

MITOGENOME ANNOUNCEMENT

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Evolutionary status of the invasive American mink *Neovison vison* revealed by complete mitochondrial genome

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ABSTRACT

The American mink, *Neovison vison*, is native to North America and listed as one of the most widely distributed invasive species into the Eurasian mainland. Even though facing serious over-hunting and habitat degradation problems, this species has successfully dispersed into most areas of northeast China in the past decades, which may have a huge impact on local species composition and structure. We determined and annotated the whole mitochondrial DNA genome of the American mink *N. vison* to better understand the evolutionary relationship of this invasive species with other *Mustelidae* distributing in China. The complete mitogenome is 16627 bp in length, includes 13 protein-coding genes, 22 tRNA genes, 2 rRNA genes and one control region. We built the phylogenetic tree of American mink and other 10 most closely *Mustelidae* species.

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KEYWORDS

American mink; evolutionary relationship; invasive species; mitochondrial DNA genome

The American mink, *Neovison vison*, a semi-aquatic species of *Mustelidae* native to North America (Wilson & Reeder 2005), has expanded its distribution to many parts of Eurasian mainland, including northeast China. As one of the most common invasive species into the Eurasian mainland (Zuberogoitia et al. 2010), it has been believed to be responsible for declines in European minks such as *Pyrenean desman* and European water vole populations in Europe (Marcin et al. 2010). As noted by Bowman et al. (2007), with rapid development of mink farming, captive minks become feral minks

soon after they escaped from farms or are released on purpose, and the territory size and dispersal speed are closely related to the distribution, density and size of farms.

Invasive American minks in northeast China may come from both Russian and Chinese mink farms in different time periods. Even though facing serious over-hunting and habitat degradation problems, this species has successfully dispersed into most areas of northeast China in the past decades. However, because no all regional species-specific surveys have ever been carried out, the impacts of invasive minks on

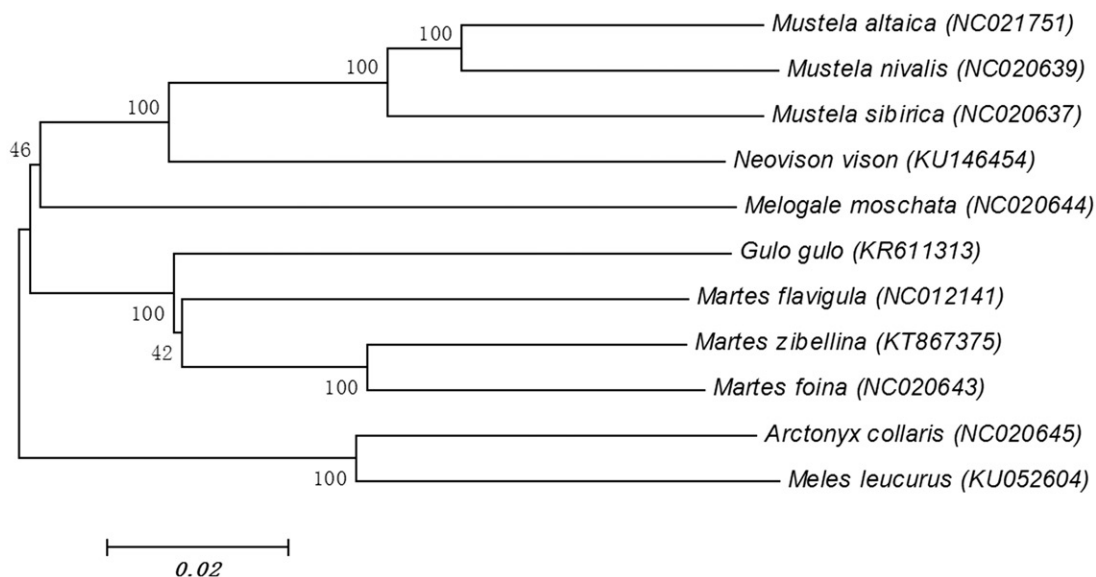


Figure 1. Neighbour-joining phylogenetic tree of American mink and other 10 species of *Mustelidae* constructed by MEGA version 6.0. Note: Complete mitogenomes of other 10 species of *Mustelidae* are downloaded from NCBI and the GenBank accession numbers are given in the bracket after the species name.

native *Mustelidae* species and prey population dynamics remain unknown.

To clarify the population sources and the genetic base of successful invasion of American minks in northeast China, we conducted a genetic research with samples from the whole range areas. And as part of the research, we determined and annotated complete mitochondrial genome of an invasive American mink *N. vison* using 13 pairs of primers. The muscle tissue used for DNA extraction and analysis was sampled from a female American mink captured in Maohe County, Heilongjiang Province, China (N: 53.14049, E: 122.62716), and the specimen is stored in the Wildlife Detection Center of Chinese State Forestry Administration, Northeast Forestry University, Harbin, China.

In addition, to reveal the phylogenetic relationship of this species, we reconstructed the complete mitochondrial genome-based neighbour-joining tree of the American mink *N. vison* and other 10 *Mustelidae* species distributed in China with Kimura 2-parameter model using MEGA version 6.0 (Tamura et al. 2013), and the tree was tested with 1000 bootstrap replications.

The complete mitogenome of *N. vison* is 16 627 bp in length (GenBank accession number KU146454), which is made up of 13 protein-coding genes, 2 rRNA genes, 22 tRNA genes and one control region. Except for the ND6 gene and 8 tRNAs, most mitochondrial genes are encoded on the H-strand as in other mammals. The overall base composition is A: 33.6%, T: 27.7%, C: 25.4% and G: 13.3%, with a much higher A + T content.

The phylogenetic neighbour-joining tree is shown in Figure 1 and we can see from the figure that the American mink *N. vison* is mostly close to the genus *Mustela* with high support. Specially, the American mink's closest relative in Eurasian mainland is the Siberian weasel *Mustela sibirica* rather the European mink *Mustela lutreola*, as demonstrated by

previous studies (Koepli et al. 2008; Yu et al. 2011), which is also shown in the figure.

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Disclosure statement

The authors declare no conflict of interests. The authors alone are responsible for the content and writing of the paper. This study was supported by Heilongjiang Province Science Foundation for Youths (QC2011C091).

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