

**Comparing pedigree- and molecular-based coefficients of inbreeding and pairwise relatedness in red squirrels (*Tamiasciurus hudsonicus*)**

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Inbreeding depression is an important issue facing the conservation of endangered species. Population declines and genetic bottlenecks result in loss of genetic diversity which can lead to increased rates of inbreeding in both wild populations and artificial breeding efforts. The goals of captive breeding programs are to enhance *ex situ* reproduction and to maintain extant genetic diversity by minimizing inbreeding. Breeding management has traditionally relied on pedigree-based estimates of genetic similarity, but advanced molecular sequencing techniques may instead allow for molecular-based management. In this study, pedigree- and molecular-based estimates of inbreeding and relatedness were compared for 171 North American red squirrels (*Tamiasciurus hudsonicus*) from a wild population near Kluane National Park, Yukon, Canada. Extracted DNA was amplified at 16 microsatellite loci by polymerase chain reaction (PCR) and sequenced. Genetic diversity was quantified and allele frequencies were used to estimate coefficients of individual inbreeding ( $f$ ) and pairwise relatedness ( $r$ ) which were compared with estimates from an existing multigenerational pedigree. Pedigree- and molecular-based estimates were moderately correlated ( $0.40 \leq r \leq 0.59$ ) for both measures ( $f$ :  $r=0.46$ ,  $P<0.001$ ;  $r$ :  $r=0.51$ ,  $P<0.001$ ). The data suggests a combined approach to breeding management would be most effective for captive breeding programs.