Journal of Genetics and Genomics
(Formerly *Acta Genetica Sinica*)
July 2007, 34(7): 600–607

Research Article

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

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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 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.

Keywords: genetic diversity; microsatellite locus; Tibetan antelope

The Tibetan antelope (*Pantholops hodgsonii*), also known as Chiru or long-horn antelope, was endemic to the Qinghai-Tibet Plateau and was primarily found at the elevation of greater than 4,000 m [1]. Although it appears similar to a typical antelope, the Tibetan antelope is most closely related to sheep, goat, and other members of the subfamily *Caprinae*, as shown by the analyses of mitochondrial ribosomal DNA[2]. Since the 1980s, intensive illegal hunting for the high-priced wool of the animal has drastically

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Received: 2006–04–24; Accepted: 2006–09–28
This work was supported by a grant from Conservation Technology for Endangered Wildlife Program, Social Service Project of the Ministry of Science and Technology (No. 2001DIB100058), and the National Key Project of 10th Five-Year Plan (No. 2001BA510B10).

① Corresponding author. E-mail: lidq@caf.ac.cn; Tel: +86-10-6288 9551 reduced all populations. In 1905, a minimum of 15,000–20,000 Tibetan antelopes were found[3]. Today, only less than 70,000 Tibetan antelopes exist and approximately 20,000 of these are slaughtered every year[3]. In addition, habitat destruction and increased human activity exacerbated the rapid decline in population distribution and size during recent decades. The decline of the Tibetan antelope has attracted attention worldwide since the 1970s and subsequently was listed as Appendix Ⅰ by Convention on International Trade in Endangered Species of Wild Fauna and Flora (CITES; http://www.cites.org/eng /app/appendices.shtml).

The means to protect the Tibetan antelope population attract a great deal of attention of the government of China and extensive concern by the international community. The different ways to effectively protect a species should include many aspects, such as understanding its distribution, community and structure, number, and genetic diversity. Previous studies on Tibetan antelope had focused on distribution of its population, individual biological characteristics, phylogenesis, parasites, disease diagnosis and treatment, hair physics and chemistry characteristics, etc[1, 2, 4–7]. The government of China had successively set up four national nature reserves, including XHNNR, Qiangtang Nature Reserve, Altun Shan Nature Reserve and Sanjiangyuan Nature Reserve (Fig. 1) to protect the population and the habitat of these endangered animals.

Genetic diversity and structure provide useful information on the population status, connectivity, and demographic history that is essential for developing the effective management plans. One of the most widely used molecular markers to understand the genetic diversity in wildlife is variable short tandem repeats (STRs) referred to as microsatellite DNA loci. These simple repetitive sequences are highly polymorphic[8], are abundant and randomly distributed throughout eukaryotic genomes[9], and inherited under Mendelian law. Furthermore, microsatellite DNA loci appeared to follow a relatively simple step-wise mutation model of evolution[10]. The inherent characteristics of microsatellite DNA loci have made it useful in the study of population genetics and greatly enhance the ability to assess genetic diversity, detect genetic structure, test parentage and relationship, and understand its population history. Microsatellite DNA loci can be identified using polymerase chain reaction (PCR) with known DNA primers from closely related

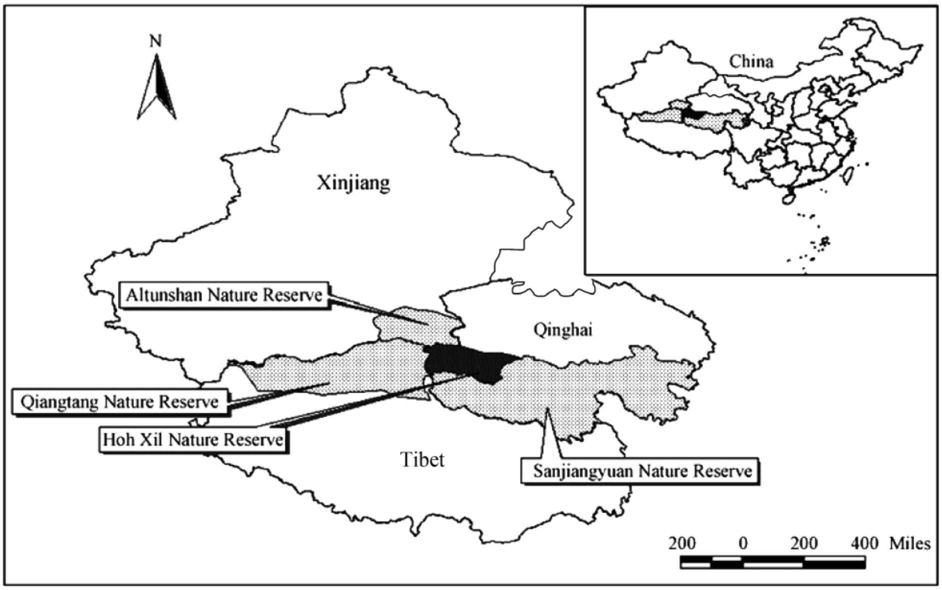

Fig. 1 Geographic distribution of Tibetan antelope in China