

What are the evolutionary origins of Kansas mammals? Community assembly dynamics through the Great Plains



Mary E Schmidt*, Kailey R Meacham, Fraser J Combe, Andrew G Hope
Division of Biology, Kansas State University, Manhattan, KS.



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Importance

The Great Plains support mammal species with generally broad distributions across North America. However, these central prairie regions are relatively poorly sampled, especially in terms of genomic resources, and the geographic distributions of genetically distinct lineages within species are not well resolved. We investigated the phylogeographic history of rodents and shrews from the Konza tallgrass prairie in northeastern Kansas to interpret community assembly through this region from an evolutionary perspective.

Hypotheses and Predictions

H₀: Lineages within small mammal species all share common phylogeographic histories; Species with shared evolutionary histories should form stable communities through long-term biodiversity connections.

H₁: Lineages have disparate evolutionary histories, with different geographic origins through North America; Mixed communities may reflect recent community assembly, turnover, and higher potential for new interactions, including transfer of parasites.

Methods

- Collected specimens of the 7 most common small mammal species from Konza long term mammal transects (Fig. 1).
- Extracted DNA from 1 to 5 individuals per species and sequenced the mitochondrial Cytochrome-b gene (Cytb).
- Downloaded, georeferenced, and pruned redundant samples from GenBank representing broadest available range-wide Cytb sampling per species.
- Estimated Bayesian phylogenies in BEAST to assign well-supported lineages, and % lineage divergence in DnaSP.

Findings

- Although the combined distributions of Konza small mammals extend across most of North America (top center map), the distinct lineages occurring on Konza (stars) have more restricted distributions, and disparate evolutionary origins.
- Great Plains endemic lineages occur within *Blarina hylophaga*, *Peromyscus maniculatus*, and *Microtus ochrogaster*. The lineage within *Reithrodontomys megalotis* has a western origin whereas that within *Sigmodon hispidus* has a southern origin. Genetic sampling within both *Cryptotis parva* and *Peromyscus leucopus* is not sufficient to resolve lineage ranges.
- The geographically most proximate genetic sequences to Konza (circled star) for *R. megalotis* and *P. leucopus* belong to different lineages.

Significance

Native grasslands of the Great Plains are becoming increasingly heterogeneous through human-associated land conversion to shrubland, woodland, agriculture, or development. This habitat mosaic will continue to promote mixing of mammals with distant origins across North America, enhancing species interactions, including spread of parasites and vector-borne zoonoses. Comparative phylogeography provides insight into levels of shared evolutionary history and the timeframe of ecological associations among species.

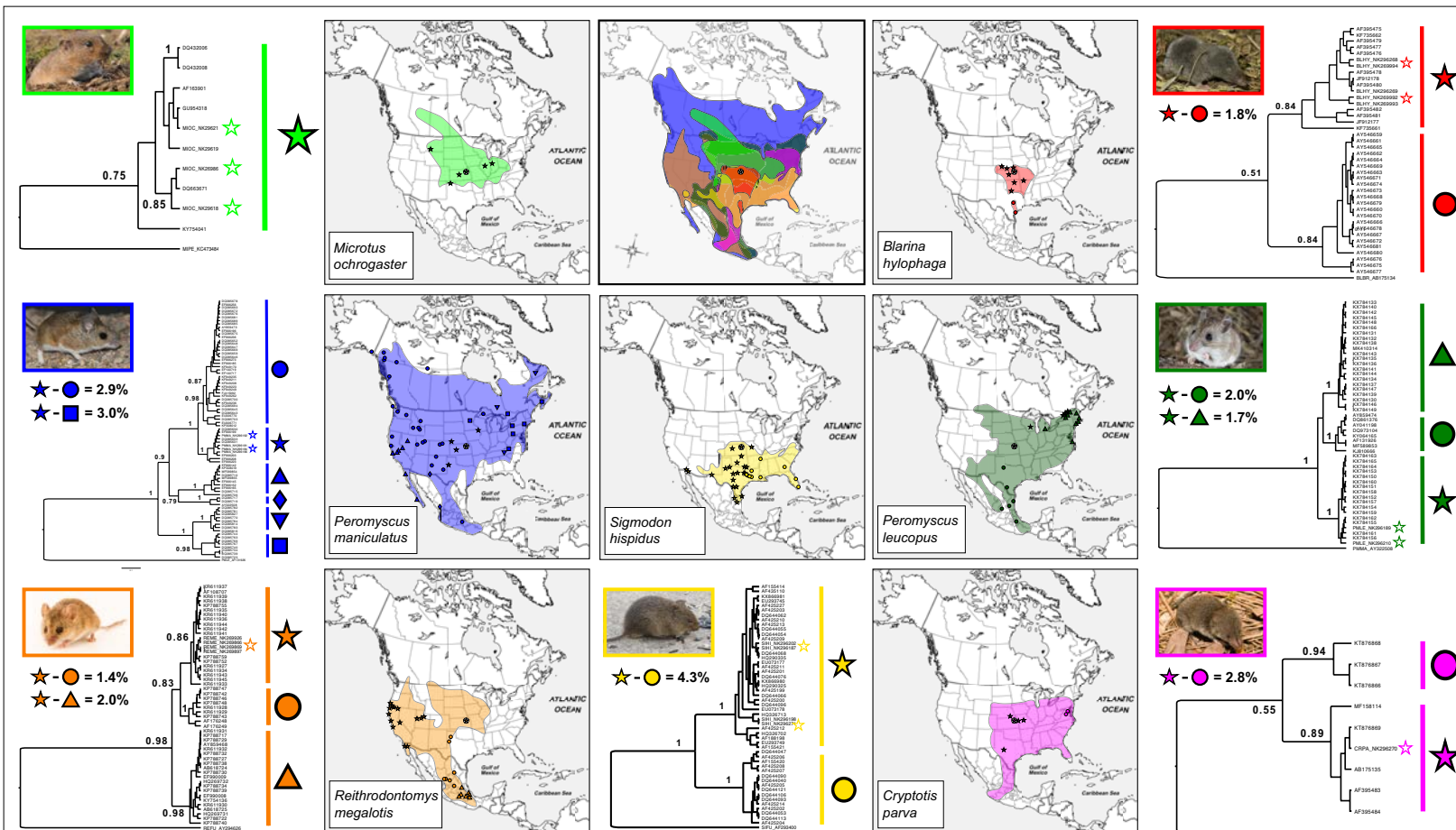


Figure 1. Geographic range and intraspecific phylogenies for the seven numerically dominant species of small mammals occurring on Konza Tallgrass Prairie in northeast Kansas (location denoted by *). mtDNA genetic lineage assignments for Konza small mammals are denoted by stars.