



# Proceedings

## Korean Journal of Veterinary Science

Vol. 48, No. 1 Supplement

April 2008



### 2008 International Joint Symposium of Preventive Medicine International Symposium on and Zoonosis, Food Safety Animal Protection and 2nd C. L. Davis Korean Symposium

- **Date:** April 25 (Fri), 2008
- **Venue:** KOFST, Seoul
- **Hosts:** Korean Society of Veterinary Science (KSVS), Korean Society for Zoonoses (KSZ), Korean Society of Veterinary Public Health (KSVPH), Korean Society of Food Hygiene and Safety (KSFHS), Korean Society of Veterinary Pathology (KSVP), Brain Korea 21 Program for Veterinary Science, SNU (BK21), Asian Association of Veterinary Schools (AAVS), Japanese Society of Mammalogy (JSM), Charles Louis Davis Foundation Korea Branch (C.L. Davis Foundation), Korean Society of Systematic Zoology (KSSZ)
- **Sponsors:** Ministry for food, Agriculture, Forestry and Fisheries, Korea Food and Drug Administration (KFDA), Korea Research Foundation, Korea Science and Engineering Foundation, The Korean Federation of Science and Technology Societies, Korean Association of Academic Societies, National Veterinary Research and Quarantine Service (NVRQS), Korea Racing Authority, Korean Veterinary Medical Association, Cargill Agripurina Korea Inc., 3M Korea, BioMerieux Korea Co. Ltd., ChoongAng Vaccine Laboratories Co. Ltd., Animal Genetics Inc. Intervet Korea, SD Co. Ltd.

The Korean Society of Veterinary Science

**Phylogeography and ecology of the  
Siberian roe deer (*Capreolus pygargus* Pallas, 1887)**

Yun Sun Lee<sup>\*,1</sup>, Inna V. Voloshina<sup>2</sup>, Alexander I. Myslenkov<sup>2</sup>, Irina Sheremetyeva<sup>3</sup>,  
Irina Kartavtseva<sup>3</sup>, Young-Jun Kim<sup>1</sup>, Mi-Sook Min<sup>1</sup>, Hang Lee<sup>1\*</sup> and Nickolay Markov<sup>4</sup>

<sup>1</sup>Conservation Genome Resource Bank for Korean Wildlife (CGRB), BK21 Program for Veterinary Science and  
College of Veterinary Medicine, Seoul National University, Seoul 151-742, South Korea

<sup>2</sup>Lazovsky State Nature Reserve, 56 Centralnaja Street, Lazo, Primorsky Krai, 692980, Russia

<sup>3</sup>Institute Biology and Soil, Far East Russian Academy Science, Porspekt Stoletiya, 159 Vladivostok-22, 690022,  
Russia

<sup>4</sup>Institute of Plant and Animal Ecology Ural Branch of Russian Academy of Sciences, 620144, 8 Marta 202,  
Yekaterinburg, Russia

The Siberian roe deer (*Capreolus pygargus*) is widely distributed in Eurasia, including Russian Siberia, Yakutia, Transbaikalia, Russian Far East, Northern Mongolia, Northern China and Korea. Ecologically, the Siberian roe deer demonstrates site-fidelity in the rut time and the period of raising young (spring and summer) with long-distance migration in autumn and winter. For most of its distribution, roe deer exist at densities of 1.2 to 8.6 ind /10 sq. Km. In a number of areas, the abundance of roe deer has been substantially decreased due to over-hunting. This has resulted in the formation of isolated populations within their range. The ecological specificity of this species emphasizes the importance of studying the genetic diversity and phylogeographic structure of the Siberian roe deer populations. However, there have been very few studies concerning these subjects up to now. In addition, the taxonomic status of the roe deer population in Jeju Island has been controversial because there seems to be considerable morphological differences between the roe deer populations on Korean peninsula and Jeju Island. In the present study, mitochondrial cytochrome *b* and control region sequences of roe deer samples from Russian Siberia, Trans-Baikal, Amurskyi region, Primorskyi Krai, Korean peninsula and Jeju Island were utilized to evaluate genetic diversity and phylogeographic structure of the species. The phylogenetic trees and network analysis indicated that there are two major phylogroups consisting of the Eurasian mainland group and Jeju Island group. There are no shared haplotypes between the two groups suggesting that the island lineage diverged early in the evolution of the species. In contrast, populations in the Eurasian continent did not show apparent phylogeographic structure suggesting gene flow among the populations. Nucleotide and haplotype diversities of *C. pygargus* in Russia were higher than those in Korea including Jeju Island. To understand their detailed phylogeographic structure, analysis with a faster evolving genetic marker such as microsatellites would be needed.