Rapid Communication

Nucleotide sequences and subtypes of hepatitis C virus genomes.

*Nobuyuki ENOMOTO, Nobuo TAKADA, Shujiro TAKASE, Akira TAKADA, and **Takayasu DATE. *Division of Gastroenterology, Department of Internal Medicine, and ** Division of Cancer Research, Department of Medical Research Institute, Kanazawa Medical University, Uchinada, Ishikawa, 920-02, Japan.

Recently, hepatitis C virus (HCV) genome was partially cloned from a Japanese patient (1). The homology of the nucleotide sequences of this clone to those of the prototype HCV of Chiron (2) was about 80 %, suggesting the presence of subtypes in HCV genomes. In this study, nucleotide sequences of our HCV clones and subtypes of HCV genomes were analyzed.

MATERIALS AND METHODS: In 24 patients with chronic non-A non-B (NANB) liver disease, HCV-RNA genomes (HCV-RNA) were detected using polymerase chain reaction (PCR) as reported previously (3). After extraction of RNA from the patient's plasma, cDNA was synthesized using reverse transcriptase. And then HCV genomes were amplified with two synthesized oligonucleotide primers, which were complementary to 400 nucleotide stretch of the prototype HCV genome, using PCR. The nucleotide sequences of the PCR products were determined by the dideoxy method, after confirmation of the amplification of 400 base pairs (bp) DNA fragments. Subtypes of HCV genomes were determined by the slot blot hybridization of the PCR products with HCV cDNA in which nucleotide sequences were already confirmed.

RESULTS: HCV-RNA was detected in 19 out of 24 cases. In 2 cases, nucleotide and amino acids sequences of the cDNA fragments were analyzed. In one case (HCV-K1), the homology of the sequences to those of the prototype HCV was 80 %in nucleotides, and 85 % in amino acids. And that in another case (HCV-K2) was 67 % and 71 %, respectively. The homology between HCV-K1 and K2 were 66 % in nucleotides and 71 % in amino acids. Using these two cDNA as the probes, slot blot hybridization was carried out on the PCR products from the 24 cases. The PCR products from 13 cases reacted with HCV-K1 and those from 6 cases reacted with HCV-K2 as shown in figure. However,

no cases reacted with both cDNA.

CONCLUSION: These results indicate that there are at least two subtypes of HCV genomes and that the major type is HCV-K1, HCV-K2 is the minor type and the prototype HCV is scarcely found in Japan. Key Words: HCV, HCV-RNA, subtype, PCR. 1) Kubo Y, et al: Nucl Acids Res. 1989; 17: 10367-10372. 2) Houghton M, et al:EP-A-O 318 216 A1. 3) Enomoto N, et al: Gastroenterol Jpn. 1990;25(4). (in press)



Received February 26, 1990. Accepted April 20, 1990. (Gastroenterol Jpn 1990;25:405) Address for correspondence: Nobuyuki Enomoto, M.D., Division of Gastroenterology, Department of Internal Medicine, Kanazawa Medical University, Uchinada, Ishikawa 920-02, Japan..