Microbial gene abundance of coastal wetland soil cores collected in June 2018 from Barataria Bay, Louisiana

Website: https://www.bco-dmo.org/dataset/840278
Data Type: Other Field Results
Version: 1
Version Date: 2021-02-10

Project
» Fate of Coastal Wetland Carbon Under Increasing Sea Level Rise: Using the Subsiding Louisiana Coast as a Proxy for Future World-Wide Sea Level Projections (Submerged Wetland Carbon)

Contributors	Affiliation	Role
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Abstract
Nine coastal wetland soil cores (150cm) collected in June 2018 from Barataria Bay, Louisiana were analyzed for microbial gene abundance

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Coverage

Spatial Extent: **Lat**:29.443547 **Lon**:-89.8998
Temporal Extent: 2018-06 - 2018-06

Methods & Sampling

Nine coastal wetland soil cores were collected in June 2018 from Barataria Bay, Louisiana, a shallow open water basin located west of the Mississippi River Delta. Soil cores were collected along three transects, roughly 1 meter apart, that consisted of three points: the coastal fringe (0 m inland), 1 meter inland, and 2 meters inland. Soil cores were collected in polycarbonate tubes via the push core method to a depth of 150 cm, and

field-extruded into 15 separate 10-cm intervals. Soils were stored in polyethylene bags on ice and immediately transported back to the laboratory, where they were kept at 4 °C until sample analysis was complete.

This dataset includes analyses of microbial gene abundance. Quantitative PCR analysis on a CFX96 Touch Real-Time PCR Detection system was used to measure the number of gene copies of bacteria (16S), sulfate reduction (dsRa), and archaea (Arch) genes.

Soil samples were sieved through a 2mm seive, then centrifuged at 4000 rpm at 25°C for 1 minute, and excess water decanted. DNA was extracted from soil subsamples (0.25 grams each) following DNAeasy PowerSoil Extraction Kit (QIAGEN, Hilden, Germany). Primers were selected to amplify specific taxonomic and functional genes of interest within the samples -- sulfate reduction (dsrA), all bacteria (16S), and all archaea (Arch). Genomic DNA from Desulfobacterium autotrophicum (Strain DSM 3382) was used to establish standard curves for both amplification of the 16S gene and the dsrA gene, while Methanococcus voltae (Strain A3) was used to establish standard curves for amplification of the Arch gene. Each 25 microliter reaction contained 5 microliters DNA, 1.25 microliters of each 0.1uM primer (forward and reverse), 12.5 microliters of SYBR green MasterMix, and 12.5 microliters of PCR-grade water. Each reaction initially proceeded through steps at 50°C and 95°C, then through 50 cycles of denaturing at 95°C, annealing, and extending at 72°C.

[For details on primers and primer annealing temperatures, see Steinmuller and Chambers (2019)].

Data Processing Description

Data processing:
All statistical analysis was performed in R (R Institute for Statistical Computing, Vienna, Austria) using RStudio (RStudio Inc., Boston, MA, USA). The Shapiro-Wilk test was used to verify assumptions of normality, and a logarithmic transformation was performed on all datasets. Levene's test was used to determine homogeneity of variance. A linear mixed-effect model (package 'lmer') was used to test the following predictor variables: depth, distance inland, and the interaction of depth and distance inland on the samples collected from the marsh. Isotopic determinations and quantitative PCR analysis was performed exclusively on the three replicate cores taken 1 meter inland, and thus depth was the only predictor variable tested for those parameters. Following determination of significance within one of the predictor variables, the package 'lsmeans' was used for post-hoc pairwise comparisons using the Tukey method.

BCO-DMO processing:
- Added a conventional header with dataset name, PI names, version date
- Adjusted parameter names to comply with database requirements.
- Units removed and added to Parameter Description metadata section.
- Added Latitude and Longitude columns, converted DMS to DD
- Added column for Date of sample collection
- Missing data entries replaced with 'nd'

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Data Files

File	
gene_abundance.csv	(Comma Separated Values (.csv), 9.69 KB) MD5:4ccfa86d7add837d4546dff3b4dca144
Primary data file for dataset ID 840278	

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Related Publications

R Core Team (2018). R: A language and environment for statistical computing. R v3.5.1. R Foundation for Statistical Computing, Vienna, Austria. URL https://www.R-project.org/
Software

RStudio Team (2018). RStudio: Integrated Development for R. RStudio 1.1.456, PBC, Boston, MA URL http://www.rstudio.com/.
Software

Sapkota, Y., & White, J. R. (2021). Long-term fate of rapidly eroding carbon stock soil profiles in coastal wetlands. Science of The Total Environment, 753, 141913. doi:10.1016/j.scitotenv.2020.141913
General

Steinmuller, H. E., & Chambers, L. G. (2019). Characterization of coastal wetland soil organic matter: Implications for wetland submergence. Science of The Total Environment, 677, 648–659. doi:10.1016/j.scitotenv.2019.04.405
Methods

Steinmuller, H. E., Dittmer, K. M., White, J. R., & Chambers, L. G. (2019). Understanding the fate of soil organic matter in submerging coastal wetland soils: A microcosm approach. Geoderma, 337, 1267–1277. doi:10.1016/j.geoderma.2018.08.020
General

Steinmuller, H. E., Foster, T. E., Boudreau, P., Hinkle, C. R., & Chambers, L. G. (2020). Characterization of herbaceous encroachment on soil biogeochemical cycling within a coastal marsh. Science of The Total Environment, 738, 139532. doi:10.1016/j.scitotenv.2020.139532
General

Steinmuller, H. E., Hayes, M. P., Hurst, N. R., Sapkota, Y., Cook, R. L., White, J. R., Xue, Z., & Chambers, L. G. (2020). Does edge erosion alter coastal wetland soil properties? A multi-method biogeochemical study. CATENA, 187, 104373. https://doi.org/10.1016/j.catena.2019.104373
General

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Related Datasets

IsRelatedTo

Steinmuller, H. E., White, J. R., Cook, R. L., Xue, Z., Chambers, L. G. (2021) **Nutrient properties of coastal wetland soil cores collected in June 2018 from Barataria Bay, Louisiana.** Biological and Chemical Oceanography Data Management Office (BCO-DMO). (Version 1) Version Date 2021-02-10 doi:10.26008/1912/bco-dmo.840293.1 [view at BCO-DMO]

Steinmuller, H. E., White, J. R., Cook, R. L., Xue, Z., Chambers, L. G. (2021) **Soil physicochemical properties of coastal wetland soil cores collected in June 2018 from Barataria Bay, Louisiana.** Biological and Chemical Oceanography Data Management Office (BCO-DMO). (Version 1) Version Date 2021-02-10 doi:10.26008/1912/bco-dmo.840246.1 [view at BCO-DMO]

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Parameters

Parameter	Description	Units
Field_Replicate	Denotation of whether core was the 1st (A), 2nd (B), or 3rd (C) core pulled from the site	unitless
Depth	Soil depth below the surface	centimeters (cm)
Plate_Replicate	Denotation of whether the plate was the 1st, 2nd, or 3rd plate run as analytical replicates	unitless
Bacteria	Abundance of 16S gene within a given subsample of soil	gene copies
dsrA	Abundance of dsrA gene within a given subsample of soil	gene copies
Archaea	Abundance of Arch gene within a given subsample of soil	gene copies
Latitude	Latitude	decimal degrees
Longitude	Longitude (west is negative)	decimal degrees
Date_collected	Date of sample collection	unitless

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Instruments

Dataset-specific Instrument Name	
Generic Instrument Name	Centrifuge
Generic Instrument Description	A machine with a rapidly rotating container that applies centrifugal force to its contents, typically to separate fluids of different densities (e.g., cream from milk) or liquids from solids.

Dataset-specific Instrument Name	
Generic Instrument Name	Push Corer
Generic Instrument Description	Capable of being performed in numerous environments, push coring is just as it sounds. Push coring is simply pushing the core barrel (often an aluminum or polycarbonate tube) into the sediment by hand. A push core is useful in that it causes very little disturbance to the more delicate upper layers of a sub-aqueous sediment. Description obtained from: http://web.whoi.edu/coastal-group/about/how-we-work/field-methods/coring/

Dataset-specific Instrument Name	CFX96 Touch Real-Time PCR Detection System
Generic Instrument Name	Thermal Cycler
Dataset-specific Description	The number of gene copies for each sample was determined through qPCR analysis on a CFX96 Touch Real-Time PCR Detection System
Generic Instrument Description	A thermal cycler or "thermocycler" is a general term for a type of laboratory apparatus, commonly used for performing polymerase chain reaction (PCR), that is capable of repeatedly altering and maintaining specific temperatures for defined periods of time. The device has a thermal block with holes where tubes with the PCR reaction mixtures can be inserted. The cycler then raises and lowers the temperature of the block in discrete, pre-programmed steps. They can also be used to facilitate other temperature-sensitive reactions, including restriction enzyme digestion or rapid diagnostics. (adapted from http://serc.carleton.edu/microbelife/research_methods/genomics/pcr.html)

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Project Information

Fate of Coastal Wetland Carbon Under Increasing Sea Level Rise: Using the Subsiding Louisiana Coast as a Proxy for Future World-Wide Sea Level Projections (Submerged Wetland Carbon)

Coverage: Coastal Lousiana

Description from NSF award abstract:
Coastal Louisiana is currently experiencing net sea level rise at rates higher than most of the world's coastlines and within the global range predicted to occur in the next 65 - 85 years, making Louisiana an ideal site to study potential future impacts of rising sea level on coastal systems. This project will use field collection and controlled tank experiments to study the changing organic carbon cycle resulting from erosion of marsh soils along with its impact on associated biogeochemical processes. The hypothesis tested in this study is that the majority of eroded soil organic carbon is converted to carbon dioxide (CO2) and released to the atmosphere, representing an addition to the anthropogenic input of CO2. This process has not been quantified and could be an important missing component in predictive models of atmospheric CO2 changes. While this process may be of only regional importance today in comparison to other sources of CO2, this study of the Louisiana coast will greatly enhance our full understanding of the potential impacts on the global carbon cycle that may result from coastal erosion as global sea level continues to rise.

The project will train graduate and undergraduate students in interdisciplinary research involving marine and wetland biogeochemistry, microbiology, and ecological modeling. It will also fund development of an interactive, educational display on the loss of coastal wetlands for the Louisiana Sea Grant's annual Ocean Commotion educational event attended by area middle and high school students, teachers, and parents. Results from this study may also inform community planners both regionally and worldwide as they prepare for sea level rise in coastal communities.

Eustatic sea level rise and regional subsidence have created a much greater rate of coastline loss in Louisiana than is being experienced in most of the world's coastal regions, reaching global rates that are predicted to occur worldwide in 65 - 85 years. This provides a unique potential to extrapolate data from Louisiana's changing coastal carbon cycle to both regional and global models of the future impact of sea level rise and coastal erosion. By quantifying and modeling the importance of CO2 emissions resulting directly from mineralized soil organic matter from eroding coastlines, a missing element can be added to climate change models. The PIs here plan to investigate the fate of the coastal wetland carbon pool as it erodes using field sampling, laboratory analysis, mesocosm manipulations, and the creation of a coupled physical-biogeochemical model for the basin being studied. Beyond quantifying increased CO2 emission, the PIs will also address the potential for increased eutrophication due to input of nutrients from eroded soils, as well as the potential for

future contribution to existing hypoxic zones in the northern Gulf of Mexico that result from excessive nutrient input from the Mississippi River watershed.

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Funding

Funding Source	Award
NSF Division of Ocean Sciences (NSF OCE)	OCE-1635837

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