Lesson Plan: Interpreting the diversification of ice crawlers through time

Prepared by Matthew Medeiros and Sean Schoville

Learning goals for this exercise:

1) Students will understand how to use DNA sequence data to estimate the evolutionary history of a group of species by building a phylogenetic tree.
2) Students will be able to use computational methods and tools to answer questions about large genetic datasets.
3) Students will be able to extend their knowledge about phylogenetic methods to a new situation or problem.
4) Students will become familiar with primary scientific literature and recognize that scientific knowledge is always advancing.

Recommended pre-lab activities:

In the week leading up to this, classroom lectures presented basic information about phylogenetic theory and methods, tree assembly using morphology (including a basic lesson to build a tree by hand), and a practice molecular tree-building run in MEGA, using MEGA's "crab RNA" example dataset. By the end of these activities, students should understand why we build trees, how to test hypotheses using trees, differences between morphological and molecular characters, and how we obtain statistical support values for trees. Students were already familiar with PCR/single-gene sequencing as well as next-generation/genomic sequencing methods, so we are in a position to discuss the pros and cons of each sequencing technique.

Interpreting the diversification of ice crawlers through time:

Step 1: Introduction to the ice crawlers (30-40 min):

Play recorded lecture by Sean Schoville (https://mediaspace.wisc.edu/media/Ice+Crawler+Diversification+Lecture/0_47euqtzc).
Read/discuss the ice crawler glaciation hypothesis (download: Schoville & Graening 2013, page 369). Our goal is to re-test this hypothesis using modern methods.

Step 2: Build a phylogenetic tree using genetic data (45 min).
Main activity to build, visualize, and annotate a tree using a genomic dataset. Please see attached document, "NextGen Sequencing of the Grylloblattidae: Hypothesis Testing using Phylogenetic Analysis" for step by step instructions. You will need to install the following software and obtain the following data set:

Install RaxML and FigTree on student computers

RaxML: https://cme.h-its.org/exelixis/web/software/raxml/index.html (scroll down to find version in Windows and MacOS)

FigTree: https://github.com/rambaut/figtree/releases

Obtain dataset gryllo_genomic_dataset.phy

Step 3: Interpret results in light of climate data and compare to original Kamp hypothesis (30 min to 1 hour).
Discuss in class and then have students write a short essay in class to assess their understanding, including generating a hypothesis about another group of organisms that students are interested in, and outlining how to test it.
Students also take a quiz to assess their overall understanding of phylogenetics (download: quiz and key).