Microbial orders comprising the core microbiome across all samples as measured by taxa prevalence, 2009-2012 (HERBVRE project)

Website: https://www.bco-dmo.org/dataset/674398
Data Type: experimental
Version: 1
Version Date: 2017-01-10

Project
» Cascading interactions of herbivore loss and nutrient enrichment on coral reef macroalgae, corals, and microbial dynamics (HERBVRE)

Contributors	Affiliation	Role
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Abstract
This dataset contains microbial orders comprising the core microbiome across all samples as measured by taxa prevalence, from Florida Keys National Marine Sanctuary. Cyanobacteria, Bacteroidetes and Actinobacteria were most abundant in all coral genera, with a core set of 13 bacterial orders in ≥95% of all samples. Published in Nature Communications (2016) doi:10.1038/ncomms11833, Supplementary Data 3a.

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Coverage

Spatial Extent: **Lat**:24.9943 **Lon**:-80.4065

Dataset Description

This dataset contains microbial orders comprising the core microbiome across all samples as measured by taxa prevalence, from Florida Keys National Marine Sanctuary. Cyanobacteria, Bacteroidetes and Actinobacteria were most abundant in all coral genera, with a core set of 13 bacterial orders in ≥95% of all samples. Published in Nature Communications (2016) doi:10.1038/ncomms11833, Supplementary Data 3a.

Natural history of the study site:
This experiment was conducted in the area of Pickles Reef (24.99430, -80.40650), located east of Key Largo, Florida in the United States. The Florida Keys reef tract consists of a large bank reef system located approximately 8 km offshore of the Florida Keys, USA, and paralleling the island chain. Our study reef is a 5-6 m deep spur and groove reef system within this reef tract. The reefs of the Florida Keys have robust herbivorous fish populations and are relatively oligotrophic. Coral cover on most reefs in the Florida Keys, including our site, is 5-10%, while macroalgal cover averages ~15%, but ranges from 0-70% depending on location and season. Parrotfishes (*Scaridae*) and surgeonfishes (*Acanthuridae*) are the dominant herbivores on

these reefs as fishing for them was banned in 1981. The other important herbivore on Caribbean reefs, the urchin *Diadema antillarum*, remains at low densities across the Florida Keys following the mass mortality event in 1982-3.

Related Reference:
Zaneveld, J.R., D.E. Burkepile, A.A. Shantz, C. Pritchard, R. McMinds, J. Payet, R. Welsh, A.M.S. Correa, N.P. Lemoine, S. Rosales, C.E. Fuchs, and R. Vega Thurber (2016) Overfishing, nutrient pollution, and temperature interact to disrupt coral reefs down to microbial scales. Nature Communications 7:11833
doi:10.1038/ncomms11833 Supplementary Information

Methods & Sampling

To identify how algal communities and nutrient pollution affected the coral microbiome, we collected DNA samples from the surface mucus layer of 80 coral colonies (genera Porites, Siderastrea and Agaricia) at approximately monthly intervals. From these samples, 478 were used for 16S ribosomal RNA (rRNA) gene amplicon analyses following quality control (Supplementary Data 2 sheets a–d). (Zaneveld, 2016)

Analysis of microbial β-diversity: Microbial community β-diversity was calculated based on the weighted UniFrac distance matrix67. This is a phylogenetic measure of community similarity that takes into account organismal abundance and phylogeny67. Phylogenetic trees used to calculate this metric were constructed in QIIME 1.8 (ref. 65) through alignment of representative sequences of each OTU with PyNAST against the greengenes core set alignment66, and approximate maximum likelihood phylogenetic inference with FastTree. We considered the pool of distances between samples within each metadata category of interest (for example, algal competition or categories of temperature) using QIIME's make_distance_boxplots.py. Significance was assessed by non-parametric t-tests, each with 1,000 Monte Carlo permutations (permutation is important in this instance to account for the non-independence of distances). The effect of this procedure is to ask whether different factors increase the dispersion of communities. PCoA plots of β-diversity were visualized in the Emperor software. When multiple categories (for example, different algal types) were tested for effects on β-diversity, the false discovery rate (FDR) for multiple comparisons was controlled at a threshold of q=0.05 using the Bejamini–Hochberg method. (Zaneveld, 2016)

Data Processing Description

BCO-DMO Processing:
- added conventional header with dataset name, PI name, version date, reference information
- renamed parameters to BCO-DMO standard

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Data Files

File
S3a_core_microbes.csv(Comma Separated Values (.csv), 4.40 KB) MD5:697a771612a3dc35ffada583b62cb828 Primary data file for dataset ID 674398

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Related Publications

Zaneveld, J. R., Burkepile, D. E., Shantz, A. A., Pritchard, C. E., McMinds, R., Payet, J. P., ... Thurber, R. V. (2016). Overfishing and nutrient pollution interact with temperature to disrupt coral reefs down to microbial scales. Nature Communications, 7(1). doi:10.1038/ncomms11833
Results

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Parameters

Parameter	Description	Units
taxonomy	microbe taxonomic identification from QIIME Greengenes 13_8	unitless
all_tmt_95pcent	95% carriage of the microbial order in coral mucus samples across all treatments	unitless
all_tmt_75pcent	75% carriage of the microbial order in coral mucus samples across all treatments	unitless
all_tmt_50pcent	50% carriage of the microbial order in coral mucus samples across all treatments	unitless
core_only_95pcent	95% carriage of the microbial order in coral mucus samples for Greengenes core set only	unitless
core_only_75pcent	75% carriage of the microbial order in coral mucus samples for Greengenes core set only	unitless
core_only_50pcent	50% carriage of the microbial order in coral mucus samples for Greengenes core set only	unitless

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Deployments

Burkepile_FL_Keys

Website	https://www.bco-dmo.org/deployment/639486
Platform	Florida Keys National Marine Sanctuary
Start Date	2009-06-01
End Date	2012-08-31
Description	Herbivore effects on reef algae

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Project Information

Cascading interactions of herbivore loss and nutrient enrichment on coral reef macroalgae, corals, and microbial dynamics (HERBVRE)

Coverage: Key Largo, Florida Keys, USA; N 24.99430, W 080.40650

Description from NSF award abstract:
Coral reefs in the Caribbean Sea are undergoing unprecedented declines in coral cover due in large part to climate change, pollution, and reductions in fish biodiversity and abundance. Macroalgae have become abundant on reefs, probably due to decreases in herbivory (e.g., through overfishing) and increases in anthropogenic inputs of nutrients. The spread of macroalgae has negative feedbacks on reef recovery because algae are often superior competitors and suppress growth of both adult and juvenile corals. A majority of reef studies to date have focused on how stressors affect macroorganisms, while relatively few have investigated how these stressors and the resultant algal-dominated states affect microorganisms. Yet, coral reef-associated microbes play significant roles in coral reef ecosystems through biogeochemical cycling and disease. Since microbes are important mutualists of corals as well as potential pathogens, it is important to understand the mechanisms that control their taxonomic and functional diversity.

The goal of this proposal is to quantify how alterations of top-down (removal of herbivorous fish) and bottom-up (inorganic nutrient addition) forces alter macrobial as well as microbial dynamics on coral reefs in order to understand the mechanisms that reinforce coral-depauperate reef systems. This work asks two main questions:

Q1. How do nutrient enrichment and herbivore removal interact to affect benthic algal abundance, coral-algal interactions, and coral survivorship and growth?

Q2. How do nutrient enrichment and herbivore removal affect bacterial abundance, taxonomic diversity, and functional diversity on and within corals?

The proposed research will directly and empirically address many of the current hypotheses about how bottom-up and top-down forces alter reef dynamics. The PIs will investigate: (1) the impact of multiple stressors over several years; (2) impacts on multiple levels of biological organization (from fishes to algae to microbes); and (3) the mechanisms underlying changes in algal-coral microbe interactions. Significantly, the approach will provide the statistical power necessary to distinguish between seasonal- and stress-induced changes in macro- and microbial diversity.

Resulting Publication:
Zaneveld, J.R., D.E. Burkepile, A.A. Shantz, C. Pritchard, R. McMinds, J. Payet, R. Welsh, A.M.S. Correa, N.P. Lemoine, S. Rosales, C.E. Fuchs, and R. Vega Thurber (2016) Overfishing, nutrient pollution, and temperature interact to disrupt coral reefs down to microbial scales. Nature Communications 7:11833 doi:10.1038/ncomms11833.
Access to data via Supplementary Information.

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Funding

Funding Source	Award
NSF Division of Ocean Sciences (NSF OCE)	OCE-1130786

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