

MITOGENOME ANNOUNCEMENT

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The complete mitochondrial genome of Marco Polo wild sheep (*Ovis ammon polii*)

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ABSTRACT

In this study, the complete mitochondrial genome of Marco Polo wild sheep was sequenced for the first time. It is 16613 bp in length and possesses 22 tRNA genes, 13 typical mammalian protein-coding genes, two rRNA genes and one D-loop region. The whole genome's base composition is 33.7% A, 25.8% C, 13.1% G and 27.4% T, and the percentage of AT-rich regions is 61.1%.

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Argali (*Ovis ammon*) are the largest wild sheep in the world and are threatened throughout their habitat in central Asia (Kenny et al. 2008; IUCN 2013). Currently, nine different subspecies are commonly recognized (Fedosenko & Blank 2005; Wilson & Reeder 2005), of which, Marco Polo Argali (*Ovis ammon polii*/*O. a. polii*) have the longest horns. Due to illegal and legal hunting, habitat loss and competition with livestock (Reading et al. 2001), they are now facing an unprecedented threat throughout their habitat (geospatial coordinates: 37°05'~39°30' N-71°0'~75°50' E), which is adjacent to the borders of China, Pakistan, Afghanistan and Tajikistan (Schuerholz 2001). This study is the first published mitochondrial genome of *O. a. polii* (GenBank accession number: KT781689), which can be used to investigate evolutionary relationships among *Ovis* species and the Argali taxonomy.

Mitochondrial DNA from one specimen of *O. a. polii* blood was collected from Tianshan Mountain Wildlife Park (Urumqi, Chian) and sequenced using Illumina Hiseq 2500 (Illumina Inc., San Diego, CA). The mitogenome was successfully assembled using six scaffolds and six gap-filling polymerase chain reaction (PCR) products from Sanger sequencing. It is 16613 bp in length, and harbours 13 protein-coding genes, 22 tRNA genes, two rRNA genes and a non-coding D-Loop RNA. Its overall elements, and the gene arrangement pattern, are similar to those of the typical vertebrate mitogenome. The overall base composition (A: 33.7%, C: 25.8%, G: 13.1% and T: 27.4%) results in a low G + C (38.9%) content. Eight tRNA were encoded on the light strand, with the remainder of the genes encoded on the heavy strand. Of the 13 coding proteins, 10 use ATG as the start codon and three use ATA. Additionally, seven open-reading frames end with TAA, three genes use T, and single gene

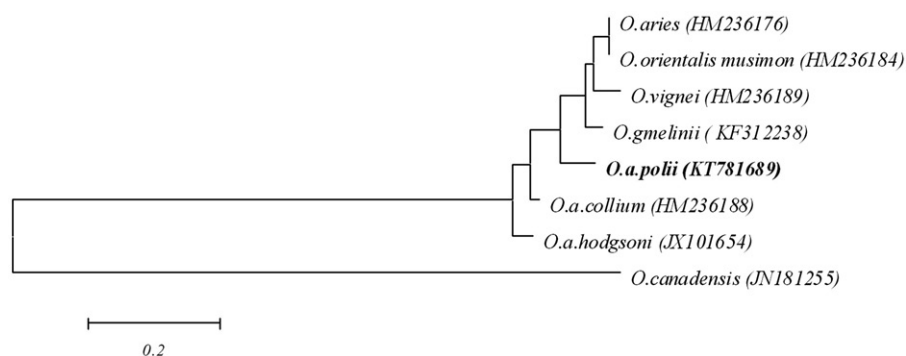


Figure 1. Neighbor-joining tree for five wild *Ovis* species and domesticated sheep based on the sequence of whole mitogenome.

uses TAG, AGA and TA as stop codons. The lengths of the 12s and 16s RNA genes located between tRNA^{phe} and tRNA^{leu} are 958 and 1575 bp, respectively.

The complete *O. a. polii* mitogenome was compared with five *Ovis* species [*O. vignei* (HM236189), *O. canadensis* (JN181255), *O. orientalis musimon* (HM236184), *O. gmelinii* (KF312238) and *O. aries* (HM236176)] and two argali subspecies [*O. a. collium* (HM236188) and *O. a. hodgsoni* (JX10165)] (Hiendleder et al. 1998; Lancioni et al. 2013; Hu et al. 2016). The gene order and base composition were conserved among these species, but the D-loop-region's sequences belong to a highly varied region among the species. The phylogenetic analysis indicated that the whole mitogenome of *O. a. polii* showed a high level of conservation with three wild species (Figure 1), *O. vignei*, *O. gmelinii*, *O. ammon* (*O. a. collium* and *O. a. hodgsoni*), as compared with domesticated sheep (*O. aries*) and bighorn wild sheep (*O. Canadensis*).

Disclosure statement

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

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