Plan Overview

A Data Management Plan created using DMPTool

Title: Assessing how disruption of the methanogenic community and their syntrophic relationships in tidal freshwater marshes via saltwater intrusion may affect CH4 emissions

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Assessing how disruption of the methanogenic community and their syntrophic relationships in tidal freshwater marshes via saltwater intrusion may affect CH4 emissions

The field site soil redox and salinity will be measured prior to constructing microcosms. After the microcosms are constructed, methane flux, carbon dioxide flux, butyrate degradation rates, sulfate concentrations, organic matter content, C:N ratio and redox data will be collected from each microcosm during the experiment. Gas flux measurements will be determined using gas chromatography, sulfate and butyrate concentrations will be determined using ion chromatography, organic matter content will be determined gravimetrically, C:N ratios will be determined using a Perkin Elmer Series II CHNS/O Analyzer 2400, and redox and salinity will be measured using a salinity redox probe. In addition total DNA/RNA will be extracted from each microcosm and the 16s gene sequence of both bacteria and methanogens will determined using Illumina sequencing. Data other than the 16s gene sequence data, all other data will be entered into excel and stored using XML formats and/or CSV formats. The environmental data will be analyzed by R and python using ANOVA, regressions analysis, t-tests, and correlated to sequence data using multivariate statistics (e.g. mantel tests). Using multiple reps and including blanks for every variable measured will maintain quality control.

Environmental data, gas flux data, and butyrate degredation data will be entered into excel and stored as both EML and CSV for ease of use in the statistical program R and python. Sequence data from Illumina sequencing will be stored in FASTQ format. The data folder will contain a readme folder the indicates the methods used to collect data on each variable, and the units for the data as well as any labeling schemes. Sequencing conditions (e.g. primer concentration and illumina protocol) will be included in the readme file)

The environmental data, gas flux measurements, butyrate degradation rates and genetic sequence data will be made available after the resulting manuscript and publication. Until then data will be stored on the VCU microbial ecology R drive and on the Franklin lab Dropbox. All raw data will be made available to Rice Center and if deemed appropriate will be stored on the University's Rice Rivers Center Google Drive. There should be no fee to access the data. Data may also be hosted on a website such as http://datadryad.org/, however the data will always be accessible by e-mailing either Dr. Rima Franklin (rbfranklin@vcu.edu) or myself, David Berrier (berrierdj@vcu.edu).

There should be no restrictions on access or reuse of the data. The data will be made avaliable after the publication or two years, which ever is first. The metagenomic sequences, and it's correlation with environmental variables may be used by future wetland ecologist to understand methane production in relation to microbial species composition.

Data will be on the Franklin Lab Dropbox and the VCU microbial ecology R drive for long-term storage. The storage of the data on these two different drives in addition to storage on the Rice Center google drive will insure that the data will be preserved. The data will be preserved indefinitely as part of the Franklin lab’s database.
