

Complete mitochondrial genome of the Eurasian collared lemming *Dicrostonyx torquatus* Pallas, 1779 (Rodentia: Arvicolinae)

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ABSTRACT

The complete mitochondrial genome of the Eurasian collared lemming was obtained by using PCR amplification and capillary sequencing (GenBank accession no. KX066190). The collared lemming mitochondrial genome is 16,340 bp long and shows the gene order, contents and gene strand asymmetry typical for mammals. The mitogenome sequence provides an important new genomic resource for the collared lemming, which is a model study species in Arctic phylogeography and biotic history.

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The Eurasian collared lemmings, *Dicrostonyx torquatus*, the northernmost species of rodents and a key species of the Arctic communities, evolved in dry landscapes of eastern Siberia and were characteristically associated with the dry and cold environment during the Pleistocene (Kowalski 1995). Nowadays collared lemmings are restricted to dry and treeless tundra and they represent the only rodent genus that inhabits the polar desert of the northernmost parts of the Arctic (Ognev 1967). The collared lemming is a model species in Arctic phylogeography to infer impacts of the past climate warming events on demographic history of the cold-adapted specialist from genetic diversity in its modern and ancient populations (Fedorov 1999). Mitochondrial DNA data available for the collared lemming are limited to restriction fragment length polymorphism (RFPL) haplotypes (Fedorov et al. 1999) and fragments of single gene or single region sequences (Fedorov 1999; Prost et al. 2010; Brace et al. 2012; Palkopoulou et al. 2016). Furthermore, circumpolar phylogeography based on partial sequences of the mitochondrial cytochrome b gene revealed relatively low genetic variation in the Eurasian collared lemmings and provided limited information content for phylogenetic and demographic history reconstructions (Fedorov & Goropashnaya 1999). Access to the complete mitogenome of this species will significantly increase the power and resolution population genetics analyses.

We present the first complete mitochondrial genome sequence of the Eurasian collared lemming, *Dicrostonyx torquatus*, which has been deposited in the NCBI GenBank database with the accession number KX066190.

The mitogenome sequenced belongs to a male collected near Yanrikintot Village, Eastern Chukotka, Russia (64.87 latitude, –172.67 longitude) and voucher specimen (UAM84102) was deposited to the Mammal Collection, University of Alaska Museum Fairbanks. The total genomic DNA was extracted from liver tissue, the mitogenome was amplified by polymerase chain reaction in two overlapping amplicons and capillary sequenced by primer walking (the primer sequences are available on request). The collared lemming mitogenome is 16,340 bp long, with a base composition on the heavy strand of 32.69% A, 26.82% C, 13.16% G, and 27.33% T and consisting of 13 protein-coding genes, 22 transfer RNA (tRNA) genes, two ribosomal RNA (rRNA) genes and a control region. The order and direction of these genes were identical to those of other Metazoa (Gissi et al. 2008). Most of the genes encoded by the heavy strand, except for *nad6* and eight tRNA genes encoded by the light strand. All tRNAs were predicted to fold into typical cloverleaf secondary structures. Of the 13 protein-coding genes, three (*nad1*, *cox3* and *nad4*) showed an incomplete stop codon which is completed by the addition of 3' A residues to the mRNA. A phylogenetic tree (Figure 1) constructed with mitochondrial genome sequences excluding hypervariable control regions shows that genus *Dicrostonyx* is equally distant from two genera of arvicoline rodents as it was suggested by phylogeny based on the cytochrome b gene (Conroy & Cook 1999).

The complete mitogenome sequence reported here provides an important new genomic resource for the model species in studies of Arctic genetic diversity and biotic history.

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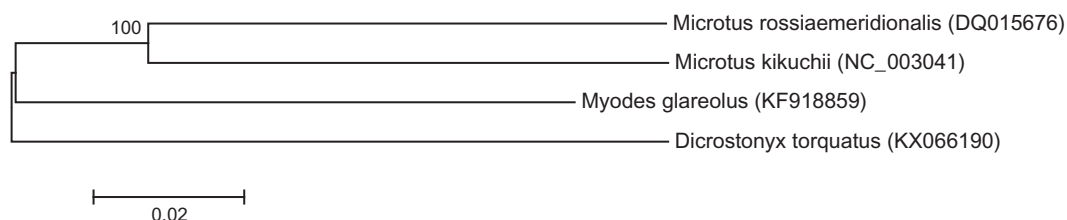


Figure 1. Neighbour-joining tree based on Tamura-Nei nucleotide distances showing phylogenetic relationships of genus *Dicrostonyx* with two genera of arvicoline rodents. Total of 15,460 bp were used in the alignment excluding hypervariable control region. Number on the node indicates bootstrap support and numbers in brackets correspond to GenBank accession numbers for complete mitochondrial genomes.

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