Deciphering the Cryptic Cycling of Methane in Sediments of a Coastal Wetland

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DATA MANAGEMENT PLAN

Types of data

We anticipate generating data from the following sources: 1) bio/geochemical data from in-situ methane emission chamber measurements, ex-situ sediment cores analyses, and in-vitro sediment slurries studies, 2) sequencing of archeal and bacterial genes from sediments, 3) micrographs from in situ hybridization and nanoscale secondary ion mass spectromity of microbial cells.

Data and metadata standards

Numerical data will be produced from bio/geochemical data (units: mol/m2, mol/L, mol/L/d). The output data file format will be Excel (.XLSX).

Visual data will be produced from in situ hybridization and nanoscale secondary ion mass spectromity (type: micrographs). The output data file format will be .TIFF and .JPG.

Molecular sequence data will be generated as FASTA files of 16S rRNA amplicon sequences and corresponding metadata.

Policies for access, sharing, re-use, and re-distribution

Field and laboratory data will be collected in notebooks, which will be electronically archived. All data will be entered into spreadsheets arranged by parameter with dates, location and units recorded. Metadata describing parameters measured, field methods, images and other descriptive data will be stored electronically and attached to all spreadsheets. Data will be stored on desktop computers and backed up on external hard drives. The PI and graduate student will share copies of all relevant data and derived products from this study.

Data sets generated will be made available through the Environmental Systems Science Data Infrastructure for a Virtual Ecosystem (ESS-DICE) and/or the Biological and Chemical Oceanography Data Management Office (BCO-DMO) within two years from the date of generation and in compliance with the NSF Sample and Data Policy. The project investigators will work with the data infrastructure managers to make project data discoverable and accessible online, and to obtain Digital Object Identifiers (DOIs). Genetic raw data will be uploaded to the National Center for Biotechnology Information Sequence Read Archive (NCBI-SRA). Per NSF guidelines, NCBI data will also be linked to the publicly-accessible project repository hosted by ESS-DICE and BCO-DMO.

Plan for archiving and preservation of access

ESS-DICE and BCO-DMO will submit the data and metadata to the National Centers for Environmental Information (NCEI) for long-term archiving. NCEI will provide public access, archiving, and discovery to the archival copy of the submitted data.