Geographic distribution and genetic variation of hantavirus in Hokkaido and Far East Russia

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A new method, the Protein-G immunofluorescence antibody assay (Protein-G IFA), was developed for serological survey of wild rodents. Wild rodents were captured in Japan and Far East Russia in 1995–1996 and the sera were tested for the presence of hantavirus antibodies by Protein-G IFA. Nucleotide sequenses of virus strains were also analyzed. The results are summarized as follows:

1. Protein-G IFA was a rapid and simple test with low non-specific reactions.

2. A total of 411 indigenous rodents were captured at Kamiiso and Tobetsu in Hokkaido and in Honshu. The sera were tested for hantaviral antibodies. Seropositive rates for rodents were high in *Cl. rufocanus bedfordiae* (15/47, 31.9% at Kamiiso; 8/87, 9.2% at Tobetsu).

3. A total of 122 rodents captured in Vladivostok in Russia were tested for hantavirus antibodies. Seropositive rodents were found in *Cl. rufocanus* (1/8, 12.5%), *M. fortis* (3/22, 13.6%), *M. arvalis* (2/66, 3.0%) and *Apodemus spp.* (2/26, 7.7%).

4. The virus genome was detected by RT-PCR from the lung in seropositive rodents. Positive individuals were found from *Cl. rufocanus* (18/21, 85.7%) captured at Kamiiso and Tobetsu, as well as *M. fortis* (1/3, 33.3%) at Vladivostok, designated the Kamiiso, Tobetsu and Vladivostok strains, respectively.

5. The entire S segments of Kamiiso and Tobetsu strains were sequenced. Kamiiso and Tobetsu strains were most closely related to the Puumala type from the identities in the nucleotide and deduced amino acid sequences. Phylogenetic analysis showed that the Kamiiso and Tobetsu strains formed an individual branch of the Puumala serotype. The partial M segment (nt 2673–3652) of the Kamiiso strain was sequenced. This also showed the strain to be closely related to the Puumala serotype.

6. Partial S segments (196 bases, nt 1034–1229) was compared among Kamiiso, Tobetsu and Vladivostok strains. Phylogenetic analysis revealed that the Kamiiso strain was distinct from the Tobetsu strain. However, within the rodent populations in an endemic focus, genetic variation was not found. The Vladivostok strain had different pattern of nucleotide sequences from Kamiiso and Tobetsu strains.

7. The recombinant nucleocapsid protein of Tobetsu was expressed in *Escherichia coli* and had epitopes similar to Puumala Sotkamo virus as recognized by Puumala-specific monoclonal antibodies.