Low Genetic Variability Across the Geographic Range of the Blanding’s Turtle (Emys blandingii)

Natalie Millspaw
Indiana University - Purdue University Fort Wayne

Follow this and additional works at: http://opus.ipfw.edu/stu_symp2014

Part of the Biology Commons

Recommended Citation

This Poster is brought to you for free and open access by the IPFW Student Research and Creative Endeavor Symposium at Opus: Research & Creativity at IPFW. It has been accepted for inclusion in 2014 IPFW Student Research and Creative Endeavor Symposium by an authorized administrator of Opus: Research & Creativity at IPFW. For more information, please contact admin@lib.ipfw.edu.
Introduction

The Blanding’s Turtle, Emys blandingii (formerly Emydoidea blandingii), is a semi-aquatic North American species that is listed as endangered on the IUCN Red List as of 2011. Its range is centered in the Great Lakes but extends from Nebraska to Nova Scotia (Fig. 1). This turtle lives up to 80 years and has a generation time of 17-25 years. The species prefers wetland habitats and uses relatively large areas while traveling among wetland complexes. Declines in populations observed across the geographic range are likely due to the loss of wetland habitat.

In addition to interest in its conservation status, there are different hypotheses concerning the genetic structure of its populations. One suggestion is that there are two major genetic groups that are divided by the Appalachian Mountains. Others have found additional genetic differences within the western portion of the geographic range.

The objective of this research is to use mitochondrial DNA sequences to test existing biogeographic hypotheses and define populations to assist future recovery efforts for the species.

Methods

Samples - A total of 33 samples from 14 localities were acquired from collaborating labs and collection from the wild in Indiana. The European pond turtle (Emys orbicularis), a sister species to E. blandingii, was used as an outgroup using sequences available in GenBank.

DNA sequences - Two partial sequences of mitochondrial DNA were assayed: control region (DES, 659 bp) and nicotinamide adenine dinucleotide dehydrogenase 4 (ND4, 894 bp). The primers used for each segment were originally designed for painted turtles (Chrysemys picta), a species within the same family.

Lab work - DNA was copied at each locus using the polymerase chain reaction (PCR). The PCR product was checked by electrophoresis in a 1.6% agarose gel. Samples that amplified were cleaned with EXOSap and sent for DNA sequencing (both directions) to the DNA Analysis Facility at Yale University.

Sequence analysis - Sequences were verified in BioEdit (v. 7.2.5) and aligned using CLC Sequence Viewer (v. 6.9.1). Phylogenetic tree construction was performed in Geneious (v. 7.1.2) using a maximum likelihood analysis. Haplotypes were defined from the sites of polymorphism found across the sample.

Results

- There was no variation among 15 turtles in ND4.
- In DES there were three polymorphic sites (sequence divergence = 0.455%) resulting in 5 haplotypes (Table 1).

Haplotype Frequency Sample Distribution
A CCA 7 (5) WI, (2) IA
B TCA 5 (5) NE
C TCG 2 (1) WI
D TCT 1 (1)

Discussion

We observed minimal variation in the mitochondrial segments analyzed and the variation observed was broadly distributed across the range. For example, a turtle from Nova Scotia shared the same genetic variant with a turtle from Iowa. This is surprising given that the closest relative of Blanding’s turtle, the European pond turtle, showed sequence variation of 0.97% for ND4 and 1.52% for DES (Velo-Antón et al., 2008). However, analysis of the mitochondrial genome of the bog turtle (Elyptemys muelenberghi) found results that mirrored our analysis (Rosenbaum et al. 2007). They found no variation among ND4 sequences and very few haplotypes within the control region.

There are two inter-related explanations that may cause the observed lack of mDNA sequence variation. First, the long generation time of the species may slow the accumulation of mutations. Second, like the bog turtle, Blanding’s turtles have a geographic range that is largely the result of recolonization following the retreat of the most recent glaciers. Species with such distributions often exhibit the loss of genetic variation (founder effect) during range expansion.

Additional documentation of mitochondrial sequence variation is needed to confirm our results. Moreover, the identification of genetic populations will likely require the analysis of genetic markers that describe more overall variation.

References