Characterization of the complete mitochondrial genome of the Pamir yak (*Bos grunniens*)

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ABSTRACT

Pamir yak (*Bos grunniens*) is a yak breed from Pamir Plateau with strong adaptation to the high-elevation, cold and anoxic environments. Its complete mitochondrial genome was determined to be 16,323 bp long with a moderately asymmetric nucleotide composition, and harbors the typical set of 37 mitochondrial genes and the noncoding control region. The PCGs start with the typical ATA or ATG codons, and end with TAA, TAG or the incomplete termination codon T. Phylogenetic analysis suggests that Pamir yak is most closely related to six other yak breeds (i.e. Datong, Pali, polled, Qilian, Seron and Sunan yaks).

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Domestic yaks (*Bos grunniens*) are mainly distributed in the Qinghai-Tibetan Plateau and adjacent regions, and are of great importance to local communities (Qiu et al. 2012). To date, many local breeds have been developed across its native distribution range (Chu et al. 2016; Guo et al. 2016; Wu, Chu, et al. 2016; Wu, Ding, et al. 2016; Fu et al. 2019; Guo, Bao, et al. 2019; Guo, Wu, et al. 2019; Wu et al. 2019; Zhang et al. 2019; Zhou, Wu, Ding, et al. 2019; Zhou, Wu, Liang, et al. 2019). Among them, Pamir yak is a local breed from Pamir Plateau with strong adaptation to the high-elevation, cold and anoxic environments. Here, we present its complete mitochondrial genome (GenBank accession number: MK922356).

A blood sample of Pamir yak were collected from Tashkurgan Tajik Autonomous County, Xinjiang Uygur Autonomous Region, China (37°10′N, 75°27′E). A voucher specimen is held in the Key Laboratory of Yak Breeding Engineering of Gansu Province, Lanzhou Institute of Husbandry and Pharmaceutical Sciences, 335 Jiangouyan, Qilihe District, Lanzhou 730050, People’s Republic of China.

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The mitochondrial genome of Pamir yak is 16,323 bp long, and encodes the typical set of 37 animal mitochondrial genes (13 protein-coding genes/PCGs, 22 tRNAs, and 2 rRNAs). Three PCGs are initiated with ATA (ND2, ND3 & ND5), while all the others use ATG as their start codon. As for the stop codons, one PCG (ND2) uses TAG, three PCGs (COX3, ND3 & ND4) use the incomplete stop codon T, while all the others are terminated with TAA. The 22 tRNAs range in length from 60 (tRNA-SerAGN) to 75 bp (tRNA-LeuUUR). The two rRNAs are 957 bp (12S rRNA) and 1571 bp (16S rRNA) long, respectively, and are separated by tRNA-Val. Besides, an 893-bp-long control region occurs between tRNA-Pro and tRNA-Phe.

A neighbor-joining (NJ) phylogenetic tree was reconstructed using the program MEGA7 (Kumar et al. 2016) to investigate its relationship with other yak breeds with sequenced mitochondrial genomes (Figure 1). All 13 PCGs were used for the phylogenetic analysis. Two Bison species, i.e., Bison bison (GU946976) (Douglas et al. 2011) and Bison priscus (KX269111) (Froese et al. 2017), were included as outgroup taxa. The result suggests that Pamir yak is most closely related to six other yak breeds (i.e., Datong, Pali, polled, Qilian, Seron and Sunan yaks).

Disclosure statement
No potential conflict of interest was reported by the authors.

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References
Al Arab M, Höner zu Siederdissen C, Tout K, Sahyoun AH, Stadler PF, Bernt M. 2017. Accurate annotation of protein-coding genes in mitochondrial genomes. Mol Phylogenet Evol. 106:209–216.
Bernt M, Donath A, Jühling F, Externbrink F, Florentz C, Fritzsch G, Pütz J, Middendorf M, Stadler PF. 2013. MITOS: improved de novo metazoan mitochondrial genome annotation. Mol Phylogenet Evol. 69:313–319.

Chu M, Wu X, Liang C, Pei J, Ding X, Guo X, Bao P, Yan P. 2016. The complete sequence of mitochondrial genome of polled yak (Bos grunniens). Mitochondrial DNA Part A. 27:2032–2033.

Douglas KC, Halbert ND, Kolenda C, Childers C, Hunter DL, Derr JN. 2011. Complete mitochondrial DNA sequence analysis of Bison bison and bison-cattle hybrids: function and phylogeny. Mitochondrion. 11:166–175.

Froese D, Stiller M, Heintzman PD, Reyes AV, Zazula GD, Soares AE, Meyer M, Hall E, Jensen BJL, Arnold LJ, et al. 2017. Fossil and genomic evidence constrains the timing of bison arrival in North America. Proc Natl Acad Sci USA. 114:3457–3462.

Fu D, Ma X, Jia C, Lei Q, Wu X, Chu M, Ding X, Bao P, Pei J, Guo X, et al. 2019. The complete mitochondrial genome sequence and phylogenetic analysis of Maiwa Yak (Bos grunniens). Mitochondrial DNA Part B. 4:1986–1987.

Guo X, Bao P, Chu M, Song R, Ding X, Wu X, Xiong L, Liang C, Pei J, Yan P. 2019. Characterization of the complete mitochondrial genome of the Yushu yak (Bos grunniens). Mitochondrial DNA Part B. 4:1853–1854.

Guo X, Pei J, Bao P, Chu M, Wu X, Ding X, Yan P. 2016. The complete mitochondrial genome of the Qinghai Plateau yak Bos grunniens (Cetartiodactyla: Bovidae). Mitochondrial DNA Part A. 27:2889–2890.

Guo X, Wu X, Bao P, Chu M, Ding X, Xiong L, Liang C, Pei J, Yan P. 2019. Characterization of the complete mitochondrial genome of the Seron yak (Bos grunniens). Mitochondrial DNA Part B. 4:2256–2257.

Hahn C, Bachmann L, Chevreux B. 2013. Reconstructing mitochondrial genomes directly from genomic next-generation sequencing reads: a baiting and iterative mapping approach. Nucleic Acids Res. 41:e129.

Kumar S, Stecher G, Tamura K. 2016. MEGA7: molecular evolutionary genetics analysis version 7.0 for bigger datasets. Mol Biol Evol. 33:1870–1874.

Qiu P, Zhang G, Ma T, Qian W, Wang J, Ye Z, Cao C, Hu Q, Kim J, Larkin DM, et al. 2012. The yak genome and adaptation to life at high altitude. Nat Genet. 44:946–949.

Wu X, Chu M, Liang C, Ding X, Guo X, Bao P, Yan P. 2016. The complete mitochondrial genome sequence of the Datong yak (Bos grunniens). Mitochondrial DNA Part A. 27:433–434.

Wu X, Ding X, Chu M, Guo X, Bao P, Liang C, Yan P. 2016. Characterization of the complete mitochondrial genome sequence of Gannan yak (Bos grunniens). Mitochondrial DNA Part A. 27:1014–1015.

Wu X, Zhou X, Ding X, Liang C, Guo X, Chu M, Wang H, Pei J, Bao P, Yan P. 2019. Characterization of the complete mitochondrial genome of the Huanhu Yak (Bos grunniens). Mitochondrial DNA Part B. 4:1235–1236.

Zhang Y, Wu Q, Yang L, Chen X, Wang C, Zhang Y, Zeng Y, Xu L, Lu C, Zeng C, et al. 2019. Characterization of the complete mitochondrial genome sequence of golden wild yak and revealed its phylogenetic relationship with 9 yak subspecies. Mitochondrial DNA Part B. 4:660–661.

Zhou X, Wu X, Ding X, Liang C, Guo X, Chu M, Wang H, Pei J, Pengjia B, Yan P. 2019. Characterization of the complete mitochondrial genome of the Xueduo yak (Bos grunniens). Mitochondrial DNA Part B. 4:1233–1234.

Zhou X, Wu X, Liang C, Guo X, Chu M, Wang H, Pei J, Bao P, Ding X, Yan P. 2019. The complete mitochondrial genome of Sunan yak (Bos grunniens) and a phylogenetic study. Mitochondrial DNA Part B. 4:1053–1054.