

Complete nucleotide sequence of a hepatitis E virus isolated from the Xinjiang epidemic (1986–1988) of China

Thein Thein Aye, Toshikazu Uchida*, Xue-Zhung Ma, Fusae Iida, Toshio Shikata, Hui Zhuang[1] and Khin Maung Win[2]

Department of Pathology, Nihon University School of Medicine, Ooyaguchi-Kamimachi, Itabashi-ku, Tokyo 173, Japan, [1]Department of Epidemiology, School of Public Health, Beijing Medical University, Beijing 100093, China and [2]Department of Medical Research, No. 5 Ziwaka Road, Dangon PO, Yangon, Myanmar

Submitted May 29, 1992 DDBJ accession no. D11092

Hepatitis E, previously called enterically-transmitted non-A, non-B hepatitis, is endemic and often provokes epidemic outbreaks in the developing world (1). It is similar clinically and epidemiologically to hepatitis A. Two strains of hepatitis E virus (HEV) were completely sequenced by Tam *et al.* (2) and us (3). The both strains originated from Myanmar (Burma). The HEV has a single-stranded, plus-sense RNA genome, 7,194 nucleotides (nt) long followed by a poly (A) tail. The HEV contains three open reading frames, flanked by 27 nt of 5′- and 68 nt of 3′noncoding region.

Here we report the complete nucleotide sequence of a HEV strain isolated from the epidemic of the south part of Xinjiang Uighur Autonomous Region, in which 120,000 patients occurred between September, 1986 and April, 1988 (4). We collected the feces from a female patient with hepatitis E in the Hetian County of the Xinjiang in 1988. The fecal extract was prepared and inoculated into rhesus monkeys as described elsewhere (5). They resulted in acute hepatitis with the excretion of the HEV into bile as the same as previously (6). The RNA in the bile juice of the second subpassage was reverse-transcribed to cDNA. Then the polymerase chain reaction (PCR) was carried out, utilizing several sets of pair primers, of which sequences were determined from the complete cDNA of Tam *et al.* (2) and us (3). The PCR product was directly sequenced by the dideoxy sequencing method (7). The strategy and method were described in detail elsewhere (3).

As a result, the full-length cDNA sequence was obtained. The nucleotide sequence identity was 93.9% to the genome reported by Tam *et al.* (2) and 93.4% to that reported by us. This identity was lower than 98.5% between the two Myanmar strains. All the differences were point substitutions and no insertion and deletion was present. The genetic organization including the three open reading frames (2, 3) and RNA-directed RNA polymerase (GDD) and helicase (GVPGSGKS and DEAP) motifs was completely conserved. The amino acid identity was between 97.5 and 100.0% in any open reading frames in the strains of the present China versus the two Myanmar strains. Although the viruses appeared to evolve differently in China and Myanmar, the genome diversity of HEV of these two countries is relatively low. This may be due to the transient infection of HEV without chronicity.

ACKNOWLEDGEMENT

This study was sponsored in part by the Japan International Cooperation Agency.

REFERENCES

1. Uchida,T. (1992) *Gastroenterology (Japan)*, in press.
2. Tam,A.W., Smith,M.M., Guerra,M.E., Huang,C.-C., Bradley,D.W., Fry,K.E. and Reyes,G.R. (1991) *Virology* **185**, 120–131.
3. Aye,T.T., Uchida,T.T., Ma,X,-Z., Iida,F., Shikata,T., Ichikawa,M., Rikihisa,T. and Win,K.M. (1992) *Virus Genes*, in press.
4. Cao,X.-Y., Ma,X.-Z., Liu,Y.-Z., Jin,X.-M., Gao,Q., Dong,H.-J., Zhuang,H., Liu,C.-B. and Wang,G.-M. (1991) In Shikata,T., Purcell,R.H. and Uchida,T. (eds), *Viral hepatitis C, D and E.* Excerpta Medica, Amsterdam. pp. 297–312.
5. Uchida,T., Win,K.M., Suzuki,K., Komatsu,K., Iida,F., Shikata,T., Rikihisa,T., Muzuno,K., Soe,S., Myint,H., Tin,K.M. and Nakane,K. (1990) *Jpn J. Exp. Med.* **60**, 13–21.
6. Uchida,T., Suzuki,K., Komatsu,K., Iida,F., Shikata,T., Rikihisa,T., Mizuno,K., Soe,S., Win,K.M. and Nakane,K. (1990) *Jpn J. Exp. Med.* **60**, 23–29.
7. Sanger,F., Nicklen,S. and Coulson,A.R. (1977) *Proc. Natl. Acad. Sci. USA* **64**, 5463–5467.

* To whom correspondence should be addressed