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ABSTRACT

Genetic diversity and origin of Chinese cattle revealed by mtDNA D-loop sequence variation

Song-Jia Lai , Yi-Ping Liu , Yan-Xing Liu , Xue-Wei Li , Yong-Gang Yao

a College of Animal Science and Technology, Sichuan Agriculture University,
Ya'an, Sichuan 625014, China

b Department of Animal Husbandry Engineering, Zhengzhou College of Animal Husbandry Engineering,
Zhengzhou 450008, China

c Laboratory of Cellular and Molecular Evolution, Kunming Institute of Zoology, Chinese Academy of Sciences, Kunming,
Yunnan 650223, China

To determine the origin and genetic diversity of Chinese cattle, we analyzed the complete mtDNA D-loop sequences of 84 cattle from 14 breeds/populations from southwest and west China, together with the available cattle sequences in GenBank. Our results showed that the Chinese cattle samples converged into two main groups, which correspond to the two species *Bos taurus* and *Bos indicus*. Although a dominant lineage was clearly discerned in both *B. taurus* and *B. indicus* mtDNAs, network analysis of the lineages in each of the two species further revealed multiple clades that presented regional difference. The *B. taurus* samples in China could be grouped into clades T2, T3, and T4, whereas *B. indicus* harbored two clades I1 and I2. Age estimation of these discerned clades showed a time range of 14,100–44,500 years before present (YBP). The phylogenetic pattern of Chinese cattle was consistent with the recently described cattle matrilineal pool from northeast Asia, but suggested that *B. indicus* contributed more to the cattle from south and southwest China. The genetic diversity of Chinese cattle varied among the breeds studied.