

DATA MANAGEMENT PLAN

Data management will be coordinated by PI Baker and co-PI Cunning, and will be carried out by all project participants. The plan encompasses three areas: data and metadata availability/archival, sample availability/archival, and use policies.

Plans for sample data and metadata availability/archival:

The primary data types that will be generated by this work include: (1) qPCR data (i.e., quantitative amplification of specific Symbiodiniaceae targets to quantify symbiont community composition), (2) ITS2 sequences; (3) photophysiological data (i.e., Fv/Fm measured with a PAM fluorometer), (4) physical environmental data (i.e., temperature and light during experimental manipulations and at field sites), and (5) gross physiological data (i.e., growth rates from buoyant weight measurements), and (6) field collections data (coral species, location, depth, etc.). Comprehensive sample metadata will map to each of the above observations. All data will be archived in the most raw format possible (e.g., “.eds” and “.pim” files for qPCR and PAM data, respectively, as downloaded directly from the instrument). Data will be archived in ASCII format on RSMAS servers with redundant back-up.

Data collected under the project will be made available to the public with as few restrictions as possible. We will typically deposit most data, with metadata, at the Biological and Chemical Oceanography Data Management Office (BCO-DMO) annually as part of our interim reporting obligations, with a publication embargo requested. As part of that effort ITS2 sequences will also be deposited on the NCBI Sequence Read Archive (SRA) at <https://www.ncbi.nlm.nih.gov/sra> with associated metadata (SRX# accession number).

In addition, data and analysis code for specific research products will be included as supplements to journal articles and/or in external, linked data repositories (e.g., GitHub, Zenodo) with Digital Object Identifiers that also link back to BCO-DMO depositions. We will also use github as a data and analysis tool to help us coordinate data analysis and interpretation between the two labs (at UM/RSMAS and Shedd). For examples of the high standard of transparency and open data and code sharing that we will apply to this work, see <http://www.github.com/jrcunning>

Sample availability/archival:

Coral samples are collected as skeletal fragments (most samples ~1cm²) with associated tissue, or as microsample tissue biopsies. We typically digest the tissue *in situ* using an SDS lysate buffer and Proteinase K.

Small aliquots of this lysate are then removed for DNA extraction on an as-needed basis. We retain archived lysates (consisting of SDS-lysed tissue and a small piece of skeleton) that are stable long-term (>20 years) at room temperature. We welcome the use of archived samples or DNA by collaborators for complementary research, subject to publication embargo (see use policies, described below).

Because corals are listed under Appendix II of the Convention on International Trade in Endangered Species (CITES) we are obliged to ensure that all samples comply with CITES regulations when shipped internationally. RSMAS is registered as a scientific institution with the CITES secretariat (Code: US 138-A) which greatly facilitates the exchange of samples between other scientific institutions worldwide.

Use policies:

We will deposit data to BCO-DMO and/or the NCBI SRA annually (see above), or at most within two years of collection. However, we will typically request an embargo on the availability of data or samples until publication. We welcome the re-use of the data following publication without restriction, but recommend users contact the PIs to ensure accuracy of use and interpretation wherever possible. Furthermore, we encourage projects that are integrally dependent on our data or samples to consider collaboration and/or co-authorship with the PIs, and to acknowledge NSF support.