

Bacteria assemblages associated with *Eurytemora affinis* in both salt and fresh water from shoreside Lee-DaSilva Lee-DaSilva Collection in the USA; Netherlands; Canada; Belgium; various locations each from 2012-2014 (CopepodMicrobiome project)

Website: <https://www.bco-dmo.org/dataset/641102>

Data Type: Other Field Results

Version: first

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Project

» [Dimensions: Uncovering the novel diversity of the copepod microbiome and its effect on habitat invasions by the copepod host](#) (CopepodMicrobiome)

Program

» [Dimensions of Biodiversity](#) (Dimensions of Biodiversity)

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Dataset Description

Bacteria in the water and bacteria from the same location but directly associated (in the cuticle) with copepods were collected from several locations world-wide with pumps and nets from saline and fresh water. The acquired DNA was sequenced and sent to GenBank. The links are here.

These data will be available after January, 2017.

Methods & Sampling

The water samples were collected this way: Approximately 10 liters of water were collected from a depth of 1 meter near the shore and filtered through a 3.0 micron filter to exclude sediment, algae, and other large particles. Then the water was passed through a 0.1 micron filter to collect bacteria. DNA was extracted from the filter with a MoBio PowerWater DNA isolation kit.

The copepods and their associated bacteria were collected this way: 100 pooled adult male and female *Eurytemora affinis* were collected via plankton tow from depth of ~1-2 meters from near the shore. These animals were isolated from the zooplankton community under a microscope, and homogenized in a glass pestle tissue grinder. DNA was extracted with a MoBio UltraClean Microbial DNA isolation kit.

Data Processing Description

There was no way to isolate bacteria from their copepod hosts, so the entire sample was processed and the DNA from the whole thing was extracted.

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Parameters

Parameter	Description	Units
collection	how the sample was collected; water by a pump; copepods and associated bacteria by a net	text
sample_name	how the sample is identified; the first initials correspond to the location and the W(water) and E(Eurytemora) indicates the method	coded text
date_start	date of start of collection	day-three letter month-four digit year
date_end	date of end of collection	day-three letter month-four digit year
site	sampling location	text
lat	latitude of the collection; N is positive	decimal degrees
lon	longitude of the collection; W is negative	decimal degrees
SRA_accession_number	Sequence Read Archive. This makes biological sequence data available to the research community to enhance reproducibility and allow for new discoveries. The identification number of the sequence submitted to GenBank.	link

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Instruments

Dataset-specific Instrument Name	Plankton net
Generic Instrument Name	Plankton Net
Dataset-specific Description	Some of the samples were collected by small boat (Blue Hammock Bayou and Lake Pontchartrain) very near the shore. The rest of the net collection was from throwing the plankton net off the dock.
Generic Instrument Description	A Plankton Net is a generic term for a sampling net that is used to collect plankton. It is used only when detailed instrument documentation is not available.

Dataset-specific Instrument Name	Water pump
Generic Instrument Name	Pump
Dataset-specific Description	Battery powered water pump dropped into the water to depth of 1 m and pumped into 25L Nalgene carboys.
Generic Instrument Description	A pump is a device that moves fluids (liquids or gases), or sometimes slurries, by mechanical action. Pumps can be classified into three major groups according to the method they use to move the fluid: direct lift, displacement, and gravity pumps

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Deployments

Lee-DaSilva Collection

Website	https://www.bco-dmo.org/deployment/641139
Platform	shoreside Lee-DaSilva
Start Date	2012-10-15
End Date	2014-05-28
Description	These samples were collected from the shore mostly, by nets and water pumps, pan-global.

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Project Information

Dimensions: Uncovering the novel diversity of the copepod microbiome and its effect on habitat invasions by the copepod host (CopepodMicrobiome)

Coverage: Atlantic Coast, Gulf of Mexico, Great Lakes, North America, Netherlands

Copepods form the largest biomass of metazoans on the planet, yet their microbiota remain largely unexplored. The microbial community associated with copepods might perform key metabolic processes that affect host fitness and ecosystem functioning. The copepod *Eurytemora affinis* is dominant in coastal habitats

throughout the world, and recently has invaded inland freshwater habitats. Associated with *E. affinis*, preliminary sequencing revealed high diversity of microbial taxa, including many undescribed genera and families. There also were parallel shifts in microbial composition during independent invasions from saline to freshwater habitats. Yet, a core set of microbial taxa remained present in all copepod populations across all locations. The copepod microbiome is likely to play fundamental roles in biogeochemical processes in many aquatic ecosystems. Microbial-host interactions could influence invasive success, and exotic microbes in the invading consortia could have vital impacts on the invaded community. This study will address the following questions: (1) What is the taxonomic composition of the copepod microbiome, and how does it shift during habitat invasions? (Taxonomy, Genetics); (2) What metabolic functions are performed by the copepod microbiome? (Function, Genetics); and (3) What is the nature of copepod host-microbial interactions, and how do these interactions shift during invasions? (Functional Integration)

Research to address these questions includes: (1) high-throughput 16S sequencing, to identify the taxonomic composition of microbial assemblages associated with the copepod host in saline and freshwater environments, (2) shotgun sequencing of metagenomes and fosmids, and also comprehensive genome sequencing of key microbial taxa, to characterize the functional repertoire of genes in the copepod microbiome, and (3) reciprocal inoculation experiments, to explore functional interactions between the copepod host and its microbiome and whether the interactions evolve during invasions into novel habitats.

Characterizing the copepod microbiome will expose a largely undiscovered realm of microbial diversity. Moreover, this gene-centric analysis will provide invaluable insights into metabolic functions of the copepod microbiome, and how these functions might shift during copepod invasions. Results are expected to yield transformative insights into the taxonomic, functional, and genetic diversity of a largely unexplored component of the ecosystem, and how this diversity might become altered following invasions into novel habitats.

This study will provide integrated insights into the taxonomic, genetic, and functional diversity of the copepod microbiome. The assembled sequences will link specific metabolic functions with particular microbial taxa, illuminating functional diversity across deeply divergent lineages. Sequence data also will reveal genetic diversity of metabolic functions within microbial taxa, and the potential sharing of functions across taxa (e.g. via horizontal gene transfer). Moreover, these findings will reveal functional integration of the microbial-host consortia, including between the microbial community and its host.

Preliminary sequencing of the *E. affinis* microbiome uncovered a wide variety of potentially pathogenic taxa, including Salmonella, Shigella, Campylobacter, *Corynebacterium diphtheriae*, Yersinia, and *Vibrio cholerae*. Thus, *E. affinis* might play an important role as a reservoir and vector of waterborne disease.

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Program Information

Dimensions of Biodiversity (Dimensions of Biodiversity)

Website: http://www.nsf.gov/funding/pgm_summ.jsp?pims_id=503446

Coverage: global

(adapted from the NSF Synopsis of Program)

Dimensions of Biodiversity is a program solicitation from the NSF Directorate for Biological Sciences. FY 2010 was year one of the program. [\[MORE from NSF\]](#)

The NSF Dimensions of Biodiversity program seeks to characterize biodiversity on Earth by using integrative, innovative approaches to fill rapidly the most substantial gaps in our understanding. The program will take a broad view of biodiversity, and in its initial phase will focus on the integration of genetic, taxonomic, and functional dimensions of biodiversity. Project investigators are encouraged to integrate these three dimensions to understand the interactions and feedbacks among them. While this focus complements several core NSF programs, it differs by requiring that multiple dimensions of biodiversity be addressed simultaneously, to understand the roles of biodiversity in critical ecological and evolutionary processes.

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Funding

Funding Source	Award
NSF Division of Ocean Sciences (NSF OCE)	OCE-1046372
NSF Division of Ocean Sciences (NSF OCE)	OCE-1046371

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