Genetic Structure of the Copperhead (Viperidae: *Agkistrodon contortrix*) at its Most Northern Distribution

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Introduction

Studies of genetic diversity and population-level parameters in North American pitvipers are largely focused on species that warrant conservation concern. Little attention, however, has been paid to the molecular ecology of the Northern Copperhead snake (*Agkistrodon contortrix mokasen*), a non-threatened pitviper species. Studying the genetic structure, mating system, and history of genetic bottlenecks of wild Northern Copperhead populations will provide baseline information for comparative studies with threatened sympatric species.

Methods and Materials

- After DNA extraction, 253 individuals were genotyped at 22 variable tetra-nucleotide microsatellite loci
- Population assessed for historical genetic bottleneck, multiple paternity, and genetic structure with the use of genetic software programs

Results

**Genetic Structure:**
- Six clusters (gene pools) detected in each of five hibernacula
- Significant admixture found in most individuals

**Historical Bottleneck:**
- Genetic bottleneck occurred during the span from 1882 to 1945
- Concurrent with building of Bradley Hubbard Reservoir

**Multiple Paternity:**
- 71% of litters were singly sired, while 29% were doubly sired

Discussion

This study details a population of North American pitvipers that has maintained genetic diversity in spite of a recent genetic bottleneck. and is the first to document multiple paternity in a wild population of Copperhead snakes. Population level parameters assessed in this study provide baseline information for comparative studies with threatened sympatric pitviper species.

Species and Study Site

- Samples collected from 5 hibernacula near Meriden, CT
  - 116 adult blood samples
  - 137 juvenile skin sheds

**Figure 1.** *Agkistrodon c. mokasen* adult ([http://siteswofford.edu/smithcf/field-and-lab-research-photos/](http://siteswofford.edu/smithcf/field-and-lab-research-photos/))

**Figure 2.** *Agkistrodon c. mokasen* tissue samples were collected from 5 hibernacula around Bradley Hubbard Reservoir in Connecticut

**Figure 3.** Example of allelic variation at 4 microsatellite loci (different colors) in 4 individuals (different rows)

**Figure 4.** Significant paternal skew (*) found in one of four double sired litters

**Figure 5.** Proportion of adult *A. c. mokasen* from five dens assigned to six genetic clusters (K) in Connecticut.

**Figure 6.** Six genetic clusters were identified, with significant admixture present in most individuals.

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References