

GENETIC VARIATION IN THE FORTH AMERICAN BLACK BEAR: EAST MEETS WEST

Steven Fain

USFWS/National Forensics Laboratory, Ashland, Oregon



The National Fish and Wildlife Forensic Laboratory of the US Fish & Wildlife Service provides analytical support for the enforcement of international, federal, and state laws enacted to conserve black bear (*Ursus americanus*) populations throughout the US. The individual typing of black bears is an important tool in linking a human suspect to a crime scene by identifying custody evidence from the victim bear or in determining the geographic source of bear parts or products in trade. To these ends, we examined eight different dinucleotide STR loci¹ to determine their suitability for the forensic identification of individual black bears.

We assessed 1,520 individuals representing 32 populations in 16 states and northern Mexico. Sample size ranged from 10 to 84 animals per population. The total number of alleles observed per locus ranged from 9 to 23 and allele size ranged from 95 bp to 220 bp. The number of alleles observed per population at a given locus ranged from a low of 2 in Oregon & California to a high of 13 in Maine.

Black bear populations exhibited significant variability at all eight loci but not all populations were equally variable. The genetic distance calculated from STR comparisons between populations is concordant with both mitochondrial DNA sequence comparisons and geographic distance. These data clearly describe three principle geographic “races” and support the subspecific distinction of the Florida black bear (*U. a. floridana*).

¹Paetkau & Strobeck 1994, *Molecular Ecology*, 3:489-495.