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Sero-epizootiological survey and genetic analysis of hantavirus in Far East Russia

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It is known that Far East Russia is an endemic area of severe HFRS, and that genera *Apodemus*, *Microtus*, and *Clethrionomys* rodents inhabit this area. However, little is known about the reservoir animals and genetic information of hantaviruses in Far East Russia. Therefore, in this study, wild rodents were captured in the suburbs of Khabarovsk, that is a main city of Far East Russia, then sero-epizootiological survey and genetic analysis of hantavirus were conducted.

In 72 rodents captured in the survey points, anti-hantavirus antibodies were detected by indirect immunofluorescence antibody assay with Hantaan and Puumala type antigens. Seropositives in each rodent species against Hantaan and/or Puumala antigen are detected as follows; *Clethrionomys (C.) rufocanus* (8/36), *C. rutilus* (3/13), *Apodemus peninsulae* (4/15), *Micromys minutus* (1/1), *Tamias sibiricus* (1/1), and *Microtus fortis* (1/1).

Hantavirus S genome segment was detected from one seropositive *C. rufocanus* by reverse transcriptase-polymerase chain reac-

tion, and the full length of the segment was sequenced. The sequence was most closely related with those of other Puumala viruses derived from *C. rufocanus* indigenous to Hokkaido and the identities were 81.4% in nucleotide and 97.9% in deduced amino acid level. The S segment detected from *C. rufocanus* in Khabarovsk was designated as Khekhchir based on the point where the host rodent was caught. The phylogenetic analysis of S genome of Khekhchir strain revealed that this virus belongs to the clade of Puumala types. Moreover, Khekhchir strain consisted a distinct lineage together with Hokkaido Puumala type viruses in *C. rufocanus*, but diverged from European Puumala viruses in *C. glareolus*.

These results indicate that Khekhchir strain detected from *C. rufocanus* in Far East Russia was Puumala type, and closely related to Puumala viruses from *C. rufocanus* in Hokkaido. The data emphasized the diversity in the hantavirus serotypes strongly depend on the host species.