DATA MANAGEMENT PLAN

Data to be generated. The proposed research will produce several types of data from six reef sites around St. Thomas, US Virgin Islands, including (1) ecological data on the response of sponge species with different morphologies to multiple stressors (e.g., two strong hurricanes and historical land-based sources), (2) ecological data on the composition of newly established sponge communities, (3) ecological data on the rate of sponge reestablishment/recruitment following removal by hurricanes, and (4) molecular characterization of the genotypic diversity within current sponge populations and individuals that recruit to newly available substrata.

All samples will be collected and manipulative experiments performed under appropriate permits from the Department of Planning and Natural Resources, Division of Fish and Wildlife, US Virgin Islands.

Data formats and storage. Field notes will be collected on underwater paper *in situ,* collated into notebooks upon return to the lab and scanned into PDF files for storage in electronic format. Databases will be maintained by the PIs at their respective institutions (University of Mississippi [UM], University of Alabama [UA], University of the Virgin Islands [UVI]) and shared with the other PIs. Digital photographs taken in the field will be downloaded after each dive, labeled appropriately, and saved on external disc drives at each institution and on shared cloud storage providers. Images will be stored in JPEG and/or TIFF formats. Image processing programs, such as CPCe and ImageJ, will be used to calculate areal coverage of sponges over time in quadrats, including new recruits and regrowth from remnant sponges.

Results from laboratory analyses will be recorded in laboratory notebooks, converted into electronic format, and stored in secure locations in the PIs' laboratories. Information stored on computers within the PIs' laboratories will be backed up on external hard drives daily. Electronic data will be archived in appropriate formats on university computers and backed up within each university's servers in sectors dedicated to the PIs for management of their data. In compliance with NSF guidelines, hard copy versions of field and laboratory data will be retained for at least three years following the award period.

Sequence data will be preserved in standard fastq and GenBank XML format and in the digital repository Dryad and the National Center for Biotechnology Information's Short Read Archive (NCBI-SRA) for maximum flexibility. Tab-delimited, plain text files will be used for data storage as they can be easily imported into various analysis programs, such as Microsoft Excel, PRIMER, R, and JMP. A variety of statistical analyses will be conducted on the resulting data and all statistical files will be retained in electronic form indefinitely.

Data access and sharing. Data access and sharing will comply with the guidelines of the NSF OCE Data and Sample Policy. Data from this study will be made available through the Biological and Chemical Oceanography Data Management Office [BCO-DMO] for broad dissemination within two years of project conclusion or immediately following publication, whichever comes first. In addition, data that will be used for comparative purposes with those generated during the course of this study, including those generated through other funding sources, will be deposited through BCO-DMO concurrently with those generated from this study. Use of this service ensures that the raw data sets will be available in useful formats in perpetuity. For data that are not immediately published, data will be embargoed through BCO-DMO for no more than two years after the grant period ends. The sequencing data will also be deposited for broader dissemination at established data portals (e.g., NCBI-SRA, Dryad). Resources at the PIs' universities will also be used to ensure redundant long-term retention of the complete datasets.

Physical samples will be preserved in RNALater for genetic analyses and in ethanol for sponge species identification. Metadata will include: sample number, collection date/time, site name/depth, and GPS coordinates. Samples will be shared upon request via a Material Transfer Agreement between appropriate parties.

Single nucleotide polymorphism and genomic sequence data for the sponge species will be stored on backed up local drives at the PIs' institutions and in Illumina's online data storage and analysis platform, BaseSpace. A free account on this platform will be created for the proposed project, and all PIs will have access. In addition, quality filtered and processed sponge sequence data will be submitted to NCBI-SRA, where it will be accessible and publicly available after a 1 year embargo or publication, whichever comes first.

User groups. We anticipate that the data generated from this project will be most useful in published formats, with broad applicability to research scientists and marine resource managers interested in sponge resilience and recovery on coral reefs. However, we recognize that some individuals may be interested in the raw data files for their own meta-analyses and/or comparative studies. The aforementioned data files will allow those analyses.