

研究报告

## 贵州黄牛mtDNA D-loop 遗传多样性研究

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### 摘要

对贵州4个地方黄牛品种共计82个个体的线粒体DNA D-loop区全序列910 bp进行分析, 检测到31种单倍型, 其核苷酸多态位点65个, 约占所测核苷酸总长的7.14%, 其中有62个转换, 2个颠换, 1个转换/颠换共存。贵州4个黄牛品种mtDNA D-loop区核苷酸多样性( $\pi$ 值)为2.16%~2.61%, 单倍型多样性(H)为0.695~0.909, 表明贵州黄牛mtDNA遗传多样性比较丰富。根据单倍型构建了贵州4个黄牛品种的NJ分子系统树。聚类表明, 贵州黄牛有普通牛和瘤牛2大母系起源, 其影响较为均一。并探讨了用核苷酸多样性 $\pi$ 值的大小来衡量黄牛群体遗传分化程度的可行性。

关键词 [贵州黄牛](#); [线粒体DNA](#); [D-loop](#); [遗传多样性](#); [起源](#)

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## Genetic Diversity of Mitochondrial DNA D-loop Sequences in Cattle Breeds in Guizhou

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### Abstract

The complete mitochondrial D-loop sequences, 910 bp in length, in 82 individual cattle from 4 breeds in Guizhou province were analyzed. The results revealed 31 mitochondrial haplotypes, 65 polymorphic sites, covering 7.14% of the entire length of the sequence. Among these polymorphic sites, there were 62 transitions, 2 transversions and 1 coexistent site of transition and transversion. The nucleotide diversity ( $\pi$ value) and haplotype diversity (H) estimated from mtDNA D-loop region in 4 cattle breeds in Guizhou varied from 2.16%~2.61% and 0.695~0.909, respectively, showing that abundant mitochondrial genetic diversity exists in Guizhou cattle breeds. The Neighbor-Joining molecular phylogenetic tree of mtDNA D-loop of 4 Guizhou cattle breeds was constructed according to the 31 haplotypes. The NJ tree indicated that the origin of cattle breeds was from *Bos taurus* and *Bos indicus* which had nearly the same influence on cattle breeds in Guizhou. The feasibility of applying nucleotide diversity ( $\pi$ value) to the evaluation of bovine genetic differentiation was discussed.

Key words [Guizhou cattle](#) [mitochondrial DNA](#) [D-loop](#) [genetic diversity](#) [origin](#)

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