THE EFFICACY OF USING SNOW TRACKS IN PROVIDING GENETIC DATA FROM WOLVERINE AND OTHER CARNIVORES^{TWS}

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Collecting noninvasive genetic samples from putative wolverine (*Gulo gulo*) snow tracks is an effective method for providing definitive species identification and more complex demographic data. We completed 54 backtracks and collected 169 hairs and 58 scats. Amplification rates of mitochondrial DNA (mtDNA) used for species identification were 74 and 24 percent for scats and hairs, respectively. Average distance to a collect a sample containing high quality mtDNA for species identification was 1331m. Genetic analysis confirmed 35 snow tracks (64%) as wolverine. The remaining 19 snow tracks consisted of 8 that did not provide samples and 11 that contained nonamplifiable samples. Collection of both hairs and scats provided 28 percent more track verifications than would have only one type of sample. We analyzed nuclear DNA (nDNA) from the same samples to produce individual genotypes. Amplification rates of nDNA from scats and hairs were 52 and 16 percent, respectively, and produced individual genotypes for 23 of the 54 snow tracks (43%). These results confirmed that snow tracking to collect noninvasive genetic samples can be used to verify species identification from snow tracks detected through any winter survey method, as well as to perform more complex monitoring such as minimum population estimates, tests of relatedness, or mark re-capture population estimates if sample sizes are large enough. While tested on wolverine, this method could be applied to other carnivores that live in snowy regions and are active during the winter months.