



# Genetic diversity and classification of Tibetan yak populations based on the mtDNA *COIII* gene

Q.Q. Song<sup>1</sup>, Z.X. Chai<sup>1</sup>, J.W. Xin<sup>2</sup>, S.J. Zhao<sup>1</sup>, Q.M. Ji<sup>2</sup>, C.F. Zhang<sup>2</sup>, Z.J. Ma<sup>3</sup> and J.C. Zhong<sup>1</sup>

<sup>1</sup>Key Laboratory of Animal Genetics and Breeding,  
State Ethnic Affairs Commission and Ministry of Education,  
Southwest University for Nationalities, Chengdu, China

<sup>2</sup>Institute of Animal Science and Veterinary,  
Tibet Academy of Agricultural and Animal Husbandry Sciences, Lhasa, China

<sup>3</sup>Institute of Animal Science,  
Qinghai Academy of Animal Science and Veterinary Medicine, Xining, China

Corresponding author: J.C. Zhong  
E-mail: zhongjincheng518@126.com

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**ABSTRACT.** To determine the level of genetic diversity and phylogenetic relationships among Tibetan yak populations, the mitochondrial DNA cytochrome c oxidase subunit 3 (*COIII*) genes of 378 yak individuals from 16 populations were analyzed in this study. The results showed that the length of cytochrome c oxidase subunit 3 gene sequences was 781 bp, with nucleotide frequencies of 29.2, 29.4, 26.1, and 15.2% for T, C, A, and G, respectively. A total of 26 haplotypes were identified, with 69 polymorphic sites, including 11 parsimony-informative sites and 58 single-nucleotide polymorphism sites. No deletions/insertions were found in sequence comparison, indicating that nucleotide mutation types were transitions and transversions. Haplotype and nucleotide

diversities were 0.562 and 0.00138, respectively, indicating a high level of genetic diversity in Tibetan yak populations. Phylogenetic relationship analysis indicated that Tibetan yak populations are divided into 2 groups.

**Key words:** Mitochondrial DNA cytochrome c oxidase subunit 3; Genetic diversity; Phylogenetic relationship; Tibetan yak