Journal of Mammalogy, 88(5):1346–1348, 2007

RELATIVE INFLUENCE OF TEMPORAL AND GEOGRAPHIC SEPARATION OF SOURCE POPULATIONS IN A SUCCESSFUL MARTEN REINTRODUCTION

BRADLEY J. SWANSON* AND CHRISTOPHER J. KYLE

Department of Biology, Central Michigan University, Mt. Pleasant, MI 48859, USA (BJS)
Natural Resources DNA Profiling and Forensics Centre/Ontario Ministry of Natural Resources, Trent University, 1600 West Bank Drive, Peterborough, Ontario K9J 8N8, Canada (CJK)

Reintroduced populations face a genetic bottleneck due to the founding event of the reintroduction. Bringing in additional animals from different locations, or at different times, can restore genetic variation to a reintroduced population and offset the founder event. The reintroduced population of martens in Michigan came from 3 different locations in Ontario and occurred over a 24-year period. The high level of genetic variation found in Michigan's reintroduced marten population could be due to the multiple source locations or the temporal separation of the reintroductions. Based on the genetic variation found in martens, the 3 source locations more likely represent subsamples from a single population and the observed level of genetic variation is due to the temporal separation of the reintroduction events.

Key words: effective population size, genetic variability, marten, *Martes americana*, microsatellites, reintroduction, translocation

Williams and Scribner (2007) address the importance of having an accurate understanding of the historical background of animal reintroductions in order to evaluate their success. However, one of the difficulties in evaluating a reintroduction is the ability to find accurate descriptions of how the reintroductions took place.

Briefly, Williams and Scribner (2007) discovered that the martens reintroduced to Michigan's Upper Peninsula came from multiple source populations. Based on this discovery, Williams and Scribner (2007) suggest that the high level of allelic diversity found in the restored martens of Michigan's Upper Peninsula (Swanson et al. 2006) is a product of multiple source populations used in the reintroduction rather than the temporal separation of reintroductions, as suggested by Swanson et al. (2006). Although we commend Williams and Scribner (2006) for the discovery of the additional documentation on the marten reintroduction, the accusation of misrepresenting the history falls short.

Due diligence is required when trying to uncover details of animal reintroductions that may have occurred decades in the past. To that end, we obtained access to the files at the headquarters of the Michigan Department of Natural Resources in Lansing, Michigan, during late 2002 (D. Etter, Michigan Department of Natural Resources, pers. comm.). We searched the files for all references to martens and fishers and did not find copies of the files cited by Williams and Scribner (2007). We searched the records of the Michigan Department of Natural Resources again in 2003 for all references regarding fishers and martens (D. Etter, Michigan Department of Natural Resources, pers. comm.) and still did not find the references cited by Williams and Scribner (2007). Given that all of the documents cited by Williams and Scribner (2007) are between 15 and 48 years old, and the sources for some of the references (e.g., a newsletter from the Wisconsin Bureau of Endangered Resources [Kohn 1991] and 2 reports by a defunct environmental research company [Churchill et al. 1981; Ludwig 1986]), it may not be surprising that this material was not in the official files. Further, personnel from the Michigan Department of Natural Resources reviewed our publication (Swanson et al. 2006) before to its submission. Nevertheless, the discovery by Williams and Scribner (2007) of additional source populations does require the critical re-evaluation of conclusions by Swanson et al. (2006) that the temporal separation of reintroductions and the subsequent translocations serve as a solid model for reintroductions of martens. The question of interest is whether the high allelic diversity in martens from Michigan's Upper Peninsula is due to temporally separated

* *Correspondent: brad.swanson@cmich.edu*

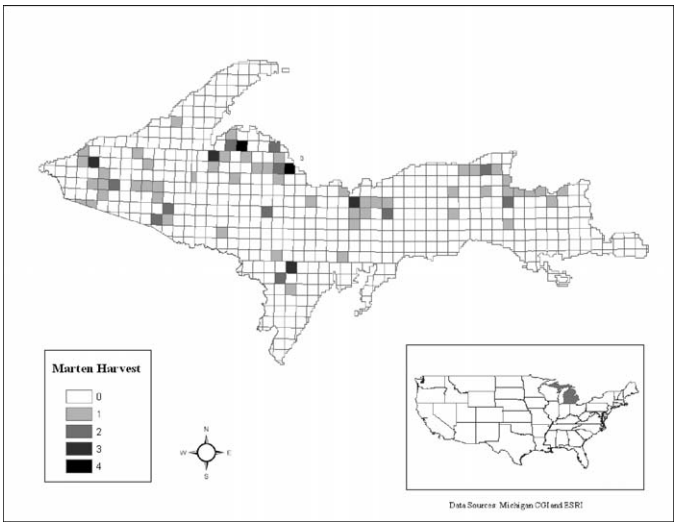

Fig. 1.—Distribution of samples of martens used by Swanson et al. (2006) for analysis of the genetic diversity of martens in Michigan's Upper Peninsula.

reintroductions (Swanson et al. 2006) or multiple source populations (Williams and Scribner 2007).

Using samples collected from across the entire Upper Peninsula (Fig. 1), Swanson et al. (2006) suggested that the high allelic diversity of the martens in Michigan's Upper Peninsula arose through multiple pathways: serial reintroductions, multiple source populations, and remnant populations of martens in Michigan's Upper Peninsula. Swanson et al. (2006) based this conclusion on their discovery of 4 alleles in martens from Michigan's Upper Peninsula that, to date, have only been found in marten populations in western Canada (Kyle and Strobeck 2003). The presence of these alleles was attributed to the 2 animals from a fur farm in British Columbia used in the initial reintroduction. Further, Swanson et al. (2006) found 3 alleles in the martens from Michigan that were not found in any of the 1,252 martens from Canada, sampled from British Columbia through Newfoundland, analyzed by Kyle and Strobeck (2003).

Swanson et al. (2006) further suggested that the serial reintroduction of martens was a major contributor to the retention of allelic diversity shown in the martens of the Upper Peninsula. The basis for their argument is that genetic drift would be a strong evolutionary force because of the relatively small size of the reintroduced populations of martens. Over time, drift would remove alleles from the populations at a rate faster than mutation could restore the alleles, until the population reached a new level of allelic diversity at drift–mutation equilibrium. By temporally segregating the reintroductions a steady influx of new alleles would occur in the population of martens, counteracting the effect of genetic drift. Similarly, the subsequent translocations of martens also would redistribute the allelic diversity throughout the Upper Peninsula.

Certainly, in many species use of multiple source populations could produce the same outcome, because each population is likely to have a unique set of alleles. However, the martens in Canada were shown to have very little genetic differentiation across mainland Canada east of the Rocky Mountains (Kyle and Strobeck 2003). This result questions the probability that the allelic diversity found by Swanson et al. (2006) could be due to the reintroduced martens coming from 3 different areas within the single province of Ontario. The 2 additional ''populations'' Williams and Scribner (2007) found to be contributors to the population of martens in Michigan span the southern boundary of Ontario from east to west. Using the original data of Kyle and Strobeck (2003) to analyze the number of unique alleles across Manitoba (site LB—Kyle and Strobeck 2003), Ontario (sites CH and PM—Kyle and Strobeck 2003), and eastern Quebec (sites EA, WA, and GT—Kyle and Strobeck 2003) supports the conclusion of Kyle and Strobeck (2003) of high levels of genetic similarity across large regions. The above sites cover a much greater area than the 3 source sites used in the Michigan reintroduction and across these sites there are only 2 unique alleles (2.5%) out of 80 alleles across 11 loci; no unique alleles were found in the loci used in common by Swanson et al. (2006) and Kyle and Strobeck (2003).

Extending this analysis to estimate the number of private alleles within any of the provinces further supports the rarity of private alleles. In order to obtain the most liberal estimates of the number of private alleles, we examined each sample location by itself rather than grouping some of the sites as did Kyle and Strobeck (2003). Analyzing the data in this fashion resulted in some sites having small sample sizes ($\bar{X} = 45.0 \pm 29.1$ *SD,* range 17–149); sites with smaller sample sizes are less likely to sample rare alleles, which would increase the likelihood of finding private alleles.

Despite analyzing the data to produce an upward bias in the number of private alleles per locus per province there is only an average of 0.81 private alleles per locus per province across all of the loci used in Kyle and Strobeck (2003). When the loci are restricted to those used in common by Kyle and Strobeck (2003) and Swanson et al. (2006) the average number of private alleles per locus per province is 0.95. This low level of allelic diversity and genetic similarity across large areas, well documented by Kyle and Strobeck (2003), indicates that it is unlikely that the additional source ''populations'' from within Ontario had any impact on the genetic uniqueness of the reintroduced animals. However, regardless of how unlikely our analysis indicates the likelihood of these 2 other ''populations'' being responsible for the observed levels of genetic variation, it is impossible to exclude the hypothesis of Williams and Scribner (2007) until these regions have been sampled.

Despite the suggestion by Williams and Scribner (2007) that the 3 reintroduction sites were genetically unique, based on the small number of private alleles found within a province, the 3 ''populations'' in Ontario from which the martens sampled in Michigan originated are most likely subsamples of a single population. The small number of private alleles found within a province supports the contention of Swanson et al. (2006) that the serial reintroduction over longer periods of time is likely the reason for the high levels of genetic variation found

in the Michigan marten population rather than the geographical location from which the animals were obtained.

Literature Cited

CHURCHILL, S. J., L. A. HERMAN, M. F. HERMAN, AND J. P. LUDWIG. 1981. Final report on the completion of the Michigan marten reintroduction program. Ecological Research Services, Inc., Environmental Report, Iron River, Michigan.

KOHN, B. E. 1991. Minnesota pine martens introduced to Wisconsin. Niche—Newsletter of the Wisconsin Bureau of Endangered Resources 5:4.

KYLE, C. J., AND C. STROBECK. 2003. Genetic homogeneity of Canadian mainland marten populations underscores the distinctiveness of Newfoundland pine martens (*Martes americana atrata*). Canadian Journal of Zoology 81:57–66.

LUDWIG, J. P. 1986. A short report on the Michigan marten reintroduction program Lower Peninsula in 1985–86: comparison to trapping success with the Algonquin Park efforts of 1980–81. Ecological Research Services, Inc., Environmental Report, Iron River, Michigan.

SWANSON, B. J., L. R. PETERS, AND C. J. KYLE. 2006. Demographic and genetic evaluation of an American marten reintroduction. Journal of Mammalogy 87:272–280.

WILLIAMS, B. W., AND K. T. SCRIBNER. 2007. Demographic and genetic evaluation of an American marten reintroduction: a reply to Swanson et al. Journal of Mammalogy 88:1342–1345.

Submitted 3 January 2007. Accepted 24 April 2007.

Associate Editor was Carey W. Krajewski.