The complete mitochondrial genome sequence and phylogenetic analysis of yellow weasel (*Mustela sibirica*)

Mengshi Yu*, Huailiang Xu**, Diyan Li*, Jiayun Wu*, Anxiang Wen*, Meng Xie*, Qin Wang*, Guangxiang Zhu*, Qingyong Ni*, Mingwang Zhang* and Yongfang Yao*

*College of Life Science, Sichuan Agricultural University, No. 46, Xinkang Road, Yucheng District, Ya'an, Sichuan 625014, PR China; **College of Animal Science and Technology, Sichuan Agricultural University, Chengdu, PR China

**ABSTRACT**

In this study, we determined the complete mitochondrial genome sequence of the *Mustela sibirica*. The complete mitogenome of *M. sibirica* is 16,529 bp in length and consist of 13 protein-coding genes (PCGs), 2 rRNA genes, 22 tRNA genes, and a D-loop region. The overall base composition of the mitochonrdial DNA is 32.88%A, 13.84%G, 27.32%T, and 25.96%C. The phylogenetic tree of the family *Mustelidae* constructed by using mitogenome sequences from 10 mustelid species of the family *Mustelidae*. These results provide necessary information for molecular phylogeny and evolutionary analysis of the *M. sibirica*.

Yellow weasel (*Mustela sibirica*) belongs to Carnivora, mustelidae. It is widely distributed in Siberia of Russia and China (IUCN 2016; Min 2018). Some weasels (*Neovison vison*, *Martes zibellina*, *M. sibirica*, etc.), are economic animal due to the value of the fur (Xu et al. 2010). In recent years, the aquaculture of the weasel is rising with the development of fur economic in China (Jian et al. 2012). In this study, we determined and analysed the complete mitochondrial genome of *M. sibirica*. This information will contribute to future phylogenetic studies of this species.

The specimen was collected from Ya'an (120°59'E, 29°58’N) and stored in Zoology laboratory of Sichuan Agricultural University, NO. 000756. The genomic DNA of *M. sibirica* was isolated from muscle tissue by using the TIANamp Genomic DNA extraction Kit. A previously published mitogenome of *M. sibirica* (HM106317) which downloaded from the National Centre for Biotechnology Information (NCBI) was used as a reference for gene annotation and primer design. The complete mitogenome sequence of *M. sibirica* which we determined was deposited in GenBank (No. MN264435).

The complete mitogenome of *M. sibirica* contains total 16,529 bp long, which consists of 13 protein-coding genes (PCGs), two rRNA genes (12S rRNA and 16S rRNA), 22 tRNA genes, and one D-loop region the same order as seen for other mammalian genes (Chun et al. 2010; Sang et al. 2017). Most PCGs are distributed on the H-strand, except for ND6 and eight tRNA genes which are encoded on the L-strand. The sequence is apparently AT biased (AT = 61.87%) with an overall base composition was 33.37%A, 28.50% T, 24.68% C, and 13.45% G. The longest PCG was the ND5 (1830 bp), whereas the shortest PCG was the ATP8 (204 bp). Ten PCGs use ATG as start codon, except for ND3 and ND5 initiate with ATA and ND2 begin with ATT. Of the 13 PCGs, the incomplete stop codons (T— or TA—) are used for termination of ND2, COX3, and ND4 (T—), ND1 and ND3 (TA—), respectively. AGA are used as stop codons in Cytb, and the other seven genes end with TAA. 12S rRNA and 16S rRNA are 959 and 1569 bp, respectively. These are located between tRNA-Pro and tRNAPhe genes and are separated by the tRNA-Val gene. The 22 tRNA genes range in length from 62 (tRNA-Ser) to 75 bp (tRNA-Leu), tRNA-Ser has lost the stem of dihydrouridine (DHU) arm. The mitochondrial control region is 1121 bp long and is laid between the tRNA-Pro and tRNA-Phe genes.

The phylogenetic tree of the family *Mustelidae* constructed using the maximum-likelihood (ML) procedures implemented in MEGA version X (Kumar et al. 2018). To further explore, the taxonomic status of the *M. sibirica* and its phylogenetic relationship within the family *Mustelidae*, a phylogenetic tree constructed using mitogenome sequences from 10 mustelid species of 3 genera (Figure 1). According to the phylogenetic tree, *M. sibirica* clustered into a clade with *M. nigripes* and *M. putorius* and all the members of the genus *Mustela* form a monophyletic group. In all, this genome will provide a molecular basis for the conservation and research of *M. sibirica*. 

CONTACT Yongfang Yao (yaoyongf@126.com) College of Life Science, Sichuan Agricultural University, No. 46, Xinkang Road, Yucheng District, Ya’an, Sichuan 625014, PR China

*These authors contributed equally to this study.

© 2019 The Author(s). Published by Informa UK Limited, trading as Taylor & Francis Group. This is an Open Access article distributed under the terms of the Creative Commons Attribution License (http://creativecommons.org/licenses/by/4.0/), which permits unrestricted use, distribution, and reproduction in any medium, provided the original work is properly cited.
Disclosure statement
The authors declare no conflicts of interest and are alone responsible for the content and writing of the article.

Funding
This work was supported by the National Natural Science Foundation of China, grant No. [31370407].

References
Chun ZX, Zhang J. Zhang Ma HH. 2010. Organization of the complete mitochondrial genome and its evolution in sable. J Beijing For Univ. 32:82–88.
Jian YW, Song SQ, Fu LT. 2012. The present situation and market prospect of special economical fur animal breeding. Shangdong J Anim Sci Vet Med. 33:69–71.
Kumar S, Stecher G, Li M, Knyaz C, Tamura K. 2018. MEGA X: molecular evolutionary genetics analysis across computing platforms. Mol Biol Evol. 35:1547–1549.
Min JP. 2018. Population quantitative and winter habitat selection of mustelidae species in Huangnihe Nature Reserve. Changchun, China: Jilin Agricultural University.
Sang JL, Hye RK, Jae YC, Yung CP. 2017. Complete mitochondrial genome of the least weasel Mustela nivalis (Mustelidae) in Korea. Mitochondrial DNA B. 2:740–741.
The IUCN Red List of Threatened Species. 2016.Version 2019-2; [accessed 2015 March 03]. www.iucnredlist.org
Xu Z, Yan L, Chang QH, Ce Z, Ling LY, Li C. 2010. Development patterns and implications from international farming industry of fur animal. For Prod Special Chin. 06:88–90.

Figure 1. Neighbour-Joining (NJ) phylogenetic tree constructed based on mitogenome sequences from 11 mustelid species of 3 genera. Numbers at the branches indicated the bootstrapping values with 1000 replications. GenBank accession numbers are given in the parentheses. Filled circle represented a sequence from this study.