
LIMITED MATERNAL GENE FLOW AMONGST ELK IN THE GREATER YELLOWSTONE ECOSYSTEM REVEALED BY MITOCHONDRIAL DNA

Brian K. Hand*, Division of Biological Sciences, University of Montana, Missoula, Montana 59812
Gordon Luikart, Flathead Lake Biological Station, Fish and Wildlife Genomics Group, University of Montana, Polson, Montana 59860.

We quantified maternal patterns of population genetic structure to help understand gene flow among elk (*Cervus elaphus*) populations across the Greater Yellowstone Ecosystem. We sequenced 596 base pairs of the mitochondrial (mt)DNA control region of 407 elk from nine populations. Our analysis revealed high mtDNA diversity within populations including 12 haplotypes per population on average, and a mean haplotype diversity (i.e., gene diversity) of 0.84. The F_{ST} from mtDNA was high (mean $F_{ST} = 0.162$; $P = 0.0001$) compared to F_{ST} for nuclear microsatellites data ($F_{ST} = 0.006$, $P = 0.125$), which suggested relatively low female movement among populations, perhaps due to female philopatry. Genetic distance (mtDNA pair-wise F_{ST}) was not significantly correlated with geographic (Euclidean) distance between populations (Mantel's $r = 0.274$, $P = 0.168$). The lack of isolation-by-distance and large genetic distance between geographically close populations (< 65 km) suggest that maternal gene flow is reduced by certain landscape features (e.g., large, non-forested valleys with roads), which is important for understanding and modeling landscape connectivity and related processes.