Fatty acid data from infauna in sediment cores at McMurdo Station, Antarctica in September, November and February of 2012 and 2013 (McMurdo Benthos project)

Website: https://www.bco-dmo.org/dataset/716455
Data Type: Cruise Results
Version:
Version Date: 2017-10-11

Project
» Microbe - Metazoan Interactions in an Antarctic Infaunal Community (McMurdo Benthos)

Contributors	Affiliation	Role
Thurber, Andrew	Oregon State University (OSU)	Principal Investigator, Contact
York, Amber D.	Woods Hole Oceanographic Institution (WHOI BCO-DMO)	BCO-DMO Data Manager

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Coverage

Spatial Extent: **Lat**:-77.846 **Lon**:166.639

Dataset Description

Fatty acid data from infauna in sediment cores collected at the “Jetty” dive site, Hutt Point, McMurdo Station, Antarctica. Seasonal sampling took place in September, November and February 2012-2013.

Methods & Sampling

Methodology:
Sample collection and field treatment: Sediment cores were collected at the “Jetty” dive site location in September, November and February 2012-2013. These were sieved on a 300-micron sieve to collect macrofauna and members of the abundant species Spiophanes tcherniai (a spionid polychaete) and Edwarsia spp. (a sand anemone) were picked under a dissecting microscope and placed in filtered seawater overnight to allow gut evacuation. At this point, individuals were frozen separately at -80 C prior to lipid extraction.

Sampling and analytical procedures:
Samples were freeze-dried and their lipids extracted using one-step extraction-transesterification procedure of Lewis et al. (2000) as used in Thurber (2014). In brief, individuals were placed in pre-cleaned and extracted sample vials, heated to 90 deg. C for one hour in a solution of methanol, chloroform, and hydrochloric acid (10:1:1 by volume) before cooling and water added to break the phase. Fatty acid methyl esters (FAMEs) were extracted in sequential addition of hexane:chloroform (4:1) and water further removed through the addition of sodium sulfate. The FAMEs were then ready for quantification on a GC-FID.

Isotopic analysis was measured on a Thermo 1310 gas chromatograph with a Flame Ionization detector using a TR-WaxMS column (30mx 0.32mm x 0.25 um). Peak identification was by comparison to known standards (for example the Supulco 32 FAME mixture).

Data Processing Description

Peak identity and area were manually checked and we report concentration as a percentage of total FAMEs for those that make up more than 1 percent of the total integrated area of the chromatogram. We have been conservative in peak identification, with multiple unidentified FAs indicated, however, these are comparable across the samples (i.e. Unident. FA # 2 is the same in all individuals analyzed).

BCO-DMO Data Manager Processing Notes:
* added a conventional header with dataset name, PI name, version date
* modified parameter names to conform with BCO-DMO naming conventions
* parameter names modified for clarity: Fatty_Acid -> Fatty_Acid_ID ; Concentration -> Fatty_Acid_Concentration ; Replicate -> Core_Replicate
* updated coordinates in data for hutt point sample site based on correspondence with data contributor.

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Data Files

File
FattyAcid.csv (Comma Separated Values (.csv), 24.99 KB) MD5:f14a38af659e73a7ef727fc2f7709a15 Primary data file for dataset ID 716455

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Related Publications

Lewis, T., Nichols, P. D., & McMeekin, T. A. (2000). Evaluation of extraction methods for recovery of fatty acids from lipid-producing microheterotrophs. Journal of Microbiological Methods, 43(2), 107–116. doi:10.1016/s0167-7012(00)00217-7 https://doi.org/10.1016/S0167-7012(00)00217-7
Methods

Thurber, A. R. (2014). Diet-dependent incorporation of biomarkers: implications for food-web studies using stable isotope and fatty acid analyses with special application to chemosynthetic environments. Marine Ecology, 36, 1–17. doi:10.1111/maec.12192
Methods

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Parameters

Parameter	Description	Units
Taxa	Species that had its fatty acid profile measured	unitless
Sample_Identifier	unique identifier for the individual that was analyzed	unitless
Sample_date	Date the sample was collected in format yyyy-mm-dd	unitless
Core_Replicate	The sample identifier for the sediment core that the individual was collected from	unitless
Fatty_Acid_ID	Identity of the fatty acid using lipid number (e.g. C16:2) which includes number of carbons in the fatty acid chain : number of double bonds in the in fatty acid chain and, where indicated, (n-x) notation indicates the location of the first double bond from the terminal end of the Fatty Acid Chain. Unidentified fatty acids (e.g. Unident. FA # 21) were assigned numeric identifiers consistent amongst all samples. See processing description section for more details.	unitless
Fatty_Acid_Concentration	Percent of total fatty acids recovered from that individual sample.	percent
lat	Latitude of sample; north is positive	decimal degrees
lon	Longitude of sample; west is negative	decimal degrees

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Instruments

Dataset-specific Instrument Name	Thermo 1310 gas chromatograph
Generic Instrument Name	Gas Chromatograph
Dataset-specific Description	Isotopic analysis was measured on a Thermo 1310 gas chromatograph with a Flame Ionization detector using a TR-WaxMS column (30mx 0.32mm x 0.25 um).
Generic Instrument Description	Instrument separating gases, volatile substances, or substances dissolved in a volatile solvent by transporting an inert gas through a column packed with a sorbent to a detector for assay. (from SeaDataNet, BODC)

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Deployments

Thurber_Hutt_Point_2012

Website	https://www.bco-dmo.org/deployment/716447
Platform	Ross Island

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Project Information

Microbe - Metazoan Interactions in an Antarctic Infaunal Community (McMurdo Benthos)

Coverage: Ross Sea, 78 S 167 E

The biota of the world's seafloor is fueled by bursts of seasonal primary production. For food-limited sediment communities to persist, a balance must exist between metazoan consumption of and competition with bacteria, a balance which likely changes through the seasons. Polar marine ecosystems are ideal places to study such complex interactions due to stark seasonal shifts between heterotrophic and autotrophic communities, and temperatures that may limit microbial processing of organic matter. The research will test the following hypotheses: 1) heterotrophic bacteria compete with macrofauna for food; 2) as phytoplankton populations decline macrofauna increasingly consume microbial biomass to sustain their populations; and 3) in the absence of seasonal photosynthetic inputs, macrofaunal biodiversity will decrease unless supplied with microbially derived nutrition. Observational and empirical studies will test these hypotheses at McMurdo Station, Antarctica, where a high-abundance macro-infaunal community is adapted to this boom-and-bust cycle of productivity. The investigator will mentor undergraduates from a predominantly minority-serving institution, in the fields of invertebrate taxonomy and biogeochemistry. The general public and young scientists will be engaged through lectures at local K-12 venues and launch of an interactive website. The results will better inform scientists and managers about the effects of climate change on polar ecosystems and the mechanisms of changing productivity patterns on global biodiversity.

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Funding

Funding Source	Award
NSF Office of Polar Programs (formerly NSF PLR) (NSF OPP)	OPP-1103428

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