could be used in the captive management of other endangered species.

扩展功能 本文信息 饲养东北虎的微卫星变异研究Genetic Diversity of Microsatellite ▶ Supporting info ▶ **PDF**(0KB) Loci in Captive Amur Tigers ▶ [HTML全文](0KB) 张于光1,2,李迪强,肖启明2,饶力群3,张学文3 ZHANG Yu-Guang1,2 LI Di-Qiang1 XIAO Qi-Ming2 RAO Li-Qun3 ZHANG Xue-Wen3 ▶参考文献 1.中国林业科学研究院森林生态环境与保护研究所,北京,100091;2.湖南农业大学生物安全科技学 服务与反馈 院,长沙,410128;3.湖南农业大学理学院,长沙,4101281. Institute of Forestry Ecology, Environment ▶把本文推荐给朋友 and Protection, Chinese Academy of Forestry, Beijing 100091, China; 2. College of Biosafety Science ▶加入我的书架 and Technology of Hunan Agricultural University, Changsha 410128, China; 3. College of Sciences of ▶ 加入引用管理器 Hunan Agricultural University, Changsha 410128, China 收稿日期 修回日期 网络版发布日期 接受日期 ▶复制索引 Email Alert 摘要 东北虎是世界上濒危动物之一,具有极其重要的研究价值和保护意义。该研究利用10个在东北虎基因组中表现多 ▶文章反馈 态性的微卫星基因座(Fca005, Fca075, Fca094, Fca152, Fca161, Fca294, Pti002, Pti003, Pti007和 ▶浏览反馈信息 Pti010)对113只饲养东北虎进行了遗传多样性检测。用非变性聚丙烯酰胺凝胶电泳检测微卫星的PCR扩增产物, 计算了10个微卫星基因座的等位基因频率、基因杂合度、多态信息含量和有效等位基因数。在113只东北虎样品 相关信息 中,10个基因座的等位基因数为3~6个,其中Fca152最多;等位基因频率处于0.009~0.767之间。基因杂合度值 ▶ 本刊中 包含"东北虎"的 在0.385~0.707间,平均为0.616,多态信息含量值在0.353~0.658间,平均为0.558,有效等位基因数处于1.629 相关文章 ~3.409之间,平均为2.784,表明所选用的10个微卫星基因座在研究样品中均为中高度多态性基因座,具有比较 明显的遗传变异。113只样品中包括75只毛发样品,23只血液样品和15只组织样品,不同样品的结果比较表明,毛卜本文作者相关文章 发、血液和组织样品均可以得到清晰的扩增结果。所以,微卫星基因座与非损伤性DNA分析方法可以成功地应用于 张于光 濒危珍稀动物的遗传多样性研究。

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Abstract:. The tiger is one of the most threatened wildlife species since the abundance and distribution of tiger have decreased dramatically in the last century. The wild Amur tiger (Panthera tigris altaica) only distributed in northeast China, the far east area of Russia and the north Korea and its size of wild population is about 450 in the world and 20 in China. Several hundred captive populations of Amur tigers are the main source to protect gene library of tiger and the source of recovering the wild populations. The Breeding Center for Felidae at Hengdaohezi and Li-Qun ZHANG Xue-Wen Ha' erbin Tiger Park in Heilongijang Province is the biggest captive breeding base in China. How t make clear the genetic pedigree and establish reasonable breeding system is the urgent issues. So we use the microsatellite DNA markers and non-invasive technology to research on the genetic diversity of captive Amur tiger in this study.

Ten microsatellite loci (Fca005, Fca075, Fca094, Fca152, Fca161, Fca294, Pti002, Pti003, Pti007 and Pti010), highly variable nuclear markers, were studied their genetic diversity in 113 captive Amur tigers. The PCR amplified products of microsatellite loci were detected by non-denatured polyacry lamide gel electrophoresis. Allele numbers, allelic frequency, gene heterozygosity(He), polymorphism information content(PIC) and effective number of allele(Ne) were calculated. 41 alleles were found and their size were ranged from 110bp to 250bp in ten microsatellite loci, Fca152 had 6 alleles, Fca075, Fca094 and Fca294 had 5 alleles, Fca005 and Pti002 had 4 alleles and the others had 3 alleles in all tiger samples, respectively. The allelic frequencies were from 0.009 to 0.767; The He ranged from 0.385 to 0.707, and Fca294 and Pti010 locus had the highest and lowest value: the PIC were from 0.353 to 0.658, Fca294 and Pti010 locus had the highest and lowest value: and Ne were from 1.626 to 3.409. Fca294 and Pti010 locus had the highest and lowest value. which showed the ten microsatellie loci had high or medium polymorphism in these Amur tigers and had high genetic diversity. At the same time, we only found even bases variability which showed the even bases repeat sequence (CA/GT) maybe the basic unit for length variability of microsatellite in all loci.

Abstract

Key words

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