

动物遗传学

中国部分牦牛品种线粒体DNA遗传多态性研究

赖松家¹, 王玲², 刘益平¹, 李学伟¹

1. 四川农业大学动科院;雅安 625014; 2. 西南农业大学荣昌校区动科院;荣昌 402460

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摘要 采用DNA测序技术首次测定了中国5个牦牛品种(类群)35个个体线粒体DNA控制区(D-loop)全序列,结果表明:牦牛线粒体DNA控制区全序列长度为891 bp~895 bp, T、C、A、G四种核苷酸的含量分别为28.5%、25.3%、32.5%、13.7%。检测到55个变异位点,约占分析位点总数的6.16%,核苷酸变异类型有转换、颠换、插入/缺失四种。确定了24种单倍型,单倍型H4和H6为中国牦牛的主体单倍型,各单倍型在品种间分布不平衡,所测定的5个牦牛品种(类群)单倍型多样性平均为 0.9697 ± 0.0180 ,说明我国牦牛D-loop单倍型类型丰富。牦牛品种内各序列平均核苷酸差异数为10.936,核苷酸多样性为1.231%;牦牛品种间核苷酸分歧度(Dxy)约为0.760%~2.155%,品种间双参数距离范围为0.000~0.029,表明我国牦牛遗传多态性丰富。对D-环序列变异的分子方差分析和单倍型网络关系图的结果表明:我国牦牛品种间出现显著的遗传分化,牦牛单倍型网络关系图聚为2个聚类簇,表明我国牦牛有2个母系来源,或者有2个主要的驯化地点。

关键词 牦牛 多态性 D-loop 单倍型

分类号

Study on Mitochondrial DNA Genetic Polymorphism of Some Yak Breeds in China

LAI Song-Jia¹, WANG Ling², LIU Yi-Ping¹, LI Xue-Wei¹

1. College of Animal Science and Technology; Sichuan Agriculture University; Ya'an 625014; China; 2. College of Animal Science and Technology; Rongchang Campus Southwest Agriculture University; Rongchang 402460; China

Abstract

This study had determined yak's complete sequence of mitochondrial DNA control region (D-loop) of 35 individuals in 5 yak breeds at first time. The result showed that the length of D-loop in yak was 891 bp~895 bp, Content of nucleotide T, C, A, G were 28.5%, 25.3%, 32.5% and 13.7% respectively. There were 55 polymorphic sites (6.16% in total analyzed sites), the transition, transversion and insertion/deletion were found in this region. 24 haplotypes was defined in this study, in which haplotype H4 and H6 were major haplotypes of Chinese yak. The distribution of all the haplotypes among the breeds was disequilibrium. The average diversity of haplotypes were 0.9697 ± 0.0180 , which indicated the abundance of haplotypes of yak's D-loop. The average nucleotide difference and the nucleotide diversity in Chinese yak breeds were 10.936 and 1.231% respectively. Nucleotide divergence and Kimura 2-parameter distance between yak breeds were 0.760%~2.155%, and 0.000~0.029 respectively. It indicated that the genetic diversity of Chinese yak was very abundant. Analysis of molecular variance and network construction results indicated that there was significant divergence among Chinese yak breeds. The network construction indicated that Chinese yak had been divided into 2 types and had probably 2 maternal origins or 2 domesticated places.

Key words Yak polymorphism D-Loop haplotype

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