

Comparative phylogeography of four *Apodemus* species (Mammalia: Rodentia) in the Asian Far East: evidence of Quaternary climatic changes in their genetic structure

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The phylogeography of four *Apodemus* species (*Apodemus agrarius*, *Apodemus peninsulae*, *Apodemus latronum*, and *Apodemus draco*) was studied in the Far East of Asia, based on sequences of the mitochondrial DNA cytochrome *b* gene. The results obtained show the existence of many different genetic lineages within the studied *Apodemus* species, suggesting the isolation and differentiation of populations in multiple refuge areas. Higher genetic diversities in some regions such as Yunnan, Sichuan (China), and eastern Russia suggest these areas are potential refuges for these species. The existence of such complex genetic structures could be linked to the presence of many biogeographic barriers (Himalaya Mountains, Tien-shan Mountains, Altai Mountains, Tibetan Plateau, Gobi desert, Yunnan Guizhou Plateau, Dzungaria basin, and others) in these regions, which were probably reinforced during the Quaternary climate changes. These barriers also played an important role concerning the low dispersal abilities of the two studied *Apodemus* species adapted to forest habitats (*A. latronum* and *A. draco*) with respect to colonizing regions other than China.

II) Co phylogeographic relationship between a rodent host species, the bank vole (*Myodes glareolus*) and one of its specific parasites, the nematode *Heligmosomum mixtum*

Nucleotide variation in 590 bp fragment of the mitochondrial DNA cytochrome *b* (*cyt b*) was used to describe the genetic variation and the phylogeographic pattern of the nematode *Heligmosomum mixtum*, a specific parasite of the Bank vole (*Myodes glareolus*). A total of 119 individuals distributed among 10 populations were studied. Fifty four haplotypes were detected. The intrapopulational genetic variability was particularly low (between 0.3-1.5%) as compared to results obtained on other nematode species (i.e. *Heligmosomoides polygyrus*). The network analyses evidenced a weak geographical phylogeographic structure. The populations of *H. mixtum* exhibit a homogenous and single lineage in Europe suggesting the survival of this species in a single glacial refugia during the last ice age maybe located in the Carpathian region.