

动物遗传学

中国驴种线粒体DNA D-loop多态性研究

雷初朝1, 陈宏1, 2, ①, 杨公社1, 孙维斌1, 雷雪芹3, 葛庆兰1, 王朝锋1, 吕宁1, 高雪1, 侯文通1

1. 西北农林科技大学动物科技学院;陕西省农业分子生物学重点实验室;杨凌 712100; 2. 徐州师范大学生物技术研究所以;徐州 221116; 3. 河南科技大学动物科技学院;洛阳 471003

收稿日期 修回日期 网络版发布日期 接受日期

摘要 利用Clustal W软件对我国5个家驴品种26个个体的mtDNA D-loop区399 bp序列进行同源序列比对,共检测到核苷酸多态位点23个,只有转换1种类型,约占所测核苷酸的5.76%。以欧洲驴D-loop作对照,我国5个家驴品种D-loop区序列的平均核苷酸变异率为1.80%,其中凉州驴的平均核苷酸变异率为0.35%,云南驴为1.25%,关中驴为2.30%,新疆驴为2.91%,佳米驴为2.20%。家驴品种内与品种间mtDNA D-loop区序列歧异度分别为0.25%~5.01%和4.51%~5.51%,说明家驴品种间D-loop区序列多态性比较丰富。在所测家驴个体中,mtDNA D-loop序列由11种单倍型组成,单倍型比例为42.31%,表明我国家驴mtDNA遗传多态性正逐步丧失,需要加强其种质资源保护。引用GenBank中亚洲野驴和欧洲家驴的序列,构建了我国5个家驴品种的NJ分子系统树,首次从分子水平证实中国家驴可能起源于非洲野驴,而与亚洲野驴无关。

关键词 [家驴](#) [线粒体DNA](#) [D-loop](#) [多态性](#) [单倍型](#) [起源](#)

分类号

Study on Mitochondrial DNA D-loop Polymorphism in Chinese Donkeys

LEI Chu-Zhao1, CHEN Hong1,2,①, YANG Gong-She1, SUN Wei-Bin1, LEI Xue-Qin3, GE Qing-Lan1, WANG Zhao-Feng1, LÜ, Ning1, GAO Xue1, HOU Wen-Tong1

1.College of Animal Science and Technology; Northwest Agriculture and Forestry University; Shaanxi Key Laboratory of Agricultural Molecular Biology; Yangling 712100; China; 2. Institute of Biotechnology; Xuzhou Normal University; Xuzhou 221116; China; 3.College of Animal Science and Technology; Henan Science and Technology University; Luoyang 471003; China

Abstract

The mitochondrial DNA (mtDNA) D-loop sequences with 399 bp in 26 individuals from 5 donkey breeds in China were analyzed. Aligned by Clustal W software, the results showed that 23 polymorphic nucleotide sites and only transition with the percentage of 5.76% of 399 bp were observed. In reference to mtDNA D-loop sequences of European domestic donkey as a control, the average percentage of mtDNA D-loop nucleotide variation in 5 Chinese donkey breeds was 1.80%. The average percentages of D-loop nucleotide variation from Liangzhou donkey (LZ), Yunnan donkey (YN), Guanzhong donkey (GZ), Xinjiang donkey (XJ) and Jiami donkey (JM) were 0.35%, 1.25%, 2.30%, 2.91% and 2.20% respectively. The average sequence divergence estimated from D-loop sequences varied from 0.25%~5.01% within breeds and 4.51%~5.51% among breeds, respectively, demonstrating that interbreed existed rather abundant mitochondrial genetic diversity in Chinese donkeys. Comparisons of the 26 sequences revealed 11 mitochondrial haplotypes, the percentage of haplotype was 42.31%. This phenomenon demonstrated that the mitochondrial genetic diversity in Chinese donkey breeds is reducing. It is urgent to protect the genetic resources of Chinese donkey. The molecular phylogenetic tree of mtDNA D-loop sequences in 5 Chinese donkey breeds, 6 sequences of Asian wild ass (Equus asinus kiang, Equus asinus kulan, Equus asinus hemionus;) and 4 sequences of European domestic donkeys from GenBank was constructed by Neighbor-Joining method. It was first proved in molecular level that the origin of Chinese donkey breeds was from African wild ass (Equus africanus africanus and Equus africanus somaliensis), not from Asian wild ass in the paper.

Key words [donkey](#) [mitochondrial DNA](#) [D-loop](#) [polymorphism](#) [haplotype](#) [origin](#)

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