Parasite abundance data collected from coral reef fishes across 19 islands in the central equatorial Pacific from 2009 to 2021

Website: https://www.bco-dmo.org/dataset/945218
Data Type: Other Field Results
Version: 1
Version Date: 2025-01-22

Project
» Collaborative Research: Decomposing the effects of diversity on the abundance of marine parasites (Diversity-disease)

Contributors	Affiliation	Role
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Abstract
The loss of biological diversity is considered one of the principal environmental challenges of the 21st century, and there are hints that this massive reorganization of food webs could affect how parasites are transmitted among hosts. Parasites are often hidden and can be easy to overlook, but they are ecologically important and ubiquitous - so it is important to understand whether we should expect more or fewer of them as biodiversity disappears. Does biodiversity loss increase the abundance of parasites by eroding natural "checks and balances" on transmission? Or does it decrease parasite abundance by removing the free-living biodiversity on which parasites depend? Answers to these questions are urgently needed if we are to mitigate or prevent an uptick in parasite transmission for ecosystems experiencing biodiversity loss. In a joint collaborative research project among the University of Washington, Scripps Institution of Oceanography at UC San Diego, and California State University Monterey Bay, we created a parasite dataset of unprecedented size and taxonomic resolution. We sampled parasites of coral reef fishes from 19 replicate islands in the central equatorial Pacific to study how biodiversity and parasite burden covary. In this dataset, we present all of the data we collected on parasite abundance in coral reef fishes. We sampled 17 species (Acanthurus nigricans, Cephalopholis argus, Cephalopholis urodeta, Chromis iomelas, Chromis margaritifer, Ctenochaetus marginatus, Ctenochaetus striatus, Paracirrhites arcatus, Plectroglyphidodon dickii, Pseudanthias bartlettorum, Pseudanthias dispar, Pseudanthias mooreanus, Pseudanthias olivaceus, Pseudanthias pascalus, Pseudanthias spp., Stegastes aureus, Stegastes fasciolatus) across three archipelagos and 19 islands (Jarvis, Kingman, Kiritimati, Palmyra, Tabuaeran, and Teraina in the Northern Line Islands; Flint, Malden, Millennium, Starbuck, and Vostok in the Southern Line Islands; Huahine, Moorea, Raiatea, Rangiroa, Tahiti, Takapoto, Tetiaroa, and Tikehau in French Polynesia), for a total of 5,251 fish. These 17 broadly distributed host species represent a large spectrum of body sizes, including multiple taxonomic and trophic groups. Included in the dataset are specimens collected from expeditions mounted in 2009, 2010, 2011, 2013, 2019, 2020, and 2021. Fish were collected with three-pronged spears and hand-nets, individually labeled and bagged, and frozen for transport before being thawed and evaluated for parasites. Parasitological dissections were designed to detect all multi-cellular (i.e., metazoan) parasites other than myxozoans, but would not have detected viral, bacterial, protozoal, or fungal parasites. Parasites were identified to the lowest possible taxonomic level and grouped into their broad parasite taxonomic grouping (i.e., Acanthocephalan, Cestoda, Copepoda, Isopoda, Monogenea, Other Crustacea, Trematoda, Nematoda) and transmission strategy (i.e., complex life cycle versus direct transmission).

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Coverage

Location: Three archipelagos of the central equatorial Pacific, encompassing 19 islands
Spatial Extent: **N**:6.46 **E**:-145.33 **S**:-17.95 **W**:-162.32
Temporal Extent: 2009 - 2021

Methods & Sampling

Fish collection

We sampled 17 species of coral reef fishes (*Acanthurus nigricans, Cephalopholis argus, Cephalopholis urodeta, Chromis iomelas, Chromis margaritifer, Ctenochaetus marginatus, Ctenochaetus striatus, Paracirrhites arcatus, Plectroglyphidodon dickii, Pseudanthias bartlettorum, Pseudanthias dispar, Pseudanthias mooreanus, Pseudanthias olivaceous, Pseudianthias pascalus, Pseudanthias* spp., *Stegastes aureus, Stegastes fasciolatus*) across three archipelagos and 19 islands (Jarvis, Kingman, Kiritimati, Palmyra, Tabuaeran, and Teraina in the Northern Line Islands; Flint, Malden, Millennium, Starbuck, and Vostok in the Southern Line Islands; Huahine, Moorea, Raiatea, Rangiroa, Tahiti, Takapoto, Tetiaroa, and Tikehau in French Polynesia), for a total of 5,251 fish. These 17 broadly distributed host species represent a large spectrum of body sizes, including multiple taxonomic and trophic groups. Due to the limitations on the natural geographic ranges of some species, not all species could be sampled on all islands; when we found that a target species was not present on a given island, we sampled a close congener instead (e.g., *Stegastes fasciolatus* instead of *Stegastes aureus*). In general, fish greater than 10 cm in total length were collected using three-pronged spears, while hand nets were used to capture fish smaller than 10 cm in length. Most fish were sampled from depths of 8 to 18 m from the leeward forereef of each island. After collection, fish were humanely euthanized using protocols in UC San Diego IACUC protocol #S09392, which provided ethical approval for this study. We then recorded morphometric data, including the total length of each fish (mm), before freezing fish immediately after collection. Fish were transported frozen back to the laboratory and were kept frozen until they were thawed for parasitological examination.

Parasite abundance assessment

We performed a comprehensive examination of each fish, designed to detect most metazoan parasites. We did not count mobile skin parasites or micropredators, as these are easily lost when the host is captured, and we did not search for myxozoan parasites, but all other metazoans should have been detected with our protocol. We adapted the dissection protocol to the morphology of each fish species (keeping the protocol consistent within species); both the generalized dissection protocol and departures from it are detailed elsewhere [see appendix E in Wood, Sandin, et al. (2014)]. Briefly, we examined the following organs individually under a stereomicroscope: fins, gills, eyes, heart, liver, spleen, gonad, gills, muscle, skin, and intestines [after Wood, Sandin, et al. (2014)]. When an organ was missing or damaged (e.g., part of fin was missing), we recorded “n/a,” not “0,”for any parasite species typically found in that organ (e.g., fin metacercariae). Photographs of each parasite species (along with detailed images of diagnostic morphological features) and voucher specimens were archived and are available for examination by request to the corresponding author. We identified parasites to the lowest possible taxonomic level using published keys [see appendix F in Wood, Sandin, et al. (2014)]: Wood CL, Sandin S, Zgliczynski B, Guerra AS, and Micheli F. 2014. Fishing drives declines in fish parasite diversity and has variable effects on parasite abundance. *Ecology* 95: 1929-46.

Data Processing Description

Data were originally entered into separate datasheets for each fish species / expedition combination, with separate columns for the number of each parasite species in each organ (e.g., separate columns for Nematode A in the stomach and Nematode A in the intestine). For each of these datasets, we first calculated the total number of parasite individuals for each parasite species across organs, summing across organs and

doubling any bilateral organs where only half was counted (e.g., if we found 3 copepods in the buccal cavity and three parasites in the gills, but only counted the right gill arches, the total number of copepods presented in the dataset will be 9). These data therefore reflect the count of each parasite species across all the organs in which they were detected.

For each dataset, we then pivoted longer, such that each row is the count of one parasite species in one fish individual. There are therefore multiple rows for each fish individual, with parasite count as one column and parasite species as a separate column. This allowed us to concatenate datasets across the fish species / expedition combinations.

BCO-DMO Curation Notes

- imported "psite_group_taxa.csv", "island_locations.csv", "fish_sp_list.csv", and "full_dataset_2025.01.17.csv" into the BCO-DMO system, replacing NAs with blanks
- joined all files into one "945218_v1_parasite_abundance_coral_fish"
- split "fish_LSID" to get "fish_AphiaID"
- renamed fields to comply with BCO-DMO system requirements and to clarify values
- export dataset as "945218_v1_parasite_abundance_coral_fish.csv"

Problem Description

NAs and blanks are used to indicate where data do not exist. For example, if a dissector forgot to measure the total length of a fish, it is recorded as NA. If a fish was missing an organ (e.g., it lost a fin when it was speared), we recorded NA for any parasite species that could have been detected in that fin. Collection date information is not available for all specimens.

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Data Files

File	
945218_v1_parasite_abundance_coral_fish.csv	(Comma Separated Values (.csv), 20.71 MB) MD5:a7602c224d3ae9e460be4868d48e995f
Primary data file for dataset ID 945218, version 1	

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Related Publications

WOOD, C. L., & LAFFERTY, K. D. (2014). How have fisheries affected parasite communities? Parasitology, 142(1), 134–144. https://doi.org/10.1017/s003118201400002x
Results

Wood, C. L., Baum, J. K., Reddy, S. M. W., Trebilco, R., Sandin, S. A., Zgliczynski, B. J., Briggs, A. A., & Micheli, F. (2015). Productivity and fishing pressure drive variability in fish parasite assemblages of the Line Islands, equatorial Pacific. Ecology, 96(5), 1383–1398. Portico. https://doi.org/10.1890/13-2154.1
Results

Wood, C. L., Sandin, S. A., Zgliczynski, B., Guerra, A. S., & Micheli, F. (2014). Fishing drives declines in fish parasite diversity and has variable effects on parasite abundance. Ecology, 95(7), 1929–1946. Portico. https://doi.org/10.1890/13-1270.1
Results

Wood, C. L., Zgliczynski, B. J., Haupt, A. J., Guerra, A. S., Micheli, F., & Sandin, S. A. (2018). Human impacts decouple a fundamental ecological relationship—The positive association between host diversity and parasite diversity. Global Change Biology, 24(8), 3666–3679. Portico. https://doi.org/10.1111/gcb.14159
Results

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Related Datasets

IsReferencedBy

Haupt, A., Barton, R., Sandin, S., Wood, C. L. (2025) **COI mtDNA sequences for trematodes from fish collections across the Northern Line Islands and French Polynesia archipelagos collected between 2009 and 2023.** Biological and Chemical Oceanography Data Management Office (BCO-DMO). (Version 1) Version Date 2025-03-03 doi:10.26008/1912/bco-dmo.953401.1 [view at BCO-DMO]

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Parameters

Parameter	Description	Units
fish_unique_code	Unique identification number for each fish individual	units
count	Number of parasite individuals of each parasite species counted in this individual fish	unitless
tract	Island tract or archipelago from which the fish was collected (FP = French Polynesia, NLI = Northern Line Islands, SLI = Southern Line Islands)	unitless
count_id	Unique identification number for the total count of species of parasite individuals in an fish individual	unitless
island	Island from which fish was collected	unitless
island_lat	Latitude of Island	decimal degrees
island_lon	Longitude of Island	decimal degrees
people	Whether the island is inhabited or uninhabited	unitless
fish_sp_code	Fish species to which this fish individual belongs	unitless
psite_unique_code	Parasite species to which parasite individual belongs	unitless
total_length	Total length of fish individual	mm
collection_date	Date on which fish individual was collected	unitless

transmission	Transmission strategy of parasite species (i.e., direct transmission, complex life cycle)	unitless
psite_group	The higher order taxonomic grouping to which parasite species belongs	unitless
psite_ScientificName	Parasite Scientific Name	unitless
fish_ScientificName	Fish Scientific Name	unitless
psite_LSID	Parasite LSID	unitless
fish_LSID	Fish LSID	unitless
psite_AphiaID	Parasite AphiaID	unitless
fish_AphiaID	Fish AphiaID	unitless

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Instruments

Dataset-specific Instrument Name	hand nets
Generic Instrument Name	Hand Net
Dataset-specific Description	In general, fish greater than 10 cm in total length were collected using three-pronged spears, while hand nets were used to capture fish smaller than 10 cm in length.
Generic Instrument Description	A hand net (also called a scoop net or dip net) is a net or mesh basket held open by a hoop. They are used for scooping fish near the surface of the water.

Dataset-specific Instrument Name	three-pronged spears
Generic Instrument Name	Manual Biota Sampler
Dataset-specific Description	In general, fish greater than 10 cm in total length were collected using three-pronged spears, while hand nets were used to capture fish smaller than 10 cm in length.
Generic Instrument Description	"Manual Biota Sampler" indicates that a sample was collected in situ by a person, possibly using a hand-held collection device such as a jar, a net, or their hands. This term could also refer to a simple tool like a hammer, saw, or other hand-held tool.

Dataset-specific Instrument Name	Leica DM1000 compound microscope
Generic Instrument Name	Microscope - Optical
Dataset-specific Description	Compound microscopes were used for parasite identification.
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	Olympus SZ61 stereomicroscope with transmitted-light base
Generic Instrument Name	Microscope - Optical
Dataset-specific Description	Stereomicroscopes were used for parasite detection.
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".

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Project Information

Collaborative Research: Decomposing the effects of diversity on the abundance of marine parasites (Diversity-disease)

Coverage: Central equatorial Pacific (Line Islands and French Polynesia)

NSF Award Abstract:

Nontechnical explanation of the project's broader significance and importance

As Earth's ecosystems experience rapid biodiversity change, disease ecologists have turned to an urgent question: how might reductions in biodiversity affect the transmission of parasites? In other words, does biodiversity loss increase the abundance of parasites by eroding natural checks and balances on transmission? Alternatively, does it decrease parasite abundance by removing the free-living biodiversity on which parasites depend? This study will constitute the first comprehensive test of these questions in any ecosystem. It will evaluate the relationship between fish biodiversity and parasite abundance across 18 replicate coral reef ecosystems. Not only will the work explore whether reductions in fish biodiversity are associated with increases or decreases in parasite burdens, it will also assess whether parasite and host traits or geographical distance influence the direction and strength of this relationship. The theories that are tested are among the most important and controversial in the rapidly growing field of disease ecology and our work represents a novel, creative approach to a long standing, but unresolved research question. The work will yield transformative insights into the nature of parasite transmission in a changing world. Furthermore, the project will intimately intermingle education with research by launching the Research Internship in Molecular Ecology at California State Monterey Bay, which will place a group of underrepresented undergraduates in a central research role, and by developing and disseminating quality educational tools for teaching about parasite

biodiversity through collaboration with the Network of Conservation Educators and Practitioners at the American Museum of Natural History. Parasites are often hidden and can be easy to overlook, but they are ecologically important and affect every population of marine animals.

Technical description of the project

The field of disease ecology is plagued by uncertainty and disagreement over whether biodiversity loss exacerbates parasite transmission, because it lacks the comprehensive, multi-host, multi-parasite, broad-spatial-scale dataset needed to formulate a convincing empirical test.

This project will answer this recalcitrant question, using a dataset of unprecedented replication and taxonomic and spatial resolution, by exploiting the advantages of a marine model system. The project is centered on a natural experiment in which the abundance of parasites across a highly resolved gradient of host biodiversity, for more than 77 parasite species and 18 replicate coral reef ecosystems will be quantified. Dataset will critically test hypotheses for the biodiversity-parasite abundance relationship, revealing how the direction, shape, and scale-dependence of this relationship vary across a diverse array of parasite taxa, and resolving questions of burning interest in the disease ecology literature - and of vital importance to marine conservation. This project will address the following questions: (Q1) For each parasite species detected, what is the direction and shape of the relationship between biodiversity and parasite abundance? (Q2) What factors (e.g., parasite traits like transmission strategy and host specificity, host traits like body size) determine the direction and shape of the relationship between biodiversity and parasite abundance? (Q3) How does spatial scale interact with parasite dispersal capacity to moderate the effects of biodiversity on parasite abundance? The work will integrate an existing dataset on fish biodiversity and abundance of coral reef fish parasites from six equatorial Pacific islands (the Northern Line Islands) with new sampling from 12 additional islands (the Southern Line Islands and French Polynesia). The resulting dataset will reflect the burden of >77 metazoan parasite taxa for seven species of coral reef fishes across18 islands. The work will provide the world's first data on the direction, magnitude, and shape of the biodiversity-disease relationship across a diversity of parasite taxa, host taxa, and spatial scales, and will comprehensively identify conditions under which biodiversity is likely to be important in determining the abundance of parasites - a fundamental contribution to ecology and to biological oceanography. The project will intimately integrate education with research by placing a group of underrepresented minority undergraduates in a central research role: performing the molecular analyses required to estimate parasite dispersal distance. A summer Research Internship in Molecular Ecology will be established at California State University Monterey Bay, a Hispanic-Serving Institution. The project will also underwrite the development of a peer-reviewed learning module on parasite biodiversity, to be developed and disseminated in collaboration with the American Museum of Natural History, and will support the training of two graduate students, one postdoctoral scholar, and several undergraduates.

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-1829509

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