Phylogenetic relationship of roe deer *Capreolus capreolus mantschurivus* revealed by complete mitochondrial genome

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\textbf{ABSTRACT}

The roe deer (*Capreolus capreolus mantschurivus*) is the main prey of the Amur tigers and leopards in the northeast of China. The population genetics of roe deer is closely related to the conservation and management of the endangered species. We first determined and annotated the whole mtDNA genome of the *C. capreolus mantschurivus* to better understand the evolutionary relationship of these sub-species. The complete mitogenome is 16,355 bp in length, includes 37 protein-coding genes, 22 tRNA genes, 2 rRNA genes, and 1 control region. We built the phylogenetic tree of *C. capreolus mantschurivus* and other 11 most closely related Cervidae species. The phylogenetic neighbor-joining tree is shown in Figure 1 and bootstrap supports for most of the tree branches are high. From the neighbor-joining tree, we can find that the phylogenetic relationship of this species, we reconstructed the complete mitochondrial genome of *C. capreolus mantschurivus* using 15 pairs of primers. The muscle tissue used for DNA extraction and analysis was sampled from a captive male roe deer in Jiaohe City, Jilin Province, China (N:43.72 E:127.33), and the sample is stored in the zoology specimen of the College of Wildlife and Protected Areas, Northeast Forestry University, Harbin, China. The sample number is NEFU-RD-M-1.

The complete mitogenome of *C. capreolus mantschurivus* is 16,355 bp in length (GenBank accession number MN 485773), which is made up of 37 protein-coding genes, 22 tRNA genes, 2 rRNA genes, and 1 control region. Except for 1 tRNAs, most mitochondrial genes are encoded on the H-strand as in other mammals. The overall base composition is A: 33.5%, T: 30%, C: 23.2%, and G: 13.3%, with a much higher A + T content.

In order to better understand the genetic and evolutionary relationship between *C. capreolus mantschurivus* and other sub-species, for the first time, we determined and annotated the complete mitochondrial genome of *C. capreolus mantschurivus* using 15 pairs of primers. The muscle tissue used for DNA extraction and analysis was sampled from a captive male roe deer in Jiaohe City, Jilin Province, China (N:43.72 E:127.33), and the sample is stored in the zoology specimen of the College of Wildlife and Protected Areas, Northeast Forestry University, Harbin, China. The sample number is NEFU-RD-M-1.

In addition, to reveal the phylogenetic relationship of this species, we reconstructed the complete mitochondrial genome-based neighbor-joining tree of the *C. capreolus mantschurivus* and other 11 Cervidae species distributed in China with Kimura 2-parameter model using MEGA version 7 (Sudhir et al. 2016), and the tree was tested with 1000 bootstrap replications.

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Disclosure statement

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