

Data Management Plan

Genetic Data

The primary data we will be collecting for the proposed research includes genetic variation among a series of protobranch bivalves at a number of loci (introns, mtDNA, and anonymous) for phylogeographic analyses, as well a variety of loci for phylogenetic analyses (18S, H3, 28S...). All results will be deposited on GenBank at the National Center for Biotechnology Information (NCBI). We have submitted completed project data to GenBank for all of our previous analyses and will continue to submit our data as we write up our results. All analytical results will be published in a timely fashion in the primary literature.

Samples

Deep-sea epibenthic sled samples were collected along a depth gradient (700-5200m) in the Western North Atlantic in June of 2008 as part of our funding in 2007. Although these are not formally part of the current proposal, we felt it was important to include our plans for those samples. We sorted out from these samples the bivalves and gastropods, and are using these for our population genetic work. The remainder of the samples are largely unsorted (although some have been sorted into major phyla) and are presently stored in 95% ethanol at -20°C. These will be moved to the Museum of Comparative Zoology at Harvard University for storage and curation (Commitment Letter from the MCZ Director was included in our 2007 proposal).

We have already made our samples available to other investigators (e.g. Bivalve Tree of Life Project, Cnidarian Tree of Life Group, The National Oceanography Centre in Southampton, The Citadel, Thoma et al. 2009 and Rex et al. 2010) as described in our Broader Impacts and we will continue to provide samples as investigators ask.

Metadata

The metadata associated with the samples (species, latitude, longitude, depth...) collected from our previous funding (not part of this proposal) were submitted to BCO-DMO in 2011.