, C. M., Hiebert, L. S., Cole, E., Wagner, J. K. S., & Van Dover, C. L. (2017). SyPRID sampler: A large-volume, high-resolution, autonomous, deep-ocean precision plankton sampling system. In Deep Sea Research Part II: Topical Studies in Oceanography (Vol. 137, pp. 297–306). Elsevier BV. https://doi.org/10.1016/j.dsr2.2016.05.007

Dataset-specific Instrument Name	Olympus EP50 Camera
Generic Instrument Name	Camera
Dataset-specific Description	Upon recovery, all SyPRID samples were immediately rinsed with 0.3-µm filtered seawater onto a 63-µm sieve, sorted into morphotypes using dissecting microscopes, imaged with an Olympus EP50 Camera mounted on an Olympus CX43 compound microscope at 40-100X magnification, and stored in 95% EtOH at -20°C for mtCO1 genotyping.
Generic Instrument Description	All types of photographic equipment including stills, video, film and digital systems.

Dataset-specific Instrument Name	McLane WTS-LV50 pump
Generic Instrument Name	McLane Pump
Dataset-specific Description	McLane WTS-LV50 pump (McLane Research Laboratories, Inc.)
Generic Instrument Description	McLane pumps sample large volumes of seawater at depth. They are attached to a wire and lowered to different depths in the ocean. As the water is pumped through the filter, particles suspended in the ocean are collected on the filters. The pumps are then retrieved and the contents of the filters are analyzed in a lab.

Dataset-specific Instrument Name	Olympus CX43 compound microscope
Generic Instrument Name	Microscope - Optical
Dataset-specific Description	Upon recovery, all SyPRID samples were immediately rinsed with 0.3-µm filtered seawater onto a 63-µm sieve, sorted into morphotypes using dissecting microscopes, imaged with an Olympus EP50 Camera mounted on an Olympus CX43 compound microscope at 40-100X magnification, and stored in 95% EtOH at -20°C for mtCO1 genotyping.
Generic Instrument Description	Instruments that generate enlarged images of samples using the phenomena of reflection and absorption of visible light. Includes conventional and inverted instruments. Also called a "light microscope".

Dataset-specific Instrument Name	dissecting microscopes
Generic Instrument Name	Microscope - Optical
Dataset-specific Description	Upon recovery, all SyPRID samples were immediately rinsed with 0.3-µm filtered seawater onto a 63-µm sieve, sorted into morphotypes using dissecting microscopes, imaged with an Olympus EP50 Camera mounted on an Olympus CX43 compound microscope at 40-100X magnification, and stored in 95% EtOH at -20°C for mtCO1 genotyping.
Generic Instrument Description	Instruments that generate enlarged images of samples using the phenomena of reflection and absorption of visible light. Includes conventional and inverted instruments. Also called a "light microscope".

Dataset-specific Instrument Name	Larval tube traps
Generic Instrument Name	no_bcodmo_term
Dataset-specific Description	To estimate larval supply to the seafloor, two replicate larval tube traps were simultaneously deployed for approximately two weeks at the base of a vent chimney at each site (except Mariner or Mata Tolu) in an animal-free patches.
Generic Instrument Description	No relevant match in BCO-DMO instrument vocabulary.

Dataset-specific Instrument Name	ROV Jason
Generic Instrument Name	ROV Jason
Dataset-specific Description	Samples within vent fields were taken with a McLane large volume pump deployed with 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

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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

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