DATA MANAGEMENT PLAN

Introduction

This data management plan has been prepared to report to the Biological and Chemical Oceanography Data Management Office (BCO-DMO) if the proposed project is funded.

Our study will generate data for bulk tissue δ^{13} C and δ^{15} N values, and δ^{15} N and δ^{13} C values from individual amino acids. These biochemical tracers will be quantified from two different types of tissues (dentin and skin) collected from an endangered and protected marine mammal species, sperm whales, and from muscle samples collected from the squid, *Dosidicus gigas*.

a) Precision of sampling and chemical preparation of samples

The Marine Analytical Laboratory at University of California Santa Cruz (UCSC) houses a New Wave Micromill for obtaining a precise amount (milligrams) of powdered dentin from each growth line from a given tooth. An integrated software system allows for communication between the digital camera and the motion control system of the microsampler, thereby allowing dentin to be obtained with high precision under specified computerized sampling paths along X-Y-Z axes.

All dentin sampling will take place at UCSC to ensure high precision during sampling and to control for contamination between growth lines. The postdoctoral researcher (Iliana Ruiz-Cooley) and her assistants will have proper training to use this system.

b) Quality of data, consistency and cross-lab comparability

Data from each tracer for a given sample will be obtained using an Isotope-Ratio Mass Spectrometers (IRMS) coupled with the corresponding Elemental Analyzer or Gas Chromatography-Combustion sampling systems at the UCSC – Stable Isotope Laboratory (SIL). At UCSC-SIL, reference gases have been calibrated relative to international reference materials obtained from the National Institute of Standards and Technology (NIST) and the International Atomic Energy Agency (IAEA) to ensure accurate measurement and reporting of isotope ratios for the selected samples. These same international standards are analyzed on a daily basis, typically at the start and finish of each analytical round. In addition, internal laboratory standards are analyzed at a much greater frequency during each analytical round to assess data quality during the course of each analytical round. The analytical error on standards measured during the course of analyses conducted for this project will be monitored and reported for each analytical round.

c) Organization and progression of isotope analysis

- Sampling of teeth will take place at the Marine Analytical Lab at UCSC.
- Preparation of samples will take place at UCSC in Koch's and McCarthy's laboratories.
- Analysis of bulk δ^{13} C and δ^{15} N will take place at the UCSC-SIL.
- Analysis of δ^{15} N and δ^{13} C for individual amino acids will take place at the UCSC-SIL.

d) Data management

The database will record 1) the preparation the sample, b) the date of stable isotope analysis, c) the results of the analysis, and d) data obtained from internal laboratory standards during each round of analysis. We anticipate two databases, one for isotope analysis of bulk tissues, and another for analysis of individual amino acids.

All data derived from these IRMS analyses will be provided electronically to the postdoctoral researcher. The databases will be stored and shared via Dropbox to ensure availability for all team members.

The bulk isotope data (samples and standards) will be integrated into a database that will be available to all team members that will have the following columns, to be used if applicable:

Sample type (i.e., sperm whale skin, sperm whale dentin, squid muscle)

Sample code/number

Sex of individual (for sperm whales only)

Year of collection

Collection site (latitude, longitude)

Calendar year of sample formation

Ontogenetic age at time of sample formation (for sperm whales only)

Pretreatment method (to account for potential changes during the project)

 $\delta^{15}N_{protein}$

 $\delta^{13}C_{protein}$

C/N ratio (atomic)

Date of protein analysis

The compound-specific isotope data (samples and standards) will be integrated into a database that will be available to all team members that will have the following columns, to be used if applicable.

Sample type (i.e., sperm whale skin, sperm whale dentin, squid muscle)

Sample code/number

Sex of individual (for sperm whales only)

Year of collection

Collection site (latitude, longitude)

Calendar year of sample formation

Ontogenetic age of sample formation

Derivitization method (to account for potential changes during the project)

 δ^{13} C of all amino acids

Date of δ^{13} C analysis

 δ^{15} N of all amino acids

Date of δ^{15} N analysis

At the end of each year, each team members will review existing data, revise timelines, and plan for the following year.

All clean and documented data will be sent to the BCO-DMO facility as instructions for format and transmission become available.