Data Management plan

We are committed to the sharing and dissemination of our results to the wider scientific, management, policy, and public communities.

Rapid Posting of Real-Time Discoveries

We will immediately establish a blog to post real-time "sampling event log" updates of the survey in Japan and the identifications of the species found on the debris, as these identifications come in from our own and cooperating laboratories. This will be similar to, but an expansion of, the blog that we have established for the NSF initiative (http://blogs.oregonstate.edu/floatingdock/) on an Oregon State University site, sharing in real time the results of our work. We believe that it is critical to rapidly post findings in order to get information to our colleagues, to managers, and to the public, relative to the variety of marine animals and plants now arriving from Japan on North American and Hawaiian shores.

Early Deposition of Metadata Project Description

We will provide BCO-DMO with a detailed metadata project description this spring, to facilitate increased interaction with other groups interfacing with JTMD. This description will include details of the work being carried out at each laboratory, and by whom, our site locations for quantitative data acquisition, and our sampling and analytical methodologies.

Plan for Long-Term Archiving, Discoverability, and Data Access

We will follow the **NSF Division of Ocean Sciences Data and Sample Policy** and specifically those guidelines set forth in the **BCO-DMO Data Management Guidelines Manual.** We will work closely with the BCO-DMO Data Management Office at the Woods Hole Oceanographic Institution for the long-term archiving, access, and discoverability of our data.

Deposition of Genetic Data

Subsamples of all tissue used for molecular analyses will be retained in ultra-low freezers or in ethanol at MLML (Dr. Jon Geller). DNA sequence data will be deposited at GenBank. We will further utilize the Barcode of Life Data Systems (BOLD) to link our DNA data with voucher material deposited at museums (below). Geller is co-PI on an NSF PIRE project involving coral reef metagenomics beginning January 1, 2013, and we will share a data structure. We will use the Metagenomics Rapid Annotation using Subsystems Technology (MG--RAST) V3.2.3 platform, which incorporates the Quantitative Insights into Microbial Ecology (QIIME) analysis pipeline for ribosomal sequence data analysis. All data will be deposited and archived under the MG--RAST data management plan.

Museum Deposition of Collected Biota

Vouchers of all species will be deposited at recognized museums, including the **California Academy of Sciences** (general invertebrates), the **Los Angeles County Museum of Natural History** (polychaetes), and the **Smithsonian Institution's National Museum of Natural History** (general invertebrates).