Characterization of whole mitogenome sequence of the Tongde yak (Bos grunniens)

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ABSTRACT

Tongde County is located in the southeast of Qinghai Province, China, harboring rich yak genetic resources. In the present study, the complete mitochondrial genome (mitogenome) of the Tongde yak (Bos grunniens) was firstly sequenced using Illumina sequencing technique and the corresponding sequence characterization was identified. Our results showed that the mitogenome of Tongde yak is a circular molecule with 16,323 bp length consisting of 37 genes (13 protein-coding genes, 2 rRNA genes, 22 tRNA genes) and a non-coding control region (D-loop), which is consistent with most bovine species. The overall nucleotide composition was found as: A (33.72%), T (27.27%), C (25.80%), and G (13.21%), respectively, yielding a higher AT content (60.99%). The complete mitogenome sequence of Tongde yak would provide useful information for further studies on its genetic resource conservation and molecular breeding programmes in the future.

Yak (Bos grunniens) is a valuable Bovine species, endemic to the Qinghai-Tibetan Plateau (QTP). In China, there are 20 officially recognized yak breeds and ~15 million yak heads are inhabited in this high-elevation ecosystem (National Committee of animal genetic resources 2021). Qinghai Province, located in the northwest of China and northeast region of QTP, has abundant yak genetic resources with more than five million individuals. Due to special geographical location, plateau climate and long history of yak breeding, some exceptional yak breeds/populations have been formed and identified recently in Qinghai province. For instance, two developed breeds (Datong and Ashidan) and four indigenous breeds (Gaoyuan, Huanhu, Xueduo and Yushu) harbor in this environment (National Committee of animal genetic resources 2021). Based on the archaeological analyses, mitochondrial and Y chromosomal variations, Qinghai is believed to be the center of origins and/or domestication for the yak (Wiener et al. 2003; Guo et al. 2006; Ma 2019). Tongde yak (Bos grunniens), harboring a strong high-altitude adaptation and resistance characteristics, with a population size of around 250,000 yak heads, is found in Tongde County of Qinghai Province. The mammalian mitochondrial genome (mitogenome) is characterized by tachyteleic evolution, simple structure and easy sequencing. The genetic characteristics of the mitogenome are one of the most important means to explore the maternal origin, diversity and migration history of mammals (Ingman et al. 2000; Shapiro and Hofreiter 2014; Reynolds et al. 2020). At present, mitogenomes of wild yak and some domestic yak breeds or populations have been successively assembled and annotated (Wang et al. 2021). However, no information is available on the mitogenome of Tongde yak. Therefore, in the current study, we sequenced and assembled its mitogenome sequence, which would provide useful basic data for the molecular genetic evaluation of this population.

Here, blood sample of one Tongde yak (Bos grunniens) was collected in Tongde County, Qinghai, China (100°20’N, 35°3’E). The voucher specimen (TD-1-20200824) is stored in the Key Laboratory of Plateau Livestock Genetic Resources Protection and Innovative Utilization of Qinghai Province, Academy of Animal Science and Veterinary Medicine, Qinghai University (Xining, Qinghai Province, China). The genomic DNA was extracted using DNA Extraction Kit (Aidlab Biotechnologies Co., Ltd, China), and stored at −20°C for later use. The complete genome of Tongde yak was sequenced using HiSeq 2000 platform (Illumina) with sequencing depth of 23.3×. The reads were aligned to the wild yak mitochondrial reference genome (Accession number:
Table 1. Summarized characterization of whole mitogenome sequence of Tongde yak (*Bos grunniens*).

| Gene       | Position | Base composition (%) | Start codon | Stop codon | Strand |
|------------|----------|----------------------|-------------|------------|--------|
| D-loop     | 1 - 476  | A 29.66% C 27.27% G 15.56% T 27.51% | ATA         | TAA        | H      |
| tRNAGly    | 950 - 10,285 | A 39.55% C 22.99% G 12.22% T 25.24% | ATG         | TAA        | H      |
| 12S rRNA   | 1,961 - 1,957 | A 39.55% C 22.99% G 12.22% T 25.24% | ATG         | TAA        | H      |
| tRNAVal    | 19,839 - 19,846 | A 39.55% C 22.99% G 12.22% T 25.24% | ATG         | TAA        | H      |
| CoX1       | 15,046 - 16,186 | A 39.55% C 22.99% G 12.22% T 25.24% | ATG         | AGA        | H      |
| CoX2       | 8,655 - 8,672 | A 39.55% C 22.99% G 12.22% T 25.24% | ATG         | TAA        | H      |
| CoX3       | 4,792 - 4,797 | A 39.55% C 22.99% G 12.22% T 25.24% | ATG         | TAA        | H      |
| ATP8       | 8,662 - 8,686 | A 39.55% C 22.99% G 12.22% T 25.24% | ATG         | TAA        | H      |
| ATP6       | 8,823 - 9,047 | A 39.55% C 22.99% G 12.22% T 25.24% | ATG         | TAA        | H      |
| CoX1       | 9,053 - 10,285 | A 39.55% C 22.99% G 12.22% T 25.24% | ATG         | TAA        | H      |
| CoX2       | 7,907 - 8,587 | A 39.55% C 22.99% G 12.22% T 25.24% | ATG         | TAA        | H      |
| CoX3       | 8,934 - 8,870 | A 39.55% C 22.99% G 12.22% T 25.24% | ATG         | TAA        | H      |
| ND4        | 10,073 - 10,771 | A 39.55% C 22.99% G 12.22% T 25.24% | ATG         | TAA        | H      |
| CoX4       | 10,287 - 10,355 | A 39.55% C 22.99% G 12.22% T 25.24% | ATG         | TAA        | H      |
| ND3        | 9,053 - 10,285 | A 39.55% C 22.99% G 12.22% T 25.24% | ATG         | TAA        | H      |
| CoX5       | 9,053 - 10,285 | A 39.55% C 22.99% G 12.22% T 25.24% | ATG         | TAA        | H      |
| ND4        | 10,772 - 11,065 | A 39.55% C 22.99% G 12.22% T 25.24% | ATG         | TAA        | H      |
| ND5        | 11,062 - 12,429 | A 39.55% C 22.99% G 12.22% T 25.24% | ATG         | TAA        | H      |
| CoX6       | 12,440 - 12,509 | A 39.55% C 22.99% G 12.22% T 25.24% | ATG         | TAA        | H      |
| CoX7       | 12,510 - 12,569 | A 39.55% C 22.99% G 12.22% T 25.24% | ATG         | TAA        | H      |
| CoX8       | 12,571 - 12,640 | A 39.55% C 22.99% G 12.22% T 25.24% | ATG         | TAA        | H      |
| ND6        | 14,451 - 14,969 | A 39.55% C 22.99% G 12.22% T 25.24% | ATG         | TAA        | H      |
| CoX9       | 14,973 - 15,041 | A 39.55% C 22.99% G 12.22% T 25.24% | ATG         | TAA        | H      |
| Cytb       | 15,046 - 16,186 | A 39.55% C 22.99% G 12.22% T 25.24% | ATG         | TAA        | H      |
| CoX10      | 16,189 - 16,258 | A 39.55% C 22.99% G 12.22% T 25.24% | ATG         | TAA        | H      |
| CoX11      | 16,258 - 16,323 | A 39.55% C 22.99% G 12.22% T 25.24% | ATG         | TAA        | H      |

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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, accession number MZ313873.

Sampling and uploading information of voucher personnel

Sample collection personnel include Guangzhen Li, Zhijie Ma, and Shengmei Chen, submitted the voucher is Guangzhen Li and Zhijie Ma. The Email of Guangzhen Li: guangzhenli6228@126.com; Zhijie Ma: zhijiema@126.com.

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