

A711

Mitochondrial DNA Restriction Fragment Patterns in Two Subspecies of Striped Field Mice, *Apodemus agrarius* Pallas (Mammalia, Rodentia), from Central China and Korea

Hung Sun Koh* and Jinxing Wang¹
Department of Biology, Chungbuk University, Korea;
Department of Biology, Shandong University, China¹

Samples of two subspecies of striped field mice, *Apodemus agrarius pallidior* from central China and *A. agrarius coreae* from Korea, were used. All 35 fragments and 12 mtDNA clones were recognized. The 12 clones were grouped into two major subgroups with the mean divergence value of 1.01%. One subgroup consisted of 51 samples from four localities in central China (= *A. agrarius pallidior*), and the other subgroup is composed of 56 samples from four localities in Korea (= *A. agrarius coreae*). Taxonomic status of these two subspecies is confirmed in this molecular study, and it is necessary to carry out further analyses with samples from other localities in eastern Asia to clarify subspecies classification of this species.

A712

Genetic Relationships of Two Subspecies of Striped Field Mice, *Apodemus agrarius* Pallas (Mammalia, Rodentia), from Korea

Hung Sun Koh*, Woo-Jai Lee¹, and Thomas D. Kocher¹
Department of Biology, Chungbuk University, Korea;
Department of Zoology, University of New Hampshire, USA¹

We obtained 282 base pairs of sequence for the mitochondrial control region from 70 individuals of striped field mice, *Apodemus agrarius coreae* and *A. agrarius chejuensis* to determine the levels of genetic divergence between these morphologically distinct taxa. The DNA sequences showed more genetic diversity in *A. agrarius coreae* (2.98%) than in *A. agrarius chejuensis* (1.86%). Phylogenetic analysis indicated that although the idea that two morphotypes are different species is not strongly supported, animals of *A. agrarius coreae* with large body size from Wan Island cluster with the large-bodied *A. agrarius chejuensis*, and should be included in that taxon. *A. agrarius coreae* is not strictly monophyletic, since the large-bodied samples cluster within the range of mitochondrial variation of this taxon. Nevertheless, the fact that the two morphotypes do not share mitochondrial haplotypes suggests that there is little gene flow between these subspecies.