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Authors
Brown, Sarah K
Blois, Jessica L

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MITOGENOME ANNOUNCEMENT

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The complete mitochondrial genome of the dusky-footed woodrat (*Neotoma fuscipes*) (Rodentia, Cricetidae)

Sarah K. Brown and Jessica L. Blois

Life and Environmental Sciences, School of Natural Sciences, University of California, Merced, CA, USA

ABSTRACT

The dusky-footed woodrat (*Neotoma fuscipes*) is an endemic North American rodent belonging to the family Cricetidae. We present here the first complete mitogenome within the *Neotoma* genus. The mitogenome is 16,199 bp in length, and has a structure and gene organization similar to other rodent species (e.g. *Mus musculus*, *Peromyscus maniculatus* and *Microtus fortis calamorum*). The overall base composition is A (35.2%), C (25.5%), G (12.3%), T (27.0%), with a GC content of 37.8%, similar to other rodents. This mitogenome serves as a foundation for future phylogenetic, phylogeographic and population genetic studies.
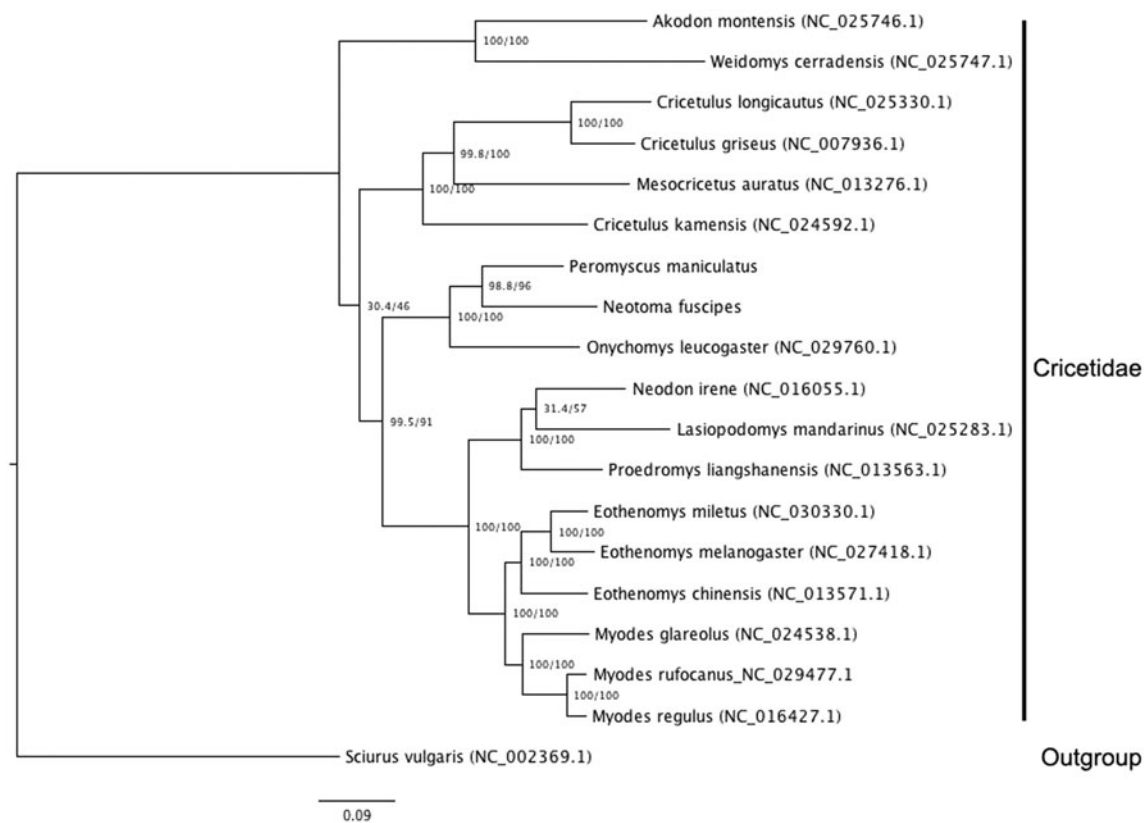
The 22 species of woodrats within the genus *Neotoma* are widespread throughout North America (Nowak 1999). They are important for paleoecological studies, serving as paleo-thermometers (Smith & Betancourt 1998) and as collecting agents for Quaternary fossils (Betancourt et al. 1990). A complete understanding of the genetic makeup of the species within *Neotoma* would thus facilitate future studies using both modern and ancient DNA. Here, we present the first mitogenome description within the genus *Neotoma*, which will help further resolve the evolutionary history of this species, and its relationship with other cricetid rodents.

We sequenced two dusky-footed woodrat (*Neotoma fuscipes*) individuals from Samwell Cave, CA (MVZ:Mamm:225109; longitude/latitude (−122.239893, 40.9176)) and the Snow Mountain Wilderness, CA (MVZ:Mamm:196404; longitude/latitude (−122.66451, 39.3450164)). DNA was extracted from muscle tissue via the Qiagen DNeasy kit (Qiagen, Valencia, CA). The complete mitochondrial genome was created through genomic library preparation using the NEBNext Ultra DNA kit (New England Biolabs, Ipswich, MA), and subsequently sequenced on a single HiSeq2000 lane (Illumina, San Diego, CA). We aligned our genomic short reads against *Mus musculus* (GenBank accession number NC_005089.1) and *Peromyscus maniculatus* (Hawkins et al. 2016) mitogenomes with BWA (v0.7.12, Li & Durbin 2009) and Samtools (v1.3, Li et al. 2009). These reads were then aligned to *Microtus fortis calamorum* (Genbank accession: JF261175.1) in Geneious (v8.1.8, Biomatters, Auckland, New Zealand). The mitogenome was annotated by the programs DOGMA (Wyman et al. 2004) and MITOS (Bernt et al. 2013), and tRNA inconsistencies were resolved with tRNAscan-SE (Lowe & Eddy 1997).

We used IQtree v1.4.3 (Trifinopoulos et al. 2016) to determine the best model of evolution amongst *N. fuscipes* and 17 other Cricetid mitogenomes, and reconstructed their phylogenetic relationships using *Sciurus vulgaris* as the outgroup.

The *Neotoma fuscipes* mitogenome (GenBank accession number KU745736) has a total length of 16,199 bp (average coverage of 3129×). The overall base composition is A (35.2%), C (25.5%), G (12.3%), T (27.0%), with a GC content of 37.8%, similar to other rodents (Partridge et al. 2007). The mitogenome arrangement is also similar to other mammals with 13 protein-coding genes, 2 rRNA genes and 22 transfer RNAs. Gene order and organization is similar to *Mus musculus* (NC_005089.1) and *Microtus fortis calamorum* (Genbank accession number JF261175.1). Annotation with DOGMA (Wyman et al. 2004) and MITOS (Bernt et al. 2013) provided fairly consistent results. tRNAscan-SE did not identify two tRNAs that were found with both MITOS and DOGMA: tRNA-VAL (1027-1097) and tRNA-SER (11606-11663). These tRNAs were added to the final annotation.

Model testing in IQtree revealed TIM2 + I + G4 to be the best-supported model of evolution. The resulting phylogeny places *Onychomys*, *Neotoma* and *Peromyscus* in a single clade, with *Neotoma* sister to *Peromyscus* (Figure 1). This placement contrasts with previous phylogenies based on one or multiple mitochondrial and/or nuclear genes (e.g. Bradley et al. 2004; Reeder et al. 2006), underscoring the uncertain placement of these taxa within Neotominae, though we note that full mitogenomes are available for only a few species. The mitogenome of *Neotoma fuscipes* will thus be useful for future phylogenetic, phylogeographic and population genetic studies.

CONTACT Sarah K. Brown ✉ brown.sarahbrown@gmail.com ▣ Life and Environmental Sciences, School of Natural Sciences, University of California, Merced, CA, USA

Figure 1. Maximum likelihood (ML) tree based on complete mitogenomes from the family Cricetidae, under the model TIM2 + I + G4. Bootstrap support at nodes depicts bootstraps in front of the diagonal (/) and ultra-fast bootstraps, after the diagonal. The number in parentheses following each specimen is the NCBI accession number, except in the case of *Peromyscus maniculatus* (from Hawkins et al. 2016) and *Neotoma fuscipes* (this study).

Disclosure statement

Acknowledgments

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