

研究报告

藏羚羊mtDNA D-Loop区遗传多样性研究

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摘要

该研究采用非损伤性DNA基因分型技术, 对可可西里地区10个藏羚羊 (*Pantholops hodgsoni*) 个体的mtDNA非编码区部分片段 (444~446bp) 进行了序列分析, 结果显示A、T含量 (61.8%) 明显高于G、C含量 (38.2%), 共发现10种单倍型, 包括48个多态位点, 其中转换位点44个、颠换位点1个、插入位点1个、缺失位点2个。单倍型间平均遗传距离为0.031, 单倍型多态性 (h) 为1.000, 核苷酸多态性 (π) 为2.96%。说明藏羚羊线粒体控制区存在着丰富变异, 最后从藏羚羊的生态习性 & 地理分布两方面对这一结果进行了分析探讨。

关键词 [藏羚羊](#); [线粒体D-loop区](#); [单倍型](#); [遗传多样性](#)

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Study on mitochondrial DNA genetic diversity of Tibetan antelope

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Abstract

With noninvasive DNA genotyping technology, we investigated genetic diversity of Tibetan antelope by analyzing mitochondrial DNA variation, those samples are collected from Hoh Xil National Nature Reserve, Qinghai province, China. A total of 444~446bp of the mitochondrial control region was sequenced from 10 individuals. The results showed that A% + T%(61.8%) was higher than C%+G% (38.2%) obviously. Ten haplotypes were identified in the 10 samples. The result showed 48 polymorphic sites after comparisons of the 10 haplotype samples, among them, including 44 transitions, 1 transversion, 1 insertion and 2 deletions. The average genetic distance of haplotypes is 0.031. The haplotypic diversity is 1.000. The nucleotide diversity is 0.0296. The average number of nucleotide differences is 13.127. It showed that the Tibetan antelope population has high variation in mitochondrial D-loop sequence.

Key words [Tibetan antelope](#) [mitochondria](#) [displacement-loop region](#) [haplotype](#) [genetic diversity](#)

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