

Data Management Plan

Basic environmental data

We will not be collecting any environmental data that will be of primary interest to a national data center.

Gene data

Raw and minimally processed data from 454 sequencing will be delivered on DVDs or an external hard drive. These data will be manipulated locally on Tarrant's personal computer (backed up daily by an automated service provided by WHOI's Computer & Information Services). Data will also be uploaded to the WHOI Biology Department bioinformatics server. All raw reads will be submitted to the NCBI Gene Expression Omnibus (GEO) database¹; the GEO project code will be included in associated publications and the link will be posted to Tarrant's personal website and the project blog.

Zooplankton data

Zooplankton net samples collected in Trondheim Fjord will be preserved in formalin after live subsamples for the proposed analyses are removed. These subsamples will be processed for 454-pyrosequencing, qPCR, jaw phase, and gonad development, and will ultimately be destroyed during analysis (i.e., homogenized or dissected). The formalin-preserved samples will be archived at the Woods Hole Oceanographic Institution BIOSPECS facility for decades. A description of these samples and enumeration data (species counts) will be submitted to the Biological and Chemical Oceanography Data Management Office (BCO-DMO).

Publications

The results of the proposed project will be published in peer-reviewed journals within 2-3 years of data collection. Both principal investigators have a solid track record of publishing, including the results of earlier studies of gene expression associated with diapause in *Calanus finmarchicus* (Tarrant et al. 2008, Aruda et al. submitted). While we anticipate a single seminal paper resulting from the project, we hope to also produce several ancillary publications on changes in gene expression and morphology during *C. finmarchicus* development. The primary data (i.e., morphometrics measurements, qPCR results, collection date and time for individual copepods from field and culture studies) will be posted as supplementary online information (.xls or .csv file) and archived with the Biological and Chemical Oceanography Data Management Office (BCO-DMO).

¹ The NCBI Short Read Archive (SRA) has been recently discontinued. NCBI has designated GEO as the appropriate archive for RNA-seq data.