

## Public Abstract

First Name:Emily

Middle Name:Elizabeth

Last Name:Puckett

Adviser's First Name:Lori

Adviser's Last Name:Eggert

Co-Adviser's First Name:

Co-Adviser's Last Name:

Graduation Term:SP 2015

Department:Biological Sciences

Degree:PhD

Title:Phylogeography and Population Genomics of the American Black Bear (*Ursus americanus*)

The American black bear (*Ursus americanus*) is one of the eight living species of Ursidae, and the only one to have speciated in North America (1.8 – 1.2 Mya). This dissertation investigates the contemporary population structure of American black bears across their range; and specifically asks how a translocation of bears affected the population genetics of individuals in the Central Interior Highlands. Black bear mitochondrial lineages began forming within the last 170 kya, whereas the eastern and western nuclear genomes diverged 67 kya. A third nuclear lineage was discovered in contemporary Alaska, which diverged from the eastern lineage 31 kya. These three lineages harbor nine genetic clusters, and potentially more in unsampled portions of the range. These nine clusters may represent evolutionary significant units for the species; however, more work would be needed before proposing taxonomic revisions. The regional population genetics of the Central Interior Highlands (Arkansas, Oklahoma, and Missouri, USA) showed that the majority of genetic diversity in contemporary populations of the Ozark and Ouachita Mountains was introduced from Minnesota, USA and Manitoba, Canada during a translocation of bears from 1958 - 1968. Analyses also indicated that the contemporary Ozark and Ouachita populations were genetically differentiated. Additionally, bears that form a low diversity genetic cluster in Missouri were highly similar to bears from the Ozarks in genomic analyses, indicating a small founding population dispersed northwards following the reintroduction. Finally, I analyzed the accuracy and precision with which the natal location of a black bear may be identified using different inference methods and dataset compositions. While samples were estimated within 201 km of their sample site and with high precision, there was a low correlation between the state or province of sampling and that estimated. These results suggest caution when using genetic data for natal inference problems in cases for trade of wildlife products.