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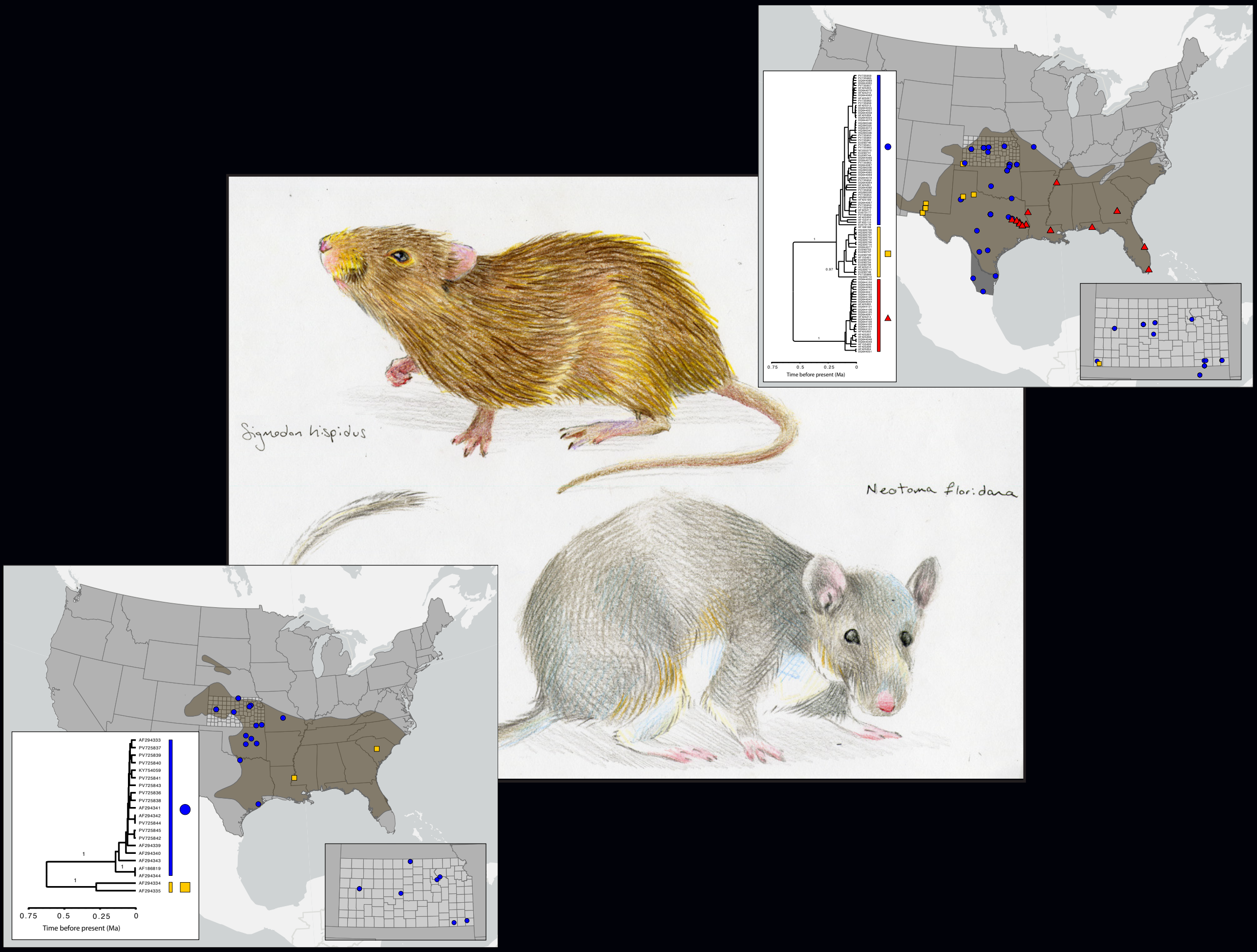
MODERN DISTRIBUTIONS AND INTRASPECIFIC DIVERSITY OF TERRESTRIAL MAMMALS OCCURRING IN KANSAS



ANDREW G. HOPE, SAM C. SPECK, LITSA T. P. WOOTEN, TOMMY M. HERRERA, KAILEY R. MEACHAM, MARY E. SCHMIDT, AND ZACKARY CORDES

Front cover: Rangewide phylogeographic history and lineage distributions of the Eastern Woodrat (*Neotoma floridana*) and Hispid Cotton Rat (*Sigmodon hispidus*) with an emphasis on Kansas. Species illustrations by Ryan Grutsch.

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MODERN DISTRIBUTIONS AND INTRASPECIFIC DIVERSITY OF TERRESTRIAL MAMMALS OCCURRING IN KANSAS

ANDREW G. HOPE, SAM C. SPECK, LITSA T. P. WOOTEN, TOMMY M. HERRERA, KAILEY R. MEACHAM, MARY E. SCHMIDT, AND ZACKARY CORDES

ABSTRACT

Kansas spans the center of the dynamic Great Plains of North America. This region is an environmental crossroad, reflecting high habitat heterogeneity. Terrestrial small and medium-sized mammals consequently constitute a diverse assemblage of wildlife distributed throughout the region that reflects distinct ecology and community associations of species, as well as evolutionary legacies originating from distinct biomes of North America through time. Herein, knowledge of the distribution of species, as well as genetic diversity within species, was used to infer responses to processes of change, both for ensuring the continued persistence of mammal species into the future and more broadly for identifying important regions for biodiversity across the central Great Plains. Field surveys were performed across Kansas between 2020 and 2024, including voucher specimen and tissue sample collections to enable multiple future research outcomes. Subsequently, distributional records and intraspecific mitochondrial lineages were assessed in the broader context of historic sampling and range-wide phylogeographic structure. Field efforts were enhanced by concurrent surveys conducted by the Kansas Department of Wildlife and Parks and associated data, which are amalgamated here. Specimens resulting from our surveys vouch for 45 mammal species detected during the five-year sampling timeframe. Six species of greatest conservation need for the state of Kansas each were sampled from at least a single locality. In addition, new records of *Geomys* pocket gopher were recorded for Kansas that are substantially genetically divergent from other described species and conceivably constitute a new and possibly endemic species to the central Great Plains, pending further evidence and a formal account. Results of genetic analyses show that current distributions of subspecies of mammals through Kansas are not well-supported. Instead, distinct genetic lineages tend to cluster in peripheral regions of the state. This often reflects the limits of a species' range within Kansas. But in multiple instances, lineage transitions highlight discrete evolutionary boundaries associated with secondary contact of evolutionarily distinct units. Multiple new county records (39 new detections from 25 species) included some extralimital records that might suggest recent distributional shifts. New records also were found for common species within their presumed distribution, highlighting that contemporary sampling can enhance understanding of even well-known species. Quantifying ongoing ecological and evolutionary trajectories will require field surveys and collections with more comprehensive spatial and temporal coverage, particularly along presumed range limits.

Key words: conservation, global change, holistic specimen, intraspecific lineages, mammal inventory, new distributional records, phylogeography, small mammals, wildlife management

INTRODUCTION

The state of Kansas spans the geographic and environmental center of North America at the heart of the Great Plains. Although often perceived as an expanse of prairie that lacks topographic relief or habitat heterogeneity, this region is biogeographically complex and boasts diverse flora and fauna that reflect the Great Plains more broadly (Burke et al. 1991; Benedict et al. 1996). Kansas is located at the crossroads of faunal communities distributed across multiple distinct ecosystems that are maintained by strong gradients of temperature (latitudinally) and precipitation (longitudinally). In terms of mammals, this translates to high total faunal diversity, but low local diversity or endemism (Jenkins et al. 2015). Reflecting these environmental gradients is a transition of mammal diversity and composition from western arid grasslands (higher richness and western-origin species) to eastern mesic grasslands (lower richness and greater influence of plains endemics, and eastern-origin species associated with broadleaf forests; Jenkins et al. 2015). Similarly, mammalian communities associated with north-temperate grassland and boreal zones dominate in the northern plains, south to northern Kansas, and species associated with subtropical and arid chapparal are prevalent in the southern plains and have their northern distributional limits in southern Kansas (Armstrong et al. 1986).

Historically, Great Plains grasslands stretched from northern Mexico to central Canada and were maintained by relatively intact and stable wildlife communities, fire regimes, and climatic gradients (Samson et al. 2004). Since colonial times, local land conversion, wholesale declines in native wildlife (Flores 2017), and global anthropogenic forcing have transformed the Great Plains and much of Kansas to an increasingly fragmented mosaic of remnant habitats, agriculture, urban zones, and woodland (Scholtz and Twidwell 2022). Impacts from contemporary global climate changes include predicted increases in the intensity and severity of extreme events, such as both storms and droughts that are more severe than in recent centuries (Cook et al. 2015). Warming average temperatures have shifted the Great Plains climatic envelope northward by more than 500 km in the last 50 years (Roberts et al. 2019). Similarly, the transition zone between arid western grasslands and eastern mesic grasslands has shifted eastward from roughly the 100th meridian to the 98th meridian longitude (Seager et al. 2018). Human land use has exacerbated environmental trends, where cessation of natural wildfire regimes has contributed to westward woody encroachment by eastern woodland flora (Ratajczak et al. 2016). Collectively, these environmental dynamics have consequences for the future integrity of mammal communities, and by extension, potential outcomes and risks associated with human health (Hope et al. 2025).

As the extent to which global environmental trends influence contemporary biodiversity are explored in more depth, it is increasingly critical to develop samples and data streams that document change and provide materials for trans-disciplinary analysis of the continuing ecological and evolutionary legacies of species (Hope et al. 2018; Schmitt et al. 2019). Kansas is a historical hub for documentation and research on mammalian biodiversity through relatively comprehensive sampling of species during early biodiversity surveys, and subsequently through the mid-20th century (summarized by Cockrum 1952). However, few spatially broad specimen-based field sampling efforts have been performed in the last 20 years as environments have continued to change dramatically. Further, modern collection and preservation of genomic resources (frozen tissues) and associated biodiversity (parasites) that can enhance our understanding of biodiversity outcomes are still sparse (Edwards et al. 2005; McLean et al. 2016). The purpose of this study is to report on recent distributions and intraspecific genetic analyses of small mammals across the state of Kansas. Provided is a modern baseline understanding of mammalian mitochondrial genetic diversity through the central Great Plains, and in the broader context of range-wide species distributions across North America.The ultimate value of these resources will be extended by continued efforts to systematically sample mammalian biodiversity across the region, providing temporally deep and spatially broad perspectives on global change (Dunnum et al. 2017).

Methods

Taxonomic focus.—Terrestrial small mammals within Kansas constitute a diverse group of resident species that occupy all terrestrial habitats. As noted from historic accounts and primary literature, most of the native small mammals of Kansas are represented by multiple subspecies occurring throughout the state, reflecting perceived biogeographic turnover, particularly from west to east (Hall 1955). In addition, due to the central location of Kansas within North America, multiple small mammal species that occur in Kansas are on the extreme periphery of their broader species ranges, thus having implications for regionally distinct populations exhibiting local endemism and adaptations (Channell and Lomolino 2000).

Eight rodent species and one lagomorph are listed as species of greatest conservation need (SGCN) in the Kansas Wildlife Action Plan (Rohweder 2022). Several of these species occur in the state at the periphery of their rangewide distributions and four are listed as species in need of conservation (SINC) in the Kansas Nongame and Endangered Species Conservation Act. SGCN species include the Black-tailed Prairie Dog (*Cynomys ludovicianus*), Franklin's Ground Squirrel (*Poliocitellus franklinii*; SINC), Fulvous Harvest Mouse (*Reithrodontomys fulvescens*), Southern Bog Lemming (*Synaptomys cooperi*; SINC), Southern Flying Squirrel (*Glaucomys volans*; SINC), Spotted Ground Squirrel (*Xerospermophilus spilosoma*), Swamp Rabbit (*Sylvilagus aquaticus*), Texas Deermouse (*Peromyscus attwateri*; SINC) and Yellow-faced Pocket Gopher (*Cratogeomys castanops*). These species collectively illustrate the critical role that Kansas plays in connecting wildlife across central North America, as they are indicators of distinct regional ecosystems with distant geographic and evolutionary origins from western arid regions, northern Great Plains, eastern forests, southern deciduous highlands, and obligate wetland associations.

The primary focus for this work included shrews, moles, lagomorphs, and rodents. In addition, incidental sampling of other groups including opossums, armadillos, raccoons, canids, felids, and weasels were included as part of the observed species accounts.

Timeline and sampling localities.—Records of mammals herein are in all cases represented by voucher specimen materials archived in either the Kansas State Biorepository (KSB) or the Museum of Southwestern Biology and are publicly searchable through the Arctos digital specimen database. Sampling was performed by three different modes: 1) site-intensive specimen-based sampling through summers 2020–2021 across 12 general sampling localities, including long-term annual sampling at one site; 2) capture-release sampling with collection of select individuals across multiple localities spanning 2020–2022 as conducted by the Kansas Department of Wildlife and Parks (KDWP); and 3) additional incidental sampling records of specimens between 2020–2024 based on efforts from both KSB and KDWP. Site-intensive sampling targeted sites across Kansas that were also coincident with historic collection localities of taxa designated as SGCN, as mined from the Kansas Mammal Atlas (https://webapps.fhsu.edu/ksmammal/). Many sites also were coincident with ecological focus areas (EFAs) designated by the Kansas Wildlife Action Plan and with state managed lands to maximize the value of recovered specimen resources for biodiversity conservation efforts (Rohweder 2022).

Fieldwork.—All site-intensive general collecting localities were sampled for 2–4 nights of general collecting by using multiple standard trap types (various combinations of Sherman live traps, museum special snap traps, Victor rat traps, pitfall cups, Havahart cage traps, and gopher/mole traps). Traps were set in transects to maximize detection of different small mammal species, sampling across all local habitats, and based on knowledge of the ecological habitat requirements of small mammals. An average of 400 traps were set per night for each site, totaling minimally 1,200 trap nights per general collecting locality (where one trap night equals one trap set for one night). Traps were set in the afternoon. Each morning, traps were checked after dawn and individuals were collected and fully processed (vouchers prepared and tissue samples preserved) in the field according to published comprehensive methods to maximize the research potential of all specimen parts (Galbreath et al. 2019).

Genetic sequencing.—Selected samples representing most species detected were used for genetic analysis to understand the distribution of distinct intraspecific genetic lineages across Kansas in relation to elsewhere through the range-wide distribution of these species. Genomic DNA was extracted from tissue for selected samples following the NEB Monarch Blood DNA extraction kit using manufacturer's instructions. The full mitochondrial cytochrome *b* gene (*Cytb*) was amplified using primers MSB05/MSB14 (Hope et al. 2010). PCR included initial denaturation at 94°C for 6 min, followed by 40 cycles of denaturation at 94°C for 25 s, annealing at 50°C for 30 s, extension at 72°C for 1 min, and final extension at 72°C for 5 min, with cooling at 15°C for 10 min. PCR products were cleaned using ExoSAP-IT (Affymetrix, Santa Clara, California) diluted 1:10. All PCR products were confirmed on a 0.8% electrophoresis gel and sequenced in both directions (on an ABI 3730) at Eurofins Genomics. Raw reads were cleaned and aligned using Geneious (versions 2020 through 2025; Kearse et al. 2012) with a focus on molecular sequences and related data types. For each species, we also downloaded existing *Cytb* sequence data from GenBank and compiled data sets that included *Cytb* sequences of focal taxa and appropriate outgroups of closely related species.

Phylogeny construction.—Bayesian phylogenetic reconstructions were produced for selected species for which samples were collected from Kansas and sufficient comparative materials were publicly available on NCBI GenBank. Phylogenetic trees were estimated via Markov Chain Monte Carlo searches in BEAST2 (Bouckaert et al. 2019), setting all parameters in BEAUti, part of the BEAST2 software package, and estimating the substitution model through use of the bModelTest package, also in BEAST2 (Bouckaert and Drummond 2017). A strict molecular clock model was applied, and the mutation rate was set to 0.05 (5% per million years; Hope et al. 2010) for all species. Although mutation rates are known to vary across species, a mutation rate was applied to anchor relative divergence among taxa as a first approximation of genetic distinctness and of the evolutionary history of taxa; for example, ancient divergence between taxa, >100 thousand years ago (ka) coincident with mid- to late-Pleistocene, versus recent, <100 ka, coincident with the Last Glacial period. Empirical base frequencies were used, along with a constant population size tree prior, with other parameters run with default settings. MCMC was run for 10 million generations, sampling every 1,000 generations, with the first 10% trees discarded as burn-in. Stationarity of MCMC runs was assessed in Tracer v1.7 (Rambaut et al. 2018). Tree files were annotated in TreeAnnotator (BEAST2 package). Chronograms were visualized with posterior probabilities and reported as a mid-point rooted tree in FigTree v1.4.4 (Rambaut 2010). Outgroups were subsequently excluded from tree figures due to often long branches that obscured detail of the focal ingroup. Lineages were identified based on strong nodal support for reciprocally monophyletic clades, or otherwise were justified as outlined in individual species accounts.

Distribution maps.—To visually assess the distribution of genetic lineages within and among species, all specimen records for which genetic sequence data was included were compiled and then georeferenced by mining locality information from associated publications through GenBank accession numbers (see Appendix for specimens examined). Distribution maps were generated by downloading and plotting the range-wide distribution hull based on IUCN distribution maps (https://www.iucnredlist.org/) and subsequently adding symbols for distinct genetic lineages corresponding to georeferenced specimen records that also had genetic information.

RESULTS

A total of 45 mammal species in the Orders Didelphimorphia, Cingulata, Lagomorpha, Eulipotyphla, Carnivora, and Rodentia was sampled from 50 counties across Kansas (Table 1). Total sampling included 231 modern records of species by county, and typically multiple records for a species at a given site. Across 25 species, 39 new county records were documented as well as one new state record of a putatively new species of pocket gopher (Table 1). Detailed field journal entries (Hope, unpublished) for many of the primary sampling sites are archived in either the Museum of Southwestern Biology or the Kansas State Biorepository. The following accounts include a synopsis of species detected, including opportunistic sampling. Comments also were included for small mammal species (lagomorphs, shrews, rodents) not recovered through new specimens to qualify absences. Along with remarks for each species, a phylogenetic tree and distribution map illustrating the geographic limits of discrete, well-supported genetic lineages are provided for most taxa.

SPECIES ACCOUNTS

ORDER DIDELPHIMORPHIA
Family Didelphidae
Didelphis virginiana
Virginia Opossum

This species was common. Samples were collected via Havahart trap or roadkill from six sites, including a new county record from Osage County, and opossums were commonly seen at additional sites, particularly associated with riparian woodlands. Much of western Kansas still lacks occurrence records for this species, but detections would likely be successful in additional counties, particularly by sampling roadkill. A large series of specimens from Osage County was recently accessioned, including pouched young of all developmental stages, that has the potential to enhance investigation of didelphid development through future research.

ORDER CINGULATA
Family Dasypodidae
Dasypus mexicanus
Mexican Long-nosed Armadillo

A roadkill specimen of this species was salvaged from Cherokee County, representing a new county record. Although the only sample obtained, this species was relatively common across southeastern Kansas and additional roadkill were observed across much of the eastern half of Kansas, including Riley County. Despite being increasingly common across Kansas, armadillos are still under-represented in museums. At the time of Hall's (1955) account of Kansas mammals, armadillos occurred only as far north as Osage County. By 1981, they were detected as far north as Russell County (Bee et al. 1981). The farthest north specimen recorded in Kansas is from 2005 in Rooks County (Schmidt et al. 2021). Additional records have been recorded by multiple authors (reviewed by Kaufman and Kaufman 2014). Recently, they have been detected in southern Nebraska, apparently as dispersing males (Roehrs et al. 2021). As such, the recognized distribution of this species in Kansas is likely outdated, and they can be presumed to be present throughout much of the state.

ORDER LAGOMORPHA
Family Leporidae
Lepus californicus
Black-tailed Jackrabbit

In 2020, Black-tailed Jackrabbits were moderately abundant through Cimarron National Grassland, although there was no evidence of this species at other sites sampled through western Kansas or farther east. Jackrabbits were once much more widespread and abundant across Kansas, and this species has experienced decline and westward contraction in recent decades (Simes et al. 2015; Schmidt et al. 2021). Observations of Black-tailed Jackrabbits from the vicinity of Marion, Marion County, were reported from 2024 (Natalie McLinden, pers. comm.). Given these combined observations coupled with ongoing trends, further study of distributional change of this species through time, based on specimen collection records, hunter surveys, or observation surveys, is warranted. The sand sagebrush habitats of southwestern Kansas are a critical habitat for supporting jackrabbits, although further studies might focus on the impacts of local land use and climate to population fluctuations (Locklear 2021).

Sylvilagus aquaticus
Swamp Rabbit (SGCN)

Although no Swamp Rabbit specimens were sampled, a large cottontail was observed in the Mined Lands Wildlife Area (WA) that might have been this species. Previous survey efforts for Swamp Rabbits in Kansas are dated and were unsuccessful (DeSanty-Combes et al. 2002). This species is considered extirpated from southwestern Missouri (Dailey et al. 1993). Further

Table 1. Mammal detections by species and county. Open circles represent additional records for a county and filled circles represent new county records based on existing museum specimen resources. Observations, either historic or present, were not included in detections. Species are listed according to phylogenetic Order and Family, then alphabetically, as reflecting the written species account.

	Barber	Barton	Chase	Chautauqua	Cherokee	Clark	Clay	Coffey	Ellis	Ellsworth	Finney	Ford	Geary	Gray	Greenwood	Harper	Jackson	Jefferson	Jewell	Kingman	Kiowa	Labette	Leavenworth	Lincoln	Linn
Didelphis virginiana					○																				○
Dasypus mexicanus					●																				
Lepus californicus																									
Sylvilagus audubonii																									
Sylvilagus floridanus																			●						
Blarina hylophaga													○												
Cryptotis parvus	○					○																			
Sorex cinereus																									
Scalopus aquaticus			●																						
Procyon lotor					○														○						○
Canis latrans					●		●		○				●	○			○	○			○		○	●	
Vulpes vulpes																									
Lynx rufus																									
Mustela nivalis																									
Taxidea taxus										○															
Glaucomys volans					○																	●			
Ictidomys tridecemlineatus																									
Marmota monax																									
Sciurus niger																									
Xerospermophilus splosoma																									
Castor canadensis																									
Chaetodipus hispidus	○					○							○			○				○					
Dipodomys ordii	○											○								○					

Table 1. (cont.)

	Barber	Barton	Chase	Chautauqua	Cherokee	Clark	Clay	Coffey	Ellis	Ellsworth	Finney	Ford	Geary	Gray	Greenwood	Harper	Jackson	Jefferson	Jewell	Kingman	Kiowa	Labette	Leavenworth	Lincoln	Linn
Perognathus flavescens																				○					
Perognathus flavus						○																			
Zapus hudsonius													●												
Cratogeomys castanops												○													
Geomys bursarius						○																			
Geomys Sp.																									
Microtus ochrogaster												○	●						○						
Microtus pennsylvanicus																									
Microtus pinetorum																									
Neotoma floridana		○		○	●							○	●						●						●
Neotoma micropus	○					○																			
Ondatra zibethicus																									
Onychomys leucogaster	○					○																			
Peromyscus attwateri				○																					
Peromyscus leucopus	○	○		○	○	○		○				○	○		○	○			○	○					○
Peromyscus sonoriensis	○	○		○	○	○						○	○			○				○					
Reithrodontomys fulvescens	○			○	○																				
Reithrodontomys megalotis													○												
Reithrodontomys montanus	○												●												
Sigmodon hispidus	○	○		○	○			○				○	○			○				○					
Synaptomys cooperi																									
Xerospermophilus spilosoma																									
Mus musculus																									
Total species by county	9	4	1	6	10	7	1	2	1	1	0	7	10	1	1	4	1	1	5	5	1	1	1	1	4

Table 1. (cont.)

	Logan	Lyon	Marshall	McPherson	Miami	Montgomery	Morris	Morton	Neosho	Osage	Osborne	Pawnee	Pottawatomie	Pratt	Republic	Reno	Riley	Rush	Scott	Shawnee	Stafford	Thomas	Trego	Wabaunsee	Washington
Didelphis virginiana										●			○				○			○					
Dasypus mexicanus																									
Lepus californicus								○																	
Sylvilagus audubonii								○																	
Sylvilagus floridanus													○				○								
Blarina hylophaga											○		○		○		○			○	○			○	○
Cryptotis parvus								○			○		●						○						
Sorex cinereus															○										
Scalopus aquaticus								○					○	○			○								
Procyon lotor																	○								
Canis latrans		○					●		●	○							○	○				●			
Vulpes vulpes				●									●												
Lynx rufus				○													●							●	
Mustela nivalis				○																					
Taxidea taxus													●				○								
Glaucomys volans																									
Ictidomys tridecemlineatus																	○								
Marmota monax													○				○								
Sciurus niger													○				○								
Xerospermophilus splosoma								○																	
Castor canadensis													○				○								
Chaetodipus hispidus								○									○		○						
Dipodomys ordii								○													○				

Table 1. (cont.)

	Logan	Lyon	Marshall	McPherson	Miami	Montgomery	Morris	Morton	Neosho	Osage	Osborne	Pawnee	Pottawatomie	Pratt	Republic	Reno	Riley	Rush	Scott	Shawnee	Stafford	Thomas	Trego	Wabaunsee	Washington
Perognathus flavescens																									
Perognathus flavus	○																		○						
Zapus hudsonius																	○								
Cratogeomys castanops																									
Geomys bursarius																			○		○				
Geomys Sp.																			●						
Microtus ochrogaster											○	●	○		○		○			○	○			○	○
Microtus pennsylvanicus															○										
Microtus pinetorum													●												
Neotoma floridana		○	○			○				○	○		○				○		○					○	○
Neotoma micropus								○																	
Ondatra zibethicus													●												
Onychomys leucogaster								○											○				○		●
Peromyscus attwateri																									
Peromyscus leucopus		○	○	○	○	○		○		○	○	○	○		○		○		○	○	○		○	○	○
Peromyscus sonoriensis		○	○	○						○	○		○	○	○		○		○	○	○		○	○	○
Reithrodontomys fulvescens														●							●				
Reithrodontomys megalotis					○			○				○			○		○		○	○	○				○
Reithrodontomys montanus										●			○				●		●				○		
Sigmodon hispidus			○	○		○		○			○	○		○			○		●	○	○			○	○
Synaptomys cooperi												●			○										
Xerospermophilus spilosoma								○																	
Mus musculus																	○		●		○			●	
Total species by county	1	4	4	5	2	3	1	12	1	6	7	5	16	4	8	1	22	1	13	7	10	1	4	8	8

survey efforts in swamp/wet habitats of southeastern Kansas that focus on obtaining voucher materials would help assess the conservation status for the most peripheral known populations of this species (Chapman and Feldhamer 1981). Additional sign surveys of latrines on logs and collection of fecal material could enhance DNA detection efforts (Brubaker et al. 2014).

Sylvilagus audubonii
Desert Cottontail

Desert Cottontails and Eastern Cottontails (*S. floridanus*) have broadly overlapping distributions throughout western Kansas, and these species are not easily distinguished based on external morphology. Given that obtaining samples of *Sylvilagus* is relatively easy, either through direct collection or salvage of material, genetic barcode sequencing could be used to confirm the presence and distributional extent of these species based on genomic resources now available from Morton County and elsewhere. Rabbits were abundant in the vicinity of Lake Scott, although samples were not obtained. Hall (1955) recognized two subspecies of *S. audubonii* in Kansas north and south of the Arkansas River. Sampling of additional rabbit specimens from across western Kansas is warranted to develop a baseline for the distribution and genomic background of Desert Cottontail, particularly considering potential for hybridization and emerging disease (e.g., Ringenberg et al. 2024).

Sylvilagus floridanus
Eastern Cottontail

This species was very common at most sites sampled. Eastern Cottontails were collected from sites across three counties, but again, no genetic analyses have been performed. The sample from Jewell County is a new county record. Hall (1955) noted the presence of four subspecies of Eastern Cottontail within Kansas, with divisions roughly coincident with the 98th meridian and 38th parallel. As such, additional samples from museum collections or from further field sampling should be analyzed to assess the validity of subspecies status in these regions.

ORDER EULIPOTYPHLA
Family Soricidae

Blarina brevicauda
Northern Short-tailed Shrew

This species was not detected during recent surveys. These shrews originally were considered to occur broadly throughout northern and eastern Kansas. Subsequent genetic and morphometric analyses recognized most occurrences as *B. hylophaga* (George et al. 1981; Thompson et al. 2011), with *B. brevicauda* being restricted to small portions of northeastern Kansas (George et al. 1986). Subsequently, Pfau et al. (2011) demonstarted that *B. brevicauda* occurred broadly throughout northern Arkansas. Given that the distribution of this species is currently coincident with the eastern border of Kansas (Brant and Orti 2003), it is likely that future specimens will confirm its presence more broadly through easternmost Kansas, which could be used to establish future changes in the known extent of this peripheral distribution.

Blarina hylophaga
Elliot's Short-tailed Shrew

This species was common across the northeastern two thirds of Kansas and samples were recovered from nine counties (Table 1). Through long-term sampling on Konza Prairie, it is evident that this species experiences major population fluctuations and is absent some years, but can reach high abundance in other years (Matlack et al. 2002). Population densities are driven by multiple factors, including precipitation (Kaufman et al. 2012). Given recent locality records outside their presumed range, this species might be experiencing shifting distributions (Fig. 1). Additional monitoring, including use of pitfalls, is warranted, particularly along the known periphery of their range in the southwestern quarter of the state. All samples with genetic information from Kansas belong to a single genetic lineage that is widespread through the range of the species (Fig. 1). Isolated populations in southern Texas are genetically divergent.

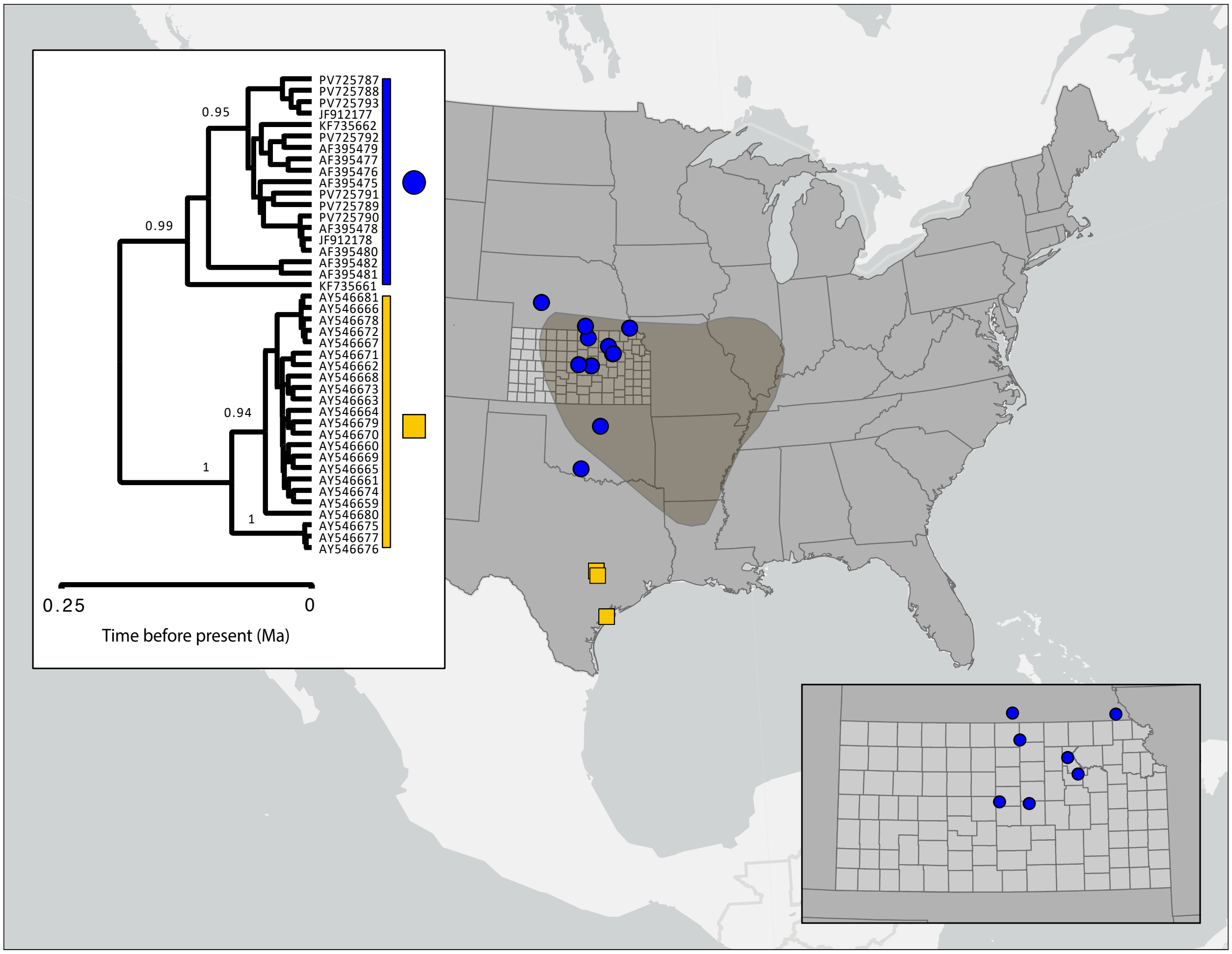

Figure 1. Phylogeographic history of *Blarina hylophaga* based on recent sampling and available sequences from GenBank for the mitochondrial cytochrome *b* gene. The Bayesian phylogeny illustrates lineage relationships with strong posterior probability support. Samples by lineage are georeferenced on the background map in relation to the IUCN range map of the species. The inset map shows individuals with genetic data from Kansas.

Cryptotis parvus
Least shrew

These tiny shrews were relatively common. Samples from Pottawatomie County represent a new county record. All samples collected from Morton County in Cimarron National Grassland were from thick mesic vegetation in proximity to standing pools near the USDA campsite. Least Shrews are difficult to sample with traditional Sherman traps, and trap success is dramatically increased through use of pitfall traps. The species is widespread throughout most available habitat but is rarely encountered. A recent phylogenomic study on Least Shrews (Galfano et al. 2025) showed that what was considered *C. parvus sensu lato* constitutes multiple distinct species, and *C. parvus sensu stricto* consists of three highly distinct lineages based on nuclear data, although not consistent with the two lineages recovered from the mitochondrial data available (Fig. 2). Populations throughout Kansas are closely related to populations from northern New Mexico eastward to the Mississippi River, whereas populations east of the Mississippi form a second distinct lineage, and populations associated with the Ciénega habitats of Bitter Lake National Wildlife Refuge in southeastern New Mexico constitute a highly divergent lineage based on both adaptive and neutral genomic loci (Galfano et al. 2025). No genetic discontinuities were found across Kansas. This species is considered to be expanding its range westward, based on multiple extralimital records in recent years (Fig. 2).

Notiosorex crawfordi
Desert Shrew

Desert Shrews are known only from a single locality in Morton County, specifically at Point of Rocks in the Cimarron National Grassland, recovered as skulls from empty bottles (Dreier et al. 2015). They were not collected during the efforts reported herein, despite both Sherman and snap traps being set at the same locality. Desert Shrews are known to be tolerant of arid conditions and might occur more broadly throughout southwestern-most Kansas (Armstrong and Jones 1972). Pitfall traps can be more effective than traditional traps for sampling this species. As recommended by Dreier et al. (2015), this species warrants consideration as a species in need of conservation within Kansas.

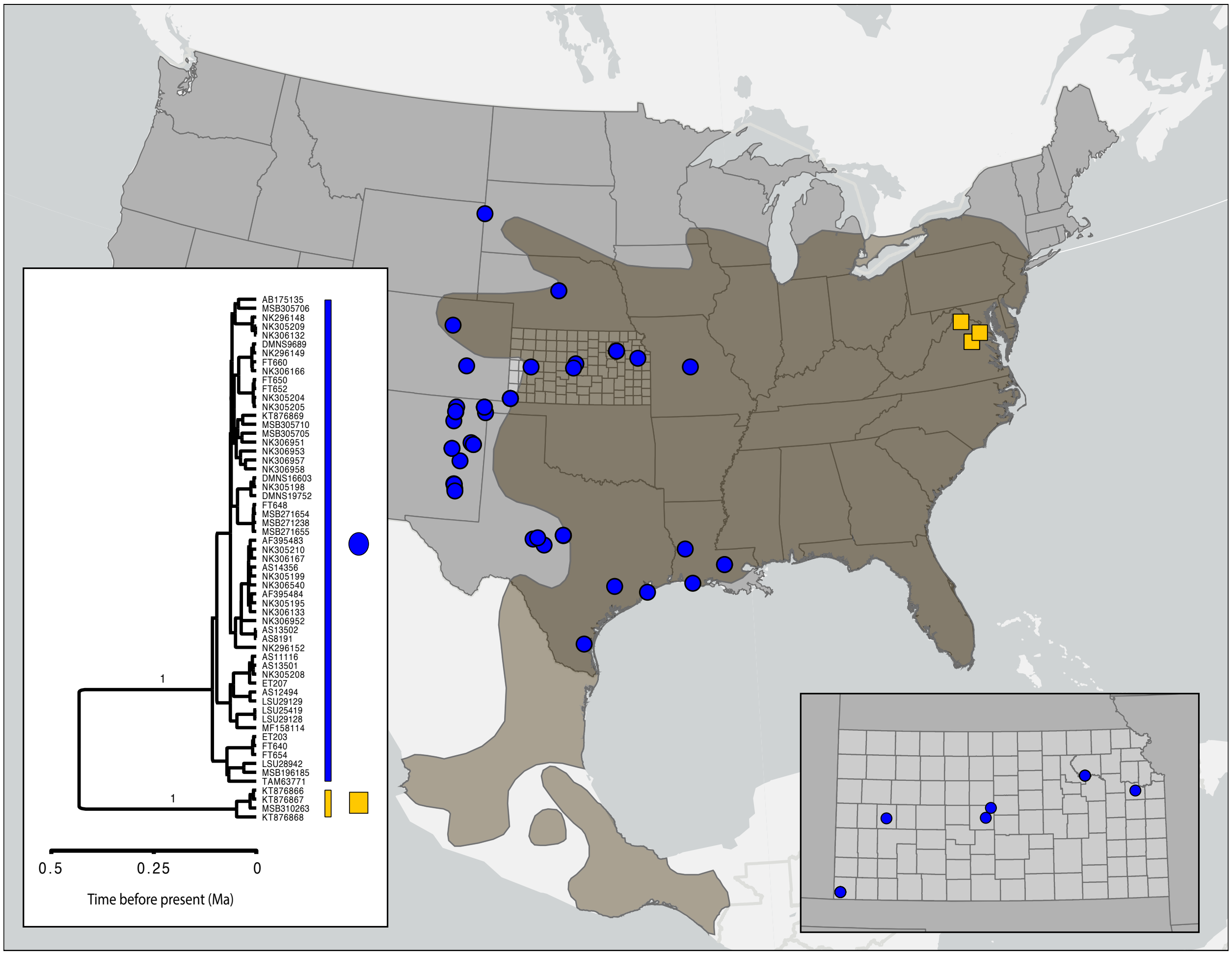

Figure 2. Phylogeographic history of *Cryptotis parvus* based on recent sampling and available sequences from GenBank for the mitochondrial cytochrome *b* gene. The Bayesian phylogeny illustrates lineage relationships with strong posterior probability support. Samples by lineage are georeferenced on the background map in relation to the IUCN range map of the species. The inset map shows individuals with genetic data from Kansas.

Sorex cinereus
Masked Shrew

The detection of Masked Shrews at Jamestown WA reflects the positive influence of wetland management for supporting mesic-associated species, and Masked Shrews have been found only in north-central portions of Kansas. Masked Shrews and Prairie Shrews (*Sorex haydeni*) are sister species and difficult to distinguish, particularly throughout the Great Plains where their distributions might significantly overlap, and considering they are known to hybridize (Brunet et al. 2002; Bartels 2007). Recent evidence based on genomic data suggests that the taxonomy of these species might need to be updated (Hope, unpublished data). Based on mitochondrial DNA evidence, specimens sampled from Republic County were aligned with *S. cinereus* (Fig. 3). The distribution of Masked Shrews in Kansas is considered to be expanding southward (Frey 1992) and additional surveys are warranted, particularly in mesic and marshy habitats, and through the use of pitfall traps. It is possible that Masked Shrew range expansion might also be related to anthropogenic land-use change associated with roadside ditches and irrigation. Two lineages

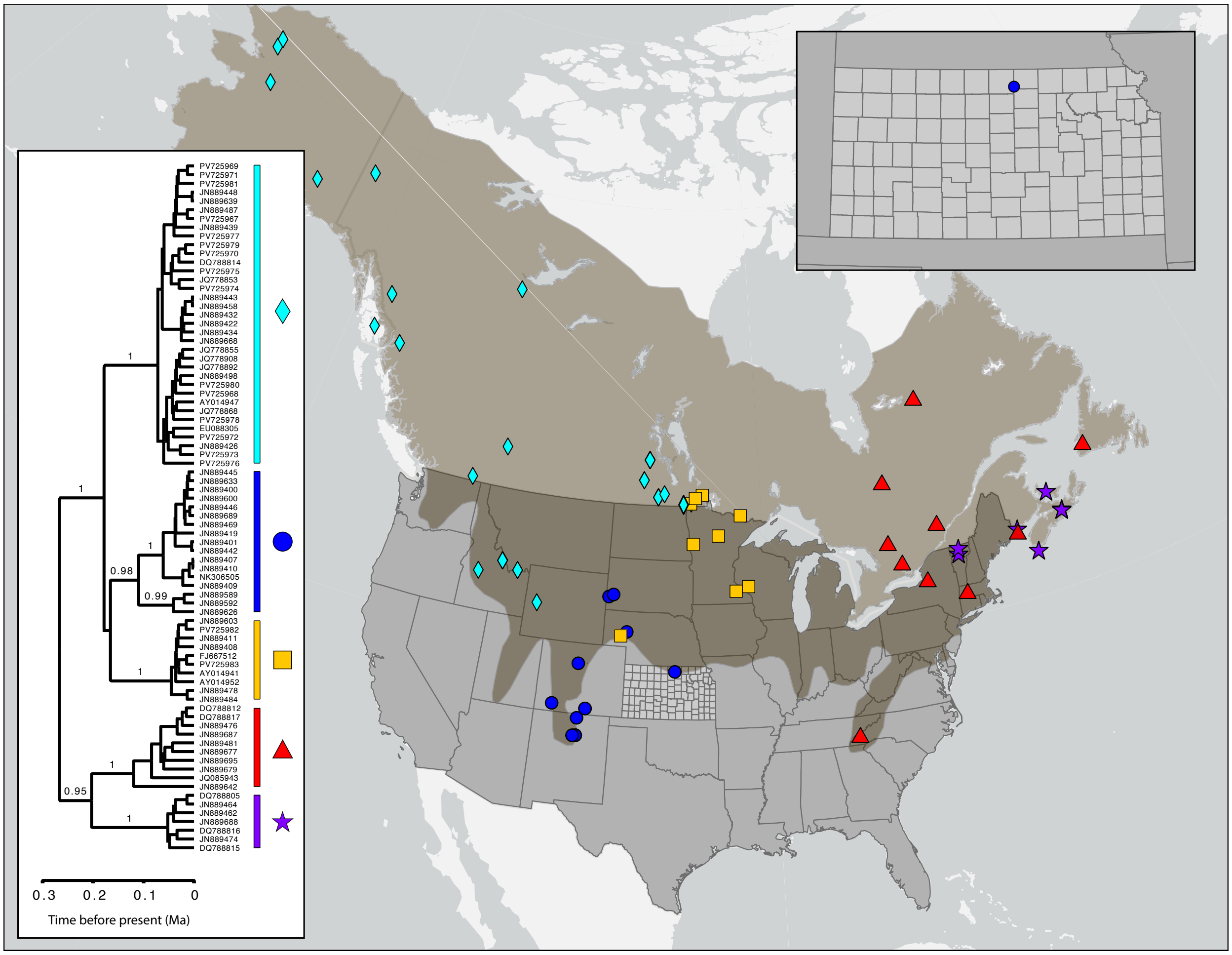

Figure 3. Phylogeographic history of *Sorex cinereus* based on recent sampling and available sequences from GenBank for the mitochondrial cytochrome *b* gene. The Bayesian phylogeny illustrates lineage relationships with strong posterior probability support. Samples by lineage are georeferenced on the background map in relation to the IUCN range map of the species. The inset map shows individuals with genetic data from Kansas.

within Masked Shrews are distributed across grassland habitats of the Great Plains. The sample sequenced from Kansas aligns with samples from throughout the Southern Rocky Mountains of Colorado and New Mexico and the Black Hills of South Dakota (Fig. 3)

Sorex haydeni
Prairie Shrew

This shrew was not sampled. Based on recent genetic work, *Sorex* shrews detected from the Lower Republican drainage were Masked Shrews and not Prairie Shrews. It is possible that Prairie Shrews do not occur within Kansas, and recent genomic surveys of long-tailed shrews from across the Great Plains have not yielded confirmation of this species (Hope et al. unpublished data). Considering their close relationship with Masked Shrews (Hope et al. 2012) and their ability to hybridize (Brunet et al. 2002), additional targeted sampling of *Sorex* across the Great Plains states is a priority to locate persistent populations of Prairie Shrews and develop adaptive conservation management.

Family Talpidae
Scalopus aquaticus
Eastern Mole

The westernmost record of Eastern Moles within Kansas are roughly coincident with the western state line in Cheyenne (northwestern) and Morton (southwestern) counties, and these constitute peripheral populations for the species (Yates and Schmidly 1978). The sample obtained from Cimarron National Grassland confirms their persistence in this area, at least as associated with the campground, which is located near permanent water sources. Samples were recovered from four additional counties, including a new county record for Chase County. Moles are limited to deep, damp soils where earthworms and other soil invertebrate food resources can be found in relative abundance. Eastern Moles likely can be found more broadly than their recognized distribution within Kansas given appropriate soil conditions along river drainages, although existing peripheral populations also could be more highly isolated and restricted to areas in proximity to perennial water in the most arid regions. Further surveys in the northwestern region of Kansas are warranted to confirm the persistence of moles associated with the Arikaree Breaks and Upper Republican drainage. The scant genetic data available suggest a single lineage across much of the range, including Kansas (Fig. 4).

ORDER CARNIVORA
Family Procyonidae
Procyon lotor
Northern Raccoon

Raccoons were sampled with Havahart traps at four sites through northern and eastern Kansas near open water. This species was abundant everywhere in proximity to water, and roadkill were extremely common. Despite their widespread occurrence throughout Kansas, this medium-sized species is relatively poorly represented in museum collections and greater geographic coverage of specimens is warranted. Little genetic work has been conducted for this species. A recent study found that there was little risk for Northern Raccoons to contract chronic wasting disease (CWD) from roadkill deer in Wisconsin (Jennelle et al. 2009), but they have been implicated in contributing to the spread of CWD prions in Mississippi (Huang et al. 2025).

Family Canidae
Canis latrans
Coyote

A single juvenile Coyote was collected as roadkill from Cherokee County, a new county record. Coyotes were seen or heard at multiple sites throughout Kansas and are extremely common. This species is highly under-represented in museums and additional specimens should be sampled and made available in museum collections. An additional 250 specimens of *Canis latrans* (skulls, tissues, and parasite data) were collected by the Kansas State Department of Veterinary Medicine (KSDVM) through trapper networks from across the Great Plains (including ~50 samples from across Kansas) for research on infection with *Echincoccus* tapeworms. Those skulls and tissues were deposited in the Kansas State Biorepository in 2024, along with infection data. Although no evidence has yet linked this species to infection with CWD (e.g., Jennelle et al. 2009), the prions of this disease have been shown to pass through Coyotes in feces following scavenging, and as such they might contribute to disease spread

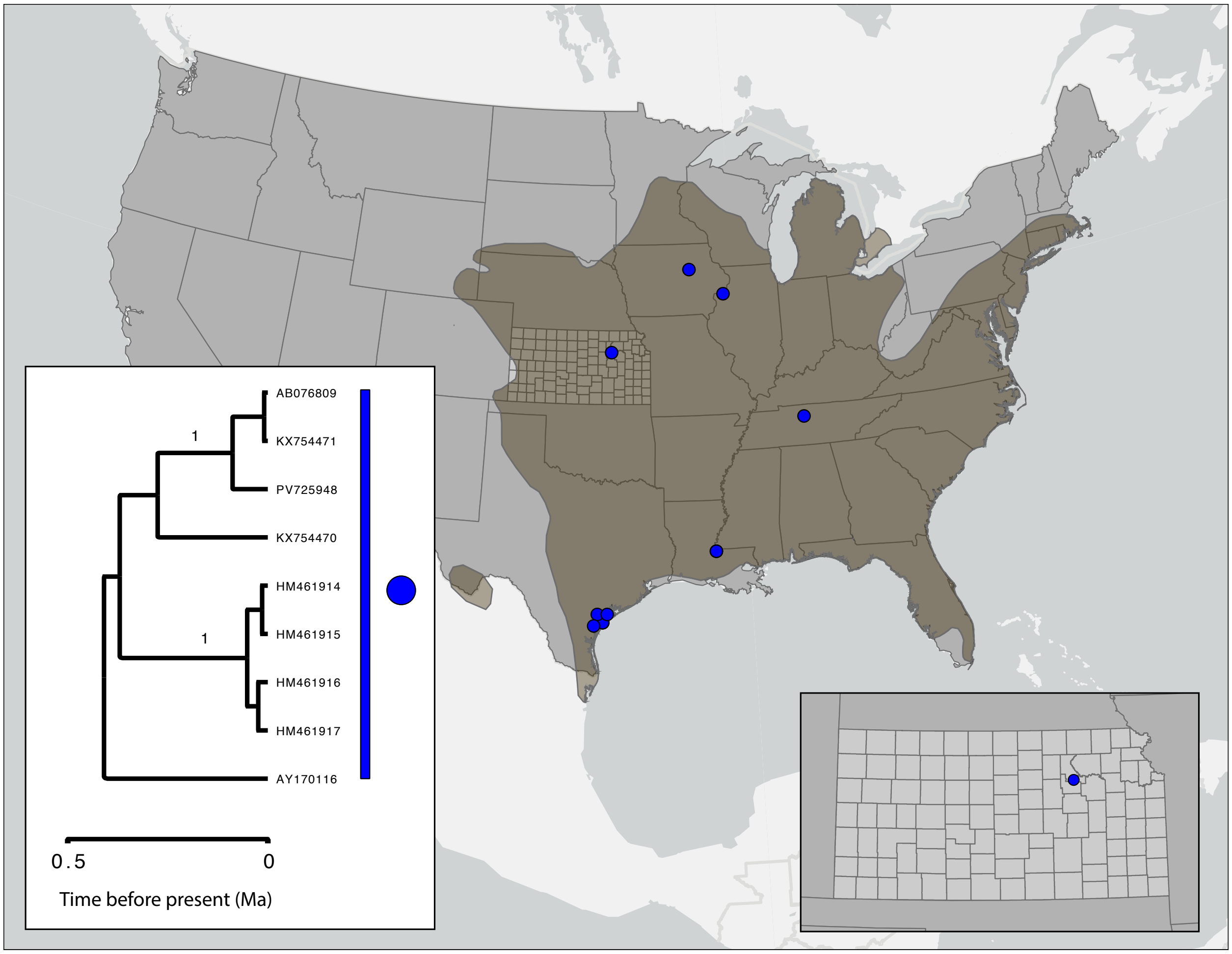

Figure 4. Phylogeographic history of *Scalopus aquaticus* based on recent sampling and available sequences from GenBank for the mitochondrial cytochrome *b* gene. The Bayesian phylogeny illustrates lineage relationships with strong posterior probability support. Samples by lineage are georeferenced on the background map in relation to the IUCN range map of the species. The inset map shows individuals with genetic data from Kansas.

(Nichols et al. 2015). Samples through time also could facilitate epidemiology of CWD spread. Coyotes also are prone to hybridization with other canid species, but this is still poorly monitored through resources including genetic sampling or GIS modeling (e.g., see Thornton and Murray 2014).

Urocyon cinereoargenteus
Northern Gray Fox

No specimens of Northern Gray Fox were detected during the surveys. However, while retrieving a roadkill Coyote specimen from Cherokee County, a law enforcement officer stopped to inspect our activities and relayed that he had seen several Northern Gray Fox in the vicinity of Baxter Springs along roads at night.

Vulpes vulpes
Red Fox

Two roadkill specimens of Red Fox each represent new records for Pottawatomie and McPherson counties. This species is widespread across Kansas and common; however, the species is difficult to sample with live traps, and although they can be easily monitored with wildlife cameras (Kays et al. 2022), few studies of canids or other meso-carnivores have been conducted within Kansas (e.g., Wait et al. 2018;

Werdel et al. 2023; Benson et al. 2024; Taraporevala et al. 2025).

Family Felidae
Lynx rufus
Bobcat

Three roadkill Bobcat specimens were collected from McPherson, Wabaunsee, and Riley counties, the latter two representing new county records. This species is common across Kansas and still collected in abundance through fur trapping, although rarely seen. Two genetic lineages of Bobcat are distributed across Kansas, one widespread and the other restricted to the southwestern corner (Reding et al. 2012).

Family Mustelidae
Mustela nivalis
Least Weasel

A single specimen of Least Weasel from the vicinity of Hutchinson, Reno County, was obtained. This constitutes one of a growing number of detections at the southern limits of the Least Weasel's range in the Great Plains and supports recent research suggesting this is one of few species with a distribution expanding southward due to multiple potential factors (Frey 1992; Campbell et al. 2025). Despite recent recorded occurrences, additional studies on Least Weasel and other small weasel species occurring across North America are warranted, especially considering perceived declines in this group (Jachowski et al. 2021)

Taxidea taxus
American Badger

Several badger specimens were recovered as roadkill through the project duration, one from Ellsworth County and additional specimens from Riley and Pottawatomie counties, the latter of which is a new county record. Additional observations of individuals included the south end of the Konza LTER site on the border of Riley and Geary counties. This species is common across Kansas but elusive, with two putative subspecies co-occurring across much of the state (Long 1973).

ORDER RODENTIA
Family Sciuridae
Cynomys ludovicianus
Black-tailed Prairie Dog (SGCN)

Prairie dogs were not sampled, although they were observed in small numbers on roadsides between Colby and Scott City and farther south between Dodge City and Sublette, mostly in vacant lots near residences. At present, very little non-agricultural habitat remains across their historic range in Kansas. Black-tailed Prairie Dogs have experienced major declines through recent decades due to loss of habitat, eradication efforts (e.g., Karl 1986), and increasing incidence of disease, especially plague (e.g., Cully et al. 2000). Black-tailed Prairie Dogs in Kansas are similarly impacted by habitat loss and eradication, although small colonies persist. Given their ecological value as a keystone species, additional samples would allow for continued monitoring of populations, particularly through disease testing and analysis of disease vectors such as fleas. Such efforts also would enhance renewed interest in reintroductions of Black-footed Ferrets (*Mustela nigripes*) within Kansas (e.g., Jachowski and Lockhart 2009), where the last individual ferret from a native population was recovered in 1957 from Sheridan County (specimen housed at KSB – KSB:Mamm:2031).

Glaucomys volans
Southern Flying Squirrel (SGCN/SINC)

These squirrels are elusive in Kansas and difficult to catch in Sherman live traps, but they are conducive to sampling via habituated nest boxes within oak woodlands during winter (Bernhardt 2025). A single specimen was sampled using a Victor rat trap from Shoal Creek WA in Cherokee County, which is the first specimen collected from this county in more than six decades. An additional two samples (based on ear punches) were included in genetic analysis from a radio-tracking project being conducted at Grand Osage WA, and subsequently roughly a dozen more individuals from this WA were sampled for ear punch tissue (Bernhardt 2025). Southern Flying Squirrels are found only within eastern forested habitats of Kansas. Very few specimens exist within museum collections, most from Shawnee, Wyandotte, and Leavenworth counties in the northeast and Crawford and Cherokee counties in the southeast. However, recent trail camera surveys throughout eastern Kansas have revealed a much broader distribution and relatively common occurrence across the distribution of large and connected stands of mast-bearing hardwood in eastern Kansas (Lydia Robbins, unpublished data). Preliminary genetic analysis showed that the Cherokee County specimen is closely related to samples from farther south in Texas and western Arkansas, but collectively are divergent from all samples, including from Grand Osage WA and farther east, including multiple sequences from Missouri (Fig. 5). Further sampling and deeper genomic analyses are currently in progress (Jackie Olexa, unpublished data) from throughout this species' range to establish the distribution of genomic diversity and demography among Kansas populations.

Ictidomys tridecemlineatus
Thirteen-lined Ground Squirrel

Only three specimens of Thirteen-lined Ground Squirrel were sampled from tallgrass prairie habitat in Riley County, although these are widespread through Kansas and can be found in a variety of habitats. Plugged burrows that were likely of this species were

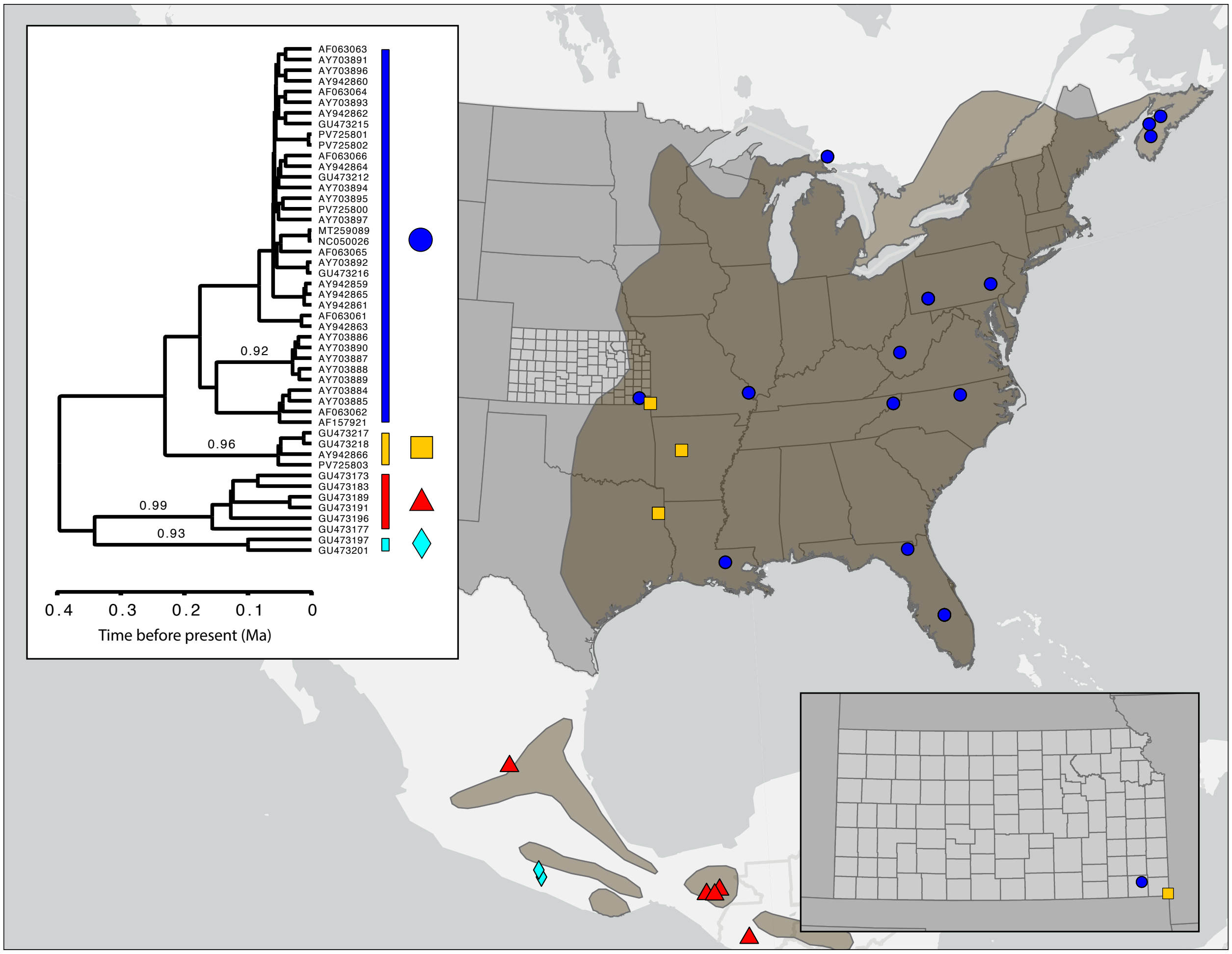

Figure 5. Phylogeographic history of *Glaucomys volans* based on recent sampling and available sequences from GenBank for the mitochondrial cytochrome *b* gene. The Bayesian phylogeny illustrates lineage relationships with strong posterior probability support. Samples by lineage are georeferenced on the background map in relation to the IUCN range map of the species. The inset map shows individuals with genetic data from Kansas.

observed along the upper Saline River in Trego County during the winter hibernation period. Additional survey efforts might clarify whether this species is currently experiencing decline. The genetic evidence based on new samples here and from Thompson et al. (2015) suggests that all Thirteen-lined Ground Squirrels within Kansas are closely related and constitute a single lineage that extends from central Texas northward across the extent of the Great Plains (Fig. 6). In Texas, *I. tridecemlineatus* experiences contact and periodic gene flow with *I. parvidens,* the sister taxon (Thompson et al. 2015).

Marmota monax
Woodchuck

A single young Woodchuck was collected from Pottawatomie County and a single adult from Riley County. This species is widespread and common through woodland and open habitats of eastern Kansas, particularly along edge habitats between meadow and woodland. Little is known of the distribution of genetic diversity within this species, but it is clearly spreading westward through time, presumably in accordance with progressive woody encroachment and human land-use (Roehrs and Genoways 2004).

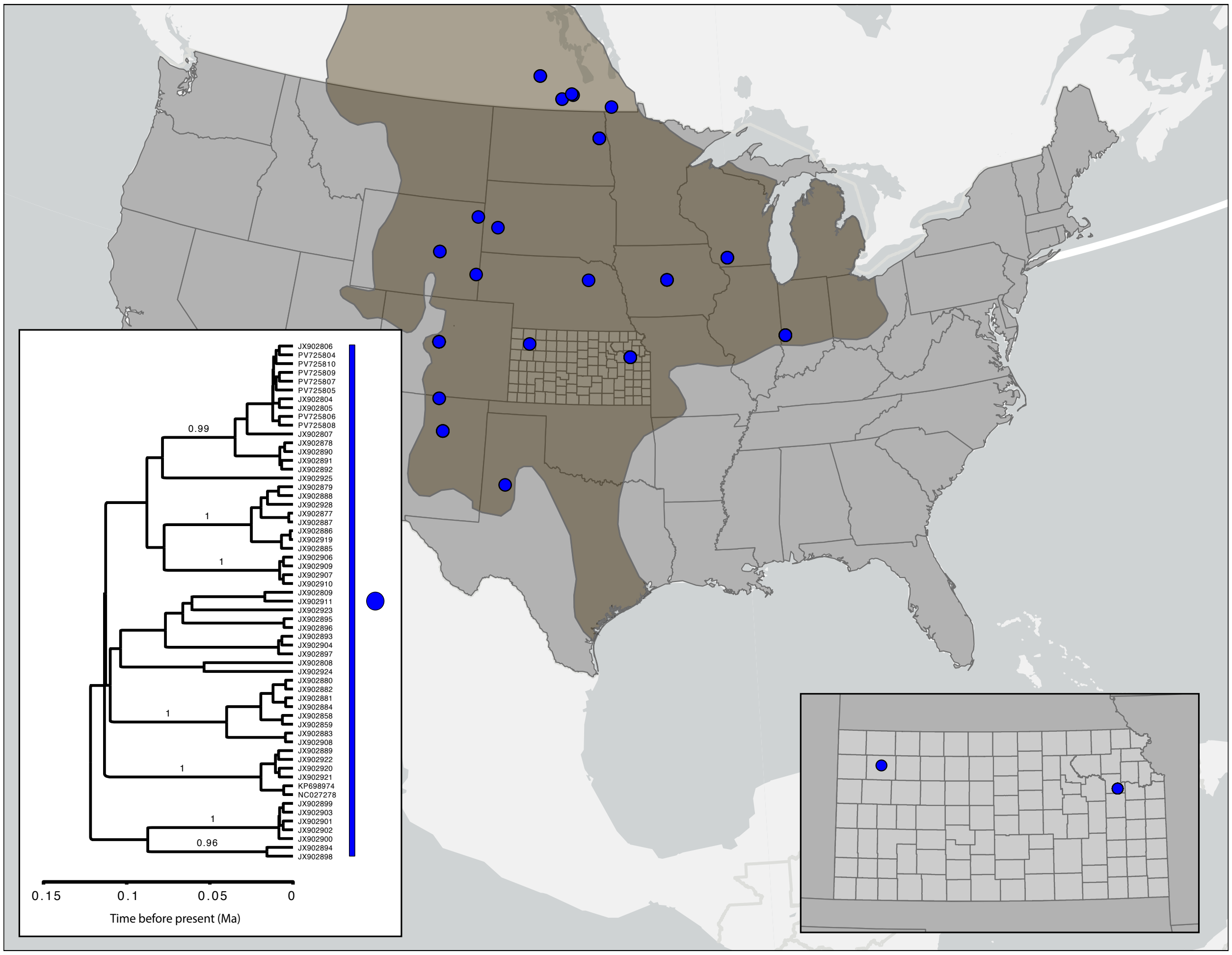

Figure 6. Phylogeographic history of *Ictidomys tridecemlineatus* based on recent sampling and available sequences from GenBank for the mitochondrial cytochrome *b* gene. The Bayesian phylogeny illustrates lineage relationships with strong posterior probability support. Samples by lineage are georeferenced on the background map in relation to the IUCN range map of the species. The inset map shows individuals with genetic data from Kansas.

Poliocitellus franklinii
Franklin's Ground Squirrel (SGCN/SINC)

The last verifiable specimen of Franklin's Ground Squirrel in Kansas dates to the late 1980's. Although this species is considered common farther north through the Great Plains and upper midwest (e.g., they were observed commonly in Nebraska at the Omaha zoo in 2023), it is possibly extirpated from Kansas. Any additional surveys for this species should focus on previous collection localities and through permissions to survey on private lands.

Sciurus carolinensis
Eastern Gray Squirrel

Eastern Gray Squirrels were not sampled, but a single observation was made of an individual on the Kansas State University campus, where they were not considered to occur. In summer 2023, a single Eastern Gray Squirrel was also sighted in the city park of Meade, Kansas, well west of their known distribution. It is possible that Eastern Gray Squirrel might be expanding westward within Kansas with forest expansion and possibly facilitated by human transport. Two subspecies are recognized, associated with the southeastern corner and with the remainder of eastern Kansas. This should be assessed from a genetic perspective.

Sciurus niger
Fox Squirrel

Fox Squirrels were abundant throughout their range within Kansas, often strongly associated with urban centers farther west. Multiple samples were collected as roadkill from Pottawatomie and Riley counties.

Tamias striatus
Eastern Chipmunk

Eastern Chipmunks were not sampled. The distribution in Kansas is considered to be limited to the extreme eastern edge. Further survey efforts in wooded areas of eastern Kansas should be conducted to establish if this species is expanding westward to occupy available hardwood forest or other woody habitats.

Xerospermophilus spilosoma
Spotted Ground Squirrel (SGCN)

Two specimens of Spotted Ground Squirrel from Morton County were sampled, confirming its continued presence in the southwestern corner of Kansas. The broader distribution of this species is closely associated with river floodplain sandy soil habitats including the Cimarron, Arkansas, Smoky Hill, and Upper Republican drainages on the westernmost edge of the state within the zone of short-grass prairie. Additional survey efforts in these regions will be critical to determine if this species persists and if it is experiencing expansion or decline. Little is known of genetic structure within *Xerospermophilus spilosoma,* although based on morphology, specimens from northwestern and southwestern populations in Kansas represent distinct subspecies. There appear to be multiple distinct lineages based on the few available sequences, and Kansas samples are associated with a lineage including samples from New Mexico, where the species is common in semiarid grassland and scrub (Fig. 7). Additional samples would allow the distribution of genetic diversity to be refined further.

Family Castoridae
Castor canadensis
American Beaver

Two American Beaver specimens from Riley and Pottawatomie counties were salvaged from furbearer trapping efforts during the survey period, although most existing samples of this species within museum collections are many decades old. Furbearing species are often underrepresented in collections. As such, little can be said of their genetic population trends, particularly from the southern half of the state. Hall (1955) suggested their presence throughout Kansas, and *Castor canadensis* are considered abundant along the Kansas River corridor.

Family Heteromyidae
Chaetodipus hispidus
Hispid Pocket Mouse

This species was sampled from eight counties and was consistently recovered from long-term sampling

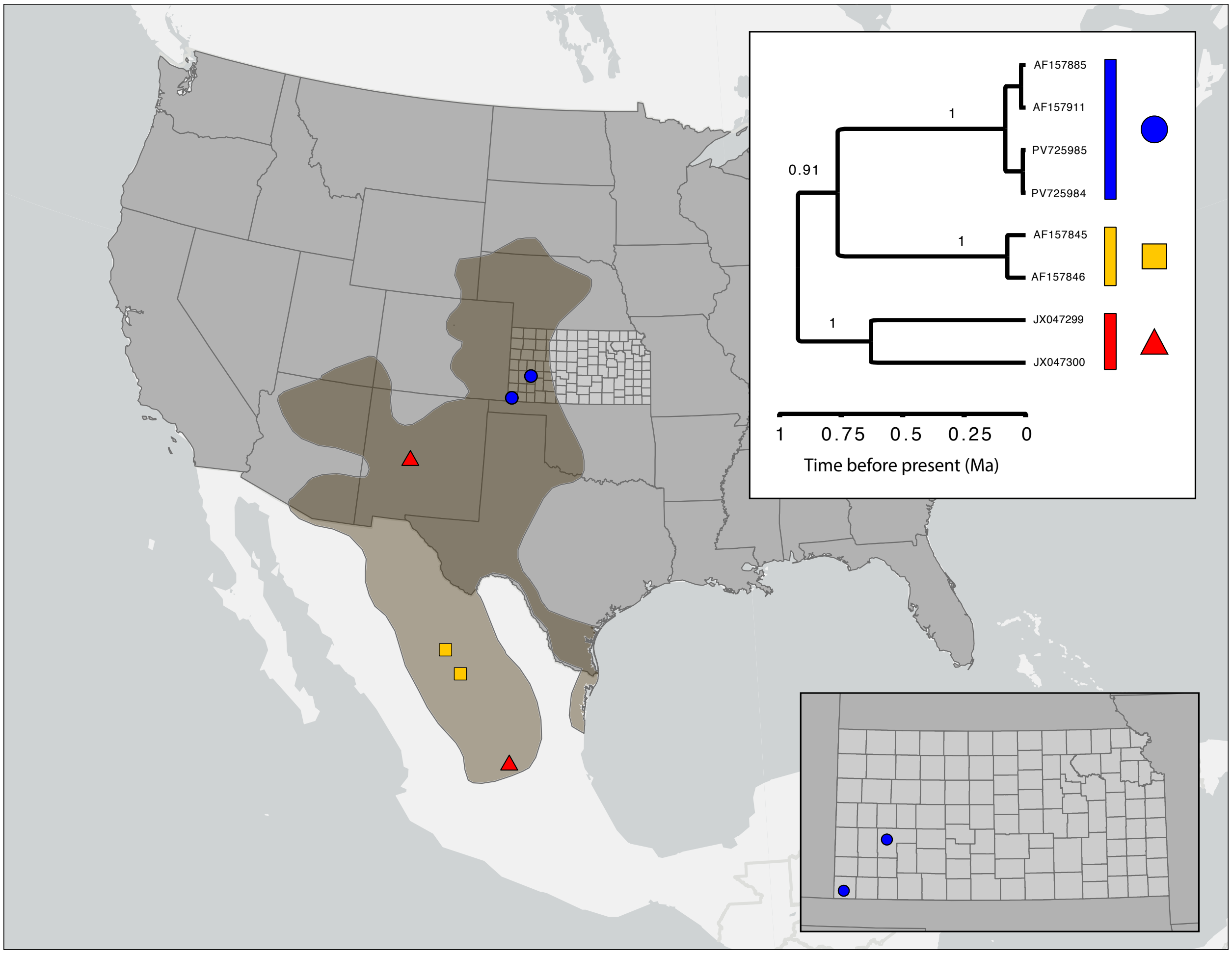

Figure 7. Phylogeographic history of *Xerospermophilus spilosoma* based on recent sampling and available sequences from GenBank for the mitochondrial cytochrome *b* gene. The Bayesian phylogeny illustrates lineage relationships with strong posterior probability support. Samples by lineage are georeferenced on the background map in relation to the IUCN range map of the species. The inset map shows individuals with genetic data from Kansas.

transects on the Konza LTER site within open tallgrass prairie, particularly in areas with shallow rocky soil, but never at high abundance. The Hispid Pocket Mouse is broadly distributed across Kansas coincident with the extent of prairie habitats. It is locally rare. Although two subspecies have been recognized within Kansas, a study of the distribution of genetic diversity by Andersen and Light (2012) clearly showed that subspecies distributions based on morphology were not supported by genetic evidence. All specimens of *Chaetodipus hispidus* from the Great Plains belong to a single lineage, including those that we collected (Fig. 8). This species is seemingly stable, although Paulson (1988) stated that it required native prairie habitats and as such might experience further decline as prairies become increasingly fragmented.

Dipodomys ordii
Ord's Kangaroo Rat

This species was sampled from five counties in south-central and southwestern Kansas and is common throughout this region. In Morton County, Ord's Kangaroo Rats were sampled within sand-sage and arid grassland habitats. This species is associated with sandy soils, often along river floodplains and adjacent

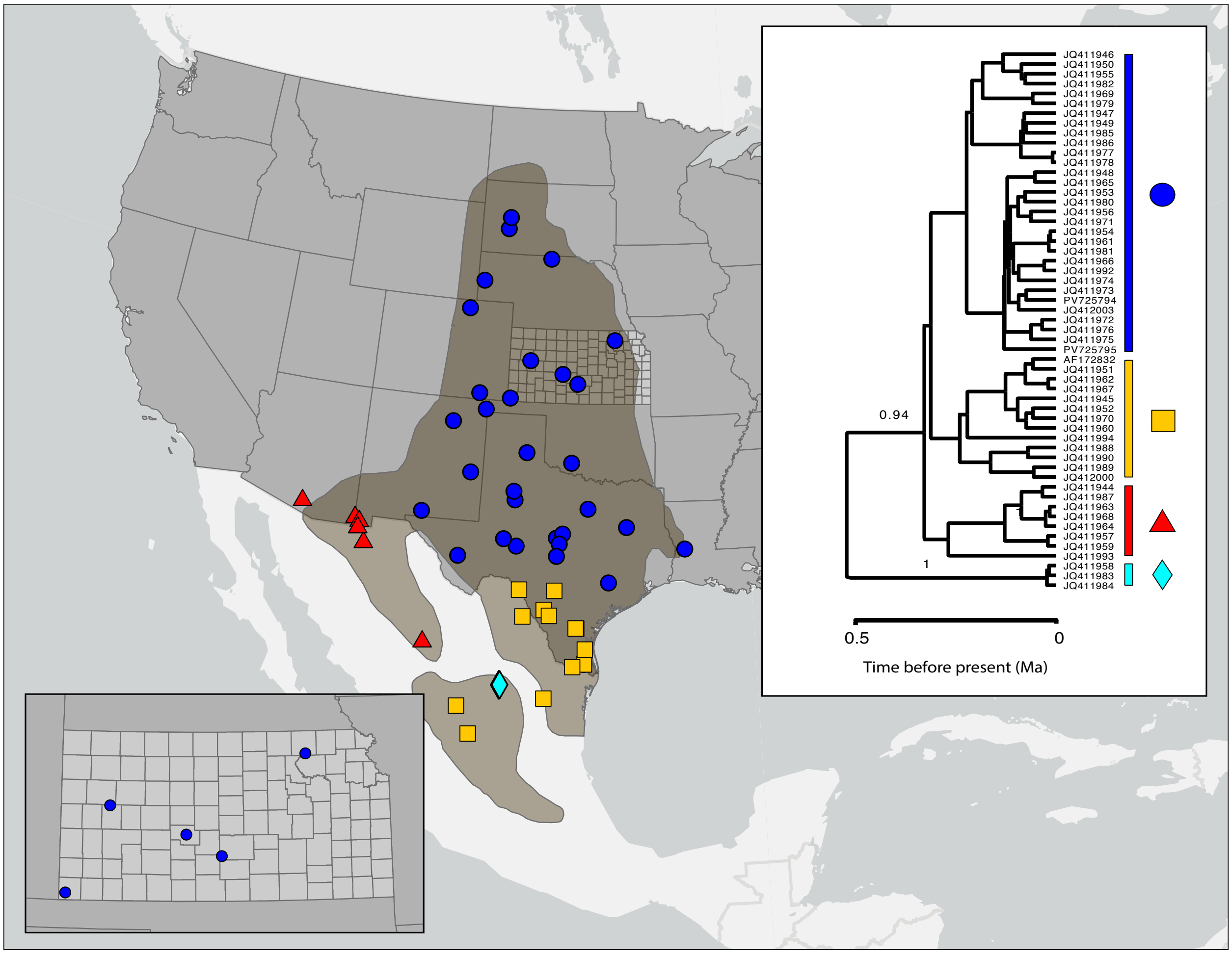

Figure 8. Phylogeographic history of *Chaetodipus hispidus* based on recent sampling and available sequences from GenBank for the mitochondrial cytochrome *b* gene. The Bayesian phylogeny illustrates lineage relationships with strong posterior probability support. Samples by lineage are georeferenced on the background map in relation to the IUCN range map of the species. The inset map shows individuals with genetic data from Kansas.

habitats, although they have been sampled within more upland and loamy soil elsewhere farther north (Kaufman and Kaufman 2015). There are minimally two distinct lineages within this species, but available genetic data is too sparse for accurate delineation of their distributions (Fig. 9). Available evidence suggests that samples from Kansas all stem from a single lineage.

Perognathus flavescens
Plains Pocket Mouse

The Plains Pocket Mouse was detected only from Kingman County and McPherson County at Maxwell Wildlife Area (the latter a new county record, but with no specimen collected), and most existing records are very old. *Perognathus flavescens* is considered to have two subspecies within Kansas in the western and central thirds of the state distributed within prairie habitats, but few samples exist in collections to qualify this. Targeted surveys for this species at previous localities of record and elsewhere are warranted, and all recent evidence suggests this species is now rare. In Nebraska, it has been found to be negatively influenced by loss of native habitat (Geluso and Wright 2012), and likely this holds true for Kansas.

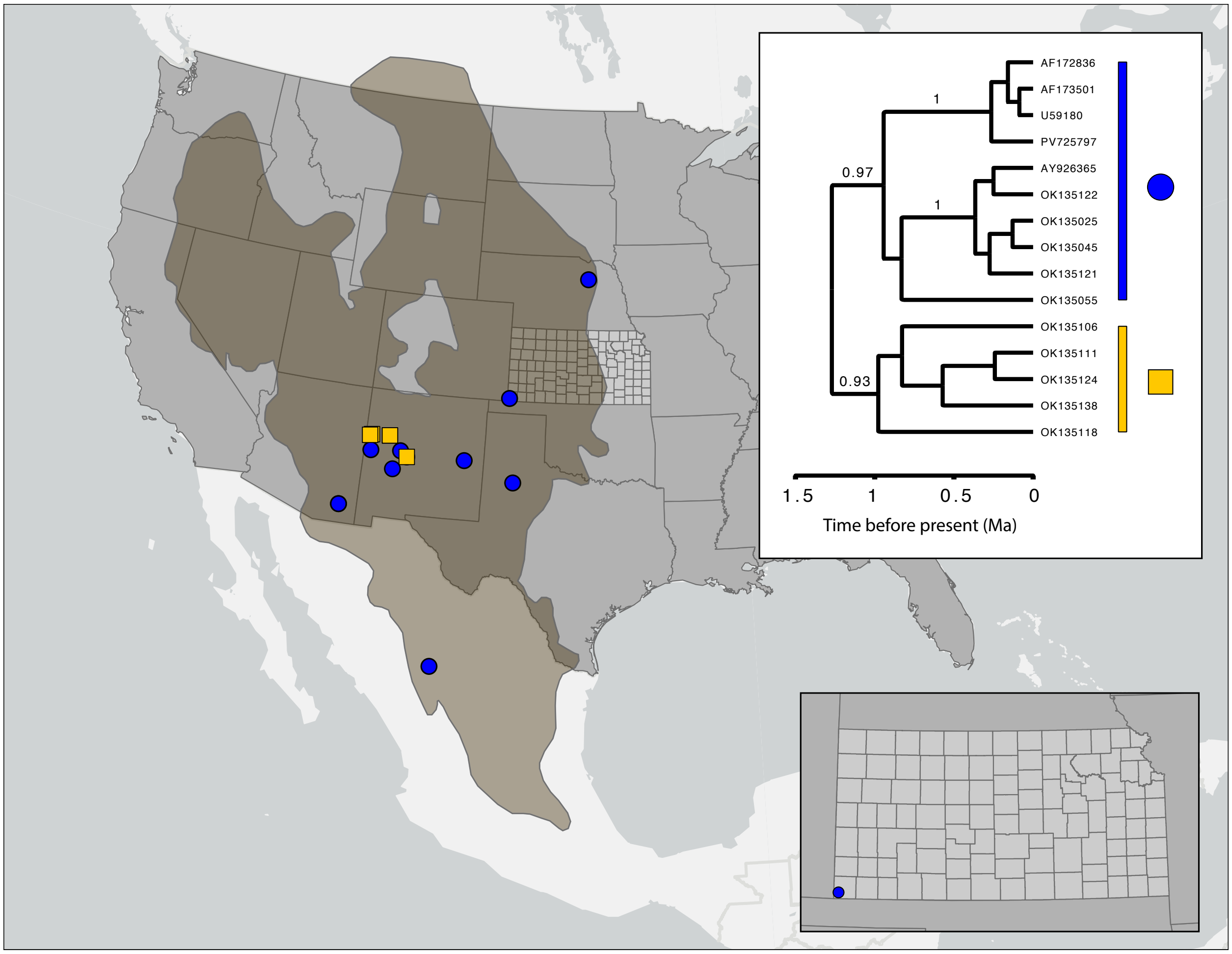

Figure 9. Phylogeographic history of *Dipodomys ordii* based on recent sampling and available sequences from GenBank for the mitochondrial cytochrome *b* gene. The Bayesian phylogeny illustrates lineage relationships with strong posterior probability support. Samples by lineage are georeferenced on the background map in relation to the IUCN range map of the species. The inset map shows individuals with genetic data from Kansas.

Perognathus flavus
Silky Pocket Mouse

Silky Pocket Mice were sampled from Clark, Logan, and Scott counties and are moderately common. Previous genetic analyses showed presence of both *P. flavus* and the sister taxon, *Perognathus merriami*, to occur in proximity in western Kansas and this zone of sympatry continues south through eastern New Mexico and western Texas (Neiswenter and Riddle 2010). *Perognathus merriami* is not currently documented from Kansas, despite its likely occurrence. Existing tissue samples and additional sampling of Silky Pocket Mice from throughout western Kansas will help to formally recognize *P. merriami* within Kansas for management considerations, and clarify how both species are distributed, spatially and ecologically.

Family Zapodidae
Zapus hudsonius
Meadow Jumping Mouse

Two specimens of *Zapus hudsonius* were collected from the Konza LTER site within mesic drainages running through tallgrass prairie, representing a new county record for Geary County, although other individuals were sampled at this site previously based on LTER mark-recapture data (Kaufman and Kaufman

2010). The Meadow Jumping Mouse is widespread across much of North America associated with mesic meadow and streamside habitats and mesic woodland habitats. It is considered to be expanding southward (Frey 1992). Although *Zapus hudsonius* can become extremely abundant in high-quality habitat, they are inherently rare within Kansas (Whitaker 1972). Additional field surveys through eastern portions of Kansas are warranted, given much of its known range in the state was not well sampled. The genetic background of jumping mice in Kansas is unknown.

Family Geomyidae

Cratogeomys castanops

Yellow-faced Pocket Gopher (SGCN)

A single specimen of this gopher was collected from the vicinity of Hain State Fishing Lake in Ford County. This species is exclusively associated with the greater Arkansas River drainage in southwestern counties of Kansas, particularly Ford, Hodgeman, Finney, and Hamilton. Most historic records occur along roadside easements, likely reflecting the ease of finding gopher mounds along mowed verge habitat (Hoffman and Choate 2008). However, most records of Yellow-faced Pocket Gophers are decades old. Extensive road surveys were conducted through this area to locate modern gopher sign but virtually none were found. Conversations with local ranchers suggested that poison had recently been used to eradicate gophers near agricultural fields through much of the region. Given very limited public land availability in this region, access to private lands will be critical to better establish the status of Yellow-faced Pocket Gophers in Kansas. Gopher mounds were found along the road adjacent to Hain State Fishing Lake, as well as around the northeastern corner of the lake. Genetic analysis of this specimen with respect to other available specimens with sequence information reflected two distinct genetic lineages (Hafner et al. 2008), and Kansas specimens belong to a northern lineage distributed through western Texas and eastern New Mexico (Fig. 10). As such, Kansas populations represent the most peripheral populations of this species and are seemingly at higher risk of extirpation than was determined based on previous surveys (Hoffman and Choate 2008). Given that gophers are inherently poor dispersers, future persistence of this species within Kansas will depend on maintaining local populations. Additionally, although this species and Plains Pocket Gophers (*Geomys bursarius*) are not thought to compete for resources, Yellow-faced Pocket Gophers are considered intolerant of human induced conversion of land use from native short-grass prairie (Birney et al. 1970; Davidow-Henry et al. 1989; Hoffman et al. 2007). Too few samples exist to assess demographic change or relative genetic diversity.

Geomys bursarius

Plains Pocket Gopher

This species was sampled from the southern and western portions of Kansas from three counties. Unlike *Cratogeomys*, *Geomys* are relatively common throughout much of Kansas based on evidence of gopher mounds at most sites visited. *Geomys bursarius* is a true Great Plains endemic species, broadly distributed through prairie and the verges of woody habitats. Gophers taken at Lake Scott were from road easements on both the north and south side of the lake. Abundant evidence of gopher activity was seen in this area. Genetic sequence data from these individuals were highly divergent from *Geomys bursarius sensu stricto* (Fig. 11). Due primarily to very low rates of dispersal among pocket gophers, their evolutionary history is complex, leading to lineages that often are morphologically indistinguishable but genetically divergent. Hall (1955) recognized five subspecies of Plains Pocket Gophers from Kansas. Subsequent to these morphological designations, a genetic analysis by Sudman et al. (2006) recognized gophers from westernmost Kansas as *Geomys jugossicularis*, and gophers from farther north in Nebraska as *Geomys lutescens*. This was supported by Genoways et al. (2008), relegating the distribution of *G. bursarius* within Kansas to a swath from south-central to northeast, as reflected by Connior (2011). However, a subsequent genetic assessment by Chambers et al. (2009) provided evidence that the distributional break between *G. bursarius* and *G. jugossicularis* was roughly coincident with Scott County. The specimens collected at Lake Scott are divergent from all described species, including *G. bursarius*, *G. lutescens*, *G. jugossicularis*, and *G. texensis*, the latter species being recently described from central Texas (Fig. 11; Cramer and Cameron 2001). These other taxa render the identity of Lake Scott specimens uncertain

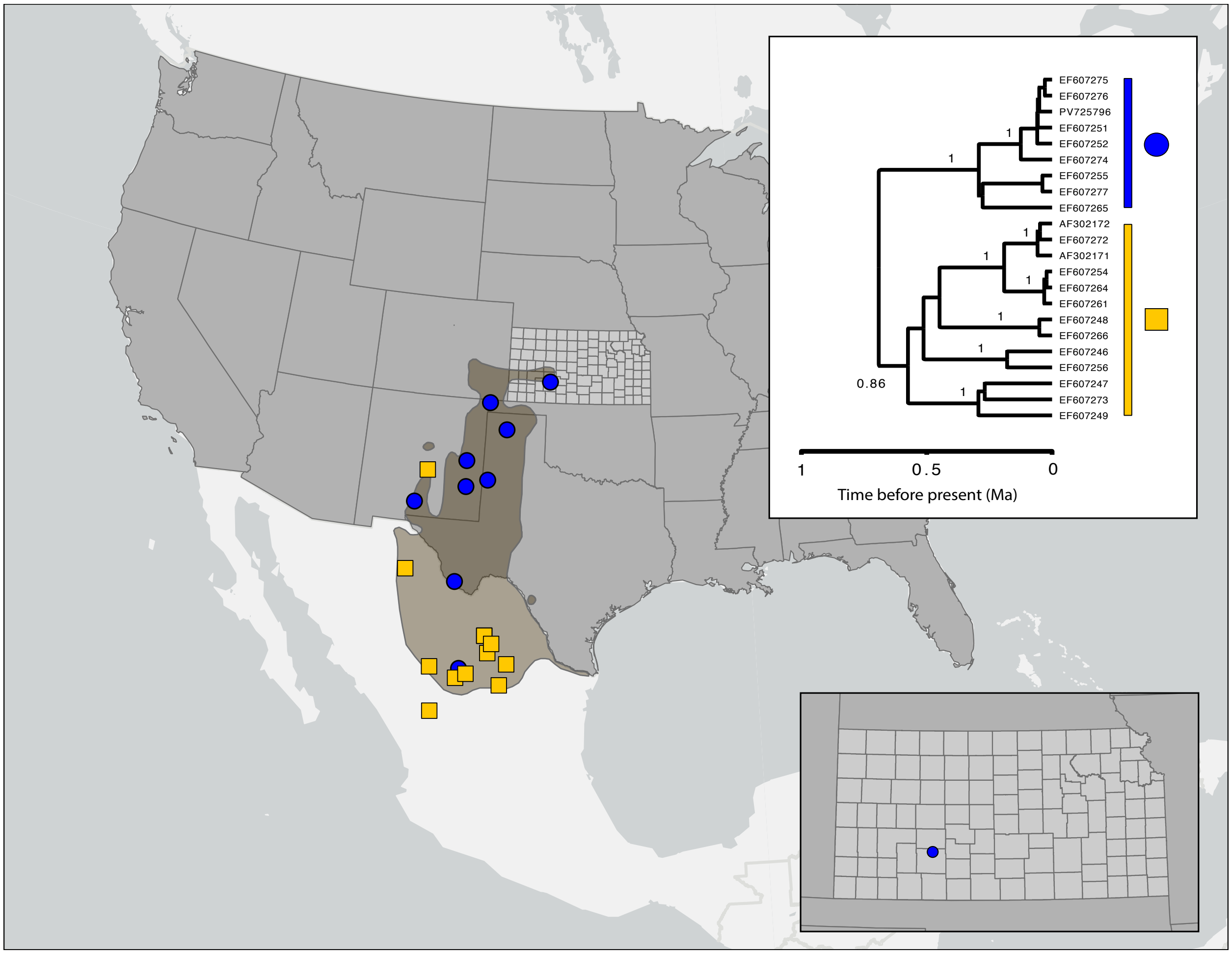

Figure 10. Phylogeographic history of *Cratogeomys castanops* based on recent sampling and available sequences from GenBank for the mitochondrial cytochrome b gene. The Bayesian phylogeny illustrates lineage relationships with strong posterior probability support. Samples by lineage are georeferenced on the background map in relation to the IUCN range map of the species. The inset map shows individuals with genetic data from Kansas.

and possibly indicate the presence of a new species of pocket gopher in Kansas that is locally endemic. Attempts to catch gophers from Morton County were unsuccessful. Additional samples of gophers from across western Kansas, and more broadly through Kansas in general, should help to resolve the taxonomy of these cryptic species.

Family Cricetidae
Microtus ochrogaster
Prairie Vole

This tawny-bellied vole is associated with prairies and grassland habitats, and compared with the Meadow Vole is more strongly associated with dry upland areas, as opposed to mesic meadows (Miller 1969). Prairie Voles were sampled from 12 counties, including two new records for Geary and Pawnee counties. Prairie Voles are rarely encountered within areas that have experienced woody encroachment (Hope 2018), and they are known to avoid recently burned prairies, preferring the buildup of plant debris in less frequently burned grasslands for maintaining runways (Clark and Kaufman 1990). Hall (1955) noted three subspecies of Prairie Voles in Kansas. Genetic analysis indicated that *Microtus ochrogaster* from Russell, Riley, and Republic counties are very similar, and collectively are similar to a small available sample of vole sequences

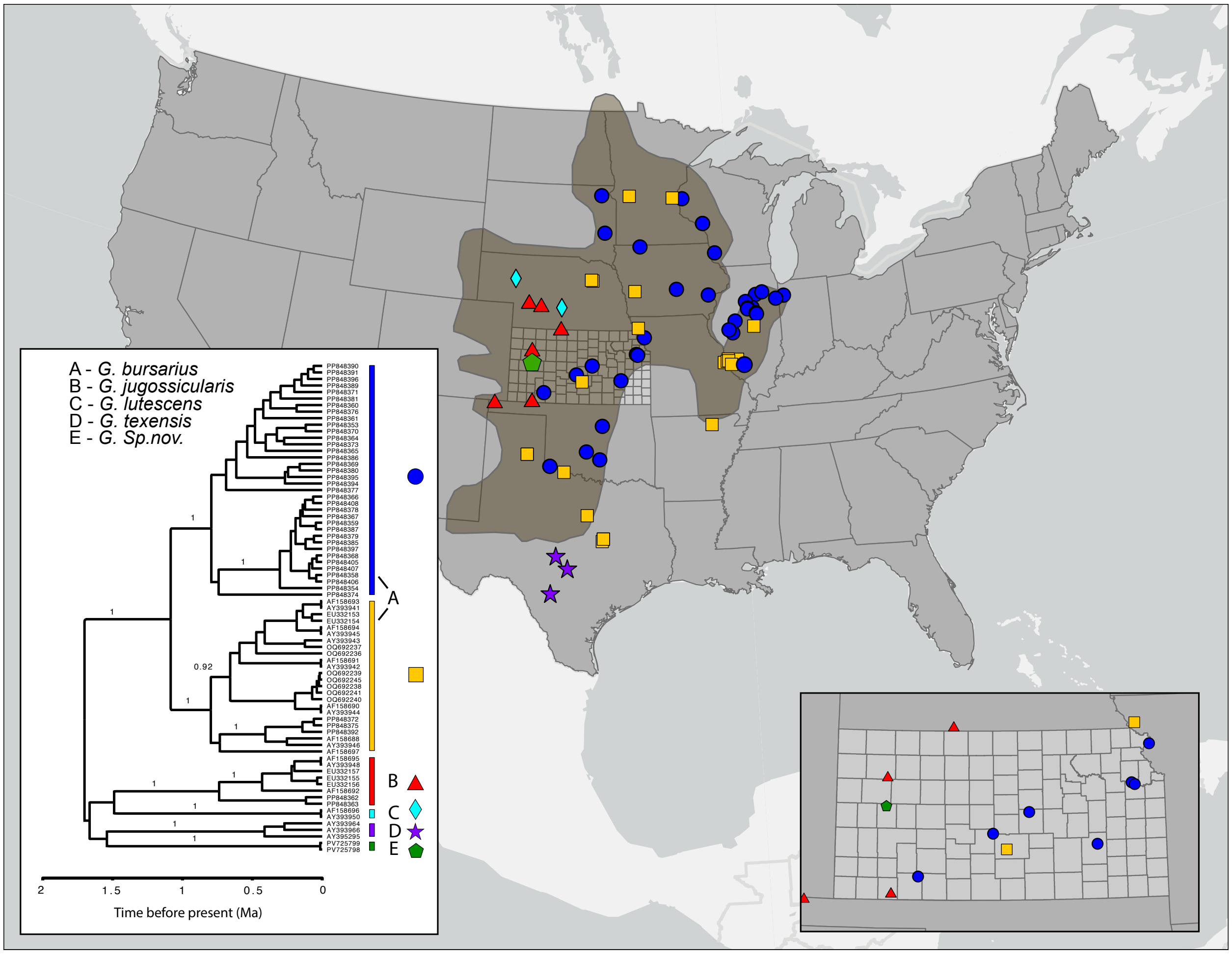

Figure 11. Phylogeographic history of closely related species of *Geomys* based on recent sampling and available sequences from GenBank for the mitochondrial cytochrome *b* gene. The Bayesian phylogeny illustrates lineage relationships with strong posterior probability support. Samples by lineage are georeferenced on the background map in relation to the IUCN range map of the species. The inset map shows individuals with genetic data from Kansas.

from elsewhere through the species' broader range (Fig. 12). However, a single specimen examined from The Tallgrass Prairie Preserve of Manitoba, Canada, is genetically divergent, and all samples from Kansas analyzed were from the range of a single subspecies. As such, additional samples from western and southwestern Kansas should be obtained, as well as from farther north through the Great Plains, to resolve the phylogeographic relationships of distinct lineages within this species. Similar to *B. hylophaga*, *M. ochrogaster* exhibits a disjunct population along the Gulf coastal plain of Texas that conceivably represents a third discrete lineage, but no samples are available for genetic analysis (Fig. 12).

Microtus pennsylvanicus
Meadow Vole

Meadow Voles, like Masked Shrews, are limited in Kansas to the Lower Republican and eastern Smoky Hill drainages, although Frey (1992) inferred an ongoing range expansion southward through time for both species. We captured Meadow Voles from Jamestown WA from low-lying wet grassy habitat, spatially separated from Prairie Voles found in higher and drier areas (Miller 1969). The genetic identity of these samples is aligned with other populations sampled from central North America, coincident with Great Plains states and

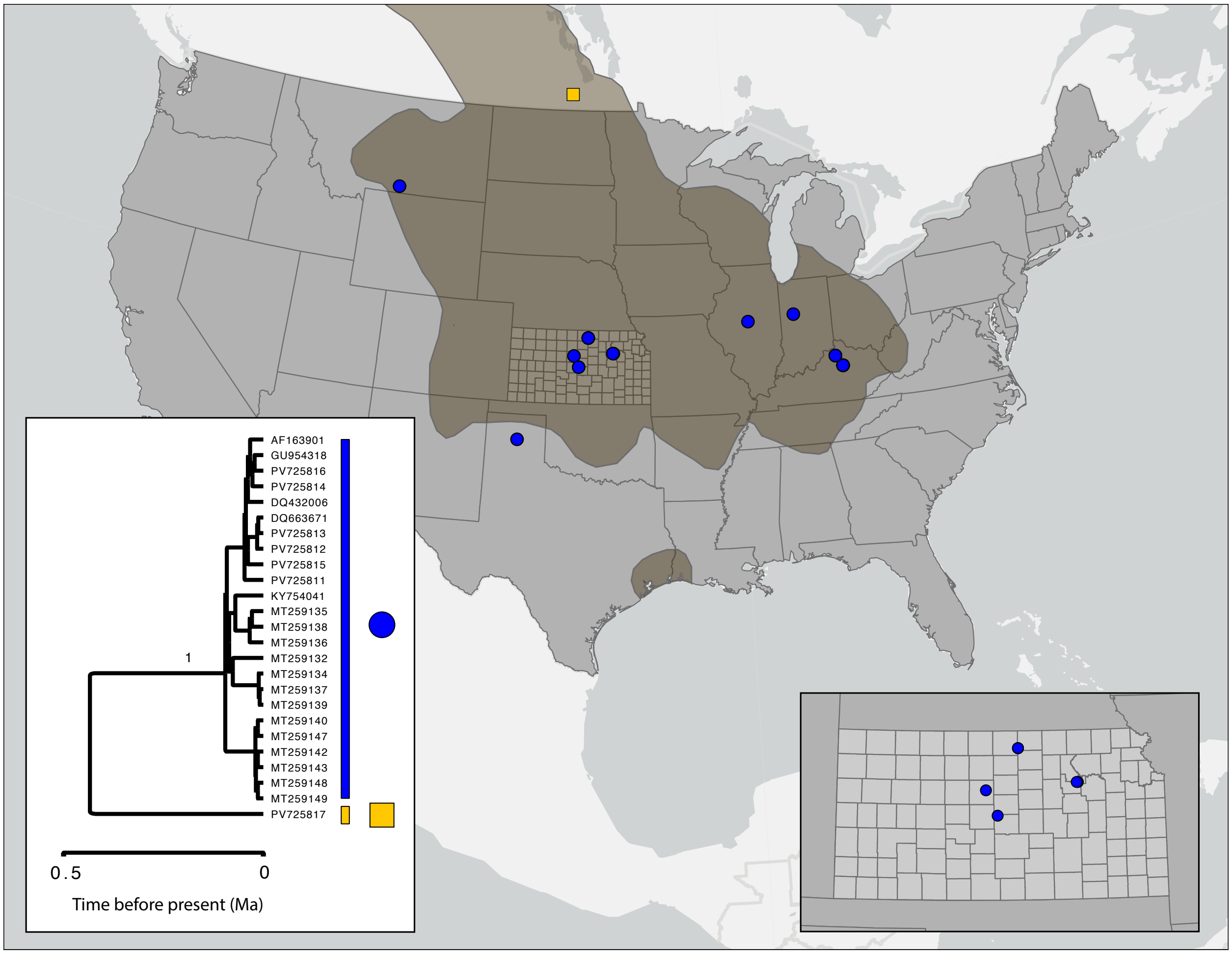

Figure 12. Phylogeographic history of *Microtus ochrogaster* based on recent sampling and available sequences from GenBank for the mitochondrial cytochrome *b* gene. The Bayesian phylogeny illustrates lineage relationships with strong posterior probability support. Samples by lineage are georeferenced on the background map in relation to the IUCN range map of the species. The inset map shows individuals with genetic data from Kansas.

provinces as well as the southwest (Fig. 13; Jackson and Cook 2020). Little is known of the biology of this vole in Kansas, and additional sampling through wetland habitats in northern and central regions is warranted.

Microtus pinetorum
Woodland Vole

Samples of this species represent new county records for Pottawatomie County. Specimens of Woodland Voles are comparatively rare within Kansas and populations represent the western periphery of the range-wide distribution. As it is associated with woodlands, its range might be expected to expand westward coincident with woody encroachment, although forest habitat associations are likely an important variable and encroachment of juniper and clonal shrubs may not reflect an expansion of preferred habitat of this species. Targeted future sampling along the western periphery of its range might reveal additional new county records. Given that these samples represent some of the only genetic resources available for this species in Kansas, additional sampling farther east within woodland habitats is advised.

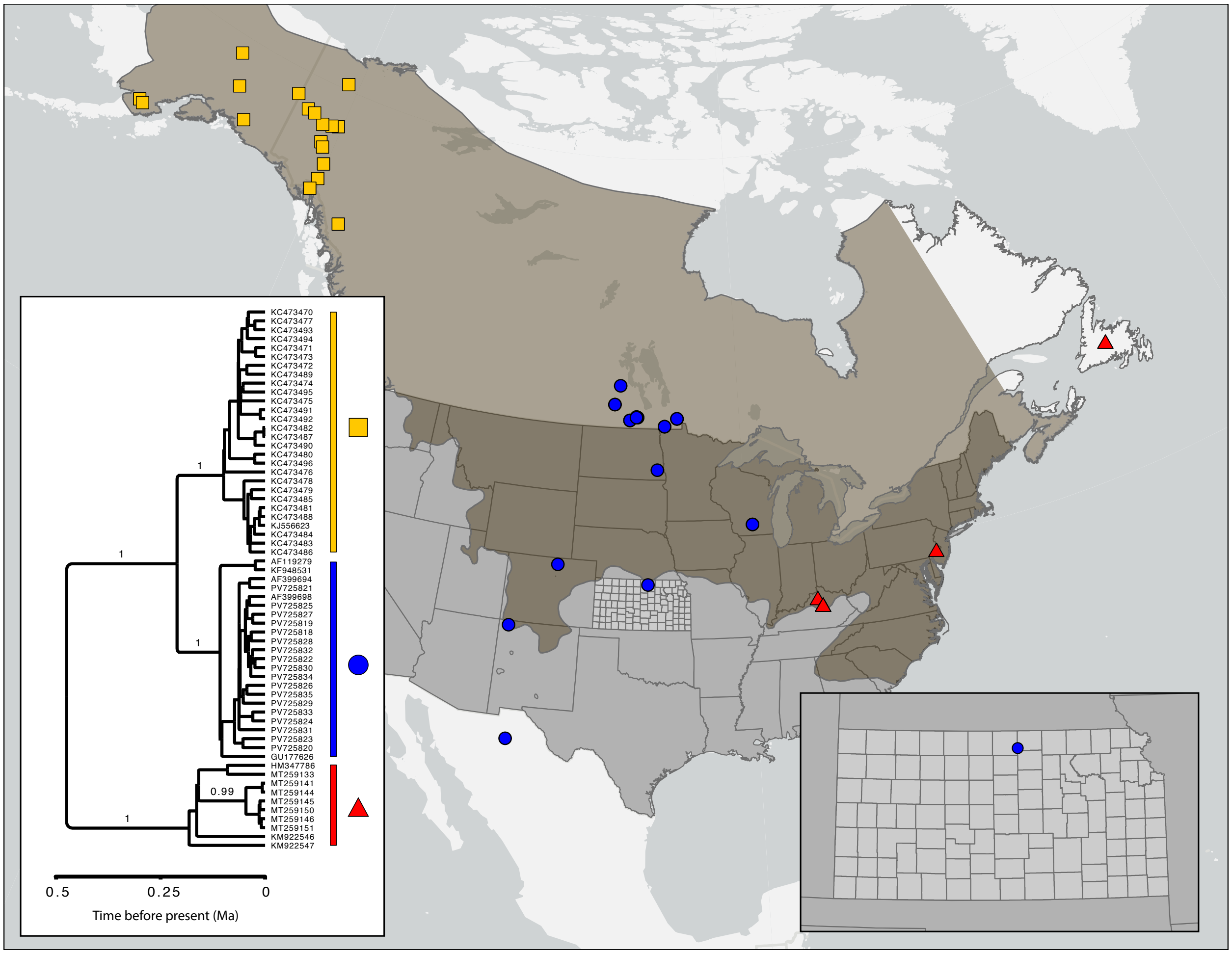

Figure 13. Phylogeographic history of *Microtus pennsylvanicus* based on recent sampling and available sequences from GenBank for the mitochondrial cytochrome *b* gene. The Bayesian phylogeny illustrates lineage relationships with strong posterior probability support. Samples by lineage are georeferenced on the background map in relation to the IUCN range map of the species. The inset map shows individuals with genetic data from Kansas.

Neotoma floridana
Eastern Woodrat

New county records of Eastern Woodrats were documented from Cherokee, Geary, Jewell, and Linn counties, as well as additional new records of locality from most of the sites sampled. Although Hall (1955) reported two subspecies of Eastern Woodrat within Kansas coincident with western and eastern halves of the state, genetic analyses show that all samples from across the state are closely related along with samples from Missouri and Oklahoma (Fig. 14). The phylogeny suggests that the Mississippi River constitutes a phylogeographic break for this species (Edwards and Bradley 2001).

Neotoma micropus
Southern Plains Woodrat

Southern Plains Woodrats were sampled from Barber, Clark, and Morton counties. This species occurs through the southwestern corner of Kansas with a northern limit coincident with the Arkansas River. Given its habitat association of semi-arid scrub brush, most historic records of occurrence are associated with sand sagebrush habitats or riparian woody com-

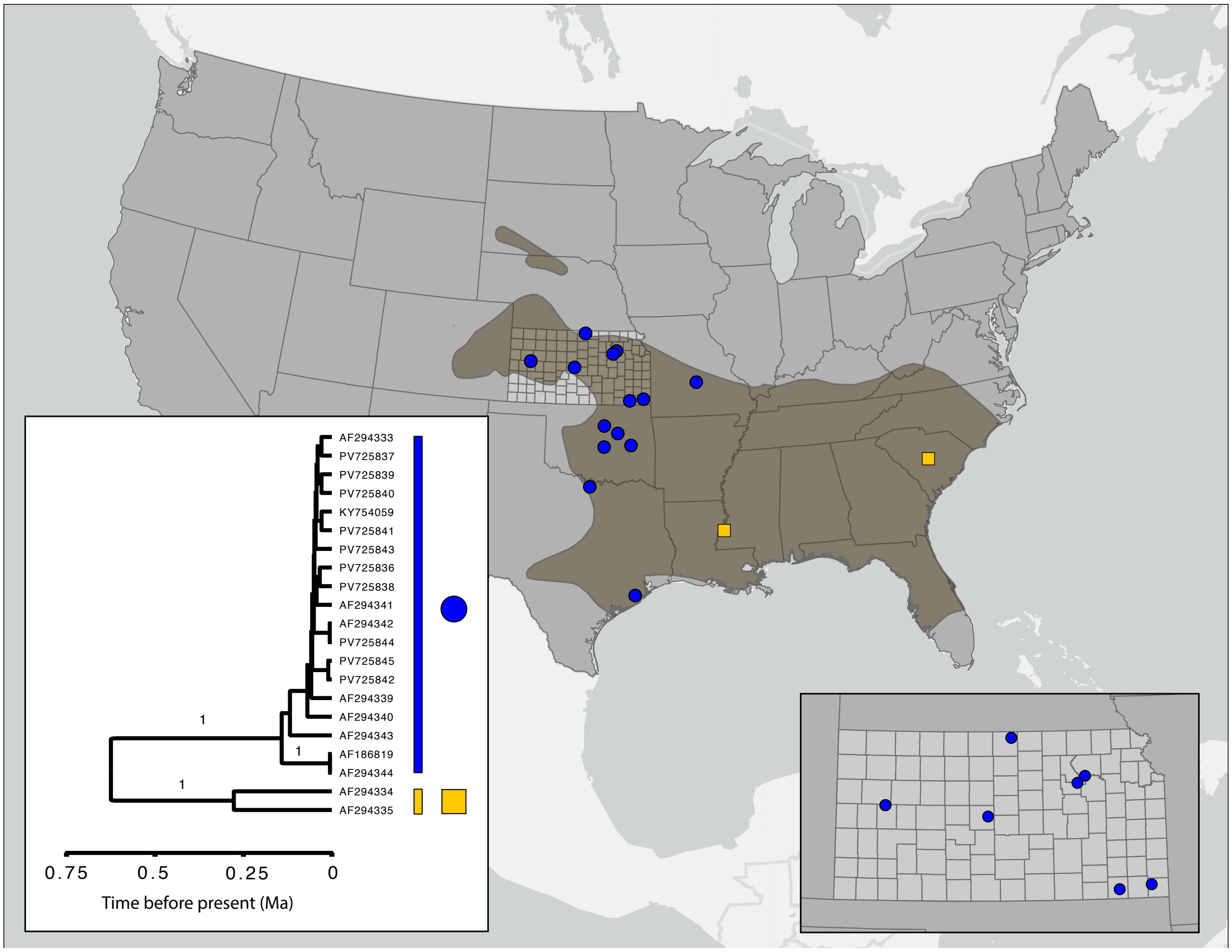

Figure 14. Phylogeographic history of *Neotoma floridana* based on recent sampling and available sequences from GenBank for the mitochondrial cytochrome *b* gene. The Bayesian phylogeny illustrates lineage relationships with strong posterior probability support. Samples by lineage are georeferenced on the background map in relation to the IUCN range map of the species. The inset map shows individuals with genetic data from Kansas.

munities. Additional surveys through areas of suitable habitat along the vicinity of the Arkansas River might substantiate if this species is expanding northward, as most occurrence records through this region are many decades old. The scant genetic evidence indicates two mitochondrial lineages that are only vaguely congruent with northern and southern geography across its range (Fig. 15). Samples from Morton County are associated with two distinct lineages.

Ondatra zibethicus
Muskrat

Muskrats were observed in Scott County in 2020, showing their persistence in western Kansas, and at Mined Lands WA in 2024, and a single specimen was salvaged as roadkill in Pottawatomie County located on high ground roughly equidistant between two dirt cattle tanks lower down to either side, suggesting potential for movement across watershed boundaries. This species is strongly associated with aquatic environments that support robust associated vegetation. It is also often coincident with presence of *Castor canadensis*, as the latter species is an engineer of aquatic habitats that Muskrat thrive in. Muskrat is known to use isolated man-made impoundments in Kansas, although occurrence is strongly negatively correlated with cattle grazing around waterways (Marchbanks 1992; Bomske et al. 2023). With deterioration of permanent flowing waterways, but an increase in isolated water impound-

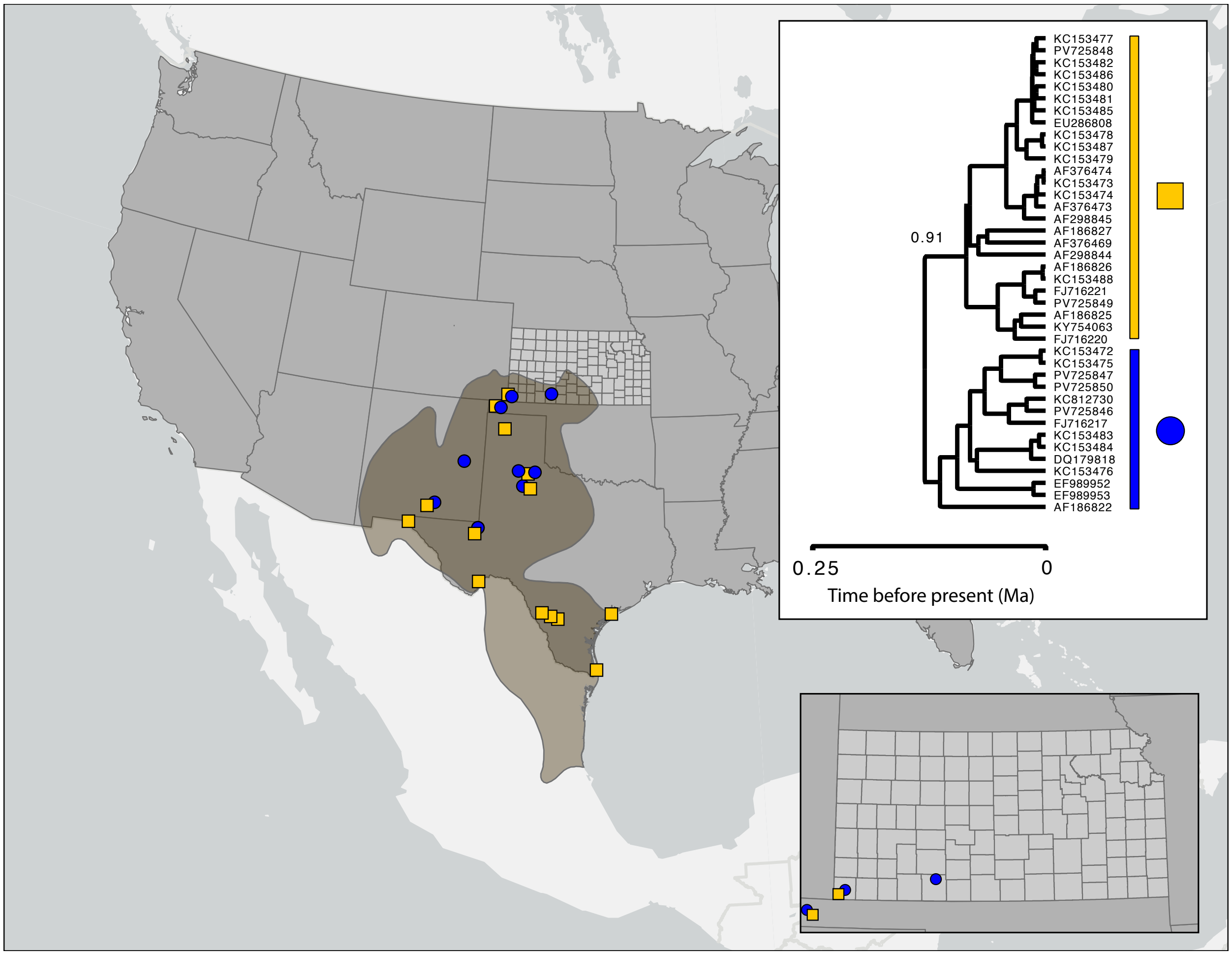

Figure 15. Phylogeographic history of *Neotoma micropus* based on recent sampling and available sequences from GenBank for the mitochondrial cytochrome *b* gene. The Bayesian phylogeny illustrates lineage relationships with strong posterior probability support. Samples by lineage are georeferenced on the background map in relation to the IUCN range map of the species. The inset map shows individuals with genetic data from Kansas.

ments, populations might increasingly lack connectivity and they are known to exhibit strong signals of isolation by distance, suggesting that small-population genetic dynamics (such as loss of diversity and inbreeding) occur among populations that have limited ability to disperse (Laurence et al. 2011). Muskrat has been documented from across Kansas but records of occurrence are generally old. Western populations are likely at higher risk of local extirpation. State lakes constitute important areas for persistence of this species. Hall (1955) recognized two subspecies in Kansas with populations in the southeastern counties being *O. z. zibethicus* and all others being *O. z. cinnamominus*. Future surveys and sampling from across the state would qualify this distinction and put into a broader perspective the genetic identity of this Kansas furbearer.

Onychomys leucogaster
Northern Grasshopper Mouse

Northern Grasshopper Mice were sampled from six localities throughout the western two thirds of Kansas. This species is associated with sandy soils in grassland or shrubland and is known to occur eastward into tallgrass prairie habitats. It has also been detected in abundance within agricultural fields (Fleharty and Navo 1983), although they primarily feed on invertebrates. Engstrom and Choate (1979) assessed the relationships among *Onychomys leucogaster* of the Great Plains and found a gradation in pelage across Kansas, being darker in eastern populations but otherwise indistinguishable. Genetic analysis grouped all specimens together, although comparative sampling for this species is poor (Fig. 16). Despite not detecting high densities of this species, relatively recent specimens have been collected from across its known range in Kansas and it is relatively common.

Peromyscus attwateri
Texas Deermouse (SGCN/SINC)

These mice were detected in relative abundance, co-distributed with *Peromyscus leucopus*, at Quivira Scout Ranch in the cross-timbers region of Kansas. This species occurs only along the southeastern border of Kansas in dry, rocky brush habitats associated with oak forest. Such preferred habitat is scarce at the

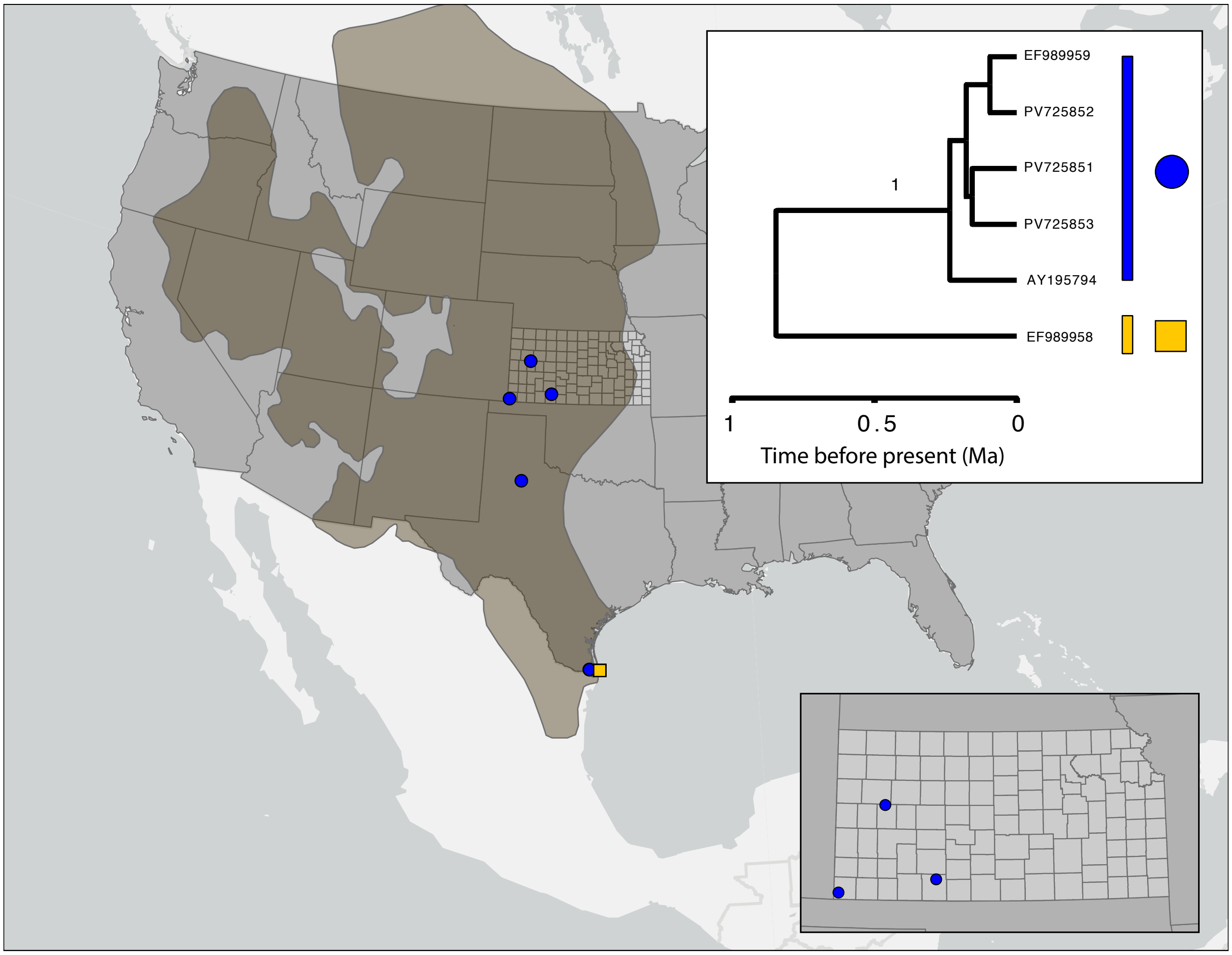

Figure 16. Phylogeographic history of *Onychomys leucogaster* based on recent sampling and available sequences from GenBank for the mitochondrial cytochrome *b* gene. The Bayesian phylogeny illustrates lineage relationships with strong posterior probability support. Samples by lineage are georeferenced on the background map in relation to the IUCN range map of the species. The inset map shows individuals with genetic data from Kansas.

northern edge of this species' distribution, and likely limits occurrence. In Cherokee County, it is possible that *Peromyscus attwateri* occurs close to Shoal Creek associated with the rocky cliffs within Schermerhorn Park. Lack et al. (2010) assessed the distribution of genetic diversity and found populations from throughout the distribution of *P. attwateri* in Texas to be similar and reflective of relatively recent population expansions. However, this species is highly habitat specific, and the preferred rocky habitats are patchily distributed through southern Kansas. Additional survey efforts associated with suitable habitats are necessary to determine the true distribution of this species.

Peromyscus leucopus
White-footed Mouse

The White-footed Mouse, since approximately the mid-2000's, has been the most common and widespread small mammal species occurring within Kansas, based on analysis of museum specimen data (Hope et al. 2025). Prior to this, *Peromyscus sonoriensis* was the most common. White-footed Mice also have rapidly expanded their range in recent decades, and both density and distribution have increased in association with woody encroachment. Historically, White-footed Mice were not known to occur in west-central Kansas (Hall 1955), but now might be considered to occur statewide (Schmidt et al. 2021). This species was sampled from 31 counties. Because it is so abundant and has shown dramatic recent demographic change throughout Kansas, it should be considered of particular concern for management from multiple perspectives. First, it is an indicator of woody expansion and land-use change within Kansas. Second, white-footed mice and their associated habitats are seemingly displacing grassland associated species (such as deermice and harvest mice; Swihart and Slade 1990) and by extension the functional roles of grassland mammals for maintaining prairie habitats (Hope et al. 2021). Third, White-footed Mice are recognized as a primary reservoir for potentially zoonotic pathogens across North America (e.g., Tufts and Diuk-Wasser 2018; Long et al. 2019), where different strains of pathogens might be associated with different lineages of mice (reflecting divergent evolutionary histories; Dragoo et al. 2006). This is pertinent, given that three recognized subspecies of *P. leucopus* have been described within Kansas, associated with the east, northwest, and southwest (Fig. 17). In addition, rapid expansion of a species such as the White-footed Mouse can have genetic consequences that impact its relative susceptibility to infection with associated disease (André et al. 2017). Finally, emerging evidence shows that Short-tailed Shrews can propagate pathogens primarily carried by *P. leucopus* (Brisson et al. 2008). These insights are new and still poorly understood but might be related to a rise of tick-borne pathogens across Kansas, especially in the eastern half of the state (Han et al. 2015). Genetic analyses reported herein with expanded sampling again reflect three distinct evolutionary lineages of White-footed Mice across Kansas, although not strictly concordant with the recognized distribution of subspecies. A single individual reflective of a fourth lineage distributed through eastern North America might reflect a long-distant unintentional human transplant (Fig. 17). Mice from the southwest constitute a lineage occurring through Texas, New Mexico, and southward through Mexico. Mice from most of the remaining sites sampled constitute a lineage distributed broadly through the Great Plains northward to southern Canada (a specimen included here represents the first record of *P. leucopus* from Manitoba, confirming that this species is expanding on multiple fronts). Sites sampled across multiple counties supported two lineages in sympatry. The robust and growing archive of specimens from this species will be of value for multiple future research priorities.

Peromyscus sonoriensis
Western Deermouse

Western Deermice were detected within 24 counties but were never as abundant as White-footed Mice. The Western Deermouse is also recognized as a primary host of potentially zoonotic pathogens that might be differentially associated with intraspecific mouse lineages (Dragoo et al. 2006). Deermice have previously been considered one of the most common small mammals through Kansas, associated with open prairie habitats. Their numerical dominance has now been reduced through loss of native prairie habitats (Kaufman et al. 2020). Our genetic analyses confirm that all samples within Kansas are similar and conform to the subspecies *P. s. bairdii* that is distributed broadly throughout the Great Plains (Fig. 18). However, Western Deermice are genetically diverse across their range

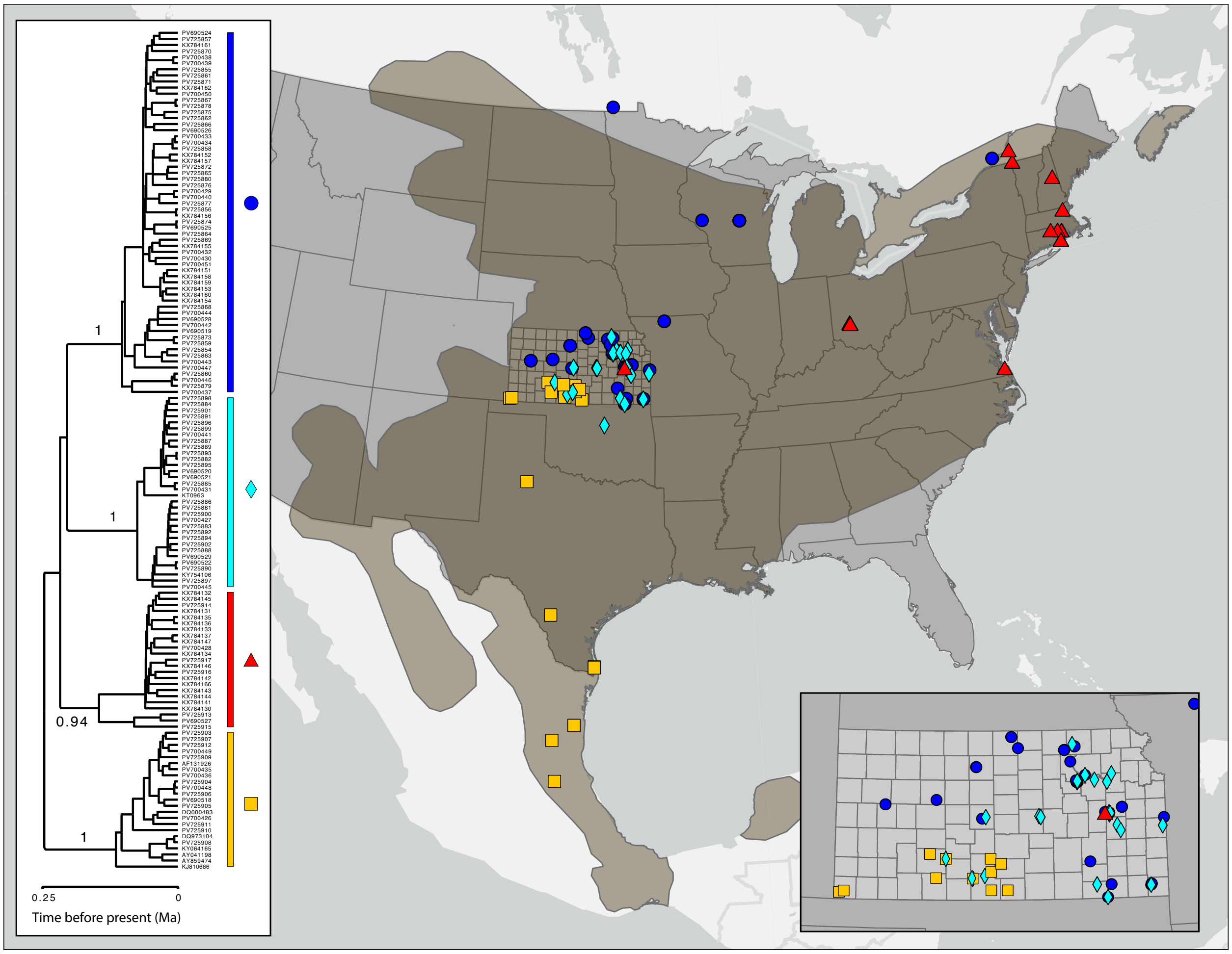

Figure 17. Phylogeographic history of *Peromyscus leucopus* based on recent sampling and available sequences from GenBank for the mitochondrial cytochrome *b* gene. The Bayesian phylogeny illustrates lineage relationships with strong posterior probability support. Samples by lineage are georeferenced on the background map in relation to the IUCN range map of the species. The inset map shows individuals with genetic data from Kansas.

and additional lineages are known to occur in Colorado/New Mexico, California, and through northern areas of the Great Plains (Fig. 18). Additional targeted surveys for *P. sonoriensis* in the north, and particularly in the southwestern corner of Kansas, would confirm if additional lineages exist.

Reithrodontomys fulvescens
Fulvous Harvest Mouse (SGCN)

Fulvous Harvest Mice were collected within five counties, including new county records for Pratt and Stafford counties, the latter north of previous distributional limits. A record from Sedgwick County from 2021 was the previous northernmost record. Southern Kansas represents the northernmost distributional limit for Fulvous Harvest Mice. Habitat associations of this species primarily include thick grassy areas and shrubby areas within grassland habitats (Spencer and Cameron 1982). There is no readily apparent competitive exclusion of this species by Hispid Cotton Rats (*Sigmodon hispidus*) or Plains Harvest Mice (*Reithrodontomys montanus*). At sites detected, this species was common. These detections provide further circumstan-

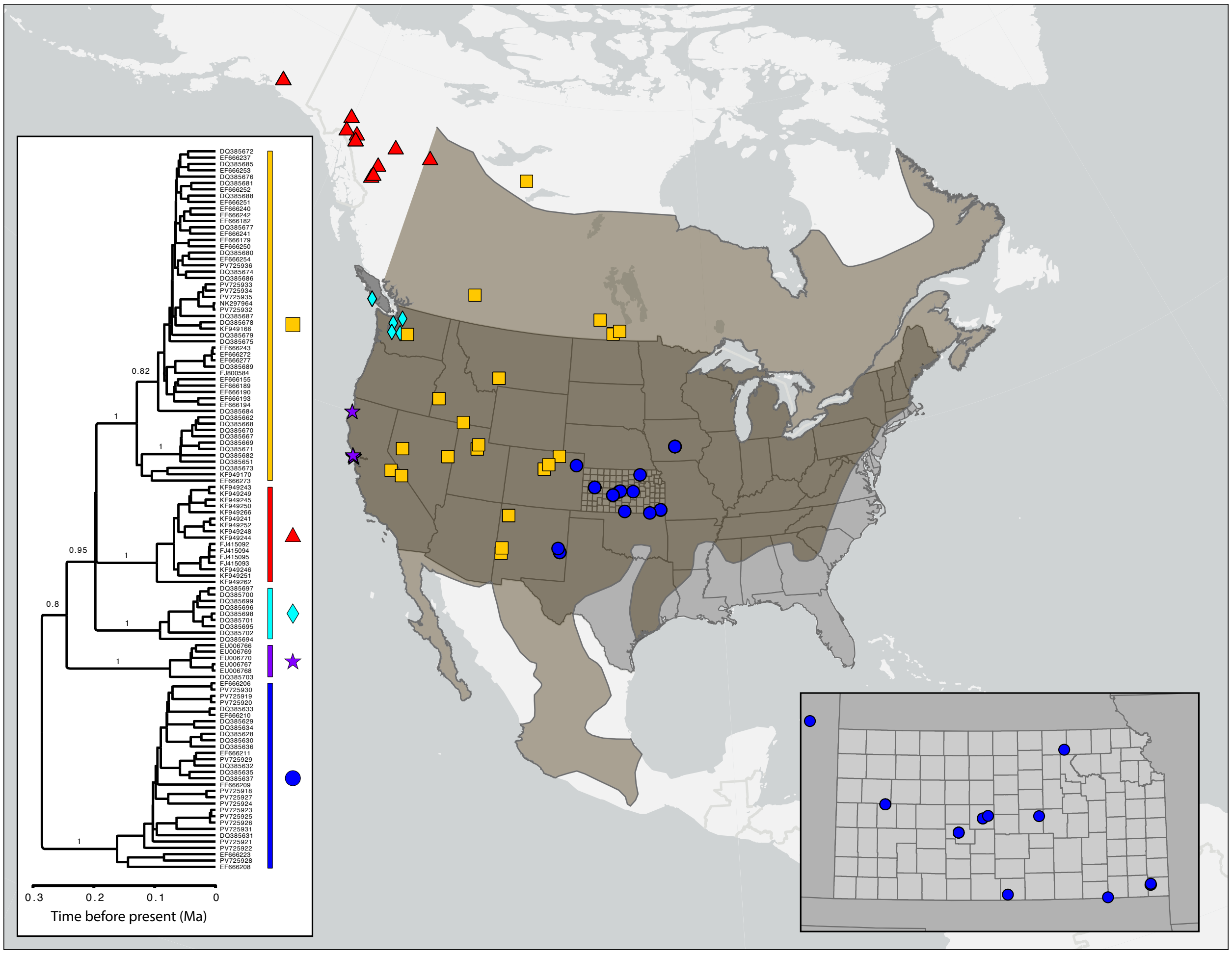

Figure 18. Phylogeographic history of *Peromyscus sonoriensis* based on recent sampling and available sequences from GenBank for the mitochondrial cytochrome *b* gene. The Bayesian phylogeny illustrates lineage relationships with strong posterior probability support. Samples by lineage are georeferenced on the background map in relation to the IUCN range map of the species. The inset map shows individuals with genetic data from Kansas.

tial evidence that this species might be expanding its range within Kansas, particularly northward. Genetic data show that Kansas specimens are associated with a lineage distributed from the Texas coastal plain northward and eastward, whereas specimens from the Edwards Plateau of Texas southward into Mexico represent a separate lineage (Fig. 19).

Reithrodontomys megalotis
Western Harvest Mouse

This species was detected within 10 counties across Kansas. Western Harvest Mice might at times be abundant and are found primarily within open grassland habitats, with a diet relying almost exclusively on grass seed (Hope and Parmenter 2007). Genetic analysis showed two lineages occurring in sympatry at Lake Scott in western Kansas (Fig. 20). Western Harvest Mice are commonly found in sympatry with Plains Harvest Mice, although the latter is more rare and morphologically difficult to distinguish. Both species were collected from Scott and Riley counties from the same grassland habitat. Interactions between Western and Fulvous Harvest Mice are not well understood, but these species likely competitively exclude each other, given their distributions are considered parapatric.

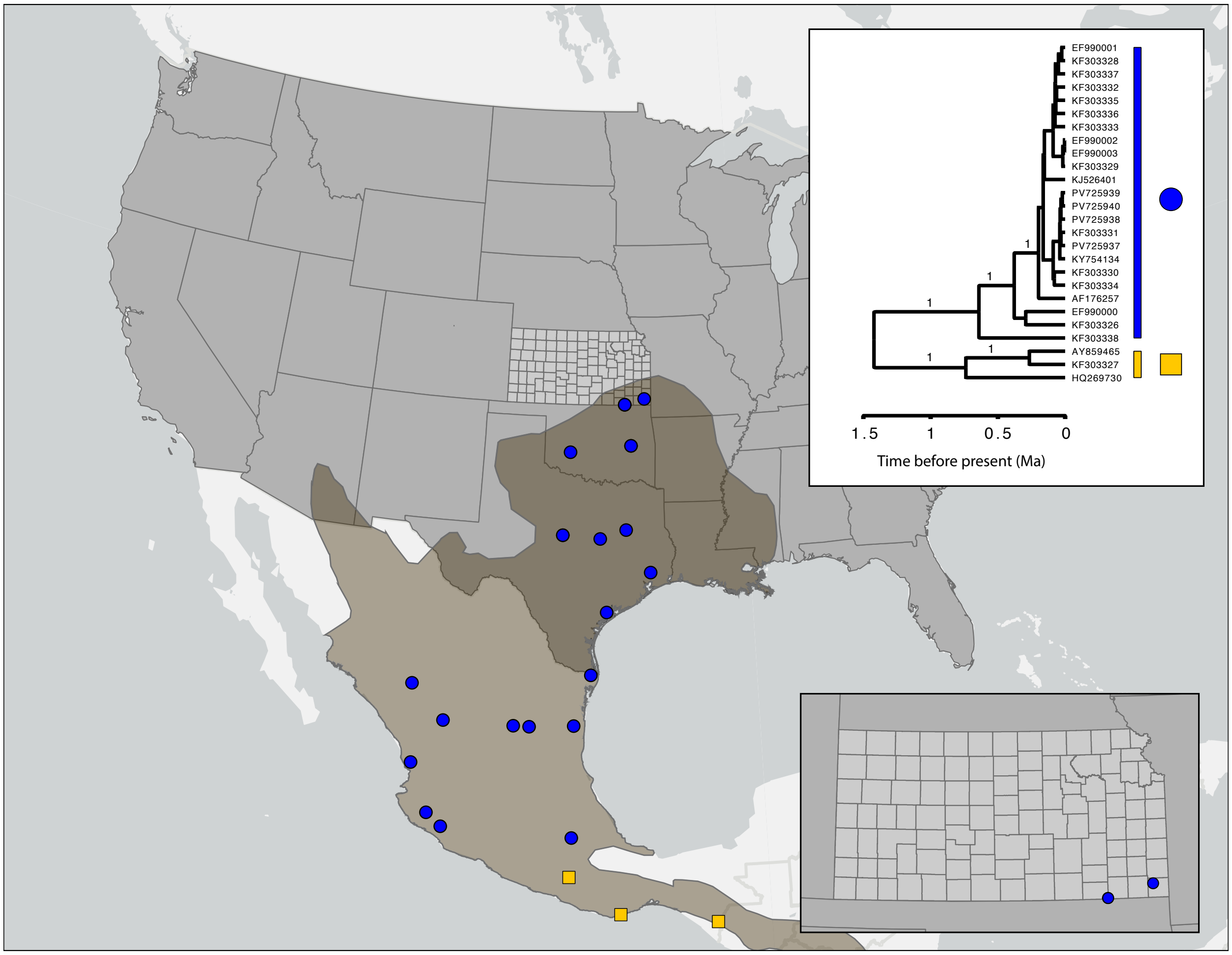

Figure 19. Phylogeographic history of *Reithrodontomys fulvescens* based on recent sampling and available sequences from GenBank for the mitochondrial cytochrome *b* gene. The Bayesian phylogeny illustrates lineage relationships with strong posterior probability support. Samples by lineage are georeferenced on the background map in relation to the IUCN range map of the species. The inset map shows individuals with genetic data from Kansas.

Reithrodontomys montanus
Plains Harvest Mouse

Specimens of Plains Harvest Mouse collected from Geary, Osage, Riley, and Scott counties represent new county records. Plains Harvest Mice are inherently rare through their distribution but have been commonly found in sympatry with both Western and Fulvous Harvest Mice. Few samples have been analyzed from a genetic perspective, and no comparative data are currently available from across their range. Two subspecies of the Plains Harvest Mouse are known from Kansas, separating western from eastern populations. We acknowledge that Plains and Western Harvest Mice are often morphologically cryptic and misidentifications might be common. Conformational barcode genetics, such as has been used effectively for identifying species of *Peromyscus*, is a viable modern option for accurate monitoring (Light et al. 2021).

Sigmodon hispidus
Hispid Cotton Rat

Multiple recent specimens of Hispid Cotton Rats have been collected from across northern Kansas and this species is rapidly expanding northward, now as far as the Platt River in Nebraska (Frisch et al. 2015). *Sigmodon hispidus* are now widespread in Kansas, al-

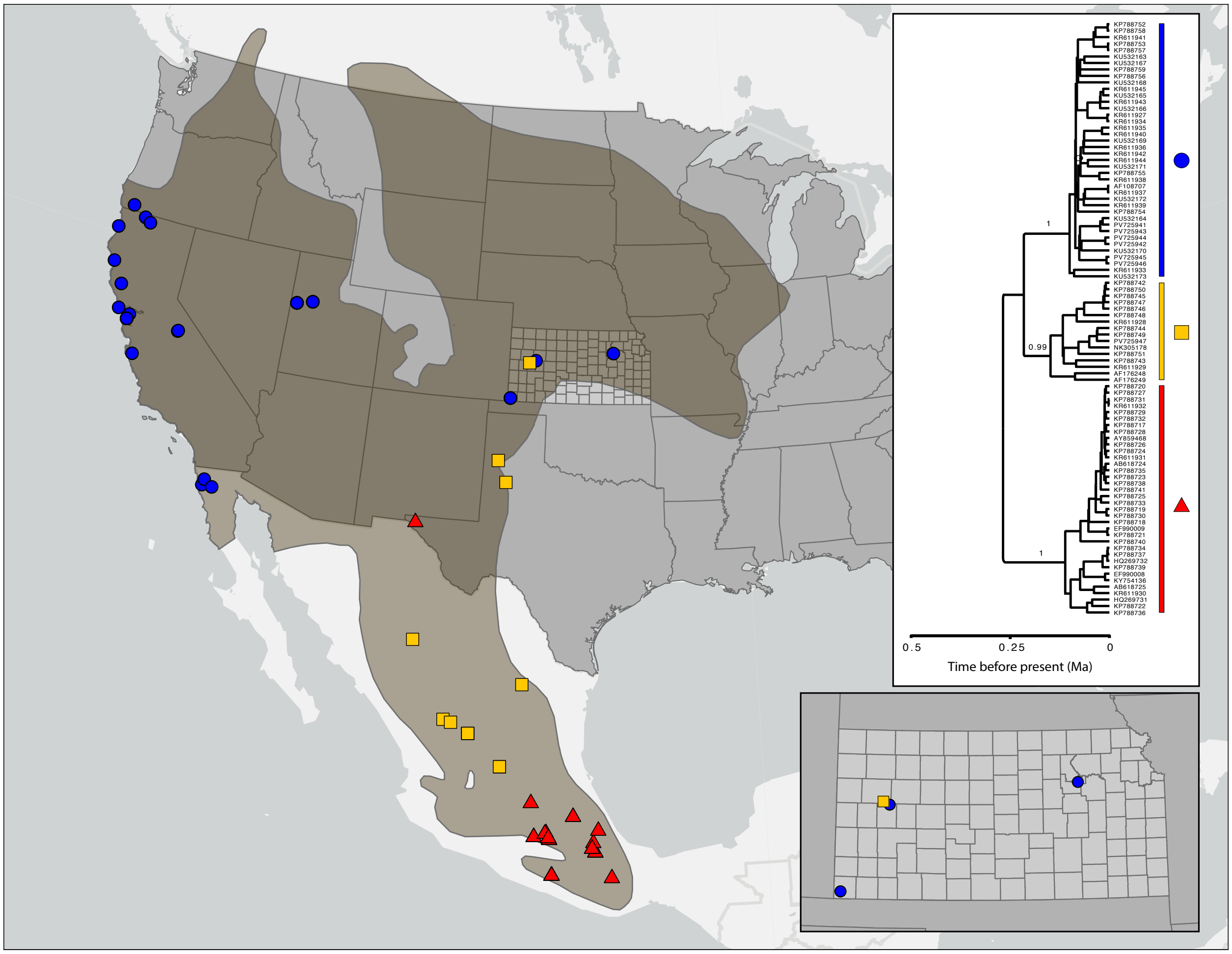

Figure 20. Phylogeographic history of *Reithrodontomys megalotis* based on recent sampling and available sequences from GenBank for the mitochondrial cytochrome *b* gene. The Bayesian phylogeny illustrates lineage relationships with strong posterior probability support. Samples by lineage are georeferenced on the background map in relation to the IUCN range map of the species. The inset map shows individuals with genetic data from Kansas.

though their first appearance in the state was as recent as the early 1900's (Thompson and Finck 2013). Hall (1955) considered them to be rare in western Kansas and absent from most northern counties. This species was sampled from 21 counties, with a new county record from Scott County. Rivers do not appear to limit dispersal, and the species is generally associated with mesic habitats including grasslands, shrubby habitats or woodlands. Hispid Cotton Rats experience dramatic cycles of population growth and decline, with very short lifespans but very high reproductive potential. At population peaks, *Sigmodon hispidus* can be the most abundant species encountered, with implications for competitive exclusion of other native species. Hispid Cotton Rats and White-footed Mice were co-dominant species during the project timeframe, and both have only recently become so widespread. These two species partition their food resources (Hope et al. 2021) and as such, might together competitively exclude other historically more abundant species within Kansas. Genetic analysis showed that samples from Morton County represent two distinct genetic lineages occurring in sympatry, further evidence of distinct biodiversity from the southwest finding their distributional limits within this part of Kansas (Fig. 21).

Synaptomys cooperi
Southern Bog Lemming (SGCN/SINC)

A single specimen of this species was collected from Jamestown WA in Republic County, a new locality for this species and one of only two records from the county. The specimen was caught in a pitfall trap set in low lying wet meadow, in sympatry with *Microtus pennsylvanicus*, *Sorex cinereus*, and *Blarina hylophaga*. Also, a new county record was documented for Pawnee County. Linzey (1984) found that competition between Southern Bog Lemmings and Meadow Voles was only apparent when Meadow Vole densities were high. The relative isolation of these populations are not known, but the Pawnee specimen represents an extralimital record for this species in the southwestern extent of its range. The exception is a relictual historic population from Meade County that has not been recorded in recent times (Wilson and Choate 1997). Another specimen was caught and released from Quivira National Wildlife Refuge in 2020. The Southern Bog Lemming is broadly distributed across northeastern North America and Kansas. It is associated with mesic habitats including both woodland and open grassland, but it is not restricted to wetlands, having been collected from upland dry prairie habitats (Rose and Linzey 2021). Evidently, suitable habitat remains throughout much of Kansas, and yet incidence of this

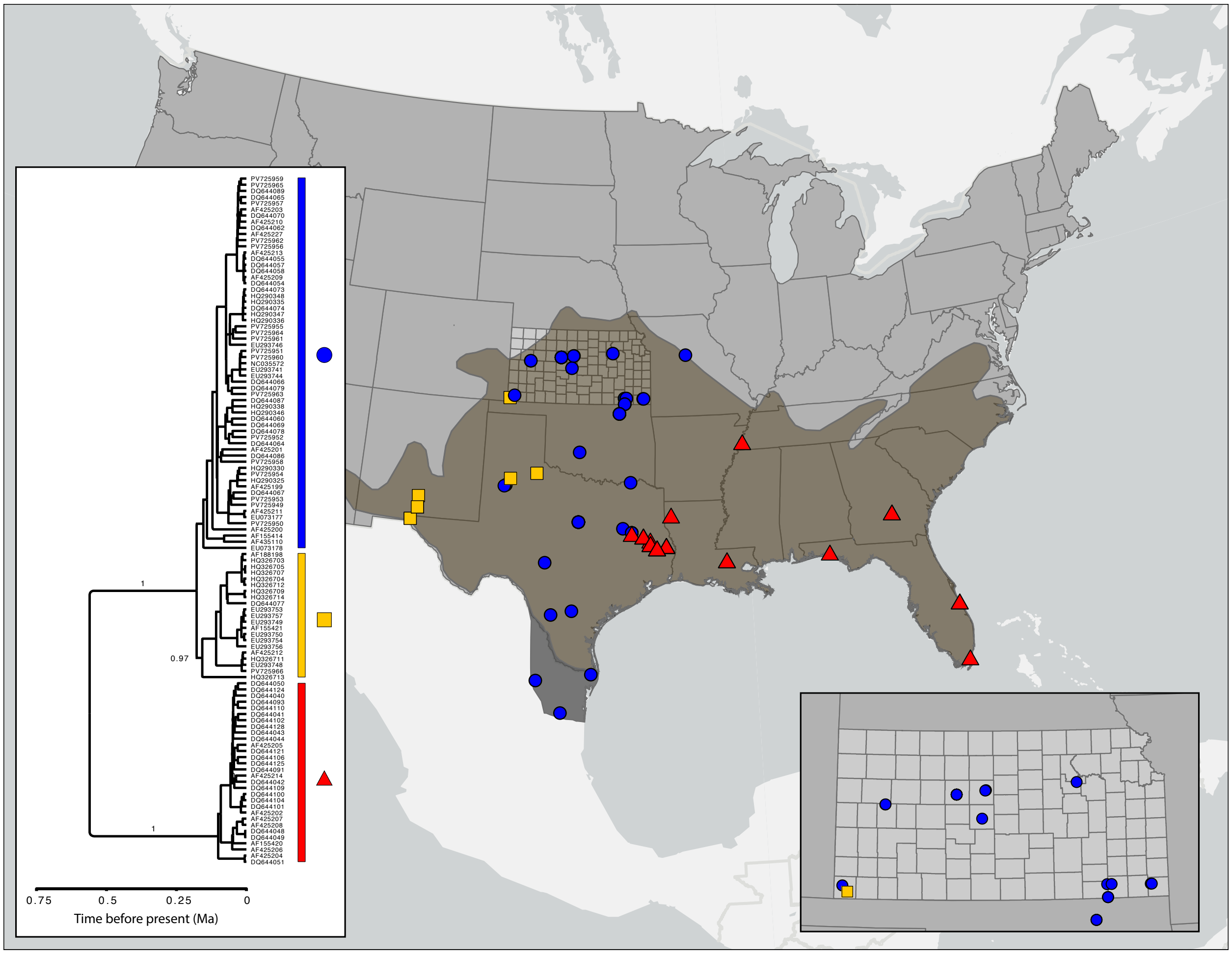

Figure 21. Phylogeographic history of *Sigmodon hispidus* based on recent sampling and available sequences from GenBank for the mitochondrial cytochrome *b* gene. The Bayesian phylogeny illustrates lineage relationships with strong posterior probability support. Samples by lineage are georeferenced on the background map in relation to the IUCN range map of the species. The inset map shows individuals with genetic data from Kansas.

species has declined in recent decades. Southern Bog Lemmings are rarely sampled from standard mammal traps, and pitfalls are an effective alternative (Hope et al. 2023). Continued monitoring for this species will be essential to understand population trajectories and to increase spatial sampling, particularly to the east and northeast of Kansas where their populations have historically been more robust. Genetic analysis showed that *Synaptomys cooperi* in Kansas are closely related to other samples from the Great Plains and upper midwest, whereas samples from eastern North America (likely east of the Mississippi River) form a distinct lineage (Fig. 22).

Family Muridae
Mus musculus
House Mouse

House Mice were collected from four counties, with new records from Scott and Wabaunsee counties. Although non-native, house mice are highly commensal with humans and readily found close to habitation, especially urban areas and agricultural infrastructure. They have been broadly sampled throughout Kansas yet are still underrepresented within museum collections.

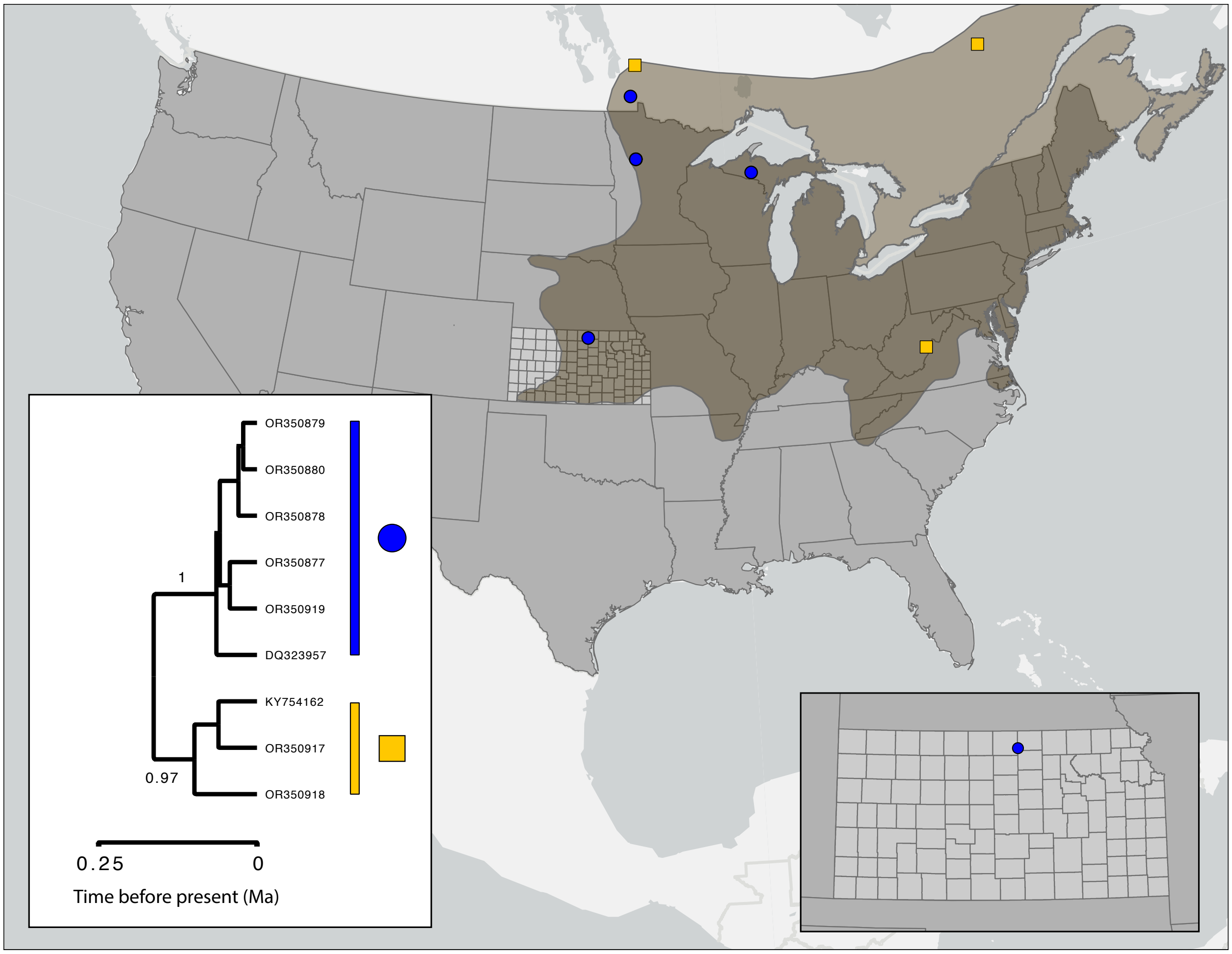

Figure 22. Phylogeographic history of *Synaptomys cooperi* based on recent sampling and available sequences from GenBank for the mitochondrial cytochrome *b* gene. The Bayesian phylogeny illustrates lineage relationships with strong posterior probability support. Samples by lineage are georeferenced on the background map in relation to the IUCN range map of the species. The inset map shows individuals with genetic data from Kansas.

Family Erethizontidae
Erethizon dorsatum
North American Porcupine

This species was not sampled. Porcupines are widespread throughout Kansas and across multiple habitat types, though often found along riparian corridors associated with cottonwood forest. Relatively recent specimens have been collected widely through Kansas and populations are considered stable (Schmidt et al. 2021).

Discussion

Small mammals are known to be valuable proxies for understanding community assembly and function through time, including processes of species turnover, shifting distributions, and changing interactions (Gerhold et al. 2015). The substantial anthropogenic induced environmental change through Kansas, and the Great Plains in general through recent decades, have not been backed up by effort towards comprehensive statewide sampling of small mammal specimen resources, that might otherwise have produced robust specimen baselines for understanding trajectories of change. This work, and other ongoing sampling efforts like it (such as the Charles Bunker resurvey efforts; A. Townsend Peterson, unpublished data), constitute modern preservations explicitly aimed at fueling emerging research priorities and preserving materials in museum collections for use into the foreseeable future (Miller et al. 2020).

Distributional records.—The gold standard for comprehensive sampling includes spatially broad, temporally deep, and site intensive effort (Dunnum et al. 2017). It is evident that spatial sampling of Kansas is far from saturated, especially in some cases for commonly occurring and widespread species. Without accurate knowledge of the distribution of species, realizing changing ranges through time is difficult. Given the lack of focus on statewide sampling of Kansas mammals in recent decades, there is also a gap in temporal depth of sampling, without which ability to track fine-scale changes in genetic diversity or the distribution of intraspecific diversity is again compromised. Development of baseline voucher sampling with modern preservation of diverse parts now, will allow for these kinds of investigations into the future, including through study of associated biodiversity and changes in disease landscapes (Thompson et al. 2021).

There also are few places in Kansas with site-focused sampling through time. The leading example of site intensive specimen-based science for mammals in Kansas currently is the Konza Prairie LTER site, with approximately 10 years of modest specimen sampling from various habitats comprising rigorous landscape scale experimental treatments (Hope et al. 2025). Site intensive sampling, at least at selected regional localities, is crucial for accurate detection of biodiversity (Hope et al. 2018). The results presented herein clearly show highest diversity of small mammals within counties that have had highest sampling effort. For instance, Riley and Pottawatomie counties, in the vicinity of Kansas State University, experience the most intensive sampling and exhibit at least double the species richness of most other sites. As such, there is little confidence in inference of community composition, diversity metrics, evenness, or abundance of small mammals, without sustained sampling across years. Species that normally are found in inherently low abundance, such as *Zapus hudsonius*, *Synaptomys cooperi*, or *Cryptotis parvus* might take multiple years for a single detection.

The data here also highlight that medium-sized mammals, including lagomorphs, carnivores, squirrels, and other large rodents (beaver, muskrat, porcupine) are still poorly sampled across Kansas. Typical mammal traps do not account for these species. Firearms are effective, but do not allow for standardized and quantifiable sampling, and are often not appropriate or permissible to use in a given setting. Trail cameras can provide much more robust data on prevalence of species and have been increasingly effective for noninvasive monitoring in recent years (Kays et al. 2022). Obtaining physical voucher specimens of these species can be effective through opportunistic salvage of specimens that have died by other means, although this practice is underused, particularly when specimens are in poor condition. It also often requires additional effort to develop a network of contacts for obtaining materials, for instance, from private landowners, district biologists, pest control, and fur harvesters. Many of our new county records for medium-sized mammals were achieved through salvage, including retrieval of roadkill.

Phylogeographic evidence.—Evidence of the distribution of intraspecific diversity is seldom included in studies of regional natural history or biodiversity assessments. However, given the relative wealth of genetic data in public databases now, even a single genetic sequence of a newly collected specimen can be put into context of the broader species diversity. These phylogeographic assessments can often pinpoint areas of a region or state like Kansas exhibiting unique diversity, with knowledge that whole species as units of analysis often are too coarse a scale to identify high priority populations or management units for localized decision-making (Coates et al. 2018).

Across multiple co-distributed species, comparative analysis of genetic structure can highlight regions that support unique diversity repeatedly across whole communities. For instance, the southwestern and western parts of Kansas are high in unique lineage diversity for *Geomys* (Fig. 11), *Neotoma micropus* (Fig. 15), *Reithrodontomys megalotis* (Fig. 20), and *Sigmodon hispidus* (Fig. 21), as well as representing the range limits across multiple species from the east (*Scalopus aquaticus*) and southwest (*Cratogeomys castanops*; *Notiosorex crawfordi*).

Phylogeographic studies emphasize not simply what the unique diversity is within species and how it is distributed now, but also reflects long-term changes through evolutionary timeframes. Geographic regionalization of genetic diversity reflects a history of divergence, often through ancient fragmentation and isolation of a species into multiple regional refugia followed by genetic differentiation and eventual reconnection (Provan and Bennett 2008). Using *Sigmodon hispidus* as an example (Fig. 21), three distinct lineages broadly distributed across southern North America now might reflect divergence of sets of populations in the southwest, southern Texas, and the southeast, respectively, during the last glacial period, that likely also have local ecological adaptations, meaning that western populations of cotton rats have essentially different life histories than eastern cotton rats.

The most striking example of lineage diversity in Kansas is provided by *Peromyscus leucopus*, as has been discussed in detail elsewhere (Hope et al. 2025). In brief, three distinct lineages of these mice in Kansas minimally reflects very high genetic diversity that is regionally unique across the state (Fig. 17). It also means that discrete lineages are interacting, potentially experiencing gene flow (intraspecific hybridization), and sharing associated biodiversity. Multiple examples demonstrate intricate changes in relationships between hosts and parasites where related mammals experience secondary contact. For instance, host swapping and differential range movement between species of gophers and their chewing lice has led to long-term changes in these intimate host-parasite relationships (Hafner et al. 2019). Reassortment of viruses is potentially more relevant for human health outcomes, such as with strains of hantavirus between lineages of *Peromyscus sonoriensis* in the southwestern US (e.g., Dragoo et al. 2006) or between hantaviruses found in *Blarina brevicauda* where shrew lineages meet (Liphardt et al. 2020).

Finally, the genetic assessments provided offer a temporal perspective into the evolution of mammals within Kansas. Each phylogeny provides an interpretation of divergence time within and among lineages. Species associated with western and southwestern ranges through North America have generally evolved over longer timeframes than species with more northern or eastern distributions that have experienced more extreme and rapid distributional shifts with glacial cycling through time (e.g., Hope et al. 2012). More rapid evolutionary responses in the past may also mean greater capacity to adapt or move in response to rapid modern change into the future, although also dependent on other factors, including relative genetic diversity, population size, and generation time (Davis et al. 2005).

C*onservation and management of Kansas mammals*.—The data presented herein offer a number of insights into biodiversity change and considerations for adjustment to current and ongoing management and conservation priorities, as well as potential for new research that may benefit both wildlife and society. Changing habitats in Kansas through the last century are undoubtedly influencing the distributions and community composition of mammals that are often habitat specialists. In addition to massive land conversion through plowing of native prairie habitats for agriculture, the biggest transformation has been a steady increase in woody cover in historical native prairie (Samson et al. 2004). However, "woody encroachment" is a broad term and often seen as a negative outcome. Perhaps more importantly, the term is a vague catchall for woody plant species, and it should be used with caution and clarity.

Encroachment is herein considered as the expansion of "weedy" wood species, including clonal shrubs (e.g., rough-leaved dogwood [*Cornus drummondii*], wild plum [*Prunus* spp.], smooth sumac [*Rhus glabra*]) and trees (e.g. eastern red cedar [*Juniperus virginiana*], honey locust [*Gleditsia triacanthos*], Siberian elm [*Ulmus pumila*]) that collectively negatively impact native grassland and promote mammal community turnover and associated cascading processes of change (Van Auken 2009). For instance, multiple new county records of *Neotoma floridana* (Table 1) likely reflects both incomplete historical sampling and an increase in densities of this species in areas where they may have occurred at lower levels in the past, due to a vast increase in weedy wooded habitat and hence carrying capacity of associated mammals. Conversely, expansion of native hardwood forest within Kansas would lend to re-establishment of historic gallery forests of oak once much more widespread in Kansas that likely supported broader distributions of mammals such as *Glaucomys volans* and *Urocyon cinereoargenteus*.

Conservation efforts through state management emphasize SGCN species as outlined in the Kansas Wildlife Action Plan (Rohweder 2022), which for terrestrial small mammals includes only one species (*Synaptomys cooperi*), which is widespread across the state, whereas other species reach their range periphery at the edges of Kansas, and collectively these species remain data deficient within Kansas. Additionally, species such as *Poliocitellus franklinii* and *Sylvilagus aquaticus* have exhibited regional declines on the periphery of their historical ranges and are at risk of loss. *Cratogeomys castanops* is also likely to be at high risk of further decline and extirpation due to a lack of preferred habitat and conflict with human land use. Based on recent survey efforts, both *Reithrodontomys fulvescens* and *Glaucomys volans* appear to be more widespread and possibly expanding their range within Kansas. Additional species of concern based on these surveys and existing specimen data include those that were historically abundant but now are rarely sampled, suggesting demographic decline despite potentially broad ranges due to various factors, including loss of semi-arid prairies (*Lepus californicus*, *Perognathus flavescens*), multi-factorial decline due to disease, habitat loss, and competition (*Urocyon cinereoargenteus*, *Spilogale interrupta*), and through direct human conflict (*Poliocitellus franklinii*, *Cynomys ludovicianus*). In general, a loss of native prairie habitats in Kansas is a driving concern for biodiversity decline, and one solution from the perspective of small mammals would be to study demographic and genomic changes in relatively common but declining species associated with these habitats, such as *Microtus ochrogaster*, *Peromyscus sonoriensis*, and *Reithrodontomys megalotis*, as these species collectively dominate in grassland habitat through partitioning the available resource base (Hope et al. 2021), space use, and habitat engineering (seed dispersal, nutrient cycling, soil perturbation; Hope et al. 2025).

CONCLUSIONS

Mammalogists are still far from an accurate understanding of the diversity or distributions of mammals and how they vary through time. Obtaining this knowledge is a prerequisite for effectively maintaining biodiversity and for gleaning insight from these species into diverse processes of change. Specimen resources in museum collections have advanced substantially from the earliest documentation of species to modern facilities that enhance knowledge and understanding that benefit the natural world as well as our own well-being (e.g., Cook and Light 2019). Concerted sampling of mammals through Kansas across a five-year period, as reported herein, clearly supports a critical need for continued robust and targeted sampling that can fuel progressive and integrative science, as well as promote diverse skillsets among the next generation of biodiversity scientists, educators, and land managers.

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Appendix

Specimens examined.—Specimens include samples that were sequenced and analyzed for the first time here, or compiled specimen records for sequences based on GenBank accessions from previously published work. For each species, new samples include the following data: lineages consistent with color and shape of datapoints presented in phylogenies and maps, respectively; higher level locality information; latitude; longitude; museum catalog number; museum tissue number; and GenBank accession number. For previously published sequences, the following data are provided: lineage; latitude; longitude; and GenBank accession. New samples with genetic data for this study are listed in bold font. New county records that were sequenced are listed as both bold font and italicized, and correspond to occurrences as reported in Table 1.

Blarina hylophaga (7 new samples; 35 previously published sequences).—Blue Circle: USA: Kansas; **Geary, 39.07, -96.61, MSB:Mamm:330611, NK269992, PV725787**; **39.07, -96.61, MSB:Mamm:330612, NK269993, PV725788**; **39.07, -96.61, MSB:Mamm:330613, NK269994, PV725789**; **Republic, 39.70, -97.92, MSB:Mamm:345500, NK306506, PV725793**; **Riley, 39.10, -96.61, MSB:Mamm:331689, NK296269, PV725790**; **39.37, -96.84, MSB:Mamm:331697, NK296268, PV725791**; **39.07, -96.57, MSB:Mamm:305558, NK269690, PV725792**; 40.18, -98.09, AF395475; 40.11, -95.70, AF395476; 38.56, -97.73, AF395477; 41.08, -100.52, AF395478; 40.11, -95.70, AF395479; 40.18, -98.09, AF395480; 41.08, -100.52, AF395481; 38.56, -97.73, AF395482; 38.60, -98.40, JF912177; 38.60, -98.40, JF912178; 34.36, -98.15, KF735661; 36.11, -97.21, KF735662; Orange Square: 30.19, -97.32, AY546659; 30.19, -97.32, AY546660; 30.19, -97.32, AY546661; 30.19, -97.32, AY546662; 30.19, -97.32, AY546663; 30.19, -97.32, AY546664; 30.19, -97.32, AY546665; 30.19, -97.32, AY546666; 30.19, -97.32, AY546667; 30.19, -97.32, AY546668; 30.19, -97.32, AY546669; 30.19, -97.32, AY546670; 30.19, -97.32, AY546671; 30.19, -97.32, AY546672; 30.19, -97.32, AY546673; 30.19, -97.32, AY546674; 28.31, -96.81, AY546675; 28.31, -96.81, AY546676; 28.31, -96.81, AY546677; 28.31, -96.81, AY546678; 30.19, -97.32, AY546679; 30.00, -97.25, AY546680; 30.00, -97.25, AY546681.

Chaetodipus hispidus (2 new samples; 52 previously published sequences).—Blue Circle: USA: Kansas; **Morton, 37.12, -101.90, MSB:Mamm:345463, NK306161, PV725794**; **Scott, 38.69, -100.94, MSB:Mamm:345742, NK306049, PV725795**; 36.61, -103.10, JQ411946; 41.84, -103.71, JQ411947; 38.18, -99.22, JQ411948; 40.67, -104.37, JQ411949; 34.00, -103.64, JQ411950; 31.50, -99.27, JQ411953; 31.10, -101.18, JQ411954; 31.37, -101.81, JQ411955; 31.67, -98.97, JQ411956; 31.06, -93.09, JQ411961; 37.25, -103.50, JQ411965; 30.56, -103.94, JQ411966; 36.02, -104.73, JQ411969; 34.58, -98.63, JQ411971; 32.99, -101.36, JQ411972; 32.25, -105.88, JQ411973; 31.26, -99.12, JQ411974; 34.94, -100.89, JQ411975; 32.71, -97.77, JQ411976; 26.32, -97.82, JQ411977; 42.86, -100.06, JQ411978; 33.34, -101.44, JQ411979; 29.70, -96.74, JQ411980; 31.98, -95.88, JQ411981; 30.75, -99.23, JQ411982; 44.01, -102.56, JQ411985; 44.47, -102.48, JQ411986; 37.80, -98.42, JQ411992; 39.60, -96.49, JQ412003; Orange Square: 26.32, -97.82, AF172832; 28.53, -99.74, JQ411945; 29.33, -99.28, JQ411951; 28.29, -99.49, JQ411952; 26.20, -98.35, JQ411960; 26.94, -97.79, JQ411962; 27.80, -98.21, JQ411967; 27.81, -98.23, JQ411970; 28.22, -100.72, JQ411988; 23.22, -102.85, JQ411989; 29.32, -100.93, JQ411990; 24.85, -99.60, JQ411994; 24.35, -103.46, JQ412000; Red Triangle: 31.81, -109.06, JQ411944; 27.04, -105.24, JQ411959; 31.67, -108.83, JQ411963; 30.83, -108.50, JQ411964; 31.40, -108.87, JQ411968; 32.17, -111.70, JQ411987; 39.49, -95.68, JQ411993; Cyan Diamond: 25.33, -101.62, JQ411958; 25.33, -101.62, JQ411983; 25.34, -101.58, JQ411984.

Cratogeomys castanops (1 new sample; 21 previously published sequences).—Blue Circle: USA: Kansas; **Ford, 37.85, -99.86, MSB:Mamm:347238, NK307116, PV725796**; 33.72, -102.77, EF607251; 34.45, -103.88, EF607252; 32.60, -106.27, EF607255; 25.58, -103.45, EF607265; 33.39, -103.82, EF607274; 35.82, -101.97, EF607275; 36.88, -102.91, EF607276; 29.47, -103.99, EF607277; 25.88, -104.81, EF607245; 26.62, -102.23, EF607246; 27.33, -102.42, EF607247; 27.33, -102.42, EF607248; 27.33, -102.42, EF607249; 25.50, -103.60, EF607253; 24.04, -104.62, EF607254; 33.94, -105.78, EF607256; 25.31, -101.62, EF607261; 26.20, -101.34, EF607264; 27.01, -102.08, EF607266; 25.70, -103.15, EF607272; 29.82, -106.36, EF607273.

Cryptotis parvus (59 previously published sequences).—Blue Circle: 31.44, -100.39, AB175135; 41.60, -99.60, AF395483; 41.60, -99.60, AF395484; 38.90, -95.27, KT876869; 38.50, -92.50, MF158114; 31.22, -99.84, PQ278313; 31.63, -98.93, PQ278314; 31.64, -98.94, PQ278315; 31.64, -98.94, PQ278316; 29.58, -96.44, PQ278318; 31.50, -100.17, PQ278319; 39.91, -105.22, PQ278320; 44.56, -104.02, PQ278321; 38.31, -104.30, PQ278322; 30.38, -91.22, PQ278324; 29.67, -92.76, PQ278325; 30.38, -91.22, PQ278326; 31.08, -93.07, PQ278327; 29.34, -94.90, PQ278330; 35.18, -103.70, PQ278331; 35.18, -103.70, PQ278336; 35.18, -103.70, PQ278337; 39.19, -96.40, PQ278338; 39.19, -96.40, PQ278339; 38.45, -100.91, PQ278340; 33.46, -104.40, PQ278342; 35.21, -103.74, PQ278349; 35.15, -103.61, PQ278350; 35.14, -103.61, PQ278351; 33.28, -104.35, PQ278352; 33.48, -104.43, PQ278353; 33.46, -104.41, PQ278354; 33.46, -104.41, PQ278355; 39.19, -96.40, PQ278358; 38.65, -98.55, PQ278359; 39.19, -96.40, PQ278360; 34.91, -104.68, PQ278361; 34.44, -104.22, PQ278366; 36.48, -103.13, PQ278367; 36.70, -103.21, PQ278369; 36.70, -103.21, PQ278370; 34.91, -104.68, PQ278371; 36.70, -103.21, PQ278373; 33.19, -104.34, PQ278378; 37.12, -101.90, PQ278379; 37.12, -101.90, PQ278380; 37.12, -101.90, PQ278381; 37.12, -101.90, PQ278383; 38.48, -98.67, PQ278384; 36.04, -104.71, PQ278385; 36.41, -104.65, PQ278386; 36.61, -104.63, PQ278387; 36.61, -104.63, PQ278388; 36.42, -104.66, PQ278390; 27.19, -97.83, PQ278394; Orange Square: 38.20, -77.60, KT876866; 38.20, -77.60, KT876867; 38.50, -77.10, KT876868; 39.08, -77.96, PQ278341.

Dipodomys ordii (1 new sample; 14 previously published sequences).—Blue Circle: USA: Kansas; **Cimmaron, 37.10, -101.94, MSB:Mamm:345816, NK306135, PV725797**; 42.07, -97.97, AF172836; 34.44, -104.01, AF173501; 25.88, -104.81, AY926365; 32.10, -109.92, OK135025; 34.36, -106.89, OK135045; 34.47, -108.71, OK135055; 34.36, -106.89, OK135121; 32.10, -109.92, OK135122; 33.67, -101.52, U59180; Orange Square: 34.36, -106.89, OK135106; 35.11, -108.76, OK135111; 35.07, -108.85, OK135118; 35.15, -107.85, OK135124; 35.15, -107.85, OK135138.

Geomys bursarius (2 new samples; 73 previously published sequences).—Blue Circle: 43.42, -95.10, PP848353; 41.29, -88.78, PP848354; 39.78, -90.15, PP848358; 38.59, -90.00, PP848359; 38.56, -97.69, PP848360; 39.04, -95.35, PP848361; 37.97, -96.16, PP848364; 39.72, -94.91, PP848365; 41.16, -87.26, PP848366; 40.77, -89.02, PP848367; 41.02, -89.36, PP848368; 36.11, -97.11, PP848369; 41.66, -93.11, PP848370; 41.38, -91.37, PP848371; 34.42, -99.71, PP848373; 34.42, -99.71, PP848374; 43.98, -97.09, PP848376; 37.42, -100.18, PP848377; 41.37, -88.43, PP848378; 40.76, -89.27, PP848379; 38.18, -98.51, PP848380; 45.52, -97.31, PP848381; 40.72, -89.27, PP848385; 39.00, -95.28, PP848386; 38.65, -90.04, PP848387; 45.36, -92.63, PP848389; 44.31, -91.50, PP848390; 44.31, -91.50, PP848391; 34.74, -97.22, PP848394; 35.05, -97.90, PP848395; 43.09, -90.90, PP848396; 40.26, -89.99, PP848397; 40.54, -88.84, PP848405; 39.92, -90.35, PP848406; 40.49, -88.81, PP848407; 41.06, -87.70, PP848408; Orange Square: 38.60, -90.70, AF158688; 34.20, -99.00, AF158690; 40.00, -89.00, AF158691; 45.50, -95.70, AF158693; 41.60, -95.40, AF158694; 36.10, -91.50, AF158697; 45.40, -93.20, AY393941; 38.70, -89.99, AY393942; 37.90, -98.20, AY393943; 32.45, -97.80, AY393944; 40.10, -95.23, AY393945; 38.73, -90.48, AY393946; 42.02, -97.73, EU332153; 42.05, -97.81, EU332154; 34.88, -100.88, OQ692236; 34.88, -100.88, OQ692237; 31.50, -97.00, OQ692238; 31.50, -97.00, OQ692239; 31.50, -97.00, OQ692240; 31.40, -97.05, OQ692241; 31.50, -97.00, OQ692245; 38.64, -90.54, PP848372; 38.66, -90.46, PP848375; 38.51, -90.32, PP848392; Red Triangle: 37.00, -102.70, AF158692; 39.20, -100.90, AF158695; 40.10, -99.40, AY393948; 41.13, -101.20, EU332155; 41.13, -101.20, EU332156; 41.02, -100.53, EU332157; 37.14, -100.78, PP848362; 37.14, -100.78, PP848363; Cyan Diamond: 42.00, -102.00, AF158696; 40.90, -99.40, AY393950; Purple Star: 29.21, -99.46, AY393964; 30.76, -99.26, AY393966; 30.26, -98.69, AY395295; Green Inverted Triangle: USA: Kansas; ***Scott, 38.67, -100.92, MSB:Mamm:345623, NK306070, PV725798***; ***38.67, -100.92, MSB:Mamm:345680, NK306019, PV725799***.

Glaucomys volans (4 new samples; 44 previously published sequences).—Blue Circle: USA: North Carolina; **Bladen, 36.15, -78.71, KSB:Mamm:2309, KT1572, PV725800**; Kansas; ***Labette, 37.26, -95.21, KSB:Mamm:2599, KT2301, PV725801; 37.26, -95.21, KSB:Mamm:2600, KT2302, PV725802***; 30.45, -91.18, AF063061; 30.45, -91.18, AF063062; 36.25, -82.16, AF063063; 36.25, -82.16, AF063064; 36.25, -82.16, AF063065; 38.26, -81.43, AF063066; 30.27, -82.49, AF157921; 27.36, -81.25, AY703884; 27.36, -81.25, AY703885; 27.36, -81.25, AY703886; 27.36, -81.25, AY703887; 27.36, -81.25, AY703888; 27.36, -81.25, AY703889; 27.36, -81.25, AY703890; 40.24, -79.47, AY703891; 40.24, -79.47, AY703892; 40.24, -79.47, AY703893; 40.24, -79.47, AY703894; 37.31, -89.52, AY703895; 37.31, -89.52, AY703896; 37.31, -89.52, AY703897; 44.43, -65.21, AY942859; 44.93, -65.07, AY942860; 45.08, -64.30, AY942861; 44.93, -65.07, AY942862; 46.60, -83.90, AY942863; 46.60, -83.90, AY942864; 46.60, -83.90, AY942865; 37.31, -89.52, GU473212; 40.24, -79.47, GU473215; 40.24, -79.47, GU473216; 40.34, -76.00, MT259089; 40.34, -76.00, NC050026; Orange Square: USA: Kansas: **Cherokee, 37.04, -94.64, MSB:Mamm:346182, NK306590, PV725803**; 35.10, -93.10, AY942866; 32.55, -94.32, GU473217; 32.55, -94.32, GU473218; Red Triangle: 14.75, -90.98, GU473173; 16.73, -92.63, GU473177; 22.12, -100.96, GU473183; 16.90, -92.09, GU473189; 16.73, -92.63, GU473191; 16.70, -92.30, GU473196; Cyan Diamond: 17.30, -99.40, GU473197; 17.60, -99.52, GU473201.

Ictidomys tridecemlineatus (7 new samples; 50 previously published sequences).—Blue Circle: CANADA: Manitoba; **49.20, -96.78, MSB:Mamm:331420, NK305107, PV725804**; **49.48, -99.85, MSB:Mamm:332122, NK304771, PV725805**; **49.48, -99.85, MSB:Mamm:332205, NK304767, PV725806**; **49.67, -99.17, MSB:Mamm:332226, NK304848, PV725807**; **49.71, -99.26, MSB:Mamm:332252, NK304884, PV725808**; **50.40, -101.28, MSB:Mamm:332653, NK297775, PV725809**; **50.40, -101.28, MSB:Mamm:332654, NK297776, PV725810**; 47.90, -97.50, JX902804; 47.90, -97.50, JX902805; 47.90, -97.50, JX902806; 47.90, -97.50, JX902807; 42.85, -106.36, JX902808; 42.85, -106.36, JX902809; 36.90, -105.57, JX902858; 36.90, -105.57, JX902859; 39.55, -87.35, JX902877; 42.08, -93.62, JX902878; 42.08, -93.62, JX902879; 39.19, -105.88, JX902880; 39.19, -105.88, JX902881; 39.19, -105.88, JX902882; 39.19, -105.88, JX902883; 39.19, -105.88, JX902884; 39.55, -87.35, JX902885; 39.55, -87.35, JX902886; 39.55, -87.35, JX902887; 39.55, -87.35, JX902888; 39.55, -87.35, JX902889; 42.08, -93.62, JX902890; 42.08, -93.62, JX902891; 42.08, -93.62, JX902892; 38.95, -95.67, JX902893; 38.95, -95.67, JX902894; 38.95, -95.67, JX902895; 38.95, -95.67, JX902896; 38.95, -95.67, JX902897; 38.95, -95.67, JX902898; 38.95, -95.67, JX902899; 38.95, -95.67, JX902900; 38.95, -95.67, JX902901; 38.95, -95.67, JX902902; 38.95, -95.67, JX902903; 39.39, -101.05, JX902904; 35.59, -105.22, JX902906; 35.59, -105.22, JX902907; 35.59, -105.22, JX902908; 35.59, -105.22, JX902909; 35.59, -105.22, JX902910; 44.04, -103.21, JX902911; 42.88, -90.20, JX902919; 42.88, -90.20, JX902920; 42.88, -90.20, JX902921; 42.88, -90.20, JX902922; 44.41, -104.38, JX902923; 42.06, -104.22, JX902924; 33.60, -101.89, JX902926; 42.07, -97.97, JX902928.

Microtus ochrogaster (7 new samples; 18 previously published sequences).—Blue Circle: USA: Kansas; **Republic, 39.70, -97.92, MSB:Mamm:345496, NK306231, PV725814**; **39.70, -97.92, MSB:Mamm:345826, NK306247, PV725815**; **39.70, -97.92, MSB:Mamm:345845, NK306232, PV725816**; **Riley, 39.08, -96.57, MSB:Mamm:330715, NK269952, PV725812**; **39.08, -96.60, MSB:Mamm:330719, NK269956, PV725813**; **Russell, 38.95, -98.66, MSB:Mamm:330565, NK234472, PV725811**; 45.28, -109.10, AF163901; 40.35, -86.82, DQ432006; 38.50, -98.40, DQ663671; 40.20, -89.30, GU954318; 35.46, -101.43, KY754041; 38.49, -84.82, MT259132; 38.06, -84.48, MT259134; 38.06, -84.48, MT259135; 38.06, -84.48, MT259136; 38.06, -84.48, MT259137; 38.06, -84.48, MT259138; 38.06, -84.48, MT259139; 38.06, -84.48, MT259140; 38.06, -84.48, MT259142; 38.06, -84.48, MT259143; 38.49, -84.82, MT259147; 38.49, -84.82, MT259148; 38.49, -84.82, MT259149; Orange Square: CANADA: Manitoba; **49.67, -99.17, MSB:Mamm:332216, NK304845, PV725817**.

Microtus pennsylvanicus (18 new samples; 43 previously published sequences).—Blue Circle: USA: Kansas: **Jewell, 39.70, -97.92, MSB:Mamm:345495, NK306230, PV725835**; North Dakota: **Ransom: 46.53, -97.31, MSB:Mamm:330590, NK234497, PV725818**; CANADA: Manitoba; **49.16, -96.72, MSB:Mamm:331370,**

NK305069, PV725819; **49.15, -96.73, MSB:Mamm:331384, NK305075, PV725820**; **49.48, -99.84, MSB:Mamm:332044, NK297939, PV725821**; **49.48, -99.85, MSB:Mamm:332045, NK297940, PV725822**; **49.48, -99.84, MSB:Mamm:332046, NK297941, PV725823**; **49.67, -99.17, MSB:Mamm:332222, NK304844, PV725824**; **49.71, -99.26, MSB:Mamm:332251, NK304883, PV725825**; **49.67, -99.17, MSB:Mamm:332285, NK304842, PV725826**; **49.67, -99.27, MSB:Mamm:332301, NK304936, PV725827**; **49.63, -95.61, MSB:Mamm:332344, NK304984, PV725828**; **49.63, -95.61, MSB:Mamm:332345, NK304985, PV725829**; **49.63, -95.60, MSB:Mamm:332347, NK304988, PV725830**; **49.16, -96.72, MSB:Mamm:332422, NK305071, PV725831**; **51.56, -100.84, MSB:Mamm:332543, NK297647, PV725832**; **50.40, -101.28, MSB:Mamm:332651, NK297773, PV725833**; **50.40, -101.28, MSB:Mamm:332652, NK297774, PV725834**; 36.73, -108.34, AF119279; 43.14, -89.44, AF399694; 43.14, -89.44, AF399698; 30.00, -107.56, GU177626; 40.61, -105.09, KF948531; Orange Square: 58.76, -155.89, KC473470; 58.76, -155.89, KC473471; 58.68, -155.42, KC473472; 65.28, -149.29, KC473473; 64.75, -141.23, KC473474; 64.75, -141.23, KC473475; 64.08, -139.44, KC473476; 62.40, -136.56, KC473477; 62.40, -136.56, KC473478; 61.10, -135.29, KC473479; 61.10, -135.29, KC473480; 60.06, -135.23, KC473481; 60.06, -135.23, KC473482; 63.84, -135.46, KC473483; 63.84, -135.46, KC473484; 63.70, -136.14, KC473485; 63.54, -137.19, KC473486; 63.54, -137.19, KC473487; 64.03, -138.58, KC473488; 66.92, -136.34, KC473489; 66.92, -136.34, KC473490; 63.19, -147.60, KC473491; 61.35, -145.30, KC473492; 59.27, -135.60, KC473493; 59.27, -135.60, KC473494; 57.82, -131.40, KC473495; 57.82, -131.40, KC473496; 62.12, -136.14, KJ556623; Red Triangle: 40.13, -75.11, HM347786; 48.80, -56.20, KM922546; 48.80, -56.20, KM922547; 38.49, -84.82, MT259133; 38.06, -84.48, MT259141; 38.06, -84.48, MT259144; 38.06, -84.48, MT259145; 38.06, -84.48, MT259146; 38.06, -84.48, MT259150; 38.06, -84.48, MT259151.

Neotoma floridana (10 new samples; 9 previously published sequences).—Blue Circle: USA: Kansas; **Barton, 38.50, -98.62, MSB:Mamm:346250, NK306547, PV725842**; ***Cherokee, 37.23, -94.99, MSB:Mamm:346276, NK306576, PV725843***; ***Jewell, 39.89, -98.07, MSB:Mamm:345815, NK306214, PV725840***; ***39.90, -98.07, MSB:Mamm:346051, NK306532, PV725841***; **Montgomery, 37.17, -95.70, MSB:Mamm:346353, NK306725, PV725844**; **Pottawatomie, 39.19, -96.40, MSB:Mamm:331736, NK296264, PV725836**; **Riley, 39.07, -96.58, MSB:Mamm:360678, NK269965, PV725845**; **Scott, 38.69, -100.94, MSB:Mamm:345538, NK306007, PV725837**; **38.69, -100.94, MSB:Mamm:345663, NK306015, PV725838**; **38.69, -100.94, MSB:Mamm:345673, NK306008, PV725839**; 37.87, -92.22, AF294333; 35.35, -95.65, AF294339; 35.28, -97.01, AF294340; 35.84, -96.32, AF294341; 33.65, -97.70, AF294342; 29.21, -95.48, AF294343; 36.14, -97.01, KY754059; Orange Square: 31.77, -91.16, AF294334; 33.82, -80.83, AF294335.

Neotoma micropus (5 new samples; 35 previously published sequences).—Blue Circle: USA: Kansas: **Morton, 37.14, -101.82, MSB:Mamm:345678, NK306163, PV725848**; Texas; **Cameron, 26.18, -97.35, MSB:Mamm:345727, NK305240, PV725849**; 28.33, -99.41, AF186825; 28.33, -99.41, AF186826; 28.33, -99.41, AF186827; 29.56, -102.90, AF298844; 29.56, -102.90, AF298845; 28.50, -96.81, AF376469; 31.81, -106.42, AF376473; 31.81, -106.42, AF376474; 35.84, -101.89, EU286808; 28.41, -99.81, FJ716220; 28.28, -99.10, FJ716221; 32.63, -105.59, KC153473; 32.63, -105.59, KC153474; 34.13, -100.71, KC153477; 34.13, -100.71, KC153478; 34.13, -100.71, KC153479; 33.60, -100.71, KC153480; 33.60, -100.71, KC153481; 33.60, -100.71, KC153482; 31.54, -103.13, KC153485; 33.60, -100.71, KC153486; 33.60, -100.71, KC153487; 28.41, -99.81, KC153488; 28.28, -99.10, KY754063; Orange Square: USA: Kansas: **Clark, 37.39, -99.78, MSB:Mamm:347230, NK307103, PV725850**; **Morton, 37.10, -101.94, MSB:Mamm:345550, NK306111, PV725846**; **37.10, -101.94, MSB:Mamm:345635, NK306162, PV725847**; 34.44, -104.01, AF186822; 34.07, -101.25, DQ179818; 31.77, -103.08, EF989952; 31.77, -103.08, EF989953; 36.79, -102.62, FJ716217; 32.63, -105.59, KC153472; 32.63, -105.59, KC153475; 34.13, -100.71, KC153476; 33.60, -100.71, KC153483; 33.60, -100.71, KC153484; 36.79, -102.62, KC812730.

Onychomys leucogaster (3 new samples; 3 previously published sequences).—Blue Circle: USA: Kansas; **Clark, 37.38, -99.78, MSB:Mamm:347285, NK307136, PV725853**; **Morton, 37.11, -101.94,**

MSB:Mamm:345789, NK306114, PV725852; **Scott, 38.69, -100.94, MSB:Mamm:345697, NK306045, PV725851**; 33.80, -101.10, AY195794; 26.13, -97.20, EF989959; Orange Square: 26.13, -97.20, EF989958.

Peromyscus leucopus (102 new samples; 36 previously published sequences).—Blue Circle: USA: Kansas; **Barton, 38.44891, -98.75089, MSB:Mamm:346153, NK306544, PV700442**; **Chautauqua, 37.01759, -95.96796, MSB:Mamm:346549, NK306737, PV700447**; **Cherokee, 37.20866, -95.00424, KSB:Mamm:1852, KT2004, PV700430**; **37.23057, -94.99105, MSB:Mamm:346265, NK306564, PV700443**; **37.22720, -94.98954, MSB:Mamm:346285, NK306565, PV700444**; **Greenwood, 37.65966, -96.33709, KSB:Mamm:775, KT0317, PV725873**; **Jewell, 39.89455, -98.07394, MSB:Mamm:345605, NK306193, PV700437**; **39.89420, -98.07378, MSB:Mamm:345836, NK306194, PV700438**; **39.89268, -98.07310, MSB:Mamm:345669, NK306205, PV700439**; **Lyon, 38.53015, -95.97262, KSB:Mamm:1464, KT1080, PV725861**; **Marshall, 39.71124, -96.62733, KSB:Mamm:234, KT0376, PV725866**; **39.70765, -96.62148, KSB:Mamm:262, KT0386, PV725867**; **Miami, 38.39880, -94.65171, KSB:Mamm:133, KT0615, PV690519**; **Montgomery, 37.24480, -95.88008, MSB:Mamm:346506, NK306713, PV700446**; **Osage, 38.60981, -95.58775, KSB:Mamm:1466, KT1083, PV690528**; **38.60996, -95.58736, KSB:Mamm:1410, KT1085, PV700429**; **38.51947, -95.88339, KSB:Mamm:1339, KT1088, PV725857**; **38.60971, -95.58776, KSB:Mamm:1366, KT1084, PV725858**; **38.51164, -95.87760, KSB:Mamm:158, KT0905, PV725863**; **Osborne, 39.36422, -98.88509, KSB:Mamm:366, KT0163, PV725868**; **39.36422, -98.88509, KSB:Mamm:493, KT0166, PV725870**; **39.36341, -98.87933, KSB:Mamm:955, KT0167, PV725880**; **Pottawatomie, 39.19496, -96.40307, KSB:Mamm:944, KT0846, PV725879**; **Republic, 39.69545, -97.92265, MSB:Mamm:345516, NK306250, PV700440**; **Riley**; **39.07348, -96.57906, KSB:Mamm:1492, KT0965, PV690524**; **39.07506, -96.59674, KSB:Mamm:1443, KT0983, PV690525**; **39.07405, -96.58958, KSB:Mamm:1220, KT1074, PV690526**; **39.07629, -96.59803, KSB:Mamm:1191, KT1059, PV725855**; **39.07381, -96.57932, KSB:Mamm:1414, KT0967, PV725859**; **39.07318, -96.57871, KSB:Mamm:1440, KT0961, PV725860**; **39.07506, -96.59674, KSB:Mamm:1508, KT1017, PV725862**; **39.10340, -96.61060, KSB:Mamm:194, KT0921, PV725864**; **39.10300, -96.61000, KSB:Mamm:195, KT0923, PV725865**; **39.10350, -96.60770, KSB:Mamm:841, KT0893, PV725874**; **39.10300, -96.60700, KSB:Mamm:845, KT0897, PV725875**; **39.10104, -96.60760, KSB:Mamm:876, KT0931, PV725876**; **39.44107, -96.73106, KSB:Mamm:93, KT0833, PV725878**; **Scott, 38.68682, -100.93713, MSB:Mamm:345521, NK305999, PV700433**; **38.68717, -100.93806, MSB:Mamm:345687, NK306036, PV700434**; **Trego, 38.77797, -99.78357, KSB:Mamm:375, KT0160, PV725869**; **Washington, 39.64879, -96.86558, KSB:Mamm:102, KT0300, PV725854**; **39.64758, -96.86312, KSB:Mamm:58, KT0312, PV725871**; **39.64758, -96.86312, KSB:Mamm:6, KT0314, PV725872**; **39.64879, -96.86558, KSB:Mamm:92, KT0302, PV725877**; Missouri; **Harrison, 40.37074, -93.82199, MSB:Mamm:347740, NK307218, PV700450**; **40.37365, -93.82480, MSB:Mamm:347808, NK307233, PV700451**; Wisconsin; **Trempealeau, 44.43800, -91.51900, KSB:Mamm:1202, KT1064, PV725856**; CANADA, Manitoba, **49.17253, -96.67281, MSB:Mamm:332417, NK305068**; 44.33751, -89.38279, KX784151; 44.33751, -89.38279, KX784152; 44.33751, -89.38279, KX784153; 44.33751, -89.38279, KX784154; 44.33751, -89.38279, KX784155; 44.33751, -89.38279, KX784156; 44.33751, -89.38279, KX784157; 44.33751, -89.38279, KX784158; 44.33751, -89.38279, KX784159; 44.33751, -89.38279, KX784160; 45.33054, -74.39468, KX784161; 45.33054, -74.39468, KX784162; Orange Square: USA: Kansas; **Barber, 37.17468, -98.55135, KSB:Mamm:687, KT0177, PV725903**; **37.38375, -98.96353, KSB:Mamm:138, KT0340, PV725907**; **Clark, 37.38864, -99.77890, MSB:Mamm:347226, NK307100, PV700448**; **Ford, 37.81508, -99.91959, MSB:Mamm:347135, NK307128, PV700449**; **37.73451, -99.56347, KSB:Mamm:120, KT0347, PV725904**; **37.73451, -99.56347, KSB:Mamm:124, KT0354, PV725905**; **37.73264, -99.56423, KSB:Mamm:125, KT0355, PV725906**; **37.73264, -99.56423, KSB:Mamm:154, KT0356, PV725909**; **Harper, 37.17264, -98.18717, KSB:Mamm:675, KT0178, PV725910**; **Kingman, 37.64459, -98.32863, KSB:Mamm:848, KT0326, PV725912**; **Morton, 37.13915, -101.82333, MSB:Mamm:345806, NK306136, PV700435**; **37.11238, -101.92808, MSB:Mamm:345467, NK306178, PV700436**; **Pratt, 37.73451, -98.56347, KSB:Mamm:142, KT0346, PV690518**; **37.49949, -98.55135, KSB:Mamm:686, KT0176, PV700426**; Texas; **Cameron, 26.22603, -97.35121, KSB:Mamm:1455, KT0998, PV725908**; **26.18189, -97.35021, KSB:Mamm:847, KT0880,**

PV725911; 33.75900, -100.81700, AF131926; 23.11343, -99.15850, AY041198; 21.39000, -98.99000, AY859474; 28.32600, -99.40800, DQ000483; 28.32600, -99.40800, DQ973104; 23.76800, -98.20800, KJ810666; 23.76800, -98.20800, KY064165; Red Triangle: USA: Kansas; **Lyon, 38.53455, -95.97232, KSB:Mamm:864, KT0926, PV725917**; Ohio; **Greene, 39.73875, -83.81384, KSB:Mamm:1409, KT1078, PV690527**; **39.73819, -83.82492, KSB:Mamm:788, KT0869, PV700428**; **39.73877, -83.81376, KSB:Mamm:1357, KT1062, PV725913**; **39.79184, -83.84926, KSB:Mamm:1358, KT1068, PV725914**; **39.73880, -83.82655, KSB:Mamm:1359, KT1069, PV725915**; **39.73599, -83.83657, KSB:Mamm:1462, KT1065, PV725916**; 36.91591, -76.19074, KX784130; 41.47069, -71.69830, KX784131; 41.83828, -71.53990, KX784132; 41.83828, -71.53990, KX784133; 41.89218, -71.74695, KX784134; 41.95268, -72.12379, KX784135; 42.64798, -71.18509, KX784136; 44.04947, -71.27383, KX784137; 41.47069, -71.69830, KX784141; 41.47069, -71.69830, KX784142; 41.47069, -71.69830, KX784143; 41.47069, -71.69830, KX784144; 41.47069, -71.69830, KX784145; 45.06207, -73.28488, KX784146; 45.06207, -73.28488, KX784147; 45.55440, -73.33683, KX784166; Cyan Diamond: USA: Kansas; **Barber, 37.43017, -98.69373, KSB:Mamm:128, KT0360, PV725883**; **37.38401, -98.96342, KSB:Mamm:1435, KT0287, PV725886**; **37.38401, -98.96342, KSB:Mamm:88, KT0342, PV725902**; **38.47570, -98.66773, MSB:Mamm:346050, NK306543, PV700441**; **Chautauqua, 37.24833, -96.20165, KSB:Mamm:793, KT0377, PV700427**; **37.01767, -95.96779, MSB:Mamm:346537, NK306709, PV700445**; **37.24833, -96.20165, KSB:Mamm:272, KT0374, PV725892**; **Cherokee, 37.20866, -95.00424, KSB:Mamm:1850, KT2001, PV690529**; **Coffey, 38.29335, -95.70874, KSB:Mamm:46, KT0307, PV725894**; **38.19887, -95.63430, KSB:Mamm:823, KT0322, PV725900**; **Ford, 37.73451, -99.56347, KSB:Mamm:121, KT0349, PV725881**; **Linn, 38.25348, -94.68842, KSB:Mamm:139, KT0650, PV690520**; **38.25357, -94.68863, KSB:Mamm:140, KT0651, PV690521**; **Marshall, 39.75028, -96.67928, KSB:Mamm:763, KT0381, PV725898**; **McPherson, 38.48322, -97.46749, KSB:Mamm:673, KT0185, PV725895; 38.46648, -97.42862, KSB:Mamm:697, KT0190, PV725896**; **38.46648, -97.42862, KSB:Mamm:700, KT0196, PV725897**; **Osage, 38.50835, -95.86148, MSB:Mamm:331800, NK296346, PV700431**; **38.51974, -95.88357, KSB:Mamm:1365, KT1082, PV725885**; **38.51880, -95.88329, KSB:Mamm:184, KT0910, PV725890**; **38.48220, -95.87707, KSB:Mamm:316, KT0847, PV725893**; **Pottawatomie, 39.19496, -96.40307, KSB:Mamm:1263, KT1026, PV725882**; **Riley, 39.07453, -96.58009, KSB:Mamm:1394, KT0963, PV690523**; **39.07450, -96.58746, KSB:Mamm:1304, KT1049, PV725884**; **39.07441, -96.58997, KSB:Mamm:1441, KT0962, PV725887**; **39.09145, -96.58222, KSB:Mamm:1496, KT0977, PV725888**; **39.09136, -96.58224, KSB:Mamm:1501, KT0981, PV725889**; **Shawnee, 39.20976, -95.80261, KSB:Mamm:736, KT0665, PV690522**; **39.06555, -95.90796, KSB:Mamm:255, KT0397, PV725891**; **39.06555, -95.90796, KSB:Mamm:84, KT0308, PV725901**; **Wabaunsee, 39.10777, -96.19262, KSB:Mamm:767, KT0393, PV725899**; 36.14500, -97.00700, KY754106.

Peromyscus sonoriensis (19 new samples; 94 previously published sequences).—Blue Circle: USA: Kansas; **Barton, 38.45, -98.74, MSB:Mamm:346049, NK306542, PV725927**; **38.45, -98.74, MSB:Mamm:346252, NK306550, PV725929**; **38.50, -98.62, MSB:Mamm:346253, NK306551, PV725930**; **Cherokee, 37.21, -95.01, KSB:Mamm:1825, KT2046, PV725919**; **37.21, -95.02, KSB:Mamm:1881, KT2060, PV725920**; **37.23, -95.01, MSB:Mamm:346154, NK306592, PV725928**; **Harper, 37.10, -98.19, KSB:Mamm:1064, KT0281, PV725918**; **McPherson, 38.48, -97.46, KSB:Mamm:674, KT0186, PV725921**; **Montgomery, 37.01, -95.97, MSB:Mamm:346558, NK306762, PV725931**; **Scott, 38.69, -100.94, MSB:Mamm:345533, NK306012, PV725923**; **38.69, -100.94, MSB:Mamm:345691, NK306039, PV725924**; **38.69, -100.94, MSB:Mamm:345701, NK306056, PV725925**; **38.69, -100.94, MSB:Mamm:345839, NK306010, PV725926**; **Washington, 39.65, -96.86, KSB:Mamm:98, KT0295, PV725922**; 34.02, -103.62, DQ385628; 34.02, -103.62, DQ385629; 34.02, -103.62, DQ385630; 34.02, -103.62, DQ385631; 34.28, -103.79, DQ385632; 41.60, -93.61, DQ385633; 41.60, -93.61, DQ385634; 41.60, -93.61, DQ385635; 41.60, -93.61, DQ385636; 41.60, -93.61, DQ385637; 38.20, -99.28, EF666206; 38.20, -99.28, EF666208; 38.20, -99.28, EF666209; 38.20, -99.28, EF666210; 38.20, -99.28, EF666211; 40.12, -102.73, EF666223; Orange Square: CANADA: Manitoba; **49.48, -99.84, MSB:Mamm:332088, NK297986, PV725932**; **49.45, -99.85, MSB:Mamm:332141, NK304790, PV725933**;

49.66, -99.16, MSB:Mamm:332214, NK304836, PV725934; **49.66, -99.16, MSB:Mamm:332237, NK304864, PV725935**; **50.40, -101.30, MSB:Mamm:332669, NK297792, PV725936**; 33.53, -108.54, DQ385651; 33.91, -108.53, DQ385662; 36.20, -108.31, DQ385667; 36.20, -108.31, DQ385668; 36.20, -108.31, DQ385669; 36.20, -108.31, DQ385670; 36.20, -108.31, DQ385671; 43.38, -116.46, DQ385672; 43.38, -116.46, DQ385673; 43.38, -116.46, DQ385674; 43.38, -116.46, DQ385675; 45.55, -111.04, DQ385676; 45.55, -111.04, DQ385677; 45.55, -111.04, DQ385678; 45.55, -111.04, DQ385679; 39.42, -118.72, DQ385680; 39.42, -118.72, DQ385681; 39.42, -118.72, DQ385682; 40.45, -112.00, DQ385684; 40.46, -112.01, DQ385685; 40.45, -112.00, DQ385686; 40.45, -112.00, DQ385687; 40.45, -112.00, DQ385688; 47.22, -120.99, DQ385689; 37.77, -119.26, EF666155; 37.58, -118.24, EF666179; 37.58, -118.24, EF666182; 39.56, -114.52, EF666189; 39.56, -114.52, EF666190; 39.56, -114.52, EF666193; 39.56, -114.52, EF666194; 39.69, -105.64, EF666237; 39.69, -105.64, EF666240; 39.69, -105.64, EF666241; 40.67, -104.37, EF666242; 40.67, -104.37, EF666243; 40.67, -104.37, EF666250; 40.67, -104.37, EF666251; 40.67, -104.37, EF666252; 40.67, -104.37, EF666253; 40.75, -111.93, EF666254; 40.02, -105.27, EF666272; 40.02, -105.27, EF666273; 40.02, -105.27, EF666277; 42.08, -113.71, FJ800584; 51.03, -115.03, KF949166; 60.01, -111.54, KF949170; Red Triangle: 61.35, -145.30, FJ415092; 61.35, -145.30, FJ415093; 61.35, -145.30, FJ415094; 61.34, -145.31, FJ415095; 57.42, -130.24, KF949241; 61.10, -135.29, KF949243; 61.10, -135.29, KF949244; 60.14, -124.06, KF949245; 60.01, -133.80, KF949246; 58.38, -129.92, KF949248; 60.06, -135.23, KF949249; 59.56, -133.67, KF949250; 59.56, -133.67, KF949251; 57.62, -130.08, KF949252; 60.10, -128.60, KF949262; 59.56, -133.67, KF949266; Cyan Diamond: 47.72, -122.72, DQ385694; 48.20, -121.92, DQ385695; 47.17, -121.76, DQ385696; 47.09, -122.60, DQ385697; 48.93, -125.55, DQ385698; 48.93, -125.55, DQ385699; 48.93, -125.55, DQ385700; 48.93, -125.55, DQ385701; 48.93, -125.55, DQ385702; Purple Star: 41.00, -124.09, DQ385703; 37.99, -122.79, EU006766; 38.01, -122.80, EU006767; 38.01, -122.80, EU006768; 38.01, -122.80, EU006769; 38.10, -122.90, EU006770.

Reithrodontomys fulvescens (4 new samples; 22 previously published sequences).—Blue Circle: USA: Kansas; **Cherokee, 37.25, -94.96, MSB:Mamm:346146, NK306662, PV725937**; **Montgomery, 37.02, -95.97, MSB:Mamm:346151, NK306688, PV725938**; **37.01, -95.97, MSB:Mamm:346171, NK306689, PV725939**; **37.01, -95.97, MSB:Mamm:346359, NK306720, PV725940**; 35.34, -95.65, AF176257; 21.85, -105.22, EF990000; 23.77, -98.22, EF990001; 31.65, -98.96, EF990002; 31.65, -98.96, EF990003; 19.04, -98.21, KF303326; 23.73, -103.98, KF303328; 31.53, -97.15, KF303329; 30.15, -94.74, KF303330; 35.05, -98.7, KF303331; 25.16, -105.5, KF303332; 28.51, -96.81, KF303333; 31.9, -95.9, KF303334; 25.9, -97.5, KF303335; 23.68, -100.18, KF303336; 23.69, -100.88, KF303337; 19.79, -104.37, KF303338; 19.25, -103.72, KJ526401; 35.34, -95.65, KY754134; Orange Square: 15.39, -92.19, AY859465; 15.77, -96.13, HQ269730; 17.35, -98.27, KF303327.

Reithrodontomys megalotis (7 new samples; 84 previously published sequences).—Blue Circle: USA: Kansas; **Morton, 37.12, -101.89, MSB:Mamm:345595, NK306150, PV725943**; **37.12, -101.89, NK306168, PV725946**; **Riley, 39.08, -96.57, MSB:Mamm:330690, NK269927, PV725941**; **Scott, 38.69, -100.94, MSB:Mamm:345540, NK306052, PV725942; 38.69, -100.94, MSB:Mamm:345686, NK306035, PV725944**; **38.68, -100.94, MSB:Mamm:345695, NK306044, PV725945**; 41.86, -122.82, AF108707; 40.06, -112.88, KP788752; 40.06, -112.88, KP788753; 40.06, -112.88, KP788754; 39.90, -113.71, KP788755; 39.90, -113.71, KP788756; 39.90, -113.71, KP788757; 39.90, -113.71, KP788758; 39.90, -113.71, KP788759; 31.86, -116.61, KR611927; 32.09, -116.55, KR611933; 31.85, -116.12, KR611934; 39.83, -123.80, KR611935; 41.21, -124.11, KR611936; 41.86, -122.82, KR611937; 42.22, -123.61, KR611938; 39.00, -123.09, KR611939; 38.03, -122.87, KR611940; 36.38, -121.56, KR611941; 41.70, -122.49, KR611942; 37.73, -119.56, KR611943; 37.75, -119.54, KR611944; 37.89, -122.23, KR611945; 37.69, -122.31, KU532163; 37.69, -122.31, KU532164; 37.69, -122.31, KU532165; 37.69, -122.31, KU532166; 37.69, -122.31, KU532167; 37.69, -122.31, KU532168; 37.69, -122.31, KU532169; 37.69, -122.31, KU532170; 37.69, -122.31, KU532171; 37.69, -122.31, KU532172; 37.69, -122.31, KU532173; Orange Square: USA: Kansas: **Scott, 38.68, -100.94, MSB:Mamm:345532, NK306011, PV725947**; 33.68, -101.86, AF176248; 34.55, -102.31, AF176249; 23.22, -102.85, KP788742; 23.22, -102.85, KP788743; 23.22, -102.85, KP788744; 23.22, -102.85, KP788745; 25.39, -100.59, KP788746; 26.93, -105.67, KP788747; 21.91, -101.38, KP788748; 21.91, -101.38, KP788749; 21.91, -101.38, KP788750; 21.91, -101.38, KP788751; 23.73, -103.98, KR611928; 23.63, -103.64, KR611929; Red Triangle: 19.03, -99.14, AB618724; 19.03, -99.14, AB618725; 31.88, -106.13, AY859468; 19.11, -99.18, EF990008; 19.11, -99.18, EF990009; 20.57, -99.97, HQ269731; 19.85, -97.36, HQ269732; 19.29, -99.33, KP788717; 17.51, -98.99, KP788718; 17.51, -98.99, KP788719; 17.51, -98.99, KP788720; 17.51, -98.99, KP788721; 17.51, -98.99, KP788722; 17.51, -98.99, KP788723; 17.51, -98.99, KP788724; 17.51, -98.99, KP788725; 17.51, -98.99, KP788726; 19.13, -99.79, KP788727; 19.13, -99.79, KP788728; 19.13, -99.79, KP788729; 19.32, -99.29, KP788730; 19.32, -99.29, KP788731; 20.04, -98.16, KP788732; 20.04, -98.16, KP788733; 18.54, -97.20, KP788734; 18.54, -97.20, KP788735; 18.54, -97.20, KP788736; 18.54, -97.20, KP788737; 18.94, -97.29, KP788738; 19.47, -97.09, KP788739; 18.70, -97.34, KP788740; 18.70, -97.34, KP788741; 17.45, -96.50, KR611930; 17.51, -98.99, KR611931; 19.29, -99.33, KR611932; 19.11, -99.18, KY754136.

Scalopus aquaticus (1 new sample; 8 previously published sequences).—Blue Circle: USA: Kansas; **Riley, 39.11, -96.66, MSB:Mamm:331650, NK296172, PV725948**; 36.18, -86.78, AB076809; 30.92, -91.58, AY170116; 28.06, -96.99, HM461914; 28.06, -96.99, HM461915; 28.06, -96.99, HM461916; 30.92, -91.58, HM461917; 42.45, -92.38, KX754470; 41.40, -90.56, KX754471.

Sigmodon hispidus (18 new samples; 93 previously published sequences).—Blue Circle: USA: Kansas; **Barton, 38.45, -98.75, MSB:Mamm:346293, NK306548, PV725958**; **Chautauqua, 37.02, -95.97, MSB:Mamm:346341, NK306707, PV725959**; **37.02, -95.97, MSB:Mamm:346429, NK306727, PV725961**; **37.02, -95.97, MSB:Mamm:346503, NK306751, PV725962**; **37.02, -95.97, MSB:Mamm:346547, NK306735, PV725964**; **37.02, -95.97, MSB:Mamm:346559, NK306764, PV725965**; **Cherokee, 37.23, -95.01, MSB:Mamm:346273, NK306573, PV725956**; **37.23, -94.99, MSB:Mamm:346277, NK306577, PV725957**; **Montgomery, 37.25, -95.98, MSB:Mamm:346349, NK306721, PV725960**; **37.25, -95.88, MSB:Mamm:346536, NK306753, PV725963**; **Morton, 37.14, -101.82, MSB:Mamm:345790, NK306115, PV725954**; **37.14, -101.82, MSB:Mamm:346046, NK306112, PV725955**; **Riley, 39.07, -96.60, MSB:Mamm:330667, NK269903, PV725951**; **Russell, 38.95, -98.66, MSB:Mamm:330562, NK234469, PV725949**; **38.95, -98.68, MSB:Mamm:330563, NK234470, PV725950**; ***Scott, 38.68, -100.94, MSB:Mamm:345534, NK306014, PV725952; 38.69, -100.94, MSB:Mamm:345752, NK306098, PV725953***; 35.03, -98.24, AF155414; 25.90, -97.50, AF425199; 28.33, -99.41, AF425200; 28.51, -98.45, AF425201; 38.97, -92.74, AF425203; 38.88, -99.33, AF425209; 31.93, -96.06, AF425210; 30.47, -99.78, AF425211; 38.88, -99.33, AF425213; 33.81, -95.68, AF425227; 33.58, -101.85, AF435110; 38.88, -99.33, DQ644054; 38.88, -99.33, DQ644055; 38.88, -99.33, DQ644057; 38.88, -99.33, DQ644058; 38.88, -99.33, DQ644060; 36.62, -96.24, DQ644062; 36.62, -96.24, DQ644064; 36.62, -96.24, DQ644065; 36.62, -96.24, DQ644066; 36.62, -96.24, DQ644067; 32.18, -98.22, DQ644069; 32.18, -98.22, DQ644070; 32.18, -98.22, DQ644073; 32.18, -98.22, DQ644074; 31.76, -95.63, DQ644078; 31.76, -95.63, DQ644079; 31.76, -95.63, DQ644086; 31.76, -95.63, DQ644087; 31.76, -95.63, DQ644089; 24.27, -98.84, EU073177; 25.59, -99.99, EU073178; 33.68, -101.80, EU293741; 33.68, -101.80, EU293744; 33.68, -101.80, EU293746; 38.88, -99.33, HQ290325; 38.88, -99.33, HQ290330; 32.18, -98.22, HQ290335; 32.18, -98.22, HQ290336; 32.18, -98.22, HQ290338; 32.18, -98.22, HQ290346; 32.18, -98.22, HQ290347; 32.18, -98.22, HQ290348; Orange Square: USA: Kansas; **Morton, 37.14, -101.82, MSB:Mamm:345849, NK306183, PV725966**; 32.55, -114.79, AF155421; 32.84, -106.10, AF188198; 34.12, -100.34, AF425212; 31.76, -95.63, DQ644077; 33.68, -101.80, EU293748; 32.55, -114.79, EU293749; 32.55, -114.79, EU293750; 32.55, -114.79, EU293753; 32.55, -114.79, EU293754; 32.55, -114.79, EU293756; 32.55, -114.79, EU293757; 31.88, -106.38, HQ326703; 31.88, -106.38, HQ326704; 32.38, -106.09, HQ326705; 32.38, -106.09, HQ326707; 32.38, -106.09, HQ326709; 32.38, -106.09, HQ326711; 32.38, -106.09, HQ326712; 32.38, -106.09, HQ326713; 32.38, -106.09, HQ326714; Red Triangle: 25.49, -80.39, AF155420; 35.36, -90.02, AF425202; 30.57, -91.10, AF425204; 32.49, -93.71, AF425205; 30.56, -86.18, AF425206; 27.85, -80.45, AF425207; 27.85, -80.45, AF425208; 31.48, -94.74, AF425214; 31.25, -93.97, DQ644040; 31.25, -93.97, DQ644041; 31.25, -93.97, DQ644042; 31.25, -93.97, DQ644043; 31.25, -93.97, DQ644044; 31.89, -82.99, DQ644048; 31.89, -82.99, DQ644049; 31.25, -93.97, DQ644050; 30.57, -91.10, DQ644051; 31.76, -95.63, DQ644091; 31.65, -95.07, DQ644093; 31.65, -95.07, DQ644100; 31.65, -95.07, DQ644101; 31.65, -95.07, DQ644102; 31.65, -95.07, DQ644104; 31.34, -94.73, DQ644106; 31.34, -94.73, DQ644109; 31.34, -94.73, DQ644110; 31.16, -94.42, DQ644121; 31.16, -94.42, DQ644124; 31.16, -94.42, DQ644125; 31.16, -94.42, DQ644128.

Sorex cinereus (18 new samples; 61 previously published sequences).—Blue Circle: USA: Kansas; **Jewell, 39.70, -97.92, MSB:Mamm:345827, NK306505**; 37.34, -105.00, JN889400; 37.34, -105.00, JN889401; 41.75, -102.42, JN889407; 41.74, -102.38, JN889409; 41.73, -102.38, JN889410; 37.45, -107.68, JN889419; 35.77, -105.59, JN889442; 36.77, -105.59, JN889445; 35.78, -105.56, JN889446; 35.76, -105.80, JN889469; 39.84, -105.90, JN889589; 43.74, -103.83, JN889592; 35.78, -105.56, JN889600; 43.87, -103.44, JN889626; 35.78, -105.56, JN889633; 35.76, -105.80, JN889689; Orange Square: CANADA: Manitoba; **49.63, -95.60, MSB:Mamm:332336, NK304975, PV725982**; **49.15, -96.73, MSB:Mamm:332389, NK305043, PV725983**; 46.87, -96.46, AY014941; 44.20, -92.65, AY014952; 48.43, -92.00, FJ667512; 41.75, -102.42, JN889408; 44.44, -91.53, JN889411; 49.46, -96.28, JN889478; 46.87, -96.46, JN889484; 47.33, -94.12, JN889603; Red Triangle: 48.37, -58.56, DQ788812; 44.88, -66.98, DQ788817; 42.44, -72.63, JN889476; 44.80, -77.67, JN889481; 53.77, -73.23, JN889642; 46.57, -73.88, JN889677; 49.45, -78.12, JN889679; 43.59, -75.76, JN889687; 35.60, -83.42, JN889695; 46.02, -78.62, JQ085943; Cyan Diamond: CANADA: Manitoba; **50.41, -101.31, MSB:Mamm:332020, NK297910, PV725967**; **49.48, -99.84, MSB:Mamm:332042, NK297937, PV725968**; **49.48, -99.84, MSB:Mamm:332060, NK297958, PV725969**; **49.48, -99.86, MSB:Mamm:332130, NK304778, PV725970**; **49.48, -99.86, MSB:Mamm:332182, NK297970, PV725971**; **49.48, -99.85, MSB:Mamm:332192, NK304811, PV725972**; **49.67, -99.27, MSB:Mamm:332295, NK304921, PV725973**; **49.17, -96.67, MSB:Mamm:332400, NK305056, PV725974**; **51.56, -100.84, MSB:Mamm:332531, NK297634, PV725975**; **51.58, -100.85, MSB:Mamm:332536, NK297639, PV725976**; **51.56, -100.84, MSB:Mamm:332597, NK297711, PV725977**; **51.56, -100.84, MSB:Mamm:332605, NK297720, PV725978**; **51.56, -100.84, MSB:Mamm:332607, NK297722, PV725979**; **51.56, -100.84, MSB:Mamm:332608, NK297723, PV725980**; **50.40, -101.30, MSB:Mamm:332667, NK297789, PV725981**; 55.75, -132.18, AY014947; 51.31, -115.19, DQ788814; 62.10, -145.62, EU088305; 42.95, -110.03, JN889422; 57.84, -131.68, JN889426; 44.57, -112.14, JN889432; 44.57, -112.14, JN889434; 49.26, -117.94, JN889439; 44.17, -115.56, JN889443; 44.95, -113.61, JN889448; 44.95, -113.62, JN889458; 55.33, -128.97, JN889487; 60.39, -117.29, JN889498; 44.97, -113.60, JN889639; 44.95, -113.61, JN889668; 67.60, -159.79, JQ778853; 64.08, -139.44, JQ778855; 68.20, -159.86, JQ778868; 54.85, -163.42, JQ778892; 65.49, -157.59, JQ778908; Purple Star: 43.47, -65.75, DQ788805; 46.47, -63.42, DQ788815; 44.98, -66.98, DQ788816; 45.24, -62.61, JN889462; 45.20, -62.65, JN889464; 44.53, -72.62, JN889474; 44.84, -72.53, JN889688.

Synaptomys cooperi (9 previously published sequences).—Blue Circle: 46.28, -88.49, DQ323957; 39.70, -97.92, OR350877; 47.02, -95.30, OR350878; 47.02, -95.30, OR350879; 47.02, -95.30, OR350880; 49.63, -95.60, OR350919; Orange Circle: 38.31, -80.01, KY754162; 50.93, -95.32, OR350917.

Xerospermophlius spilosoma (2 new samples; 6 previously published sequences).—Blue Circle: USA: Kansas; **Morton, 37.14, -101.82, MSB:Mamm:345765, NK306177, PV725984**; **37.14, -101.82, MSB:Mamm:345809, NK306134, PV725985**; 38.06, -100.89, AF157885; 38.06, -100.89, AF157911; Orange Square: 26.63, -104.13, AF157845; 25.68, -103.37, AF157846; Red Triangle: 22.15, -100.97, JX047299; 34.38, -106.71, JX047.