Characterization of the complete mitochondrial genome of the Dayu yak (Bos grunniens)

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ABSTRACT
Dayu yak (Bos grunniens) is a long-furred yak breed from the Qinghai-Tibetan Plateau, and is highly adapted to local high-altitude and cold environments. In this study, its mitochondrial genome was characterized via high-throughput sequencing technology. The genome is 16,323 bp long with an AT-biased base composition (61.0% A + T; light strand), and harbors the typical set of 37 mitochondrial genes and a noncoding control region. Its gene arrangement is identical to those of other bovid taxa. Phylogenetic analysis suggests that Dayu yak is most closely related to Maiwa, Niangya, Qinghai Plateau, Xueduo and Yushu yaks.

As an iconic symbol of the Qinghai-Tibetan Plateau, domestic yaks (Bos grunniens) have long been exploited for meat, milk, transportation and other necessities by local communities (Qiu et al. 2012). Dayu yak is a long-furred yak breed with its distribution mostly restricted to Haibei Tibetan Autonomous Prefecture, Qinghai Province, China, and is highly adapted to local high-altitude and cold environments. To facilitate its genetic assays, its complete mitochondrial genome was assembled and annotated via high-throughput sequencing technology in this study. Furthermore, phylogenetic analysis was also conducted to ascertain its relationship with other taxa within the subfamily Bovinae. The annotated genomic sequence has been deposited into GenBank under the accession number MT649465.

The blood sample of Dayu yak were collected from Yeniugou Township, Qilian County, Haibei Tibetan Autonomous Prefecture, Qinghai Province, China (38.35°N, 99.34°E). The voucher specimen (DAYU20200528) is stored in the Key Laboratory of Yak Breeding Engineering of Gansu Province, Lanzhou Institute of Husbandry and Veterinary Station of Xitan Township in Menyuan County, Menyuan, Qinghai Province of the People’s Republic of China.

The complete mitochondrial genome of Dayu yak is 16,323 bp long with an AT-biased base composition (33.7% A, 25.8% C, 13.2% G and 27.3% T; light strand), and harbors the typical set of 37 animal mitochondrial genes (13 protein-coding genes, 22 tRNAs and two rRNAs) and one non-coding control region. Its gene arrangement is identical to those of other bovid taxa. The PCGs start with the typical ATA (ND2, ND3 and NDS) or ATG (the 10 other PCGs) initiation codons, and end with TAG (ND2), the incomplete T (COX3, ND3 and NDS) or TAA (the nine others) termination codons. The tRNAs range in size from 60 (tRNA-Ser安阳) to 75 bp (tRNA-Leuvariable) with a total length of 1509 bp. The two rRNAs are 957 bp (12S rRNA) and 1,571 bp (16S rRNA) long, respectively, and are separated by tRNA-Val. The control region is 893 bp long, and is present between tRNA-Pro and tRNA-Phe. Besides, a 31-bp-long origin of the L-strand replication is identified between tRNA-Asn and tRNA-Cys.

To investigate the relationship of Dayu yak with 42 other taxa within the subfamily Bovinae, a neighbor-joining phylogenetic tree was reconstructed using the concatenated sequences of all 13 protein-coding genes (alignment size: 11,370 bp) with MEGA7 (http://www.megasoftware.net/) (Hall 2013; Kumar et al. 2016) (Figure 1). Bootstrap support values were estimated from 1000 random samplings. The outgroup
taxa included in the phylogenetic analysis are three species from the subfamily Caprinae, i.e. *Hemitragus jayakari* (FJ207523) (Hassanin et al. 2009), *Naemorhedus goral* (JX188255) (Yang et al. 2013) and *Ovis ammon* (KX609626) (Mao et al. 2017). The result suggests that Dayu yak is more closely related to five local yak breeds (Maiwa, Niangya, Qinghai Plateau, Xueduo and Yushu yaks) than to the other 37 taxa within the subfamily Bovinae (Figure 1).

**Disclosure statement**

The authors declare that there are no financial and personal relationships with other people or organizations that can appropriately influence...
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**Data availability statement**

The data that support the findings of this study are openly available in GenBank of NCBI at [https://www.ncbi.nlm.nih.gov](https://www.ncbi.nlm.nih.gov), reference number MT649465.

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