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Nucleotide sequence of the M genome segment of hemorrhagic fever with renal syndrome virus strain B-1

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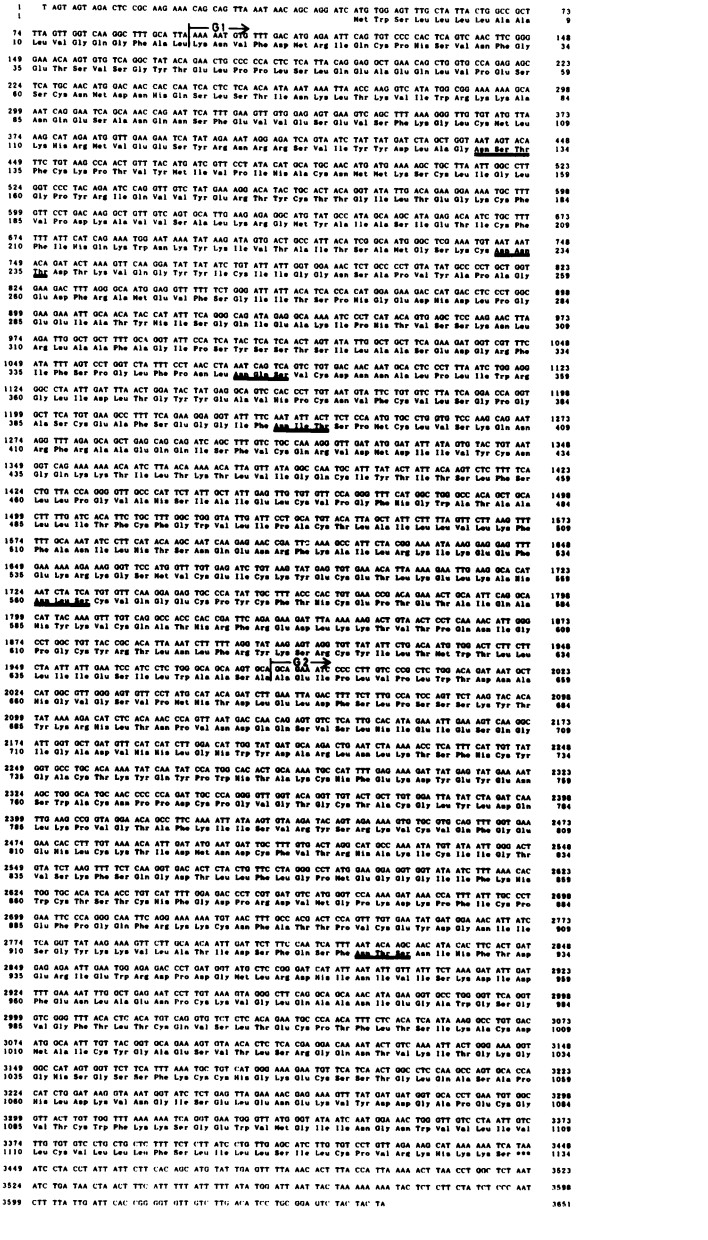
Submitted June 21, 1990

EMBL accession no. X53861

The medium (M) segments of the genomic RNA of Hantaan virus (HTN) (1), Nephropathia epidemica virus (NEV) (2) and Sapporo rat virus (SR-11) (3), each of which belongs to different serotypes of *Hantavirus* genus (4), have been cloned and sequenced. Here, we presented the nucleotide sequence of the M segment of Biken 1 virus (B-1), whose serotype is the same as that of SR-11. The cDNA was cloned and sequenced by the use of the cassette method of PCR that we have recently devised (5). The M segment determined consists of 3616 nucleotides and the cDNA has a single large open reading frame (ORF) capable to code a polypeptide of 1133 amino acids. Comparison of the M segments of B-1 and SR-11 strains revealed a 96% homology in the overall nucleotide sequence and a 97% homology in the nucleotide sequence of ORF. The homology of the deduced amino acid sequence of G1 envelope glycoprotein is 98% between B-1 and SR-11 and that of G2 is 99%. Moreover, six potential asparagine-linked glycosylation sites (=) are identified in both strains at the same positions. On the other hand, a significant difference is seen between the nucleotide sequences of the non coding regions of the M segments of these two strains. These results indicate that the serotype of B-1 and SR-11 reflects the homology of the structure of G1 and G2 proteins.



ACKNOWLEDGEMENTS

This work was supported by a Grant-in-Aid for General Scientific Research and a Grant-in-Aid for Developmental Scientific Research from the Ministry of Education, Science and Culture of Japan.

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