Homogeneity test for the Pacific sleeper shark (Somniosus pacificus): Project update

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Abstract

A test of homogeneity will be conducted on Pacific sleeper shark (Somniosus pacificus) samples from the north Pacific Ocean in an attempt to determine the genetic stock structure of this species. Collections are represented by 107 tissue samples ranging from areas of high to low shark occurrence within three IPHC charter regions. Extraction of mitochondrial DNA, polymerase chain reaction (PCR) amplification, and sequencing have been completed. Analysis of the data is currently underway.

Introduction

The population dynamics of Pacific sleeper sharks (Somniosus pacificus) within the northeast Pacific are not well documented. Preliminary tagging studies have indicated that at least some sleeper sharks display a resident behaviour, and likely have relatively small home ranges. To test this assumption, tissue samples were collected during the 2004 International Pacific Halibut Commission (IPHC) standardized stock assessment survey. A simple test of homogeneity will compare samples collected from regions of high species occurrence to peripheral regions of lesser occurrence.

Mitochondrial DNA polymorphisms will be used as the initial genetic marker system to investigate genetic differentiation among the sampling locations. The objective of this study is to test if mobility in sleeper sharks has led to genetic homogeneity within this sampling range. Alternately, heterogeneity could indicate some degree of site fidelity. Knowing the population structure of a species can be very useful when dealing with concerns of conservation. The IPHC general survey has one of the best spatial designs for encountering sleeper sharks over a wide area, and thus was solicited to supply tissue samples for this experiment.

Results and Discussion

Tissue samples were collected during the 2004 IPHC standardized stock assessment survey. Biopsy tips mounted on pole spears were utilized to collect tissue samples of approximately 5 by 100 mm in size. These were immediately placed in 2-ml micro-vials containing 95% EtOH. A total of 118 samples were collected: 40 samples from the Unalaska charter region, 51 samples from
the Shelikof charter region, and 27 samples from the Ommaney charter region. Data collected included date, charter region, station number, and animal’s condition. The animal’s condition was based on whether the sample was collected from a dead specimen or a live specimen. Length and sex data were also collected when possible.

DNA extraction and PCR amplification occurred at the Department of Biochemistry and Microbiology at the University of Victoria, British Columbia. Mitochondrial DNA was extracted from 118 samples with the use of a DNeasy Blood and Tissue kit®. PCR amplification and purification of the DNA target chain occurred using an 869 bp fragment of the mitochondrial cyt-b gene amplified with Somniosus-specific primers Somn-CYTB-H2 and Somn-Glu-L1 (Murray et al. 2008). Eleven of the 118 samples failed to amplify. A total of 107 samples were submitted to the DNA Sequencing Facility on campus at the University of Washington in Seattle, Washington. The resulting data are now currently undergoing statistical analysis.

Statistical analysis will be by way of $\chi^2$ and Analysis of Molecular Variance (AMOVA) probabilities of haplotype homogeneity across sampling sites. As the name suggests, AMOVA is a method for studying molecular variation within a species. AMOVA works on such data to create a distance matrix between samples in order to measure the genetic structure of the population from which the samples were drawn. In statistical terms, AMOVA is a testing procedure based on permutational analysis and involves few assumptions about the statistical properties of the data.

References