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# Complete nucleotide sequence of hepatitis delta virus RNA in Japan

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We have previously reported the partial nucleotide sequence and characterization of hepatitis delta virus (HDV) RNA in isolates from Japanese patients M and S (1). We present here the complete nucleotide sequence of delta virus RNA from the same isolate of patient S using polymerase chain reaction (PCR) (2) and direct nucleotide sequencing (3). The full length of the HDV RNA was estimated to be 1683 nucleotides from the sequence analysis of overlapping PCR products. Four open reading frames more than 100 amino acids in both genomic and anti-genomic strands were found. One of them in anti-genomic strand, which can code for 195 a.a., might correspond to the HDAg.

The sequence of this Japanese strain showed 76–78% identity to the sequences previously obtained from three other strains of HDV (4–6), while there was 83–86% identity among the three known delta virus RNA sequences (4–6). Thus, the nucleic acid sequence obtained from, Japanese patient S (39-year-old male with chronic active hepatitis) was the most diverged of those studied.

The sequence divergence is distributed over the entire genome, however, there are two highly conserved regions among the four HDV strains: nucleotides 678 to 751 around the autocatalytic

cleavage site of the genomic RNA (7) and nucleotides 858 to 919 around the autocatalytic cleavage site of the anti-genomic RNA (8). Synthetic oligonucleotides located in these highly conserved regions of HDV sequences could be very useful as primers for PCR in diagnosis of delta virus infection.

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