OCE-1129553
Tebo - *"Understanding microbial manganese-oxidizing communities and physiological mechanisms in metal oxide-rich hydrothermal sediments using a metagenomic and metatranscriptomic approach"*

DATA MANAGEMENT PLAN

1. Types of Data and Sample Inventory

a) *Molecular/Sequence Data*: The primary data that we will collect on this project will be sequence data from rRNA and functional gene libraries and metagenomic and transcriptomic sequencing of microbial mat samples and enriched Mn oxide samples from Loihi Seamount and the Lau Basin.

b) *Cultures*: We will be making enrichment cultures and attempting to isolate Bacteria and Archaea in pure culture.

c) *Geochemical Data*: We will be making measurements of total and dissolved iron and manganese for the samples collected for metagenomic and transcriptomic sequence analysis. This dataset will represent only a few measurements.

2. Data and Metadata Standards

a) Sequence data will be archived in data and metadata formats compliant with MIGS/MIMS (Minimum Information about a (Meta)Genome Sequence-Genomics Standards Consortium).

b) Geochemical data will be archived using data and metadata standards as required by the Biological and Chemical Oceanography Data Management Office (BCO-DMO) (http://www.bco-dmo.org/).

3. Data Access and Sharing Policies

All data will remain proprietary for no more than two years after completion of this grant, until after publication, or as required by other participating organizations (e.g., the Joint Genome Institute for sequence data), whichever comes first. The data will be freely accessible after this period. Access and sharing will be provided for all data that are published and/or as required for scholarly data publication.

4. Policies for Re-use, Re-distribution and Production of Derivatives

Data re-use and redistribution and the production of derivatives will be encouraged through publishing, and open data access and sharing.

5. Data and Sample Archival and Access

a) Scientifically interesting organisms isolated as part of our work will be maintained in frozen or other stored culture collections in the laboratory. Organisms on which we publish will be submitted to the American Type Culture Collection (ATCC http://www.atcc.org/) which will decide whether to acquire them and we will provide those organisms to other researchers upon request. Additionally, any extra samples (usually frozen at -80°C) that we are not using, we will make available to other researchers to use.

b) We will make all the metagenomic/metatranscriptomic data that we generate broadly available to the research community by depositing and publishing the data in CAMERA (http://camera.calit2.net/). CAMERA accepts all data forms (raw reads and/or contigs and scaffolds). CAMERA also has the ability to deposit the metadata with the sequences and CAMERA is MIGS/MIMS compliant (http://gensc.org/gc_wiki/index.php/MIGS/MIMS) and fully indexed based on a semantic database for ease of querying. We will also deposit specific sequences of interest (e.g., ribosome RNA gene sequences and RuBisCo) into GenBank (NCBI) as typically necessary for publication.

c) The geochemical data we collect on specific samples will be deposited and made publicly available through the Biological and Chemical Oceanography Data Management Office (BCO-DMO) (http://www.bco-dmo.org/), however, we don't expect this to represent very significant amounts of data.