



multi-use forest landscapes. Between 2007 and 2010, we deployed Argos satellite telemetry collars on 26 fishers in north-central Idaho. We assessed resource selection at the home range scale using a synoptic modeling approach in which the home range and resource selection are estimated simultaneously. We developed a suite of *a priori* models of habitat selection based on current knowledge of the ecology and habitat requirements of fishers. We used LANDFIRE and VMAP GIS habitat layers in Program FRAGSTATS to calculate habitat composition and configuration metrics and evaluated support for our competing models in an information theoretic framework. We expected that habitat selection would differ between sexes due to differences in reproductive strategy and that resource selection at the home range scale might not be consistent with patterns of habitat selection documented at other spatial scales (i.e., landscape and micro-site). As predicted, resource selection differed between sexes; however, individuals exhibited marked variation in selection for vegetation resources across our study area. We discuss how managers of private and public forests can use this type of information in planning forest harvest strategies that will facilitate occupancy of fishers.

SCHWARTZ, MICHAEL, USFS Rocky Mountain Research Station, Missoula MT, 59801; J. Sauder, Idaho Department of Fish & Game, 3316 16th St, Lewiston, ID, 83501. **FISHER RESEARCH IN THE US ROCKY MOUNTAINS: A CRITICAL OVERVIEW.**

In this talk we review the recent fisher research and monitoring efforts that have occurred throughout Idaho and Montana in past 2 decades. We begin this talk with a summary of the habitat relationship work that has examined fisher habitat use at multiple scales. These have largely been conducted using radio and satellite telemetry, although a new, joint effort to use GPS tags on fisher to understand their habitat use in multiple-use, xeric stands is underway. Next we discuss our progress in the arena of molecular genetics and genomics. We note the progress that has been made in the realms of phylogenetics and taxonomy, population genetics, landscape genetics, and understanding gene flow. We also discuss needs to begin to examine genomic markers under selection to better understand how fishers that we reintroduced into Idaho and Montana from both British Columbia and the Midwestern United States have adapted compared to fishers that have native genes that persisted in the Bitterroot Mountains. Subsequently, we review several fisher species distribution modeling efforts, including efforts to project these models under various climate change scenarios. Finally we review our multiple agency monitoring work, describing what these efforts can tell us about fishers (i.e., distribution) and what we still need to understand (i.e., trends). We end this discussion with an honest critique of our progress to date on these research areas, and provide some open-ended questions to help us develop a research agenda for this rare carnivore for the coming decade.

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This talk provides a population and landscape genetic overview of fishers in Idaho and Montana. We start by discussing some of our initial findings using mitochondrial DNA (Vinkey et al. 2006, Schwartz 2007, Knaus et al. 2011). On balance these results demonstrate the uniqueness of a native haplotype that persisted in the Bitterroot – Selway Ecosystem. They also show the mixing of this native type with reintroduced individuals from British Columbia and the Midwest United States. Subsequently, we examine the genetic substructure of fishers throughout the Rocky Mountains using a panel of microsatellite (nuclear) DNA markers. These data also show a strong break between areas where fishers have been reintroduced and where the native populations persisted. We end this talk presenting some preliminary landscape genetic analyses that examine how coarse landscape features such as mesic and xeric forests influence gene flow at multiple scales.