

CYCLES AND NON-CYCLES IN VOLE POPULATIONS:
THE GREY-SIDED VOLE IN HOKKAIDO AS AN EXAMPLE

Abstracts

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of

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presented at

Ninth International Mammalogical Congress (IMC 9)

A lecture will start with a synopsis of small rodent cycles since Charles S. Elton's pioneering work in the 1920s. The lecture will then focus on much ecological research in north-eastern Hokkaido, Japan. The abundance of the grey-sided vole in Hokkaido will then be the subject of the lecture after these introductory remarks. Observed results from statistical time-series analysis of these monitoring data will then be interpreted ecologically and compared with findings from studies using other approaches. A local topic of the lecture will be the effects of different seasonal processes (and the length of the various seasons) affect the over-annual dynamics of the population. The lecture will close with some reflections on where we ought to go next, both with respect to Hokkaido as well as with respect to more general topics.

Roles of Mammalogy on Coexistence of Wild Mammals and Human

by works: monitoring data, population dynamics, statistical time-series analysis, rodent density cycle

July 31- August 5, 2005

Sapporo, Hokkaido, Japan

Organized by

The Science Council of Japan and The Mammalogical Society of Japan

Website: <http://www.imc9.jp>

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Site-specific highly repetitive DNA sequences, which comprise constitutive heterochromatin, is a useful marker for both taxonomic and phylogenetic studies in mammals on account of the evolutionary features as rapid evolving sequences. To clarify chromosomal organization and phylogenetic relationships in the Cricetinae, we molecularly cloned new families of site-specific repetitive DNA sequences from the Syrian hamster (*Mesocricetus auratus*) (2n=44), Chinese hamster (*Cricetulus griseus*) (2n=22), Djungarian hamster (*Phodopus sungorus*) (2n=28) and Triton hamster (*Tscherskia triton*) (2n=28). The repetitive sequences were characterized by chromosome *in situ* hybridization and filter hybridization. They were classified into six different types of repeated sequence families according to chromosomal distribution and genome organization; 1) centromeric major satellite DNA, 2) sex chromosome-specific repetitive sequences, 3) repetitive sequences in the telomeric regions of heterochromatic arms of autosomes and sex chromosomes, 4) repetitive sequences in the interstitial regions of autosomes, and 5) LINE 1-like and 6) non LINE 1 repeats predominantly distributed in the heterochromatic arms of autosomes and sex chromosomes. The sequence homologies were compared among seven or eight species of four genera in the Cricetinae and one species of the Calomyscinae. The centromeric major satellite DNA, and sex chromosome-specific and telomeric region-specific repetitive sequences were conserved in the same genus but divergent in different genera. The repetitive sequences in the interstitial regions of autosomes were conserved in the same genus and other closely related genera. On the other hand, the repetitive sequences on the heterochromatic arms of chromosomes were conserved through the subfamily Cricetinae or both the Cricetinae and Calomyscinae. These results indicate that the nucleotide divergence of the site-specific repetitive sequences was well correlated with the phylogenetic relationships of the Cricetinae, which were inferred from the nucleotide sequences of the mitochondrial and nuclear genes, and each sequence has been independently amplified and diverged in the same genome.

S4803

B CHROMOSOMES POLYMORPHISM IN CONTINENTAL AND INSULAR POPULATIONS OF THE KOREAN FIELD MOUSE *Apodemus peninsulae*

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B chromosomes (Bs) of *Apodemus peninsulae* from 47 continental (Russia) and 9 insular (Russky, Stenin, Sakhalin and Hokkaido Islands) populations were analyzed. Polymorphism of Bs was observed in all continental and two insular (Russky and Hokkaido) populations. Bs of studied samples differed in number, size and morphology. The variation of number of Bs was wider in mice from Siberia and Hokkaido Island. Similar C-banding patterns of banded Bs were observed in mice from Russky Island and continental Far. Banded Bs from Hokkaido and Siberia showed also similar C-banding patterns. Low frequency of specimens without B was registered in Khabarovsk Region (0.23), Primorsky Region (0.06), Siberia, Russky and Hokkaido Islands (0). However, no B was found in populations from Sakhalin and Stenin Islands. DNA composition analysis of Bs from Siberia and the Far-East was performed by DNA-probe generation with chromosome microdissection of different Bs followed with FISH of obtained DNA-probes on A and B chromosomes from different localities. The hypothesis of a possible multiregional origin of Bs has been suggested. Distribution of Bs in population of *Apodemus peninsulae* in different continental and insular localities, probably, reflects the population history and particularities of genomes of mice from these populations. This study was supported by the Grants of Far East Branch Russian Academy of Science 05-1-P12-001; Siberian Branch of the Russian Academy of Science Integration project 48.