Evaluating statewide marten (*Martes spp.*) distribution and habitat use in Montana

Federal Aid in Wildlife Restoration Grant W-190-R

Annual report, September 2026

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Note: All results should be considered preliminary and subject to change; please contact the authors before citing or referencing these data.

Background and Summary

The American and Pacific marten (*Martes americana* and *M. caurina*; hereafter marten) are widespread forest carnivores whose presence is often considered an indication of forest health (Macfarlane 1994). Marten are associated with late seral stage forests, increased canopy cover, complex understories, and persistent, deep snowpack (Cheveau et al. 2013, Wiebe et al. 2014, Martin et al. 2021). These habitat characteristics offer an abundance of prey, nesting and denning sites, cover from predators, and subnivean space for thermoregulation and hunting during winter. However, reliance on these features make marten particularly sensitive to forest disturbance (e.g., timber harvest; Cheveau et al. 2013, Woollard et al. 2024).

In Montana, marten are important harvestable furbearers. Marten trapping provides an entry point to learn the art of trapping and many seasoned trappers consider marten an important target species. Despite marten having both ecological and monetary value on the landscape, there are gaps in our knowledge about their status and distribution in Montana. Declines in trapper harvest of marten, particularly in Montana Fish, Wildlife & Parks' (MFWP) Region 1 (Fig. 1), have prompted the need to develop effective monitoring techniques to improve MFWP's ability to manage marten populations. Further, marten in North America were recently reclassified as two distinct species (*Martes americana* and *M. caurina*) with a suspected hybrid zone centered along the Clark Fork Valley in Montana, where the Clark Fork River, I-90 highway, and unforested valleys may limit dispersal and contact between the two species (Colella et al. 2019, Lucid et al. 2020). Lastly, MFWP wildlife managers have begun efforts to restore marten populations to previously occupied portions of their range, which could be informed by improved understanding of the distribution of each marten species and development of effective methods to monitor restored populations.

This project is designed to address these information gaps regarding marten distribution, species taxonomy and hybridization, and field methods for monitoring population status. MFWP currently collects harvest location information for marten from all trappers. We leveraged these data as well as occurrence data obtained from the Montana Natural Heritage Program (MNHP) to develop a statewide distribution model for marten that helped guide efforts to monitor occupancy. Additionally, we have begun collecting samples of marten muscle tissue from participating trappers in cooperation with MFWP regional furbearer biologists. We are collaborating with the National Genomics Center for Wildlife and Fish Conservation at the USDA-USFS Rocky Mountain Research Station (RMRS) to extract DNA from those samples and use a genomic approach to quantify the breadth of the hybrid zone, the distribution of both marten species, and the extent of introgression occurring between the species. Additionally, we aim to evaluate habitat relationships, functional responses in habitat selection, and the effects of forest disturbance on marten occupancy. This project will provide MFWP with tools to design long-term monitoring and management actions for marten, including translocation efforts and harvest management.

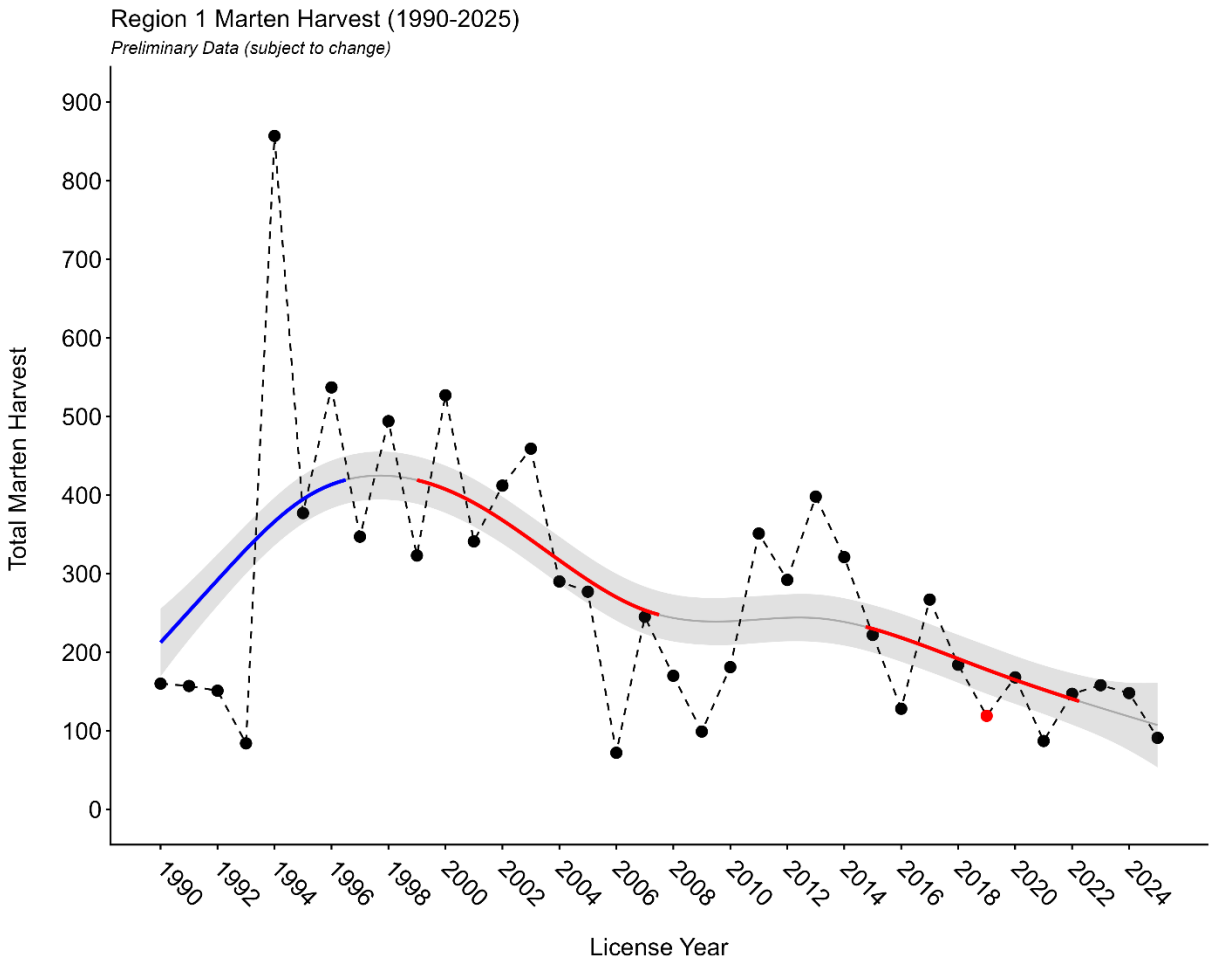


Figure 1. Annual marten (*Martes* spp.) harvest (circles) in Montana Fish, Wildlife & Parks' Region 1, Montana, 1990-2024. The red circle indicates when a 10-martens-per-person harvest limit was implemented in Region 1.

Location

Field studies are occurring in Regions 1, 2, and 3 of Montana and genetic samples are being collected throughout these regions as well. Marten distribution models utilize occurrence data throughout western Montana.

Study Objectives

This project has 3 primary objectives: 1) development of a statewide habitat model to guide future monitoring and reintroduction efforts, 2) development of a methodology and framework for occupancy monitoring with statewide implications, and 3) a statewide assessment of the genetic differentiation and distribution of both marten species, the breadth of the hybrid zone, and the extent of introgression in Montana.

Objective #1: ***Species distribution modeling***

Species distribution models are a popular tool for wildlife conservation and management. Species distribution models use presence-only, presence-absence, or detection-non-detection data to make inferences about species-habitat relationships and predict habitat both spatially (e.g., throughout a species range) and (or) temporally (e.g., under future climate scenarios). Species distribution models can be used to guide translocation and survey efforts (Eyre et al. 2022), identify habitat for rare species of conservation concern (Helmstetter et al. 2021), and predict range shifts under future climatic conditions (Johnston et al. 2012).

We developed a statewide distribution model for the pooled distribution across both marten species. We compared habitat use (i.e., occurrence records) to availability (i.e., background points), enabling spatial predictions of marten habitat throughout western Montana. We used presence-only data including harvest data obtained from MFWP and occurrence records obtained from the MNHP collected between the years 2012 – 2021. MFWP requires all trappers to report the public land survey system (PLSS) township range and section number where martens were harvested. The MNHP is a repository for additional species occurrence records and includes opportunistic sightings or sign of species, as well as occurrence data from camera traps and hair snare surveys. Species-level distinctions were not available within these data and thus they represented the pooled combination of both marten species across the state.

Sampling effort is often unknown for presence-only data collected by the public, which can introduce sampling bias in the form of confounding, additional variation in the densities of occurrence records among regions. This bias typically stems from accessibility, with sampling effort concentrated in areas near human population centers or areas containing roads, drainages, and gentle topography. Patterns of marten occurrence within both the MFWP harvest data and the MNHP data likely suffer from such biases. Sampling bias can make it difficult to disentangle whether observed patterns in the data reflect true ecological differences or are artifacts of uneven sampling effort (Phillips et al. 2009). Moreover, such biases can lead to models that overfit conditions in areas with high sampling effort, thereby reducing the ability of the model to predict relative probability of occurrence to new areas or areas with fewer occurrence records (i.e., poor transferability, Phillips 2008).

We explored two approaches to address the effects of sampling bias. For the first approach, we down-weighted occurrence records located in regions with high sampling intensity (Elith et al. 2010) and randomly selected 10,000 background locations from within a minimum convex polygon around occurrence records. Down-weighting occurrences in this manner helps to prevent model predictions from being overly influenced by spatial clustering in areas with high sampling effort. For the second approach, we selected background points using a targeted background approach that mimicked the spatial sampling bias exhibited by the occurrence data (Phillips et al. 2009). Specifically, we selected 10,000 background points in proportion to the estimated sampling effort.

We used 7 environmental variables in the model believed to be predictors of marten habitat at broad spatial extents: annual canopy cover, the standard deviation of annual canopy cover, snow depth, historical forest disturbance, average minimum temperature, topographic positioning index, and topographic ruggedness index (Wiebe et al. 2014, Chmura et al. 2024, Martin et al. 2021, Viau et al. 2024, Woollard et al. 2024). All environmental variables were measured as raster data and we matched the resolution of the harvest data by taking the average of each environmental variable within a 2.56-km^2 buffer (i.e., the area of a PLSS section) around occurrence records and background points. Canopy cover can change over time; thus, we matched the year the occurrence record was recorded to the raster data from the prior year. Because marten may respond to forest disturbance for several years after a

disturbance (Volkmann and Hodges 2021), we quantified the proportion of forest disturbance within each 2.56-km² buffer as the cumulative area disturbed between the year 2001 and the year the occurrence record was recorded. We assigned a random year to background points based on the distribution of years from the occurrence records and repeated the processes described above for the canopy cover and disturbance covariates. All other variables were either static (e.g., topographic position index) or were averaged across all available years (e.g., snow depth and minimum temperature).

We fit models using LASSO regression and performed model selection on subsets of the data (Hastie et al. 2009, Gerber and Northrup 2020). LASSO, or the least absolute shrinkage and selection operator, is a continuous model selection method that applies a penalty term to shrink coefficient estimates toward zero. As the penalty increases, more coefficients are reduced to zero, effectively selecting only the most informative variables (Hastie et al. 2009). We used cross-validation to identify the penalty value that best balanced model complexity and predictive performance, exploring both traditional random cross-validation and spatially explicit cross-validation. We then evaluated the predictive ability of the top models on a spatially distinct subset of the data excluded from the model selection process using the Area Under the Receiver Operating Characteristic Curve (AUC) and Spearman's rank correlation coefficient. We delineated four spatially distinct regions based on inferred dispersal barriers for marten (i.e., large open valleys and river corridors; Fig. 2) and used these regions to implement spatially explicit cross-validation and final model evaluation. This approach accounted for broad-scale variation throughout western Montana by forcing the model to predict into novel areas, both during model selection (when using spatially explicit cross-validation) and during final evaluation of the top models. We iterated the model selection and evaluation process until all four spatially explicit regions (Fig. 2) were incorporated in both stages.

We evaluated three species distribution models: 1) weighted random: a model where we down-weighted occurrence records in areas with high sampling intensity and performed model selection using random cross-validation, 2) weighted spatial: a model where we down-weighted occurrence records in areas with high sampling intensity and performed model selection using spatially explicit data and 3) targeted spatial: a model where we used unweighted occurrence records, incorporated background points selected using a targeted approach to reflect sampling bias, and performed model selection using spatially explicit data. For all three models, we evaluated predictive ability using spatially explicit data.

Our results highlight that both the weighted random and weighted spatial models predicted relative probability of marten occurrence better than the targeted spatial model (average AUC 0.74, 0.73, and 0.64 respectively; Table 1). However, all distribution models predicted relatively poorly within the Bitterroot Mountains of western Montana (Table 1). All three models had a Spearman's rank correlation coefficient of 1, indicating that points predicted to have higher relative probability of occurrence tended to correspond with occurrence records, even if the exact probability values varied.

Canopy cover and snow depth influenced relative probability of occurrence more than other covariates used in the model. Our results suggest martens selected for increased canopy cover and the relative probability of occurrence showed a curvilinear relationship with snow depth, peaking at intermediate snow levels. Martens appeared to favor cooler average minimum temperatures while avoiding temperature extremes. We found a positive relationship for standard deviation of canopy cover and a negative relationship for topographic positioning index, indicating that martens selected for areas with heterogeneity in canopy cover and topography characterized by drainages and depressions. Other environmental variables included in the model showed relatively small effect sizes on the relative probability of occurrence.

Our model predicted the relative probability of marten occurrence well throughout some portions of western Montana (Fig. 3), including the areas we selected for occupancy surveys. We used this model to inform study design for Objective #2 (see below).

Evaluating the model on spatially explicit regions of data allowed us to identify areas where the model's predictive performance was poor. We attempted to improve this model by incorporating additional occurrence records from Idaho and camera-trap surveys conducted in northwestern Montana, as well as by evaluating additional covariates (e.g., forest type and canopy height). However, these modifications did not substantially improve model transferability, and predictions remained poor in some regions. Nevertheless, our statewide distribution model will be useful for informing ongoing marten reintroduction efforts and surveys designed to monitor populations following reintroductions. We also plan to use the distribution model to investigate functional responses in habitat selection across broad spatial extents.

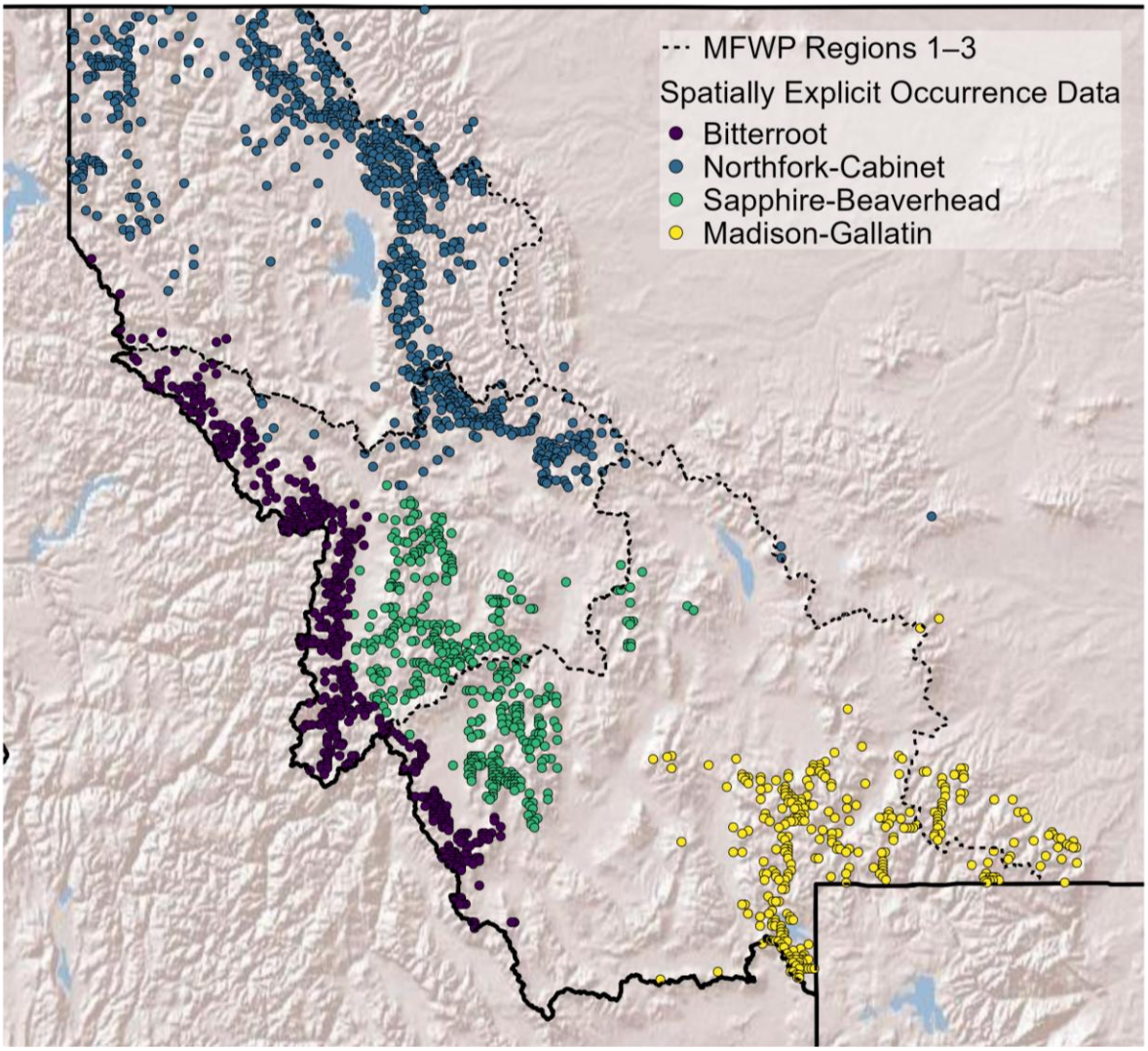


Figure 2. Marten occurrence records divided into spatially explicit regions (different colors), delineated based on inferred dispersal barriers. We used these regions to evaluate the predictive performance of species distribution models.

Table 1. AUC values for each cross-validation fold and average AUC value calculated for each species distribution model. We show the occurrence records from each individual test fold above each column.

Model	Madison-Gallatin	Northfork-Cabinets	Sapphire-Beaverhead	Bitterroots	Average AUC
Weighted Random	0.80	0.79	0.76	0.62	0.74
Weighted Spatial	0.80	0.79	0.76	0.58	0.73
Targeted Spatial	0.64	0.60	0.60	0.61	0.61

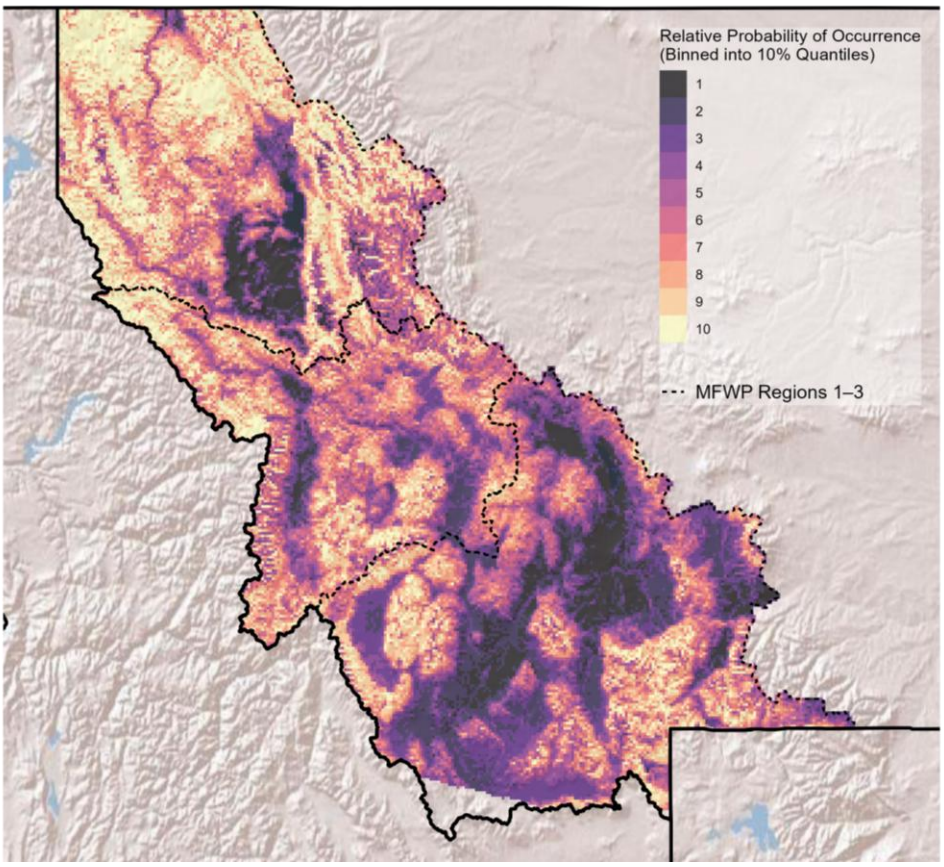


Figure 3. Predictions of the relative probability of marten occurrence across the state of Montana, based on the weighted spatial distribution model in which occurrences in areas with high sampling intensity were down weighted and the model was trained and tested on spatially explicit occurrence records and background points. The predicted values were divided into quantiles, with each quantile representing 10% of the predicted probabilities. For example, a value of 1 corresponds to the lowest 10% of the predicted probabilities, while a value of 10 represents the highest 10%.

Objective #2: ***Marten monitoring and occupancy modeling***

Quantifying how habitat heterogeneity influences wildlife abundance and demographic parameters is critical for developing effective management strategies (Tyre et al. 2001, Morrison et al. 2012). Methods for quantifying such relationships, however, are often more adept at smaller spatial extents than are of interest for wildlife managers (Pollock et al. 2002). For example, capture-recapture studies that estimate changes in abundance or vital rates across ecological gradients are logistically challenging to implement over broad spatiotemporal extents (Saracco et al. 2010). Consequently, wildlife managers often rely on estimates of occupancy (i.e., the proportion of sites occupied) to elucidate habitat relationships and population trends (Mackenzie et al. 2017).

During FY26, we began work to meet this Objective, using a combination of field data collection and occupancy modeling to evaluate habitat relationships for marten throughout their range in Montana and explore how disturbance (e.g., timber harvest) influences occupancy. Additionally, having a fine resolution picture of the breadth of the hybrid zone and the distribution of both marten species (Objective #3) will allow us to discern whether habitat relationships differ or whether functional responses are influencing patterns in habitat selection.

We used a camera-based occupancy sampling design to assess marten occurrence across study areas in Western Montana (Fig. 4). We divided each study area into 14-km^2 grid cells that served as sampling units for occupancy and aimed to deploy one sampling station within each cell (Fig. 4). For each study area, the survey period extends from December 1 through March 31, with stations deployed from August through October because of winter access limitations. We selected study sites to capture the range of variation in habitat characteristics that marten occupy throughout Montana, as well as variation in forest disturbance, including wildfire and timber harvest. The 14-km^2 cell size reflects the home range size of female martens (Lukas et al. 2020). Additionally, this grid cell is nested within other grid-based sampling protocols for mesocarnivores (e.g., fisher, wolverine, and lynx) in Montana, thereby ensuring that data collected on non-target species may also be informative.

We used the predictive distribution model developed in Objective #1 to guide the selection of camera locations within grid cells. Specifically, we used the model to identify grid cells with a mean relative probability of occurrence above the 70th percentile. Within each selected cell, we also used the distribution model to guide camera placement, aiming for locations that had the highest predicted probability of occurrence. Additionally, we assessed grid cells based on records of historical timber harvest and fire to incorporate variation in disturbance across the study area. We coordinated with U.S. Forest Service personnel and received authorization to conduct research activities within designated Wilderness areas following agency review under the Framework for Evaluation of Proposals for Research and Scientific Activities. We also collaborated with US Forest Service and State Forest personnel to identify timber harvest projects scheduled during our surveys.

During FY26, we deployed 157 sampling stations (comprised of cameras, scent dispensers, and hair snares) across the Region 1 study sites (the Whitefish Range and Lower Middle Fork Flathead; Fig. 5). We retrieved the stations in spring and summer 2026 and will re-deploy them in the Region 2 and 3 study areas (Rock Creek-Flint creek and Madison-Gallatin; Fig. 4) in fall 2026. We expect to have preliminary results in FY27 based on data collected in Region 1.

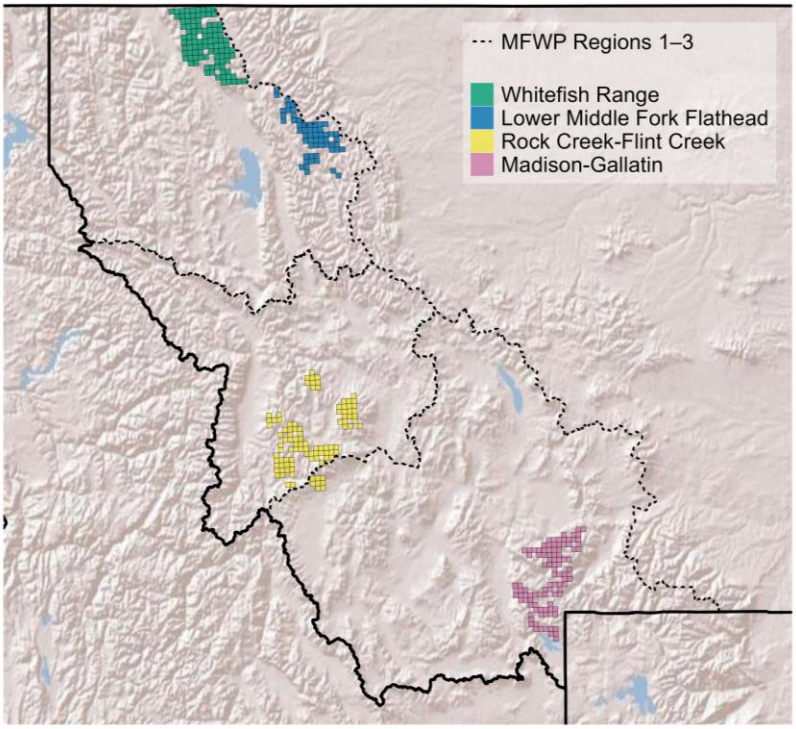


Figure 4. Study areas for marten occupancy monitoring in Montana. Each grid cell is 14 km^2 and represents a sampling unit for occupancy.

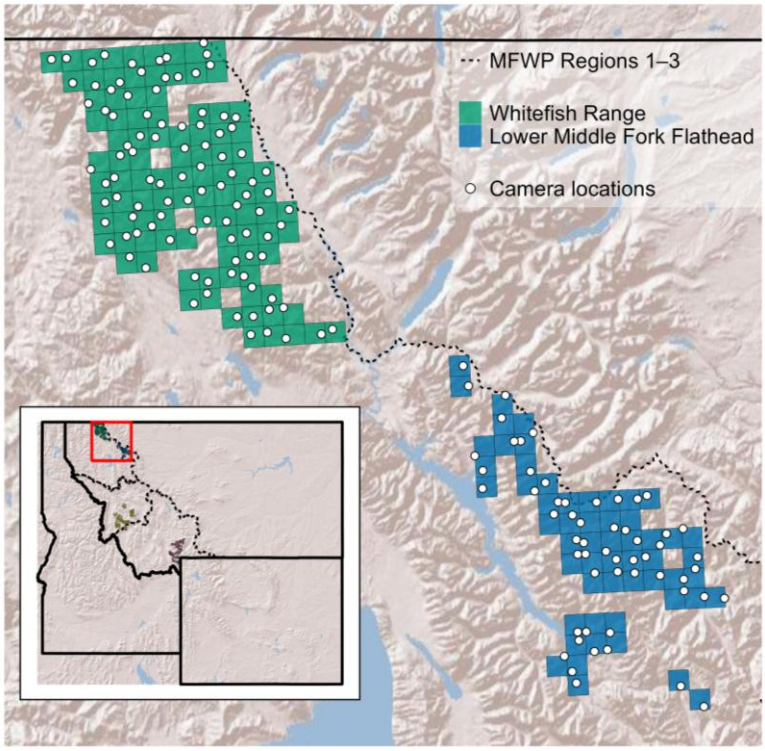


Figure 5. Marten survey station locations in two study sites, the Whitefish Range and the Lower Middle Fork of the Flathead. We deployed 157 sampling stations in these areas in FY26 and retrieved them in spring and summer of 2026.

Objective #3: *Marten genetics*

Martens currently occupying North America have recently been delineated as two species (*Martes americana* and *M. caurina*) and several studies have identified northwestern Montana as a mixing zone where the two ranges meet (Wright 1953, Colella et al. 2019). These studies have primarily relied on a small number of microsatellite genetic markers (i.e., nuclear DNA) in conjunction with mitochondrial DNA to assign individuals according to species or hybrid status. Although these techniques can provide a probabilistic way of identifying species and hybrids, they cannot readily separate ancient from historically recent hybridization. For example, studies based on microsatellites have detected few individuals with mixed nuclear ancestry in a narrow band around the Clark Fork Valley in Montana, suggesting limited interbreeding between the two species (Lucid et al. 2020). Microsatellites, however, can only identify the first few generations of hybrids and thus may mischaracterize hybrid zones as overly narrow. Other studies investigating marten distributions and hybridization have observed mito-nuclear discordance (e.g., a marten with an *M. americana* microsatellite assignment and a *M. caurina* mitochondria) across a broader region in northwestern Montana (Chmura et al. 2024; Colella et al. 2024). Such mito-nuclear discordance confirms introgression occurred sometime in the past but offers no insight into the frequency of events involving recent or ongoing hybridization. This ambiguity highlights the need for a more refined, high-powered genomic approach to better evaluate marten species distributions and hybridization.

MFWP collected marten muscle tissue from participating trappers throughout Regions 1, 2, and 3 during trapping seasons 2021/2022 – 2024/2025. Additionally, we collaborated with Idaho Department of Fish and Game (IDFG) to include tissue samples collected from trappers by IDFG in Idaho as part of this work. To date, 537 samples of marten muscle tissue have been collected from 75 trappers in Montana, and 169 samples have been collected from trappers in Idaho (Fig. 6). We are using genomic approaches to evaluate the distribution of both marten species and putative hybrids. Specifically, we are sequencing genomic DNA using the bestRAD protocol to generate genome-wide single nucleotide polymorphism (SNP) data for American and Pacific marten. We will also quantify the breadth of the hybrid zone and extent of introgression between the two marten species.

During this reporting period, we extracted DNA from a subset of samples representative of the spatial distribution of samples collected to date and sequenced those samples. Sequence data were processed using the Stacks bioinformatics pipeline (Catchen et al. 2013). Briefly, PCR duplicates were removed and reads were demultiplexed, quality filtered, and aligned to the *Martes flavigula* reference genome. Single Nucleotide Polymorphisms (SNPs) were identified and genotyped, and quality filters were applied to generate a high-confidence SNP dataset for downstream analyses. The final filtered dataset consisted of 51,462 biallelic SNPs distributed across 31,673 independent RAD loci. Lastly, we used the Bayesian clustering program ADMIXTURE (Alexander et al. 2009) to estimate individual ancestry proportions and identify putative hybrids (Fig. 7). Our preliminary results are geographically consistent with the previously identified distributions of American and Pacific marten (Dawson et al. 2017) and suggest that hybridization between the two species occurs along the Clark Fork Valley, MT and throughout the Seeley-Swan Valley, MT (Fig. 7). However, the observed pattern of admixture (mixed genetic ancestry resulting from hybridization between *Martes americana* and *M. caurina*) appears to be more geographically restricted than previously suggested (Chmura et al. 2024, Colella et al. 2024).

As of this report, we are no longer collecting tissue samples from trappers across all occupied areas of Montana and Idaho. However, a gap in our genetic sampling still exists where previous research has shown that American and Pacific marten are sympatric (e.g., Swan Valley, MT; Lamar and Mayernik 2023). Thus, during FY27, we will live-trap marten and collect ear biopsy samples to fill gaps in our

genetic sampling. Additional sampling in this region will provide information on the factors that may maintain the hybrid zone, as well as the extent of hybridization where the two species are sympatric.

Results supporting this objective will assist on-going translocation efforts by helping to identify species (and hybrid) distributions to target (and avoid) when seeking to restore native marten populations. Additionally, a finer resolution picture of the distribution of each species and the breadth of the hybrid zone will assist in quantifying habitat selection for both species (Objective #2).

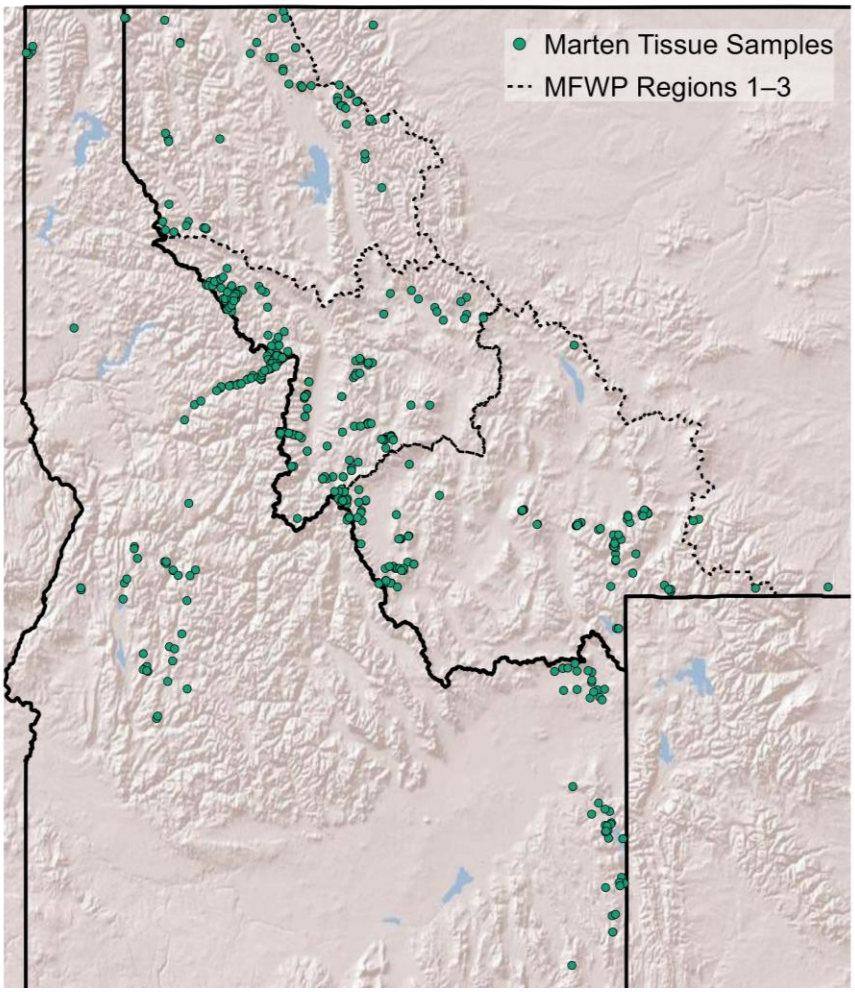


Figure 6. Locations in Montana and Idaho where marten muscle tissue samples were collected by participating trappers during trapping seasons 2021/2022 – 2024/2025.

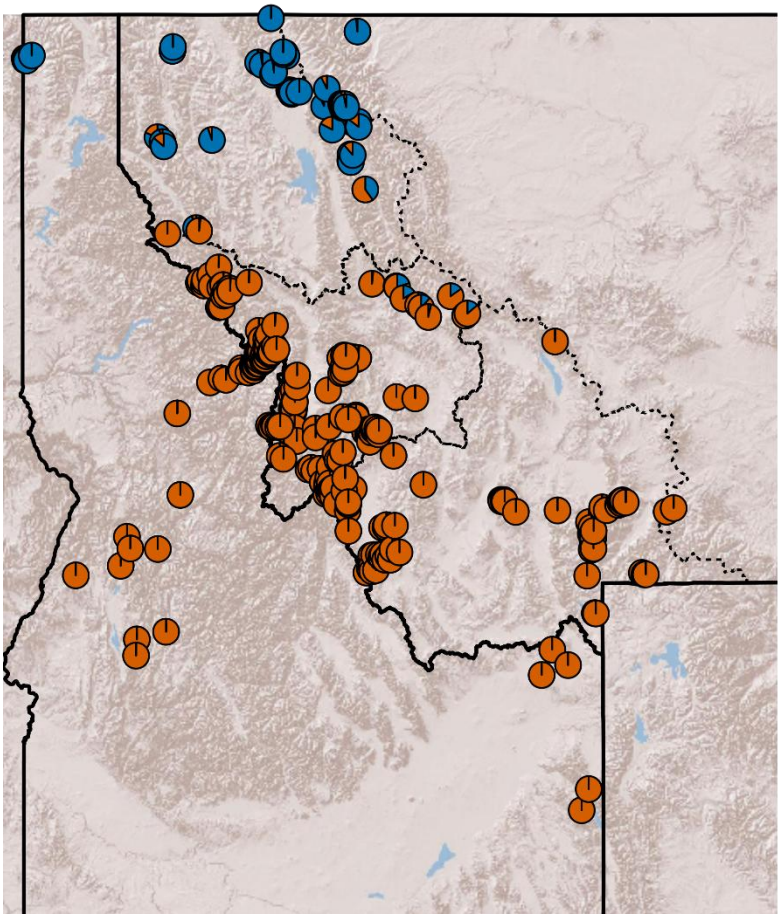


Figure 7. Preliminary results of marten genetic analyses conducted by partners at the National Genomics Center for Wildlife and Fish Conservation, USDA Forest Service Rocky Mountain Research Station. Pie charts represent individual martens, with blue and red indicating the estimated proportion of genetic ancestry assigned to two genetic clusters associated with American and Pacific martens, respectively. Individuals with ancestry assigned to both genetic clusters indicate potential admixture between the two species.

Deliverables: Reports and Presentations

Reports:

Helmstetter, N., A. Litt, N. DeCesare, and J. Coltrane. 2025. Evaluating statewide marten (*Martes* spp.) distribution and habitat use in Montana. Annual report, Federal Aid in Wildlife Restoration Grant W-190-R Annual report. https://fwp.mt.gov/binaries/content/assets/fwp/hunt/trapping/2025 report/3---msu-fwp-marten-study-annual-report-2025.pdf.

Helmstetter, N., A. Litt, N. DeCesare, and J. Coltrane. 2024. Evaluating statewide marten (*Martes* spp.) distribution and habitat use in Montana. Annual report, Federal Aid in Wildlife Restoration Grant W-190-R Annual report. https://fwp.mt.gov/binaries/content/assets/fwp/hunt/trapping/1--msu fwp-marten-study-annual-report-2024.pdf.

Presentations:

Helmstetter, N. 2026. Evaluating Marten Distributions, Habitat Selection, and Hybridization. Montana Fish, Wildlife & Parks and Montana Trappers Association Annual Meeting Region 1, Kalispell, MT.

Helmstetter, N. 2026. Evaluating Marten Distributions, Habitat Selection, and Hybridization. Montana Fish, Wildlife & Parks and Montana Trappers Association Annual Meeting Region 2, Missoula, MT.

Helmstetter, N., A. Litt, J. Coltrane, and N. DeCesare. 2025. Confronting challenges in distribution modeling for marten in western Montana. Contributed paper, Annual meeting of the Montana Chapter of The Wildlife Society, Billings, MT.

Helmstetter, N. 2025. Evaluating Marten Distributions, Habitat Selection, and Hybridization. Montana Fish, Wildlife & Parks and Montana Trappers Association Annual Meeting Region 1, Kalispell, MT.

Helmstetter, N. 2025. Evaluating Marten Distributions, Habitat Selection, and Hybridization. Montana Fish, Wildlife & Parks and Montana Trappers Association Annual Meeting Region 3, Whitehall, MT.

Helmstetter, N. 2025. Evaluating Marten Distributions, Habitat Selection, and Hybridization. Western Association of Fish and Wildlife Agencies Forest Carnivore Subcommittee Spring Meeting. Missoula, MT.

Helmstetter, N. A. 2025. Update on Marten Monitoring in the North Fork Flathead Valley. Summer Interlocal Agreement Meeting in the North Fork Flathead Valley.

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