

## Genetic Analysis of Two Subspecies of Reeves' Muntjac (Cervidae: *Muntiacus reevesi*) by Karyotyping and Satellite DNA Analyses

Pei-Yi Chiang<sup>1</sup>, Chyi Chyang Lin<sup>2,3</sup>, Shu-Ju Liao<sup>2</sup>, Lie-Jiau Hsieh<sup>2</sup>, Shuan-Yow Li<sup>1</sup>, Ming-Chieh Chao<sup>4</sup>, Yueh-Chun Li<sup>1,\*</sup>

<sup>1</sup>Department of Life Sciences, Chung Shan Medical University, Taichung, Taiwan 402, R.O.C.

<sup>2</sup>Department of Medicine Research, China Medical University Hospital, Taichung, Taiwan 404, R.O.C.

<sup>3</sup>Department of Medicine and Pathology, University of Alberta, Edmonton, Alberta, T6G 2B7 Canada

<sup>4</sup>Taipei Zoo, Taipei, Taiwan 116, R.O.C.

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**Pei-Yi Chiang, Chyi Chyang Lin, Shu-Ju Liao, Lie-Jiau Hsieh, Shuan-Yow Li, Ming-Chieh Chao, Yueh-Chun Li (2004)** Genetic analysis of two subspecies of Reeves' muntjac (Cervidae: *Muntiacus reevesi*) by karyotyping and satellite DNA analyses. *Zoological Studies* 43(4): 749-758. We analyzed the karyotypes of the Formosan muntjac (*Muntiacus reevesi micrurus*) including G-banding, C-banding, and NOR-staining analyses. The results showed the species has a  $2n = 46$  chromosome complement. The G-banding patterns as well as the localizations of rRNA gene clusters and constitutive heterochromatins were similar to those of Chinese muntjac (*M. reevesi reevesi*). In addition, satellite DNA analysis was also carried out. The restriction periodicity of FM-sat1 revealed a 0.75-kb register indicating that this deer species belongs to the plesiometa-carpalia division. Finally, the FISH study demonstrated that the Formosan and Chinese muntjacs have similar localizations of satellite I DNA in their respective genomes. Although the Formosan and Chinese muntjacs share almost identical results of cytogenetic analyses, Southern blot and FISH studies revealed some sequence divergence of satellite I DNA between these 2 species supporting the classification of the Formosan muntjac as a subspecies of, not the same species as, the Chinese muntjac. Furthermore, the data suggest that satellite I DNA of the Formosan muntjac and that of the Chinese muntjac may have originated from different ancestral sequences or that they may have experienced different homogenization patterns in the course of evolution. <http://www.sinica.edu.tw/zool/zoolstud/43.4/749.pdf>

**Key words:** Phylogeny, Cervid satellite I DNA, Muntjac karyotyping, Fluorescence in situ hybridization (FISH).

Muntjac deer (Muntiacinae, Cervidae) are classified into 9 known species: *Muntiacus crinifrons*, *M. feae*, *M. gongshanensis*, *M. muntjak*, *M. putaensis*, *M. reevesi*, *M. rooseveltorum*, *M. truongsongensis*, and *M. vuquangensis* (Shi and Ma 1988, Amato et al. 1991, Nowak 1991, Evans and Timmins 1994, Timmins et al. 1998, Gao et al. 1998, Wang and Lan 2000). Based on the morphological and anatomical studies, these species of the genus *Muntiacus* demonstrate quite-similar appearances, and a sterile hybrid was produced from 2 closely related species, *M. muntjak* and *M. reevesi* (Shi et al. 1980). However, these morphologically similar and close-

ly related species have significant diversity in diploid chromosome numbers and karyotypes from  $2n = 6$  (female Indian muntjac; *Muntiacus muntjak vaginalis*) to  $2n = 46$  (Chinese muntjac, *M. reevesi reevesi*) (Fontana and Rubini 1990). Such chromosomal divergences are not uncommon within species, such as in lemurs (Dutrillaux 1979), mole rats (Nevo et al. 1994), and gibbons ( $2n = 38, 44, 50, \text{ and } 52$ ) (Jauch et al. 1992) or within races, such as in the house mouse (*Mus musculus domesticus*) (Nachman et al. 1994). Those studies suggest that karyology might be an excellent model for investigating speciation. More recently, molecular phylogenetic studies were performed to

\*To whom correspondence and reprints requests should be addressed. No. 110 Chien-Kuo N. Rd., Sec. 1, Taichung, Taiwan 402, R.O.C. Tel: 886-4-24730022 ext. 1814. Fax: 886-4-23248109. E-mail: ycl@csmu.edu.tw