

AN EVALUATION OF FISHER INTRODUCTIONS IN MONTANA^{TWS}

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Translocations play a crucial role in the conservation and restoration of wildlife populations. We investigated the impact of translocations on the distribution and genetic structure of fisher (*Martes pennanti*) populations in Montana. We documented the presence of fisher in the Cabinet Mountains, 10 years after the release of 110 fishers from the upper Midwest. Verifiable detections were made in four of 17 systematically surveyed sampling units. Surveys indicated that fishers are rare, but present and reproducing in an area where they were believed absent prior to the introduction. To approximate the occupied range of fisher throughout Montana, we mapped fisher distribution using contemporary occurrence data (harvest, sighting, and tracking records). The spatial and temporal extent of these records demonstrated that translocations have been successful in establishing, and/or augmenting, fisher populations in the state. To investigate the origin of extant populations in Montana tissue samples from Montana, British Columbia, Minnesota, and Wisconsin fishers were collected and two regions of the mitochondrial DNA genome were examined. Haplotype frequencies differed significantly by region with four haplotypes unique to British Columbia, two to the Midwest, and one to west-central Montana. The distribution of these haplotypes in Montana suggests that fisher populations in the state have multiple origins reflecting the history of translocations and the influence of native populations. Analysis of mitochondrial DNA sequence data indicated that fisher may not have been extirpated from Montana prior to the translocations. Fisher populations in west-central Montana appear to be descended from both native and introduced animals.