

Preproposal Submitted for the 2013 State Wildlife Grant Program, Arkansas

Project Title: Distribution and status of the long-tailed weasel in Arkansas

Project Summary: Anecdotal evidence suggests that long-tailed weasels may have become rare in Arkansas, and information on their distribution and status is lacking. We propose to use scat-detecting dogs to conduct broad-scale surveys for weasel presence at ≥ 100 sites, including all major ecoregions in Arkansas. Presence data will be compared with local landcover and landscape features in an occupancy modeling framework to produce a map of predicted weasel occupancy. In year 2, we will conduct intensive scat surveys at 10 sites, 5 sites where weasels were detected in year 1 and 5 sites predicted to be occupied by the map. Our objective will be to generate a genetic mark-recapture estimate of local weasel abundance at each intense-survey site. This study will provide valuable data on the known and predicted distribution of long-tailed weasels in Arkansas, as well as site-level estimates of weasel abundance and genetic status.

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Budget Summary:

	35% Match	50% Match
State Wildlife Grant Program (Federal)	\$131,938	\$107,697
Match (Southern Illinois University)	\$ 71,045	\$107,697
Total	\$202,983	\$215,394

Need: The long-tailed weasel (*Mustela frenata*) is one of the most widespread mammals in the western hemisphere, its presence is rarely obvious because it is cryptic and generally occurs at low population densities. The Arkansas Wildlife Action Plan prominently highlights a lack of data regarding the statewide distribution and status of long-tailed weasels. This project will provide broad-scale data on presence of long-tailed weasels across Arkansas ecoregions, as well as estimates of local abundance in a subset of those areas.

Purpose and Objectives: Our objectives are: 1) to document the distribution of long-tailed weasels at ≥ 100 sites across the 7 ecoregions of Arkansas, 2) generate a predictive map of weasel occupancy statewide, 3) assess local abundance of weasels at sites known and predicted to be occupied based on genetic detection of unique multilocus weasel genotypes.

Location: We will survey sites across the state, representing all ecoregions. Sites will include state, private, and federally owned lands. Within each region, we will choose sites with some component of brush, grassy, wetland, or wooded cover. Intensive surveys to quantify local abundance will be conducted in ten 20-km² sites, half of which will be sites where weasel presence was confirmed and half will be sites predicted to have weasel presence.

Approach: Weasels often occur at low population density, have very large home ranges for their body size, and live-trapping studies and telemetry studies generally report low trap success and small sample sizes (Gehring and Swihart 2004, Richter 2005, St.-Pierre et al. 2006, Hajduk 2008). Such studies also devote extensive effort to gain information about few localized areas. Noninvasive surveys can provide an efficient alternative for assessing the distribution and abundance of cryptic species over large areas, and the use of dogs in detecting scat has proven highly effective in surveys for species ranging from ground squirrels (Duggan et al. 2011) to whales (Rolland et al. 2006).

In year 1, we will employ trained scat-detection dogs (trained and handled by the EcoDogs program at Auburn University; <http://ecodogs.auburn.edu/>) for 7 weeks (6 weeks for 50% match) to detect long-tailed weasel presence at ≥ 100 sites across Arkansas. These sites will be selected using a stratified random sampling approach, distributing survey sites among the 7 ecoregions in proportion to the area of each. Within each ecoregion, we will use a geographic information system (GIS) to generate random points and examine landcover around them. We will exclude points < 5 km from another point; points with $< 10\%$ combined coverage of grassland, brushland, wooded, and wetland cover (“natural cover”) within 1 km (e.g., points in the middle of extensive crop fields or urban areas); and points where we are unable to secure permission to conduct surveys. At each site, we will survey for scat along a triangular transect 1.5 km total length, focusing on areas of natural cover. The routes followed by the dogs and scat locations will be documented using a global positioning system (GPS) device. We will return to a subset of sites and re-run the same transects to quantify repeatability of results. Scat samples collected will be preserved and stored for later analysis.

We will analyze the detection data in an occupancy-modeling framework (MacKenzie et al. 2006) to test hypotheses regarding local and regional factors (e.g., ecoregions, distance to

water, landcover of the transect, local road density, slope, etc.) affecting weasel occupancy, estimate statewide and regional probability of occupancy (i.e., fraction of the area that weasels), and generate a map highlighting areas where weasel occupancy is predicted to be high or low.

Scat samples will be identified to species to insure that all specimens analyzed are *M. frenata* and to test scat-dog specificity. We will isolate genomic DNA from scats using commercial kits and sequence a portion of the mitochondrial cytochrome b gene using primers described in Harding and Dragoo (2012). We will test published mustelid microsatellite DNA primers listed in Zuberogoitia et al. (2013) to develop a multilocus panel of markers with sufficient variation to reliably distinguish individual weasels. To augment genetic material for primer development, we will conduct focused trapping in sites where multiple scats were found and also solicit tissue samples from Arkansas trappers.

In year 2, we will conduct intensive scat surveys to assess local weasel abundance and genetic diversity at 10 sites – 5 sites where weasels were detected in year 1 and 5 sites where weasel occupancy is predicted on the basis of occupancy modeling. The distribution of those sites within the state will depend on the results of year 1, but we will attempt to maximize the number of ecoregions represented. Long-tailed weasels have home ranges typically on the order of 20-100 ha (0.2-1 km²; Gehring and Swihart 2004, Richter 2005, Hajduk 2008), so examining local abundance requires surveying an area several times larger. We will survey for scat with detector dogs on 20 transects within a 20-km² area at each site, and will also deploy hair snares to provide additional genetic material. The samples collected will be genotyped to identify individuals, and samples from unique weasels will represent “captures” for mark-recapture abundance estimation (Waits and Paetkau 2005, Williams et al. 2009).

Expected Results and Benefits: Weasels are important generalist predators in many ecosystems, yet their activities can cause economic harm and nuisance to some stakeholders. The study we propose will provide reliable information on the distribution and status of the long-tailed weasel, enabling informed decision-making with regards to their status as furbearers and the need (or lack of need) for conservation efforts. Genetic data obtained during this study will facilitate future studies of genetic status and abundance of weasel populations. Recent scientific work has suggested that Arkansas may lie at the geographic boundary between two major genetic groupings of weasels (occupying western and eastern North America), and our study has the potential to reveal the distribution and extent of intermixing of these two groups. Samples collected during the study have the potential to contribute to a broad range of future analyses, including assessment of contaminant and parasite burdens, identification of prey, and measurement of hormone levels associated with stress and reproductive status.

Literature Cited

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BUDGET (\$)	35% Match			50% Match		
	SWG (Federal)	Match (SIUC)	Total	SWG (Federal)	Match (SIUC)	Total
Salaries & Benefits ¹	38,249	22,333	60,582	19,272	52,784	72,056
Commodities ²	31,500	0	31,500	31,500	0	31,500
Travel	5,500	0	5,500	5,500	0	5,500
Contractual ³	44,695	0	44,695	41,635	0	41,635
Indirect Costs ⁴	11,994	48,712	60,706	9,790	54,913	64,703
Total	131,938	71,045	202,983	107,697	107,697	215,394

¹We request SWG funds to cover stipend for a graduate assistant (12 months per year for 35% match, 6 months per year [remainder match] for 50% match). Tuition waiver by SIU plus salary & benefits associated with effort on this project by Drs. Schaubert and Heist included as match.

²Consumables to develop primers (\$5,000) and analyze mtDNA and microsatellite loci (\$80/sample, 320 samples total) plus field supplies (\$900).

³Training and handling detection dogs to collect reliable occupancy data requires specialized expertise, so we will contract with the Auburn University EcoDogs program (\$2500 to train, \$2500/week during surveys (6 [50% match] or 7 [35% match] weeks in year 1, 5 weeks in year 2), plus travel & lodging for dog & handler). Also included is \$1,500 per year for maintenance & calibration of laboratory equipment.

⁴10% indirect cost rate included in SWG funds. Unrecovered indirect costs (37.5% of SWG funds, plus federally negotiated 47.5% of matching salaries & benefits) included in match.

Qualifications of the Individuals and Organizations Involved:

SIUC Cooperative Wildlife Research Laboratory (CWRL) has for over 60 years fulfilled its mission of training graduate students to conduct high-quality, management-relevant wildlife research. The CWRL maintains a fleet of field vehicles and has amassed a large collection of field equipment including traps, animal handling equipment, surveying and navigation equipment, telemetry receivers and antennas, water craft, and remote cameras. The CWRL also maintains The Spatial Analysis and Computer Laboratory, a state-of-the-art facility dedicated to the interpretation, analysis, and predictive modeling of wildlife and their habitats, through application of Geographic Information Systems (GIS) and access to a wide variety of geographic and ecological data layers.

SIUC Conservation Genetics Laboratory is a fully-equipped genetic analysis facility for obtaining and analyzing DNA fragment and sequence data. Facilities include multiple freezers, refrigerators, automated pipets, centrifuges, and vacuum manifolds for DNA isolation, four thermal cyclers for PCR amplification of DNA, and an Applied Biosystems 3130XL automated DNA analyzer for resolving DNA fragments (e.g. microsatellite) and sequences in-house. Computing facilities include both Windows computers loaded with Genescan and Genotyper software for microsatellite analysis and a Macintosh computer with Sequencher software for analyzing DNA sequences.

Personnel:

Eric Schaubert, Ph.D. is a wildlife ecologist with over 24 years of experience in field studies of wildlife, particularly mammals, and expertise in rigorous quantitative data analysis. He received his B.S. in 1992 from University of Massachusetts Amherst, M.S. in 1994 from Oregon State University, and Ph.D. in 2000 from University of Connecticut. He has published over 40 peer-reviewed scientific papers and book chapters. He has supervised two Master's theses on long-tailed weasels in Illinois, and co-supervised one Ph.D. dissertation on noninvasive techniques to monitor broad-scale carnivore occupancy.

Ed Heist, Ph.D. is a conservation geneticist who runs the Conservation Genetics Laboratory at SIUC. He earned his Ph.D. in 1994 from the College of William and Mary and has since published more than 40 peer-reviewed manuscripts on conservation and population genetics of aquatic and terrestrial organisms including sturgeon, sharks, bobcats, woodrats, and bark beetles. Dr. Heist is an expert on the use of DNA microsatellites for individual and population identification.