


## The first complete mitogenome of *Cervus canadensis nannodes* (Merriam, 1905)

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### ABSTRACT

*Cervus canadensis nannodes* (Merriam, 1905) is one of the subspecies of elk distributed only in California, USA. We completed the first mitogenome of *C. canadensis nannodes*. Its length is 16,428 bp, which is in middle among 24 available *Cervus* mitogenomes. It contains 37 genes (13 protein-coding genes, 2 rRNAs, and 22 tRNAs). Phylogenetic trees show that *C. c. nannodes* was clustered with some subspecies of *C. elaphus*. Number of inter-subspecific variations between *C. c. nannodes* and *C. e. alxaicus* are relatively small in comparison to intraspecific variations of insect and fish mitogenomes and plant chloroplast genomes.

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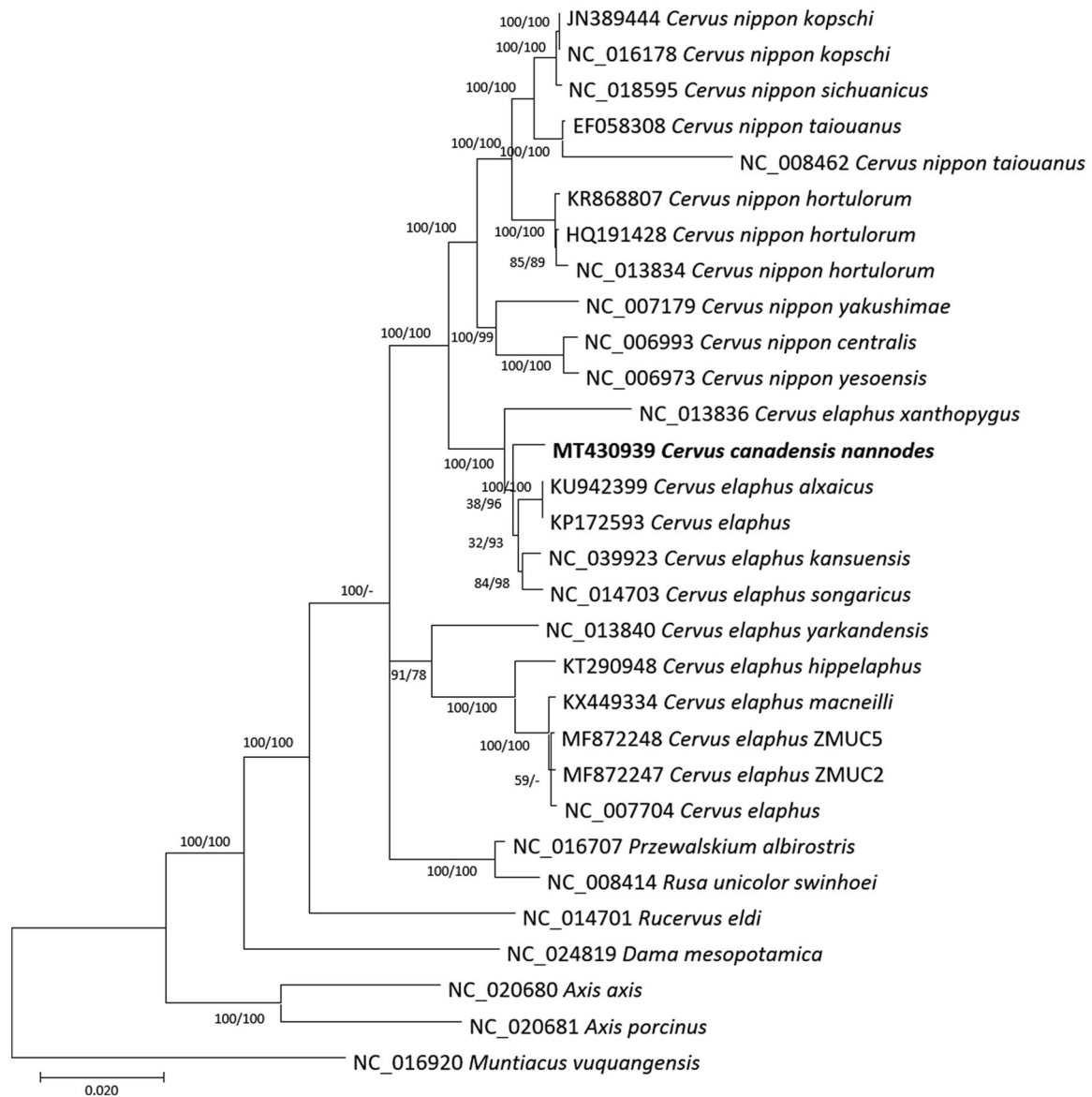
*Cervus canadensis nannodes* (Merriam 1905), a subspecies of elk, is distributed only in California, USA. This subspecies was considered as *Cervus elaphus nannodes* as one of the *C. elaphus* four subspecies (Schonewald 1994) based on the previous systematic descriptions (Merriam CH 1897; Nelson 1902; Merriam C 1905; Bailey 1935) as well as morphological classification studies (McCullough D 1969; Lowe and Gardiner 1989). Now, *C. e. nannodes* was changed to *C. c. nannodes* to clarify the origin of tule elk (Mizzi et al. 2017). Tule elk was near extinction until 1870s; however, a single breeding pair was discovered in southern San Joaquin Valley in 1874–1875 (McCullough DR et al. 1996) and now wild population is recovered. Because of the lack of its mitogenome despite of its available whole genome sequences (Mizzi et al. 2017), we completed *C. c. nannodes* mitogenome.

The brain tissue of *C. c. nannodes* collected in Namhaegun, Gyeongsangnamdo, Korea (Voucher in Animal and Plant Quarantine Agency, Korea; APQA-R-19FC020; 36.125833 N, 128.199515E) was used for extracting DNA with DNeasy Blood & Tissue Kit (QIAGEN, Hilden, Germany). Genome sequencing was performed using HiSeqX at Macrogen Inc. Mitogenome was completed by Velvet 1.2.10 (Zerbino and Birney 2008), SOAPGapCloser 1.12 (Zhao et al. 2011), BWA 0.7.17 (Li 2013), and SAMtools 1.9 (Li et al. 2009). Geneious R11 11.0.5 (Biomatters Ltd, Auckland, New Zealand) was used for annotation based on *Cervus elaphus alxaicus* mitogenome (KU942399).

The mitogenome of *C. c. nannodes* (GenBank accession is MT430939) is 16,428 bp, in middle size among 24 available

*Cervus* mitogenomes (16,350 bp to 16,663 bp). It contains 37 genes (13 protein-coding genes, two rRNAs, 22 tRNAs) and GC ratio is 38.0%.

Twenty-nine complete mitogenomes of subfamily Cervinae and one outgroup species, *Muntiacus vuquangensis*, were used for constructing bootstrapped neighbor-joining (and maximum-likelihood trees with MEGA X (Kumar et al. 2018) based on complete mitogenomes alignment conducted by MAFFT 7.450 (Katoh and Standley 2013). Phylogenetic trees presented that *C. c. nannodes* was clustered together with some of the subspecies of *C. elaphus* with high bootstrap value, even four *C. elaphus* subspecies were clustered with low bootstrap value (Figure 1). Inter-subspecific variations on mitogenome between *C. c. nannodes* and *C. e. alxaicus* in Cervinae display 145 SNPs and 77 INDELS, which is larger than that of inter-subspecific variations of *Alces alces* (subfamily Odocoileinae; 21 SNPs and 1 INDEL between KP405229 and NC\_020677); however, it is smaller than intraspecific variations of mitogenomes of fishes (e.g. *Rhynchocypris oxycephalus* (Park, Kim, Xi 2019)) and insects (e.g. *Chilo suppressallis* (Park, Xi, et al. 2019), *Spodoptera frugiperda* (Seo et al. 2019), and *Laodelphax striatellus* (Park, Jung, et al. 2019)) and plant chloroplast genomes (e.g. *Goodyera schlechtendaliana* (Oh et al. 2019), *Gastrodia elata* (Park et al. 2020), *Abeliophyllum distichum* (Park, Kim, Xi, et al. 2019), and *Pyrus ussuriensis* (Cho et al. 2019)), indicating a relatively lower level of inter-subspecific variations on its mitogenomes. Moreover, phylogenetic trees displayed that the two major



**Figure 1.** Neighbor-joining (bootstrap repeat is 10,000) and maximum-likelihood (bootstrap repeat is 1,000) phylogenetic trees of 30 complete mitogenomes: *Cervus canadensis nannodes* (MT430939 used in this study), *Cervus elaphus alxaicus* (KU942399), *Cervus elaphus* (NC\_007704 and KP172593), *Cervus elaphus kansuensis* (NC\_039923), *Cervus elaphus songaricus* (NC\_014703), *Cervus elaphus yarkandensis* (NC\_013840), *Cervus elaphus hippelaphus* (KT290948), *Cervus elaphus macneilli* (KX449334), *Cervus elaphus* (MF872248 and MF872247), *Cervus nippon yesoensis* (NC\_006973), *Cervus nippon centralis* (NC\_006993), *Cervus nippon yakushimae* (NC\_007179), *Cervus nippon hortulorum* (NC\_013834), *Cervus nippon hortulorum* (HQ191428), *Cervus nippon hortulorum* (KR868807), *Cervus nippon taiouanus* (NC\_008462), *Cervus nippon taiouanus* (EF058308), *Cervus nippon sichuanicus* (NC\_018595), *Cervus nippon kopschi* (NC\_016178), *Cervus nippon kopschi* (JN389444), and *Muntiacus vuquangensis* (NC\_016920) as an outgroup. Phylogenetic tree was drawn based on the maximum-likelihood tree. The numbers above branches indicate bootstrap support values of maximum-likelihood and neighbor-joining phylogenetic trees, respectively.

clades of *C. elephas* subspecies exists and *C. nippon* subspecies was separated from them (Figure 1).

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## Data availability statement

Mitochondrial genome sequence can be accessed via accession number MT430939 in the NCBI GenBank.

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