

## Complete mitochondrial genomes of the North American collared lemmings *Dicrostonyx groenlandicus* Traill, 1823 and *Dicrostonyx hudsonius* Pallas, 1778 (Rodentia: arvicolinae)

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### ABSTRACT

The complete mitochondrial genomes of two species of the North American collared lemmings were obtained by using PCR amplification and capillary sequencing (GenBank accession nos. KX712239 and KX683880). The collared lemming mitochondrial genomes are 16,341 and 16,338 bp long and show the gene order, contents and gene strand asymmetry typical for mammals. The mitogenome sequences provide an important genomic resource for the collared lemmings, which are model study species in Arctic genetic diversity and biogeographic history.

### ARTICLE HISTORY

Received 14 October 2016  
Accepted 23 October 2016

### KEYWORDS

Arctic; collared lemming;  
*Dicrostonyx groenlandicus*;  
*Dicrostonyx hudsonius*;  
mtDNA

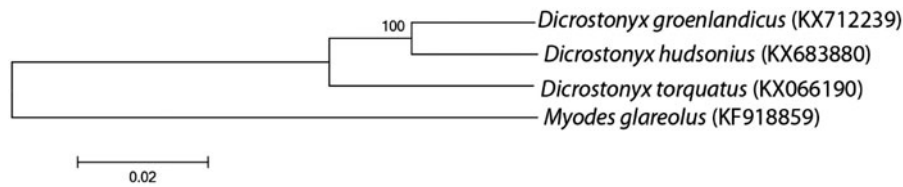
The North American collared lemmings, *Dicrostonyx groenlandicus* and *D. hudsonius*, key species of the Arctic communities, inhabit treeless tundra in Alaska and North Western Canada. Mitochondrial DNA data available for these species are limited to fragments of single gene or single region sequences (Fedorov & Goropashnaya 1999; Ehrich et al. 2000; Fedorov & Stenseth 2002). The North American phylogeography based on partial sequences of the mitochondrial cytochrome b gene and control region revealed relatively low genetic variation in the collared lemmings and provided limited information content for inferring demographic history (Fedorov & Stenseth 2002). Access to the complete mitogenomes of these species will facilitate high resolution population genetics analyses.

We present the first complete mitochondrial genome sequences of the North American collared lemmings, *Dicrostonyx groenlandicus* (NCBI GenBank database accession no. KX712239) and *Dicrostonyx hudsonius* (GenBank accession no. KX683880). The mitogenomes sequenced belong to *D. groenlandicus* collected in Alaska (coordinates: 68.338/–158.727) and *D. hudsonius* from Ungava Peninsula, Canada (coordinates: 62.333/–73.667), and voucher specimens (UAM:Mamm:56332 and UAM:Mamm:57927) were deposited to the Mammal Collection, Museum of the North, University of Alaska 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 mitogenomes are

16,341 bp and 16,338 bp long, with a base composition on the heavy strand of A – 33%, C – 27%, G – 13%, T – 27%, and consist 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.

Phylogenetic tree (Figure 1) constructed with mitochondrial genome sequences excluding hypervariable control regions shows that the North American *D. groenlandicus* and *D. hudsonius* form well-supported monophyletic group relatively the Eurasian *D. torquatus* as it was shown by phylogeny based on the cytochrome b gene (Fedorov & Goropashnaya 1999). This implies one colonization event from Eurasia through the Bering Land Bridge to North America followed by vicariant separation by the Pleistocene ice sheets. Monophyly of the North American species does not support the hypothesis that the morphologically primitive *D. hudsonius* is a relict of an earlier colonization of North America from Eurasia while *D. groenlandicus* represents second colonization event (Guilday 1963).

The complete mitogenome sequences reported here provide a new genomic resource for the model species in studies of Arctic genetic diversity and biotic history.



**Figure 1.** Neighbour-joining tree based on Tamura-Nei nucleotide distances showing phylogenetic relationships among the Eurasian *D. torquatus* and North American *D. groenlandicus* and *D. hudsonius*. The mtgenome of vole *Myodes glareolus* was included as outgroup. Total of 15,442 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.

## Acknowledgements

We thank L. E. Olson, Mammal Collection Museum of the North University of Alaska Fairbanks for providing tissue samples.

## Disclosure statement

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

## Funding

An Institutional Development Award (IDeA) from the National Institute of General Medical Sciences of the National Institutes of Health under grant number 10.13039/1000000057 [P20GM103395]. The content is solely the responsibility of the authors and does not necessarily reflect the official views of the NIH. National Science Foundation 10.13039/100000001 [EPS-0346770].

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