Sampling locations and identifications for larvae collected near three deep-sea hydrothermal vent fields from 2007 to 2017

Website: https://www.bco-dmo.org/dataset/839476
Data Type: Cruise Results
Version: 1
Version Date: 2021-02-02

Project
» RAPID: Larval Abundance, Behavior and Dispersal at Deep-sea Hydrothermal Vents in the Southern Mariana Trough (Mariana Back-arc Vents)
» Trajectories in functional diversity after disturbance at vents on the East Pacific Rise (EPR Functional Diversity)
» Metacommunity Dynamics at Hydrothermal Vents (Metacommunity Dynamics)

Contributors	Affiliation	Role
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Abstract
This dataset provides the sampling locations and identifications for larvae collected near three deep-sea hydrothermal vent fields and used in a microbiome study by Carrier et al. (2021). This dataset provides metadata for larval and microbiome genetic sequence data in another repository (Carrier et al., 2021, doi.org/10.5061/dryad.sqv9s4n18). The data table is structured as a Darwin Core occurrence table so that it can be harvested by the Ocean Biodiversity Information System (OBIS) and Global Biodiversity Information Facility (GBIF). In addition to the data table, photographs are provided for some of the specimens.

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Coverage

Spatial Extent: **N**:23.957 **E**:-108.8625 **S**:9.8401 **W**:143.6296
Temporal Extent: 2007-11-29 - 2017-11-02

Dataset Description

This dataset provides the sampling locations and identifications for larvae collected near three deep-sea hydrothermal vent fields and used in a microbiome study by Carrier et al. (2021). This dataset provides

metadata for larval and microbiome genetic sequence data in another repository (Carrier et al., 2021, doi.org/10.5061/dryad.sqv9s4n18). The data table is structured as a Darwin Core occurrence table so that it can be harvested by the Ocean Biodiversity Information System (OBIS) and Global Biodiversity Information Facility (GBIF). In addition to the data table, photographs are provided for some of the specimens. A .zip file of images is attached containing the .JPG files referenced by column "associatedMedia".

Larvae were collected near three different hydrothermal vent fields with locality, Location, and waterBody (N. Pacific) specified in the data: East Pacific Rise, 9 50 N vent field, Tica vent site at N EPR; Mariana Back-Arc, Snail and Archaean vent fields in Mariana Trough; and Pescadero Basin, Auka vent field in Gulf of California.

Methods & Sampling

Larval collection:
These larvae were collected near hydrothermal vent fields on the East Pacific Rise (EPR 9°50'N vent field), on the Mariana Back-Arc Spreading Center (near Snail or Archaean vent fields), and in Pescadero Basin (Auka vent field) in the Gulf of California. The EPR specimens were from McLane WTS-LV50 plankton pumps deployed on-axis near Tica vent site on LADDER 3 cruise AT15-26 in 2007. The pump sampled for 24 hr over a 63 micron mesh at a rate of 30 L/min at a position about 3 meters above bottom. The Mariana specimens were from the same plankton pumps with same configuration deployed on-site or off-site but within 300 m of active hydrothermal vents on R/V Yokosuka cruise YK10-11 in 2010. The Pescadero specimens were from the suction (slurp) sampler on ROV Hercules on E/V Nautilus cruise NA091 in 2017. The slurp sampled for 10 min over a 63 micron mesh at a rate of ~100 L/min at a position about 1 meter above bottom, while the ROV was parked on-site at an active vent ("intensive sampling station", or ISS). ISS 2 was during ROV dive H1657, and ISS 4 was during ROV dive H1658.

We acknowledge the sample collection permits CONAPESCA PPFE/DGOPA-010/17 and INEGI: Autorización EG0072017 associated to the Diplomatic Note number SRE 17-1087 (CTC/06727/17).

Shipboard sample processing:
Pump and slurp samples were processed within an hour upon recovery on deck, with many specimens alive. The sample was washed off the filter using 95% non-denatured ethanol into a 250 mL jar (brand new or rinsed with ethanol, but was not autoclaved).

Laboratory sorting and morphological identification:
Portions of the sample were extracted with a wide-mouthed pipette into a petri dish for sorting under a dissecting scope at magnifications up to 50X (although most tools were rinsed with ethanol, none were autoclaved). Specimens were sorted into vials by major taxa (i.e., all the gastropod larvae together), in some cases with separate vials for those retained on 300um or 63um sieve. Vials were brand new or rinsed with ethanol, but were not autoclaved. Individuals were identified to morphotypes at lowest taxonomic level. Some morphotypes contain morphologically indistinguishable larvae from multiple species (e.g., polychaete nectochaetes).

Specimens selected for DNA extraction:
We selected specimens in several major taxonomic groups (gastropods, polychaetes, crustaceans, and a bivalve) for DNA extraction. The amount of time the larval specimens had been stored in ethanol at the time of DNA extraction was ~10, ~7, and ~1 yrs, respectively, for EPR, Mariana, and Pescadero specimens. Only the Mariana specimens had been stored at 4 degrees C, while the others were at room temperature. Working in a laminar flow hood, we used sterile techniques to place 25 individuals from EPR and 25 individuals from Mariana into separate 1.5 mL vials with 95% ethanol. We thank Diana Franks for helping with sterile techniques. Pescadero specimens were provided in 2 vials each with 5 individuals of the same morphotype using sterile tools but not in a laminar flow hood.

DNA extraction and amplification are described by Carrier et al. (2021), and 28S rRNA larval genetic sequences and 16S rRNA bacterial genetic sequence data are in the Dryad repository (Carrier et al., 2021, doi.org/10.5061/dryad.sqv9s4n18). The 28S larval sequences were compared to those in the NCBI GenBank database using a BLAST search to assist with matching morphotypes to lowest taxonomic level. Results from the BLAST search were insufficient to provide additional taxonomic resolution; therefore, the 28S genetic results were primarily used as support for the morphological identification. We'd like to thank Bethany Fleming for conducting the BLAST searches.

Additional genetic evidence to assist with larval identification:
We'd like to thank Dr. Hiroka Hidaka, Dr. Shigeaki Kojima, and Dr. Hiromi Watanabe for providing histone 3 and

Dr. Florence Pradillon for providing cytochrome oxidase subunit 1 (CO1) sequences for other Mariana larval specimens from the same collections. The Canadian Centre for DNA Barcoding provided CO1 sequences for other Pescadero specimens from the same collections; these results may be viewed in the Barcode of Life Data System (BOLD) Public Data Portal using the project search PESPL.

Data Processing Description

Data Processing:
The raw data table was created in a Google spreadsheet which was imported directly into a script that removed extraneous columns, added an asterisk to 6 of the TubeIDs, constrained the latitude and longitude to 4 decimal places, and exported the table to a comma-separated values file: https://github.com/sbeaulieu/EPR-traits/blob/master/subset_Google_Sheet_BCODMO_Beaulieu_Carrier.R. The data table is structured as a Darwin Core occurrence table so that it can be harvested by the Ocean Biodiversity Information System (OBIS) and Global Biodiversity Information Facility (GBIF). Note for the column linking to the microbiome genetic sequence data in the Dryad repository, we considered using the Darwin Core term associatedOrganisms but found other studies in which the link to microbiome data was made using an Occurrence Core with an extension for ResourceRelationships.

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Data Files

File	
deep_sea_larvae.csv Primary data file for dataset ID 839476	(Comma Separated Values (.csv), 22.99 KB) MD5:4a02a0e4ce0649a2681d822548febe61
Specimen images associated with dataset 839476 filename: 839476_images.zip Images associated with dataset 839476; refer to column "associatedMedia" in dataset for the image corresponding to each occurrenceID.	(ZIP Archive (ZIP), 210.82 MB) MD5:f9e617bc5af683d1a85b68fcab104b5b

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Related Publications

Carrier, T. J., Beaulieu, S. E., Mills, S. W., Mullineaux, L. S., & Reitzel, A. M. (2021). Larvae of Deep-Sea Invertebrates Harbor Low-Diversity Bacterial Communities. The Biological Bulletin, 241(1), 65–76. doi:10.1086/715669
Results

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Related Datasets

IsRelatedTo

Beaulieu, S., Mills, S., Mullineaux, L. (2022) **Larvae collected near Mariana Back-Arc hydrothermal vents in 2010.** Biological and Chemical Oceanography Data Management Office (BCO-DMO). (Version 1) Version Date 2022-08-05 doi:10.26008/1912/bco-dmo.877284.1 [view at BCO-DMO]
Relationship Description: A subset of specimens identified in dataset 877284 ("Larvae collected near Mariana Back-Arc hydrothermal vents in 2010") with 28S rRNA sequences is described in dataset 839476 ("Deep-sea larvae for microbiome study").

Carrier, T., Beaulieu, S., Mills, S., Mullineaux, L., & Reitzel, A. (2021). Larvae of deep-sea invertebrates harbor low-diversity bacterial communities (Version 2) [Data set]. Dryad. https://doi.org/10.5061/DRYAD.SQV9S4N18

Different Version

Beaulieu, S., Mills, S., Mullineaux, L., Carrier, T., & Reitzel, A. (2021). Larvae collected near deep-sea hydrothermal vent fields for microbiome study. United States Geological Survey. Occurrence dataset https://obis.org/dataset/b920c161-c295-4a73-b9a4-96ab1ab0b357

Beaulieu, S., Mills, S., Mullineaux, L., Carrier, T., & Reitzel, A. (2021). Larvae collected near deep-sea hydrothermal vent fields for microbiome study [Data set]. United States Geological Survey. https://doi.org/10.15468/D8PACG

Parameters

Parameter	Description	Units
TubeID	Identifier for the tube containing a single larval specimen for DNA extraction. An asterisk indicates the 6 EPR specimens lost during preparation for sequencing.	unitless
Location	A spatial region, using regions from the InterRidge Vents Database Ver. 3.4 https://doi.org/10.1594/PANGAEA.917894. Darwin Core term https://dwc.tdwg.org/terms/#location based on Dublin Core term http://purl.org/dc/terms/Location	unitless
waterBody	The name of the water body in which the Location occurs, corresponding to ocean in the InterRidge Vents Database Ver. 3.4 https://doi.org/10.1594/PANGAEA.917894. Darwin Core term http://rs.tdwg.org/dwc/terms/waterBody	unitless
locality	The specific description of the place near the sampling event, using names of vent fields and sites in the InterRidge Vents Database Ver. 3.4 https://doi.org/10.1594/PANGAEA.917894	unitless
habitat	We describe the habitat as "hydrothermal vent" ENVO term http://purl.obolibrary.org/obo/ENVO_00000215 for those taxa for which we are confident that the adults live at a hydrothermal vent, otherwise NotDetermined. We are not describing the sampling event habitat per se, thus deviating from the definition of Darwin Core term http://rs.tdwg.org/dwc/terms/habitat	unitless
Deployment_Fraction	Numbered deployment (pump mooring or ROV station) with sorting fraction indicated for some samples to help identify the vial into which the specimen was sorted	unitless
eventID	An identifier for the set of information associated with a sampling event. For the EPR and Mariana specimens, the eventID is built from a cruise identifier and the deployment; for the Pescadero specimens the eventID is the E/V Nautilus sample identifier. Darwin Core term http://rs.tdwg.org/dwc/terms/eventID	unitless
decimalLatitude	The geographic latitude in decimal degrees of the sampling near the locality. Positive values are north of the Equator, negative values are south of it. Darwin Core term http://rs.tdwg.org/dwc/terms/decimalLatitude	degrees

decimalLongitude	The geographic longitude in decimal degrees of the sampling near the locality. Positive values are east of the Greenwich Meridian, negative values are west of it. Darwin Core term http://rs.tdwg.org/dwc/terms/decimalLongitude	degrees
Bottom_Depth_Meters	Depth below sea level of the seafloor under the sampling event	meters (m)
minimumDepthInMeters	The lesser depth of a range of depth below sea level for the sampling event. Darwin Core term http://rs.tdwg.org/dwc/terms/minimumDepthInMeters	meters (m)
maximumDepthInMeters	The greater depth of a range of depth below sea level for the sampling event. Darwin Core term http://rs.tdwg.org/dwc/terms/maximumDepthInMeters	meters (m)
eventDate	The date of the sampling event. Darwin Core term http://rs.tdwg.org/dwc/terms/eventDate. Format: YYYY-MM-DD	unitless
Higher_level_taxon_name	Higher level taxonomic name either Bivalvia, Crustacea, Gastropoda, or Polychaeta	unitless
Lowest_level_taxon_name_or_morphotype	Name used to identify the taxon or morphogroup to the lowest level, not necessarily a scientific name	unitless
scientificName	Name from World Register of Marine Species at the lowest level that matches the Lowest_level_taxon_name_or_morphotype. Darwin Core term http://rs.tdwg.org/dwc/terms/scientificName	unitless
scientificNameID	Machine-readable Life Science Identifier (LSID) that pairs the AphiaID from World Register of Marine Species to the scientificName. Darwin Core term http://rs.tdwg.org/dwc/terms/scientificNameID	unitless
occurrenceID	A unique identifier for the Occurrence record to be provided to OBIS and GBIF. The occurrenceID concatenates the eventID with the TubeID. Darwin Core term http://rs.tdwg.org/dwc/terms/occurrenceID	unitless
occurrenceStatus	A statement about the presence of the taxon in the Occurrence record, using controlled vocabulary term present. Darwin Core term http://rs.tdwg.org/dwc/terms/occurrenceStatus	unitless
lifeStage	The life stage of the specimen at the time the Occurrence was recorded, using biological entity development stage terms larvae, zoeae, and juvenile from controlled vocabulary http://vocab.nerc.ac.uk/collection/S11/current/. Darwin Core term http://rs.tdwg.org/dwc/terms/lifeStage	unitless
basisOfRecord	The nature of the Occurrence record, using controlled vocabulary term PreservedSpecimen. Darwin Core term http://rs.tdwg.org/dwc/terms/basisOfRecord	unitless
associatedSequences	Link to the larval 28S genetic sequence data in the Dryad repository doi:10.5061/dryad.sqv9s4n18 with specimen identifier, associated with the taxon in the Occurrence record. Darwin Core term http://rs.tdwg.org/dwc/terms/associatedSequences	unitless
microbiome_16S_Dryad	Link to the microbiome 16S genetic sequence data in the Dryad repository doi:10.5061/dryad.sqv9s4n18 with specimen identifier	unitless

associatedMedia	A list (concatenated and separated) of filenames of images associated with the Occurrence. Filenames often include specimen identifier and magnification. Darwin Core term http://rs.tdwg.org/dwc/terms/associatedMedia	unitless

Instruments

Dataset-specific Instrument Name	McLane Large Volume Pumping System WTS-LV
Generic Instrument Name	McLane Large Volume Pumping System WTS-LV
Generic Instrument Description	The WTS-LV is a Water Transfer System (WTS) Large Volume (LV) pumping instrument designed and manufactured by McLane Research Labs (Falmouth, MA, USA). It is a large-volume, single-event sampler that collects suspended and dissolved particulate samples in situ. Ambient water is drawn through a modular filter holder onto a 142-millimeter (mm) membrane without passing through the pump. The standard two-tier filter holder provides prefiltering and size fractioning. Collection targets include chlorophyll maximum, particulate trace metals, and phytoplankton. It features different flow rates and filter porosity to support a range of specimen collection. Sampling can be programmed to start at a scheduled time or begin with a countdown delay. It also features a dynamic pump speed algorithm that adjusts flow to protect the sample as material accumulates on the filter. Several pump options range from 0.5 to 30 liters per minute, with a max volume of 2,500 to 36,000 liters depending on the pump and battery pack used. The standard model is depth rated to 5,500 meters, with a deeper 7,000-meter option available. The operating temperature is -4 to 35 degrees Celsius. The WTS-LV is available in four different configurations: Standard, Upright, Bore Hole, and Dual Filter Sampler. The high-capacity upright WTS-LV model provides three times the battery life of the standard model. The Bore-Hole WTS-LV is designed to fit through a narrow opening such as a 30-centimeter borehole. The dual filter WTS-LV features two vertical intake 142 mm filter holders to allow simultaneous filtering using two different porosities.

Dataset-specific Instrument Name	dissecting scope
Generic Instrument Name	Microscope - Optical
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	
Generic Instrument Name	ROV Hercules
Dataset-specific Description	ROV Hercules multi-chamber slurp sampler was used to collect specimens
Generic Instrument Description	ROV Hercules is operated via E/V Nautilus. Hercules is outfitted with features that allow it to perform intricate tasks, including two manipulator arms, a variety of sensors and samplers, a high-definition video camera, several LED lights, and high-resolution mapping tools. The submersible receives power from the surface through a fiber-optic cable, which also transmits data and video, to allow pilots located in the shipboard control van to "fly" the ROV in any direction through the use of its six thrusters. Other sensors located on Hercules measure pressure, depth, water temperature, oxygen concentration, and salinity to accommodate requests from scientists both onboard and onshore. Hercules is equipped with multiple cameras, including the high-definition video camera that allows for real-time telepresence. The ROV is built to withstand pressures at a depth of 4,000 meters with more than 6,000 pound-force per square inch (psi) for up to three days. See more: https://nautiluslive.org/tech/rov-hercules

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Deployments

AT15-26

Website	https://www.bco-dmo.org/deployment/734071
Platform	R/V Atlantis
Report	http://datadocs.bco-dmo.org/docs/Larval_Supply_EPR_Vents/data_docs/AT15-26_LADDER-3_Cruise_Report_Feb4_36252.pdf
Start Date	2007-11-13
End Date	2007-12-03
Description	Part of Ridge Interdisciplinary Global Experiments (Ridge2000).

YK10-11

Website	https://www.bco-dmo.org/deployment/783909
Platform	R/V Yokosuka
Report	http://www.godac.jamstec.go.jp/catalog/data/doc_catalog/media/YK10-11_all.pdf
Start Date	2010-09-03
End Date	2010-09-15
Description	For more cruise information, visit http://www.godac.jamstec.go.jp/darwin/cruise/yokosuka/yk10-11/e and http://www.marine-geo.org/tools/search/entry.php?id=YK10-11.

NA091

Website	https://www.bco-dmo.org/deployment/839503
Platform	E/V Nautilus
Start Date	2017-10-30
End Date	2017-11-05
Description	Cruise DOI: 10.7284/908553 See more information at the Rolling Deck to Repository (R2R) at https://www.rvdata.us/search/cruise/NA091 and on the expedition website at https://nautiluslive.org/cruise/na091.

Project Information

RAPID: Larval Abundance, Behavior and Dispersal at Deep-sea Hydrothermal Vents in the Southern Mariana Trough (Mariana Back-arc Vents)

Coverage: Southern Mariana Trough

NSF Award Abstract:
Summary: Since the discovery of deep-sea hydrothermal vents over thirty years ago, scientists have been perplexed by the question: How are these vent sites colonized and, more specifically, How are the faunal populations established and maintained at these very discrete and often ephemeral habitats. For animals that are sessile or have limited mobility as adults, dispersal to these habitats occurs early in the life cycle, as planktonic larvae in the water column. Due to the difficulties in sampling deep-sea larvae, including low abundances (dilute concentrations), we have very few quantitative estimates of larval dispersal between or larval supply to hydrothermal vents. We also have little to no knowledge of the behavior of vent larvae. The PIs will use large-volume plankton pumps to collect larvae near vents in the southern Mariana Trough in a collaborative effort to quantify larval abundance, behavior, and dispersal in this little-studied region. The collaboration combines the PI's strengths in the collection and morphological identification of larvae and quantifying and modeling dispersal between deep-sea vents, and those of Japanese partners in rearing larvae of hydrothermal vent fauna, molecular genetic identification of larvae, and population genetics of vent fauna.

Intellectual merit: The southern Mariana Trough is a very interesting region in which to study dispersal of vent-endemic fauna, due to the proximity of vents in the back-arc spreading center to vents along the Mariana Arc. These two tectonic settings create different habitat conditions and support vent communities with different species composition. Vent sites the PIs will visit, in the axis and just off-axis of the back-arc spreading center are as close as 25 km to vents on the arc, yet 600 km south of the other known vents in the back-arc. In addition to the new information on larval abundance, diversity, behavior, and dispersal that will be gained for this little-studied region of the world's ridge system, this project has direct relevance to the integration and synthesis goals of the U.S. Ridge 2000 Program. The PI's lab group has conducted previous work at the Ridge 2000 East Pacific Rise (EPR) Integrated Studies Site (ISS). They will be making a direct comparison of the larval abundance and diversity at the EPR ISS to this very different setting along the global 'baseball seam' of oceanic spreading centers. No other such comparison has been possible due to the lack of sampling effort for larvae with large-volume pumps. Also, they are proposing the first experiments with live vent larvae (to the best of our knowledge - with the exception of brachyuran megalopae at 1 atm) to estimate swimming and sinking rates that are important for adding behavioral information to models of larval dispersal.

Broader Impacts: The project involves reciprocal training and cultural exchange - the PIs will learn field and laboratory research techniques from the Japanese PIs, and they will learn from the U.S. PIs. The project will also benefit the career development of a junior researcher (Beaulieu). The proposed activity broadens the participation of both U.S. and Japanese women scientists in sea-going, oceanographic research. The PIs will broadcast the cruise activities in a web log posted by the international InterRidge Program Office, and they anticipate at least three scientific publications will emerge. New species will be added to the online photographic identification guide for vent larvae and included in the second edition of the printed guide.

Additional cruise data and information are available from MGDS: http://www.marine-geo.org/tools/search/entry.php?id=YK10-11

Trajectories in functional diversity after disturbance at vents on the East Pacific Rise (EPR Functional Diversity)

Coverage: East Pacific Rise

NSF Award Abstract:
Hydrothermal vents support oases of life in the deep sea and are inhabited by unusual organisms that use chemical energy instead of photosynthesis as the basis of their food web. However, because the vents occur in geologically active areas of the seafloor, entire communities can be eradicated by catastrophic natural disturbances such as eruptions. The main objectives of this project are to quantify how quickly these communities recover from catastrophic disturbance and to determine what processes influence their resilience. The project focuses on both the structure (species diversity) and function (trait diversity) of the communities. The investigators will examine vents on an active segment of the East Pacific Rise where eruptive disturbance occurs on decadal time scales. These activities will create an unprecedented long-term (>14-year) quantitative time-series of colonist species composition and function. The application of trait-based analysis to the question of biological succession at vents has the potential to change the way we think about resilience in other patchy, transient and regionally-connected ecosystems. By considering how traits change over time, the researchers can untangle which species-level characteristics most influence abundance and distribution. The project objectives have broad significance with the growing potential for human-caused disturbances at deep-sea vents through deep-sea mining. Additional impacts include strengthening participation of under-represented minorities in marine science and contributing to international database development for functional traits of deep-sea vent species.

The unique, chemosynthesis-fueled fauna inhabiting deep-sea hydrothermal vents are subject to tectonic and eruptive disturbance that can eradicate entire communities. The main objectives of this project are to quantify how quickly these communities recover from catastrophic disturbance and to determine what processes influence their resilience. The focus is on vents on an active segment of the East Pacific Rise where eruptive disturbance occurs on decadal time scales. Field data on colonization and larval supply are used to characterize not only species succession but also the trajectory of functional diversity after a recent (2006) eruption. A new, promising approach to the colonization studies comes from incorporating trait-based analysis of functional diversity. Functional trait analysis is increasingly recognized in terrestrial and freshwater systems as a tool to holistically answer ecological questions, but trait analysis has not been often applied to marine systems. By considering how traits of incoming colonists change over time, the investigators can untangle which species-level factors most influence abundance and distribution. This project will create an unprecedented long-term (>14-year) quantitative time-series of colonist species composition and function. It includes multiple vent sites to encompass the full diversity of habitat conditions, and assesses both local processes and regional connectivity through larval supply. Field observations at individual sites contribute to broader questions when placed in the context of metacommunity theory. In this theoretical framework, field data such as this can be used to answer such questions as how the eradication of the vent community at a particular site affects the persistence of the metacommunity overall, and which vent sites contribute most to regional biodiversity.

Metacommunity Dynamics at Hydrothermal Vents (Metacommunity Dynamics)

NSF Award Abstract:
In this project, the researchers will develop new mathematical models to study the population dynamics of organisms that live at deep-sea hydrothermal vents, areas of the seafloor where volcanic activity causes hot, chemical-rich fluids to exit. The discovery of these vents in 1977 revealed unexpectedly novel and diverse organisms, challenging the prevailing view of the deep sea as a sparsely populated desert. Recent international efforts to mine hydrothermal vent deposits rich in copper, gold, silver and zinc are intensely debated, as deep-sea mineral mining can destroy diverse vent communities and alter the surrounding seafloor habitat. The investigators will extend their models to analyze the potential effects of mining activities. Results from new models will be synthesized to meet the needs of potential stakeholders, including organizations that advise, manage, and conduct activities related to seafloor mining and Marine Protected Areas. Research products will be disseminated as reports and in stakeholder meetings such as those organized by the International Seabed

Authority and the Deep Ocean Stewardship Initiative. The research team will work with graphic artists, video producers, and educators to develop new educational presentations for the NOAA Science on a Sphere® (SOS) system. This new content will be distributed via open access to the entire SOS Users Network and incorporated into SOS programs at over 100 science centers across the U.S. and in 20 other countries. Undergraduate students will participate in the project through the Woods Hole Oceanographic Institution's Summer Student Fellowship Program and the Woods Hole Partnership Education Program. These two programs provide students with authentic research experiences; the PEP program attracts underrepresented minority students, and offers them a short course in marine science and a research internship along with a 6-wk research project.

Metacommunity theory offers important advantages over alternative approaches in modeling vent ecosystems, and the proposed work will advance both our understanding of these communities and strategies for developing models of metacommunities more generally. The proposed work substantially expands earlier metacommunity models for vent systems developed by the researchers in innovative ways. The analyses will remove many initial constraints and add important considerations including site-dependent transition probabilities and clustering of nearby sites with shared characteristics. The options for modeling dispersal properties with two alternative dispersal kernels will also advance understanding. The researchers will examine recognized successional patterns not considered in the previous work using patch occupancy models, and they will carry out sensitivity analyses to evaluate the role of parameters for which uncertainty is high, such as larval duration and dispersal distance, patch disturbance rates and recovery times. This element of the work plan will serve to prioritize future field research, emphasizing the role that models can play in guiding research programs.

Funding

Funding Source	Award
NSF Division of Ocean Sciences (NSF OCE)	OCE-0424953
NSF Division of Ocean Sciences (NSF OCE)	OCE-1028862
NSF Division of Ocean Sciences (NSF OCE)	OCE-1829773
NSF Division of Environmental Biology (NSF DEB)	DEB-1558904