

Analysis of complete mitochondrial genome and its application to phylogeny of *Caryomys inez* (Rodentia: Cricetidae: Arvicolinae)

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ABSTRACT

In this study, the complete mitochondrial genome of Inez's red-backed vole *Caryomys inez* was sequenced and analyzed as the first species in genus *Caryomys*. The complete mitochondrial genome of *C. inez* is 16,354 bp in length and shows a typical vertebrate pattern with 13 PCGs, 22 tRNAs, 2 rRNAs and 2 non-coding regions. To gain a clear phylogenetic position of *C. inez*, a ML phylogenetic tree was constructed based on 12 PCGs on H-strand from 23 rodent species except for *ND6* gene which is on L-strand. As a result, *C. inez* is clustered with genera *Eothenomys* and *Myodes*, showing their close phylogenetic relationships. The present study may facilitate further investigation of the taxonomic studies and phylogenetic analyses of the genus *Caryomys*.

ARTICLE HISTORY

Received 25 March 2016
Accepted 26 March 2016

KEYWORDS

Caryomys inez; complete mitochondrial genome; phylogeny

The Inez's red-backed vole, *Caryomys inez*, is a Chinese native species and is distributed in central and northern China (Li & Xue 2008). Genus *Caryomys* is similar to genus *Eothenomys* in external morphology and was once regarded as a subgenus of *Eothenomys* (Allen 1940). Ma and Jiang (1996) reinstated *Caryomys* as a valid genus and had been accepted by system-

atists (Luo et al. 2000; Wang 2003; Wilson & Reeder 2005). Liu et al. (2012) confirmed this view based on morphology and two mitochondrial genes (*CO1* and *Cytb*). In this study, we captured a specimen of *C. inez* in Lingchuan, Shanxi Province (N35.565°, E113.366°), China, and sequenced its complete mitochondrial genome (GenBank accession no. KU200225),

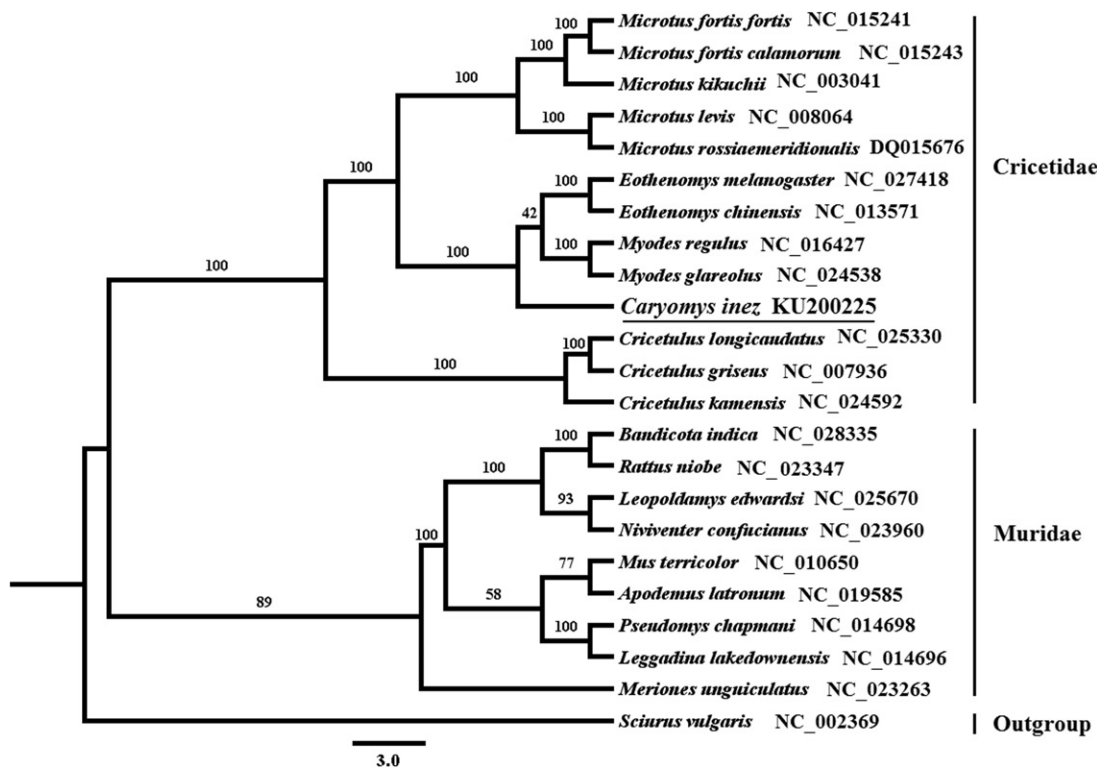


Figure 1. Maximum likelihood (ML) phylogenetic tree based on 12 PCGs located on the H-strand under GTR + I + G model. Numbers represent node support inferred from ML bootstrap analyses.

and analyzed its phylogenetic relationships to close genera *Eothenomys*, *Myodes*, *Microtus* and *Cricetulus* in family Cricetidae. The voucher specimen was labelled as S0862 and deposited at Shandong University (Weihai).

The complete mitochondrial genome of *C. inez* is 16,354 bp in length and consists of 13 protein-coding genes (PCGs), 22 tRNAs, 2 rRNAs and 2 non-coding regions, with a base composition of 33.25% A, 26.99% T, 26.80% C and 12.96% G. Apart from *ND6* which is on the L-strand, all PCGs are encoded on the H-strand.

The nucleotide sequence data of 12 H-strand PCGs of *C. inez* and other 22 rodent species were used for phylogenetic analyses with *Sciurus vulgaris* as outgroup taxa. The best-fitting model (GTR+I+G) of sequence evolution was obtained by the software jModelTest 2.1.3 (Darriba et al. 2012) under the Akaike Information Criterion (Akaike 1974). The phylogenetic tree of Maximum likelihood (ML) was constructed in RAxML-VI-HPC (Stamatakis 2006) with 1000 bootstrap replicates (Figure 1), the 22 ingroup species used in ML analysis belong to two families, Cricetidae and Muridae. Our analysis shows that the Cricetidae species examined here forms a well-supported monophyletic group and the monophyly of the family Muridae is also supported with high bootstrap value. In our ML phylogenetic tree, *C. inez* is clustered with genera *Eothenomys* and *Myodes* (bootstrap value=100). This study firstly provided the complete mitochondrial genome of species in genus *Caryomys*, and we expect our data and result may facilitate further investigation of the taxonomic studies and phylogenetic analyses of the genus.

Acknowledgements

We would like to thank the anonymous reviewers for providing valuable comments on the article.

Declaration of interest

The authors report no conflicts of interest. The authors alone are responsible for the content and writing of the article.

Funding information

This research was funded by the Major International (Regional) Joint Research Project of NSFC (Grant No. 31110103910).

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