American Black Bear Population Fragmentation Determined Through Pedigrees in the Trans-Border Canada-United States Region

Michael F. Proctor, Birchdale Ecological Ltd., Kaslo, British Columbia

Wayne F. Kasworm*, US Fish and Wildlife Service, Libby, MT

Chris Servheen, US Fish and Wildlife Service, College of Forestry and Conservation, University of Montana, Missoula

Justin E. Teisberg, US Fish and Wildlife Service, Libby, MT

Thomas G. Radandt, US Fish and Wildlife Service, Libby, MT

David Paetkau, Wildlife Genetics International, Nelson, British Columbia

Katherine C. Kendall, United States Geological Survey–Northern Rocky Mountain Science Center, Glacier Field Station, West Glacier, MT

Richard D. Mace, Montana Fish, Wildlife, and Parks, Kalispell

Mark S. Boyce, Department of Biological Sciences, University of Alberta, Edmonton

Fragmentation of species with large numbers of individuals in adjacent areas can be challenging to detect using genetic tools as there often is no differentiation because genetic drift occurs very slowly. We used a genetic-based pedigree analysis to detect fragmentation in the American black bear (*Ursus americanus*) across 2 highways with large adjacent populations. We used 20 locus microsatellite genotypes to detect parent-offspring and full sibling pairs within a sample of 388 black bears. We used the spatial patterns of capture locations of these first order relatives relative to US Highway 2 in northwest Montana and Highway 3 in southeast British Columbia to estimate the number of close relatives sampled across the highways (migrants/km of highway length) as an index of fragmentation. We compared these values to an expected migrant/km rate derived from the mean values of simulated fractures in the Highway 2 and Highway 3 region. We found evidence that these highway corridors were fragmenting black bear populations, but not completely. The observed migrant/km rate for Highway 2 was 0.05, while the expected rate was 0.21 migrants/km. Highway 3 had an observed migrant/km rate of 0.09 compared to the expected rate of 0.26. None of the 16 bears carrying GPS radio collars for 1 year crossed Highway 2, yet 6 of 18 crossed Highway 3. Pedigree and telemetry results were more closely aligned in the Highway 2 system evidencing more intense fragmentation than we found along Highway 3. Our results demonstrate that pedigree analysis may be a useful tool for investigating population fragmentation in situations where genetic signals of differentiation are too weak to determine migration rates using individual-based methods, such as population assignment.