

mitochondrial DNA control region and cytochrome b gene. In the sequence analysis of mtDNA control region, Korean racoon dog appeared to be distinct from Japanese racoon dog with average 90% sequence similarity and 0.110 pairwise distance of Kimura 2-parameter. In the sequence analysis of mtDNA cytochrome b gene, they showed average 98% similarity and 0.010 pairwise distance. It was revealed that Korean racoon dog is distinct in the mtDNA sequence. Therefore, it is concluded that Japanese racoon dog (*Nyctereutes procyonoides viverrinus*) is a subspecies which is different in chromosomal karyotype and morphometry from Chinese racoon dog (*Nyctereutes p. procyonoides*) and in mtDNA sequences from Korean racoon dog (*Nyctereutes p. koreensis*). However, in order to clarify the subspecific status of Korean racoon dog, samples of Chinese one is needed for further analyses.

A717

Taxonomic Status of Korean Hare based on Mitochondrial DNA Cytochrome B Gene Comparison

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After the analysis with partial sequence of mtDNA cytochrome b gene of Korean hare (*Lepus coreanus*) from Mt. Weolak, we compared this sequence with those of Chinese hare (*Lepus sinensis*) and Manchurian hare (*Lepus mandshurinus*) obtained from Genbank. It was revealed that Korean hare is more similar with Manchurian hare than Chinese hare in their mtDNA sequences, and it is confirmed that Korean hare is not a subspecies of Chinese hare but a distinct species of *L. coreanus*, as concluded by Jones and Johnson (1965). Moreover, it becomes necessary to carry out

further mtDNA sequence analysis with additional specimens of Manchurian and Korean hares in order to decide that Korean hare is a subspecies of Manchurian hare, as noted by Flux and Angermann (1990).

A718

Mitochondrial DNA Cytochrome b Sequence of Korean Red Squirrel (*Sciurus vulgaris coreae*)

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We compared the partial sequence of mtDNA cytochrome b of Korean red squirrel (*Sciurus vulgaris coreae*) resulted from this study with those of red squirrel from Korea (*S. v. coreae*), Hokkaido (*S. v. orientis*), Transbaikalia (*S. v. fusconigrans*), and Italy (*S. v. vulgaris*) obtained from Genbank. It was revealed that Korean red squirrel is more or less similar with Transbaikalia and Italy red squirrel, and that Hokkaido red squirrel is different from other three subspecies. Therefore, it is confirmed that *S. v. coreae* and *S. v. fusconigrans* are the synonym of *S. v. vulgaris*, as noted by Corbet (1978). Moreover, it is concluded that *S. v. orientis* is a distinct subspecies, as suggested by Corbet (1978).

A719

Isolation and Phylogeny of Endogenous Retroviral Elements Belonging to the HERV-K LTR in cDNA Library of Human Fetal Brain and Xq21.3 Region Linked to Psychosis

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HERV-K family of human endogenous retroviral sequences has been originally cloned from Syrian hamster intra-cisternal A type particles, has homology to mouse mammary tumour virus (MMTV), and includes sequences that are expressed in normal placenta. The HERV-K LTR elements have randomly transposed across the chromosomes in the course of human evolution. We identified five HERV-K LTR elements from the cDNA library of human fetal brain. Two of them (FB-1 and FB-5) are closely related to the human specific HERV-K LTR elements by phylogenetic analysis. We also investigated such an elements within the Xq21.3 region linked to psychosis that was replicated on the Y chromosome after the separation of the chimpanzee and human lineages. Four element of HERV-K LTR were identified in that region. Two of these elements (K-X10-5 and K-X13-1) have a high degree of sequence similarity to the human specific HERV-K LTR. To locate such elements and determine their possible relationship to genes that have contributed to late developments in human evolution provides a strategy for investigating the role of retroviruses/retrotransposons in species-related hominid characteristics.

A720

Molecular Phylogeny of Cobitidae Inferred from Mitochondrial DNA Cytochrome b Sequences

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Phylogenetic relationships between Korean loaches (Cypriniformes:Cobitidae) were investigated by comparing cytochrome b gene

sequences from 10 species, among which 8 were newly sequenced. Results generally agree with previous morphological studies, but new interesting relationships were found. It is remarked that two genera *Orthrias* and *Lefuna* appeared to be paraphyletic in Cobitidae observed. Also the present results supported that the species of *Iksookimia* and *Cobitis melanoleuca* were early diverged respectively. Intergeneric sequence divergences of Cobitidae ranged from 0.097 to 0.282. Interspecific sequence divergence between *I. Koreensis* and *I. pumila* was 0.011 and that of between *C. sinensis* and *C. melanoleuca* was 0.112. Interfamilic sequence divergences between Cobitidae and Cyprinidae ranged from 0.184 to 0.272.

A721

Two New Species of the Genus *Coelotes* from China (Araneae: Amaurobiidae)

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Two new species, *Coelotes wugeshanensis* sp. nov. and *C. yanlingensis* sp. nov. are described based on the specimens collected from Hunan Province, China. *Coelotes wugeshanensis* male is similar to *Coelotes argenteus* Wang et al., 1990, but differs in the form of median apophysis and the tibial apophysis of the palpal organ. *Coelotes yanlingensis* sp. nov. is allied to *Coelotes variegatus* Wang et al., 1990, but it can be distinguished by the ball-shape of spermatheca, that of the latter kidney-shaped. All the measurements are in mm. The type specimens are deposited in Hunan Biological Research Institute, Hunan Normal University.