

A109

한국산 송사리집단의 분자지리계통 연구
강태욱^P, 김무상¹, 김창배^C

한국생명공학연구원 생물다양성정보실, 대전 305-333

염색체수, 형태, 체색, 생태 등의 분류정보에 의하면 한국에는 대륙송사리(*Oryzias sinensis*)와 송사리(*O. latipes*)가 지역적으로 경계를 이루며 분포한다고 한다. 대륙송사리는 서해안으로 흐르는 하천과 서해안의 도서 지방과 중국 대륙에 분포하며, 송사리는 낙동강, 동해안으로 유입하는 하천 및 서남해의 도서 지방과 일본에 분포하는 것으로 알려져 있다. 이는 한국의 지리적 특성에 의한 결과임을 추측할 수 있다. 본 연구에서는 이를 더 명확하게 하기 위하여 분자생물학적 방법을 적용하였다. 경기도 팽성, 충청남도 부여, 전라북도 운봉, 경상남도 김해, 창녕, 밀양 지역에서 각각 10개체씩 송사리를 채집하여, 미토콘드리아 유전체 control region 1.2kbp DNA 부분을 PCR cloning 한 후, 그 염기서열을 새로이 확보하였다. 이 염기서열들을 clustalX program으로 multiple alignment하였고, 이를 바탕으로 MEGA2 program의 neighbor-joining method로 계통수를 작성하였다. 그 결과 팽성, 부여, 운봉 지역에서 채집된 송사리들은 중국의 대륙송사리 집단과 더욱 유사하였고, 김해, 창녕, 밀양 지역에서 채집된 송사리들은 일본 송사리집단들과 더 유사한 것으로 확인되었다.

A110

Molecular Phylogenetic Status of the Korean Goral and Japanese Serow Based on the Partial Sequence of Mitochondrial Cytochrome b Gene

Mi-Sook Min¹, Hideo Okumura², Jung-Hwa An¹, Dong-Jun Cho^P, Kyung-Seok Kim¹, Chang-Bae Kim², Chang-Hoon Han³, Inna V. Voloshina³, Hang Lee^C

^{PC1} College of Veterinary Medicine and School of Agricultural Biotechnology, Seoul National University, Seoul 151-742; ²FFPRI, Tsukuba, Ibaraki 305-8687, Japan; ³Korea Research Institute of Bioscience and Biotechnology, Taejon 305-333; ¹Seoul Grand Park, Gwacheon 427-702; ³Lazovsky State Nature Reserve, Primorsky Krai 692890, Russia

To investigate the molecular phylogenetic status of the Korean goral, *Nemorhaedus caudatus*, and Japanese serow, *Capricornis crispus*, partial sequences of the mitochondrial cytochrome b gene from twelve Korean gorals and sixteen Japanese serows were determined and compared with those of the major lineages of Rupicaprinae species including two other goral species of *Nemorhaedus* and two other serow species of *Capricornis*. The Korean gorals examined displayed very low intraspecific variation for the cytochrome b gene, showing nucleotide differences in only one position. The Japanese serows showed slightly higher diversity with five haplotypes. Sequence comparisons and the molecular phylogenetic tree indicated that the Korean goral was more closely related to the Himalayan goral, *N. goral* than to the long-tailed goral, *N. caudatus*. The present data highlight the necessity of reexamining the taxonomic status of Korean gorals. The present study also clearly showed the sufficient distance between serows and gorals to be separated into two genera. Of the three species of genus *Capricornis*, the Formosan serow, *C. swinhoei* more closely related to the serow, *C. sumatraensis* than to the Japanese serow. It seems appropriate that the Formosan serow is considered a distinct species. Preliminary data on the intraspecific genetic variation of the Japanese serow have also been reported.

A111

Polymorphic Microsatellites Developed by Cross-species Amplifications for Population Study of Korean Goral (*Nemorhaedus caudatus*)

Kyung-Seok Kim¹, Mi-Sook Min¹, Jung-Hwa An^P, Hang Lee^C

College of Veterinary Medicine and School of Agricultural Biotechnology, Seoul National University, Seoul 151-742

Korean goral (*Nemorhaedus caudatus*) is an endangered species and requires a high priority of conservation in South Korea. To develop microsatellite markers useful for population studies on the Korean goral, cross-species amplifications were performed. Thirty-four microsatellite primer pairs designed from domestic Bovidae were tested on test panel of six Korean gorals and ten domestic goats. After the optimization of PCR condition, 29 (85.3%) of the microsatellite primers produced amplification products in the Korean goral and 27 (79.4%) in domestic goats. Of the amplified products, 17 (58.6%) were polymorphic in the Korean goral and 25 (92.6%) in domestic goats. The expected mean heterozygosity and number of alleles per locus was 0.363 and 2.6 in the Korean goral and 0.617 and 4.6 in domestic goats, respectively. Sequencing of the PCR product of TGLA126 primers, which produced an unusual amplification product in the Korean goral, displayed a long CA repeats motif, revealing a typical of microsatellite. Considering a low level of genetic diversity of Korean goral obtained from our preliminary data, systematic population management and conservation of this species are urgently required. The result also indicates that cross-species amplification of domestic Bovidae microsatellite primers could be employed for population genetic studies on the Korean goral, allowing population studies in endangered Caprinae species.

A112

Phylogenetic Study of Korean Otter, *Lutra lutra*, Based on the Partial Sequence of Mitochondrial Cytochrome b Gene

Mi-Sook Min^P, Sungyong Han², Chang-Hoon Han³, Jung-Hwa An¹, Hang Lee^C

^{PC1} College of Veterinary Medicine and School of Agricultural Biotechnology, Seoul National University, Seoul 151-742; ²Wildlife Institute of Korea, Kyungnam 631-442; ³Seoul Grand Park, Gwacheon 427-702

Korean Otter, *Lutra lutra*, is an endangered species and has been designated as a Natural Monument species by the Cultural Properties Administration of Korean Government. To investigate the molecular phylogenetic status of the Korean Otter, partial sequences of the mitochondrial cytochrome b genes from 8 specimens were analyzed. Although an approximately 505 bp partial region of the mitochondrial cytochrome b gene were sequenced for Korean Otter, only 290bp was compared with the other otters' sequences obtained from Genbank and our data. As a result, four different haplotypes of the cytochrome b gene were recognized in Korean Otter. Sequence comparisons and the molecular phylogenetic tree indicated that the Korean Otter was more closely related to the European Otter than other from Japan.