

研究论文

可可西里自然保护区藏羚羊的微卫星多态性研究

周慧^{1, 2}, 李迪强¹, 张于光¹, 杨涛², 刘毅²

1. 国林业科学研究院森林生态环境与保护研究所, 国家林业局森林生态环境重点实验室, 北京 100091;

2. 湖南农业大学动物科学与技术学院, 长沙 410128

收稿日期 2006-4-24 修回日期 2006-9-28 网络版发布日期 2007-7-10 接受日期

摘要 藏羚羊是我国特有的珍稀濒危动物, 对其开展遗传多样性的研究具有非常重要的科学价值。为了获取足够的遗传信息并进一步研究藏羚羊在核基因水平上的遗传多样性, 对来自可可西里地区的75个藏羚羊干皮张样本进行了微卫星遗传多样性研究。研究从来自牛和绵羊的25个微卫星基因座中筛选到9个具有高度多态性的微卫星基因座(MCM38, MNS64, IOBT395, MCMAI, TGLA68, BM1329, BMS1341, BM3501 和 MB066)。用非变性聚丙烯凝胶电泳检测微卫星的PCR扩增产物, 计算了这9个微卫星基因座的等位基因频率、多态信息含量、基因杂合度等指标并估算了种群数量。结果在75只藏羚羊中共检测到85个等位基因, 9个微卫星基因座的等位基因数为7~12个, 平均每个基因座检测到9.4个等位基因, 有效等位基因数为处于4.676~9.169之间, 平均为6.519; 基因频率分布在0.007~0.313之间, 多态信息含量在0.753~0.881之间, 平均为0.818; 观察杂合度为0.791~0.897, 平均为0.844, 期望杂合度为0.786~0.891之间, 平均为0.838±0.0132, 各基因座观察杂合度与期望杂合度比较接近。固定指数为-0.269~-0.097, 平均为-0.163。Shannon's 指数为1.660~2.315, 平均为1.990。种群数量的估算结果显示这75个体均来自同一种群。结果表明该种群在核基因水平仍具有丰富的遗传多样性。

关键词 藏羚羊; 微卫星基因座; 遗传多样性; 可可西里自然保护区

分类号

Genetic Diversity of Microsatellite DNA Loci of Tibetan Antelope (*Chiru, Pantholops hodgsonii*) in Hoh Xil National Nature Reserve, Qinghai, China

Hui Zhou^{1, 2}, Diqiang Li^{1, ①}, Yuguang Zhang¹, Tao Yang², Yi Liu²

1. Institute of Forestry Ecology, Environment and Protection, and the Key Laboratory of Forest Ecology and Environment of State Forestry Administration, Chinese Academy of Forestry, Beijing 100091, China;

2. Hunan Agricultural University, Changsha 410128, China

Abstract

The Tibetan antelope (*Pantholops hodgsonii*), indigenous to China, became an endangered species because of considerable reduction both in number and distribution during the 20th century. Presently, it is listed as an Appendix I species by CITES and as Category I by the Key Protected Wildlife List of China. Understanding the genetic diversity and population structure of the Tibetan antelope is significant for the development of effective conservation plans that will ensure the recovery and future persistence of this species. Twenty-five microsatellites were selected to obtain loci with sufficient levels of polymorphism that can provide information for the analysis of population structure. Among the 25 loci that were examined, nine of them showed high levels of genetic diversity. The nine variable loci (MCM38, MNS64, IOBT395, MCMAI, TGLA68, BM1329, BMS1341, BM3501, and MB066) were used to examine the genetic diversity of the Tibetan antelope (n = 75) in Hoh Xil National Nature Reserve (HXNNR), Qinghai, China. The results obtained by estimating the number of population suggested that all the 75 Tibetan antelope

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samples were from the same population. The mean number of alleles per locus was 9.4 ± 0.5300 (range, 7–12) and the mean effective number of alleles was 6.519 ± 0.5271 (range, 4.676–9.169). The observed mean and expected heterozygosity were 0.844 ± 0.0133 (range, 0.791–0.897) and 0.838 ± 0.0132 (range, 0.786–0.891), respectively. Mean Polymorphism Information Content (PIC) was 0.818 ± 0.0158 (range, 0.753–0.881). The value of Fixation index (Fis) ranged from -0.269 to -0.097 with the mean of -0.163 ± 0.0197 . Mean Shannon's information index was 1.990 ± 0.0719 among nine loci (range, 1.660–2.315). These results provide baseline data for the evaluation of the level of genetic variation in Tibetan antelope, which will be important for the development of conservation strategies in future.

Key words [genetic diversity](#) [microsatellite locus](#) [Tibetan antelope](#)

DOI:

通讯作者 周慧 zhouhui0402@163.com