

## DATA MANAGEMENT PLAN

**Data Policy Compliance:** The project investigators will comply with the data management and dissemination policies described in the NSF Award and Administration Guide (AAG, Chapter VI.D.4) and the NSF Division of Ocean Sciences Sample and Data Policy.

### Description of Data Types

**Observational datasets:** Observational data and photographs will be collected twice over the course of one year from the reefs surrounding Heron Island, Great Barrier Reef, Australia. All data recorded by hand onto log sheets will be photographed and transcribed into Excel spreadsheets. File types: .jpg, .xlsx, .csv. Repository: BCO-DMO.

Seawater temperature will be collected using HOBO Onset temperature loggers. All data will be downloaded and backed up locally immediately following instrument recovery. All relevant metadata (dates of deployment and collection, deployment depth and gps coordinates) will be recorded and saved with the data files. File types: .csv, .txt. Repository: BCO-DMO, PennBox.

Benthic community composition and coral bleaching data: Benthic community composition and individual coral colony bleaching severity will be assessed from photographs taken with underwater digital cameras and color standards. Metadata including date, time, gps location, coral species, and observer name will be recorded by hand on log sheets. Images (.jpg, .tiff) will be archived on PennBox. Data extracted from the images will be exported as .xlsx or .csv files. Repository: BCO-DMO, PennBox.

### Experimental datasets

Coral fragments: Photographs of each colony will be taken using a digital underwater camera. Coral fragments will be flash frozen in liquid nitrogen for later analysis of host tissue and symbiont metrics (symbiont abundance, chlorophyll content, host biomass, total protein, skeletal surface area) as well as gene expression at the PIs lab in Philadelphia. Assay results will be stored in their raw unaltered output files with all metadata from the flow cytometer and spectrophotometer. Archival skeletal samples will be stored in the PIs lab. File types: .xlsx, .csv, .jpg. Repository: BCO-DMO.

Genetic sequencing. A small chip of each coral colony will be preserved in the RNALater stabilization solution. Coral host genetic identification and symbiont ITS2 rDNA data (coupled with the phylogenetic analyses of psbA sequences) will be archived on GenBank, National Center for Biotechnology Information (NCBI) (fasta format). All raw coral gene expression (TagSeq data) will be archived at the Sequence Read Archive (SRA), NCBI. File types: .sra, .fasta. Repository: NCBI; accession numbers provided to BCO-DMO.

Statistical analyses. All statistical analysis, visualization, and formatting/data-carpentry will be completed in R. The code will be saved as a R markdown file. File types: .csv, .txt, .Rmd, .ai. Repository: Dryad, Github, BCO-DMO.

### Data and Metadata Formats and Standards

Field observation data (temperature) will be stored in flat ASCII files, which can be read easily by different software packages. Field metadata will include date, time, latitude, longitude, and depth. Metadata will be prepared in accordance with BCO-DMO conventions (i.e. using the BCO-DMO metadata forms) and will include detailed descriptions of collection and analysis procedures.

### **Data Storage and Access During the Project**

All laboratory protocols are hosted on benchling.com as a laboratory wide resource to maintain consistency. Data is backed up monthly. All data generated by this project will be stored on the investigators' computers, and backed up on external hard drives and using the PennBox cloud storage system. PennBox allows secure data storage and backup, and will be used to facilitate the sharing of data files and analyses between investigators.

### **Mechanisms and Policies for Access, Sharing, Re-Use, and Re-Distribution**

Field observational data and metadata will be submitted to BCO-DMO upon submission of manuscripts. All datasets and statistical code will be uploaded and made publicly available on GitHub upon submission of manuscripts, and pushed to Dryad for permanent doi upon acceptance for publication. RNA sequences will be deposited at the Sequence Read Archive (SRA), National Center for Biotechnology Information (NCBI) upon submission of manuscripts. GenBank accession numbers will be provided to BCO-DMO in an Excel spreadsheet or .CSV file and metadata will be provided using the BCO-DMO Dataset Metadata submission form. Data sets produced will be made available through the BCO-DMO data system within two-years from the date of collection. The project investigators will work with BCO-DMO data managers to make project data available online in compliance with the NSF OCE Sample and Data Policy. Data, samples, and other information collected under this project can be made publicly available without restriction once submitted to the public repositories. Data produced by this project may be of interest to biological oceanographers, ecologists, and biologists. We will adhere to and promote the standards, policies, and provisions for data and metadata submission, access, re-use, distribution, and ownership as prescribed by the BCO-DMO Terms of Use.

### **Plans for Archiving**

After data contributed to BCO-DMO are online and fully documented, BCO-DMO ensures that the data are archived properly at the appropriate National Data Center (e.g. NCEI) for long-term archive preservation. The PI will work to ensure data are archived appropriately with the complete metadata. Archived coral samples will be made available two years after the end of the project, or following publication of the data in the peer-reviewed literature, whichever is sooner. Because corals are listed under Appendix II of the Convention on International Trade in Endangered Species (CITES), we are obligated to ensure that all samples comply with CITES regulations when shipped internationally.

### **Roles and Responsibilities**

The PI will be responsible for ensuring the data are shared among the project participants in a timely fashion. The postdoc will submit the resulting sequences to the National Center for Biotechnology Information's (NCBI) SRA database. The PI will coordinate the overall data management and sharing process, and will work along with the postdoc to submit the project data, including SRA accession numbers and metadata to the Biological and Chemical Oceanography Data Management Office (BCO-DMO), who will be responsible for forwarding these data and metadata to the appropriate national archive.

*Created using DMPTool. Last modified 9 April, 2024*