Assessing potential CWD spillover from cervid species to small rodents: implications for new disease vectors

Anjali R. Aaluri[1], Sarah C. Vrla[1], Emily A. Wright[1], Emma K. Roberts[1,2], Matthew J. Buchholz[3], Daniel M. Hardy[2], Warren C. Conway[3], and Robert D. Bradley[1,4]

[1]Department of Biological Sciences, [2]Health Sciences Center, [3]Department of Natural Resources Management, [4]Natural Science Research Laboratory

Introduction

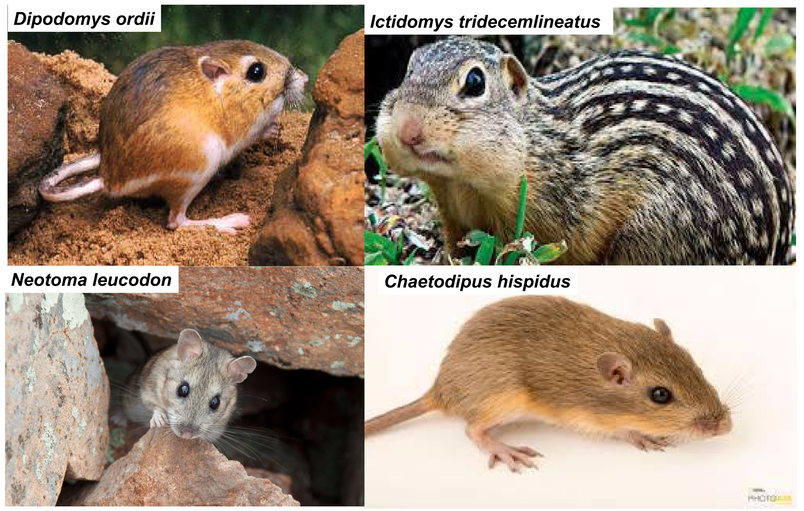
- Prion diseases are caused by an alternative isoform of the protein (PrP) that is encoded for by exon 3 of the prion protein gene (*PRNP)*.
- Certain AA changes infer susceptibility or resistance in ungulates.
- Transmission of prion diseases can occur via ingestion of organic matter containing prions (potentially leading to cross-species infection), familial inheritance, exchange of bodily fluids, spontaneous misfolding of the prion protein, etc.
- Chronic Wasting Disease (CWD) is a prion disease of deer species. It is believed that CWD may have either developed spontaneously or been derived from scrapie, a prion disease of sheep and goats. CWD is widespread, occurring internationally.
- It is not entirely clear if, or how, CWD could spread to non-deer species. One hypothesis is that small mammals (i.e., rodents) that overlap with cervid species could be exposed to CWD-like prions through contact with infected organic matter and act as vectors to spread the disease.
- Assessing *PRNP* sequences in rodent species could help to assess if rodents could act as disease vectors spreading CWD, leading to higher prevalence rates of CWD and a decline in deer populations that in turn could lead to economic losses from reduced levels of big game hunting and potentially human health risks from consuming infected deer meat.

Objectives

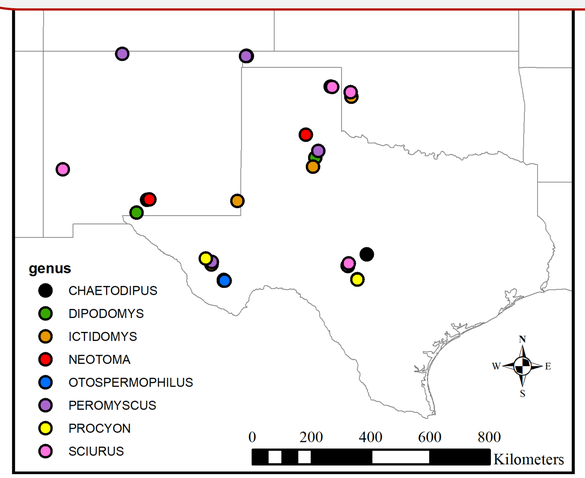
Determine if the susceptibility variant of the *PRNP* gene is present in rodent genera (*Chaetodipus, Dipodomys, Ictidomys, Neotoma, Otospermophilus, Peromyscus,* and *Sciurus*) in areas where CWD is known to affect deer populations (i.e. Texas, Oklahoma, and New Mexico), and to examine the possibility of interspecies spillover of CWD from deer to rodents.

Methods

1. Obtain muscle or liver samples (genera *Chaetodipus, Dipodomys, Ictidomys, Neotoma, Otospermophilus, Peromyscus,* and *Sciurus*; **Fig. 1**)
2. Extract genomic DNA from tissue samples using a DNeasy Blood and Tissue Kit
3. Amplify *PRNP* by PCR
4. Purify PCR products using ExoSap-IT
5. Cycle sequence PCR amplicons
6. Sequences were proofed using chromatograms and annotated using the program Sequencher
7. Phylogenetic analyses used MrBayes v3.2.6 (10 million generations, burn-in of 25%, sampling frequency every 1000 trees, 50% consensus rule).



Examples of rodents that are sympatric with deer and were analyzed in this study.



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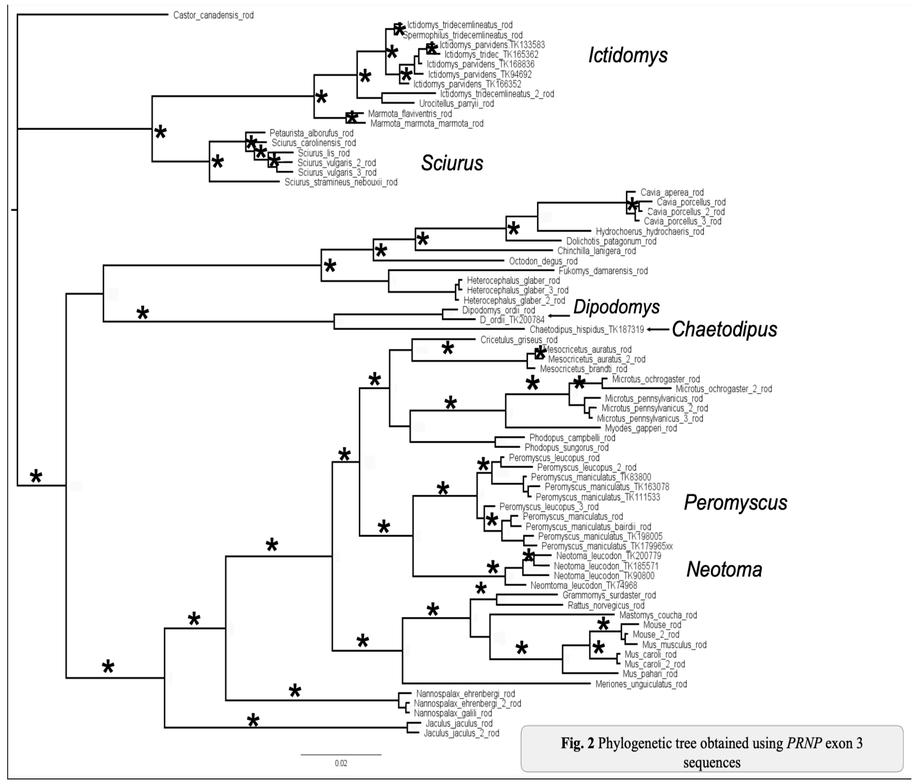

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Results

- Sequences successfully generated and compared to those of other species of in the Order Rodentia.
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- Preliminary results indicate a high level of genetic divergence in the *PRNP* gene, illustrated by branch length and phylogenetic structure.

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- We recovered substantial variation in the *PRNP* gene, which is in contrast to results obtained from the *PRNP* gene in studies of ungulates (deer species).
- Determine if any AA substitutions signal susceptibility or resistance of CWD in rodents.
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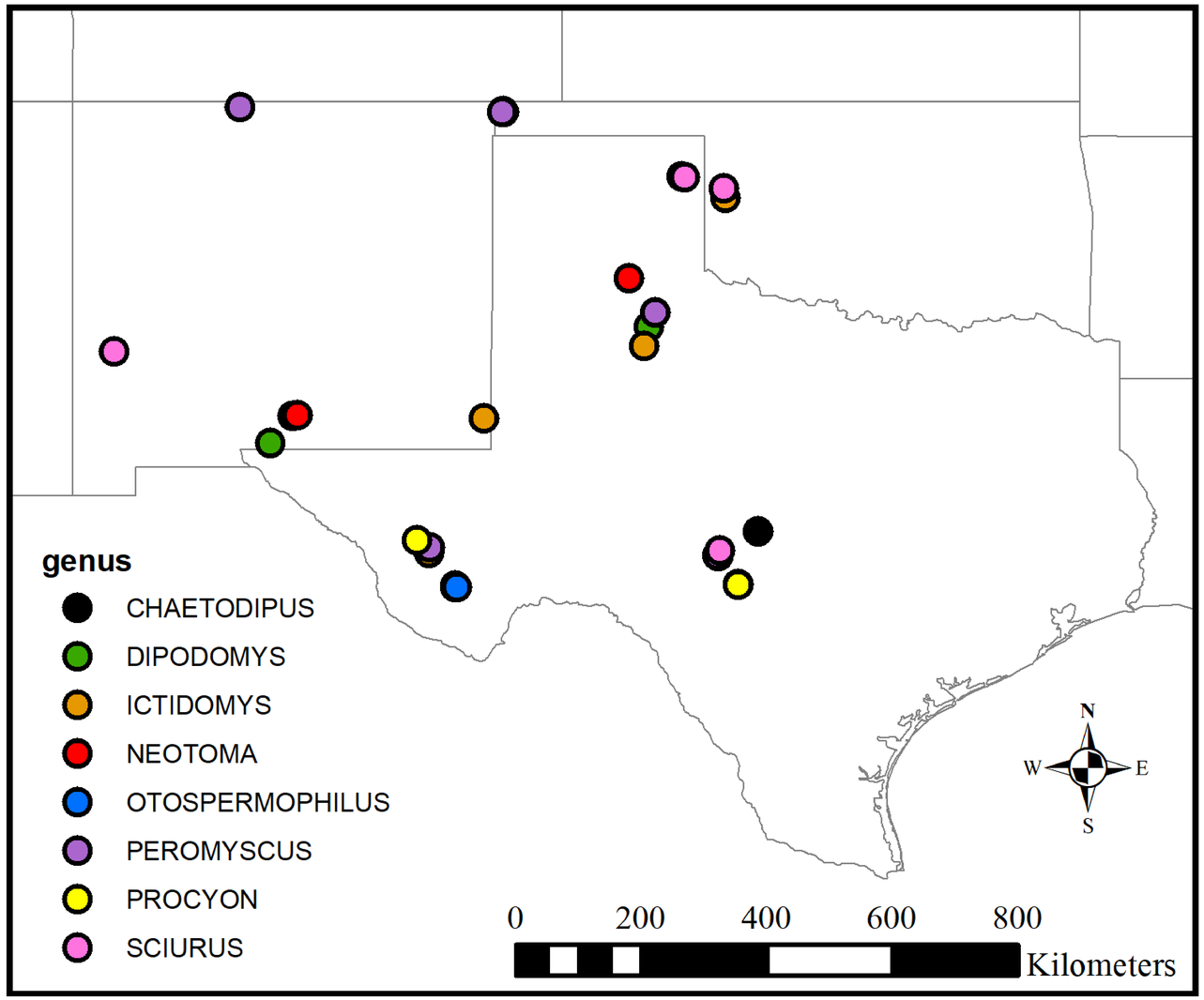

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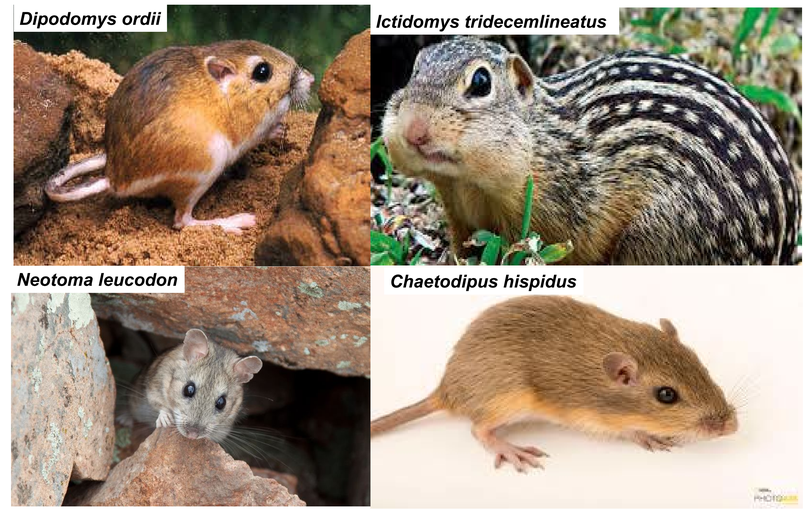

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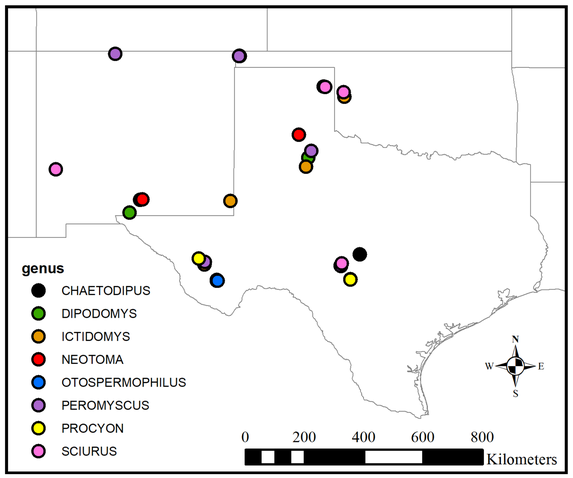

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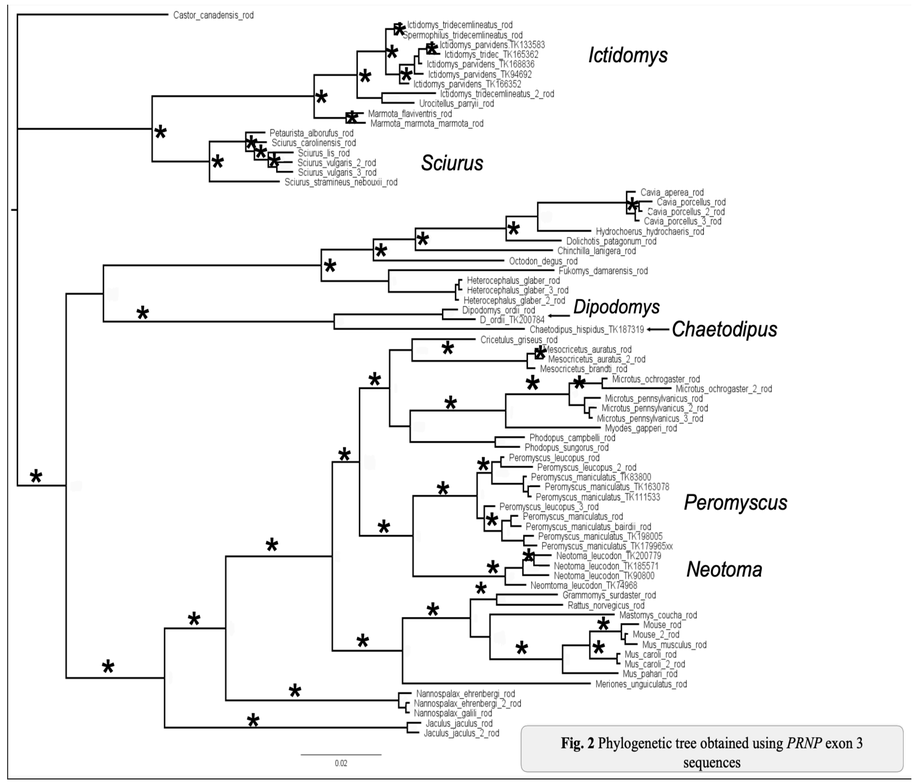

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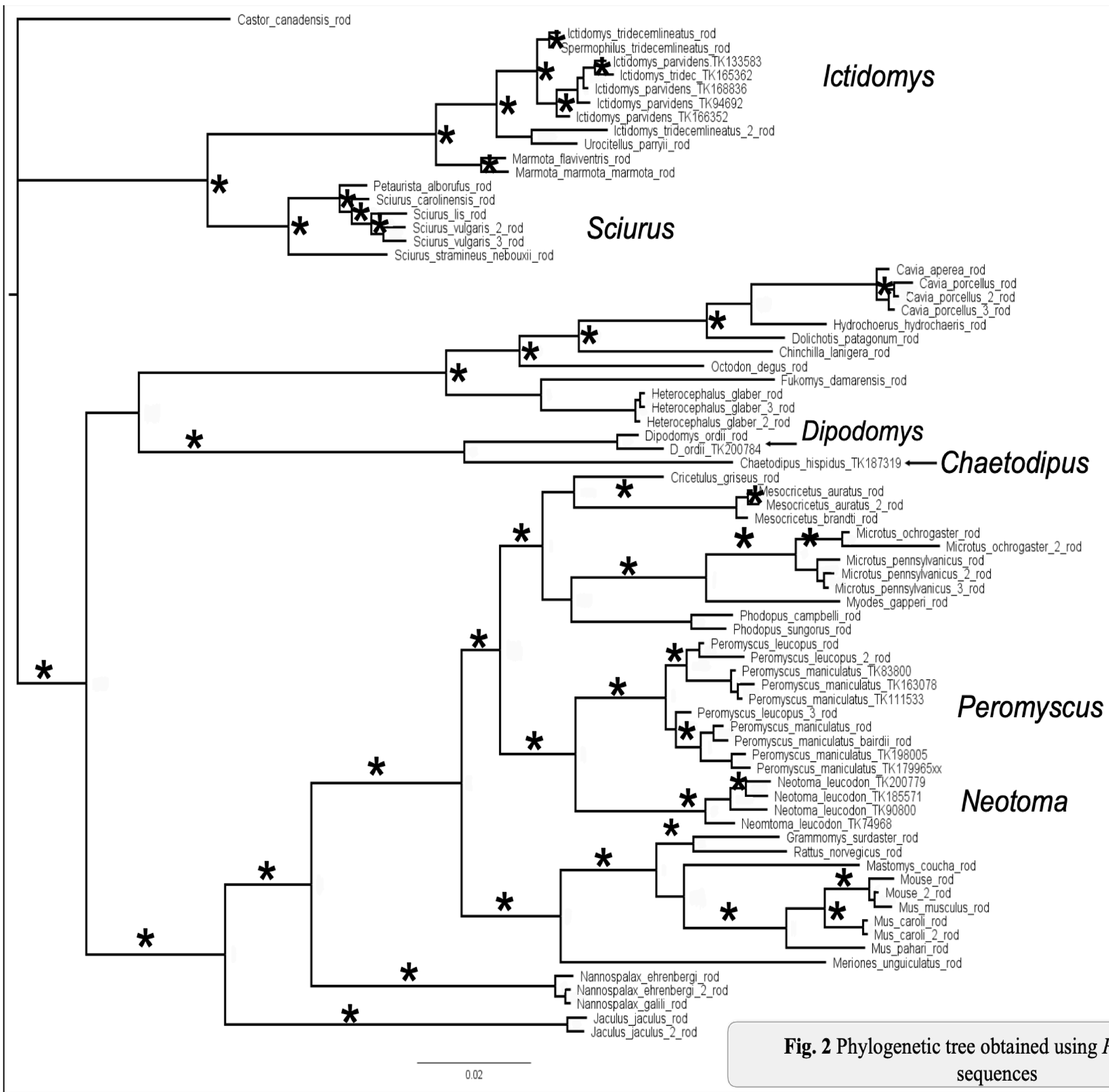

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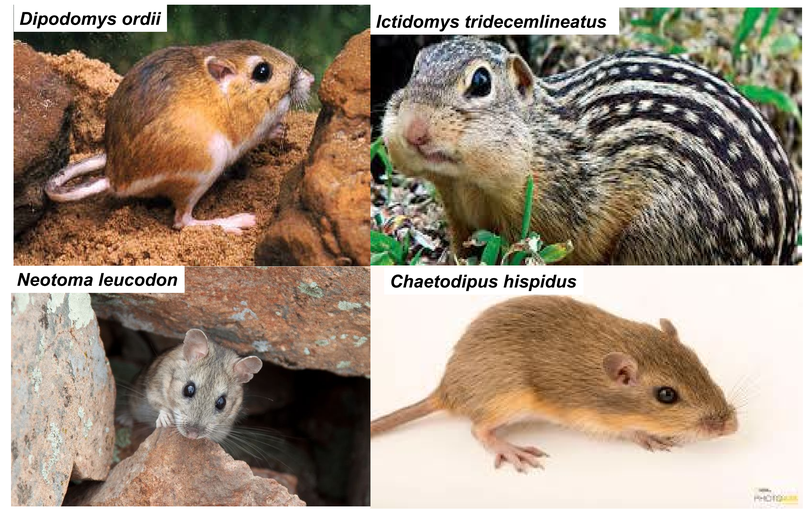

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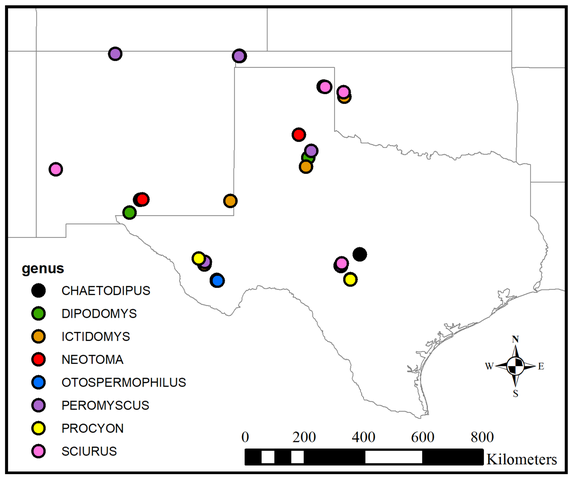

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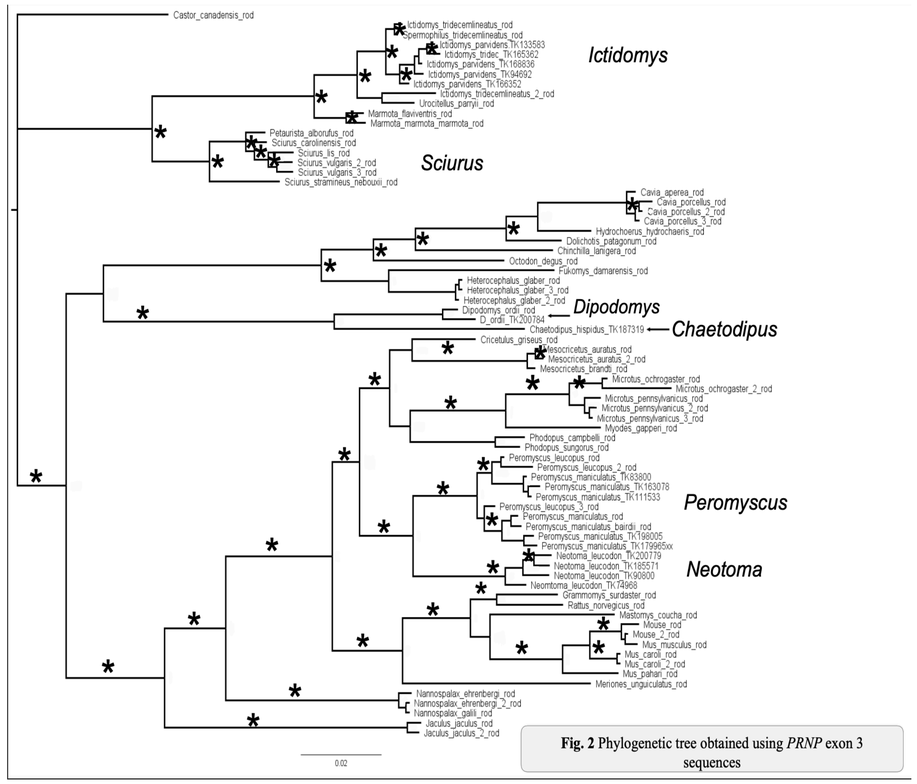

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