Name(s)	Project Number
Rachel L. Dault	34359

Project Title

DNA Barcoding

Abstract

Objectives/Goals

My objective was to assemble and submit two professional quality reference DNA Barcode records to BOLD for publication in NCBI/GenBank. As a citizen scientist, I contributed to the world's largest Biodiversity genomics project (iBOL).

Methods/Materials

In order to do this I isolated total DNA from specimen tissue (previously identified by Milton Love, taxonomist from UCSB, obtained and stored through Coastal Marine Biolabs), purified the genomic DNA, examined the gDNA using gel electrophoresis, amplified the CO1 Barcode region from the template, used a spin-column to purify the CO1 amplicons, and confirmed the length of the amplicons by use of gel electrophoresis. DNA samples were sent for sequencing. I then assembled the reference barcode record in BOLD-SDP.

In my research, I compared four families of the Sebastes fish to see which were most closely related according to their nucleotide sequences and amino acid sequences. I compared the specific percentages of base pairs for each specimen and used the bioinformatics tools on the BOLD-SDP workbench.

Results

Of the total 21 samples sent to our lab, 19 provided adequate DNA results to be analyzed. I was able to generate high quality sequences for one of the two samples, the other sample had too little DNA to provide an adequate barcode. There was a total of five families of the Sebastes fish present from our samples, I analyzed four of these.

Conclusions/Discussion

I was able to successfully isolate gDNA, purify it, amplify the CO1 amplicon and upload the trace file into BOLD. I created a DNA Barcode for the Sebastes paucispinis that is currently waiting for second- and third-tier validation for inclusion into NCBI.

Summary Statement

Isolating, purifying and analyzing DNA sequences the Sebastes species of rockfish.

Help Received