Abstract:

The northern long-eared bat (*Myotis septentrionalis*) is one of many species of hibernating bats in North America affected by a recently discovered fungal disease called white-nose syndrome (WNS). Northern long-eared bats seem to be extremely susceptible to the disease with mass fatalities occurring among populations in eastern North America. Researchers in the eastern distribution of this species have performed mtDNA analysis to identify the population structure of the species; however, genetic analysis has yet to be done in western parts of its distribution. The goal of this study is to create a better understanding of the genetic makeup of this species in Nebraska, as little is known about the genetic diversity of *M. septentrionalis* in this part of its range. From 29 June to 14 July 2017 we traveled to four separate sites in the state (south-central, east-central, northeastern, and northwestern Nebraska) and used mist nets to capture *M. septentrionalis*. Once captured we recorded information on each bat and proceeded to take two 2mm tissue punches from the tail membrane. These tissue samples were placed into small holding tubes, which contained silica beads, and then placed in a freezer for storage. We captured and sampled tissue from 31 northern long-eared bats: 4 from Elm Creek (south-central Nebraska), 18 from Ponca State Park (northeastern Nebraska), 3 from Larrabee Creek (northwestern Nebraska), and 6 from Fontenelle Forest (east-central Nebraska). After acquiring our tissue samples, we attempted to amplify a portion of hypervariable region II (HVII) of mitochondrial DNA (mtDNA). To extract DNA from tissue samples we used the Qiagen DNeasy blood and tissue kit. We attempted to initially amplify this gene segment from 6 samples; however, the gene segments obtained were approximately 1250bp in comparison to the target 400bp fragment. The exact cause of experimental error is unknown at this point in time, but we suspect that either we had an error with the extraction process and/or our primers did not work properly during PCR. We will adjust the extraction protocol with our next samples and attempt to test our primers with a positive control to determine whether they are working correctly.