We report two patients with chronic liver disease – a 46-year-old man and a 52-year-old woman, both from eastern India – who were found to be infected with hepatitis C virus genotype 6 strains. These strains have been previously reported only from Hong Kong and Southeast Asia. [Indian J Gastroenterol 2005;24:72-73]

Determining the identity of the infecting hepatitis C virus (HCV) genotype has important implications for deciding the duration of antiviral therapy and ascertaining prognosis for the patient. Of the six HCV genotypes, genotype 6 was thought to be restricted to countries of Southeast Asia, previously having been reported from Hong Kong1 and Thailand.2 We report here, for the first time, HCV genotype 6 strains identified in two Indian patients with chronic liver disease.

**Case Reports**

*Patient 1* was a 46-year-old man from eastern India who presented for evaluation after a positive HCV antibody test. He provided a history of four episodes of jaundice, in 1981, 1982, 1992 and 2000, the first episode occurring after having received blood transfusion. He had received injections in vaccination camps conducted in his state.

His ALT level at presentation was 39 U/L (64 U/L is the upper limit of normal as estimated in healthy, volunteer blood donors at our hospital3). Liver biopsy showed mild chronic hepatitis with mild periportal fibrosis (modified HAI score 6/18, fibrosis score 2/6). The viral load *(Amplicor HCV Monitor, version 2.0, Roche Diagnostics, USA)* was $2.4 \times 10^5$ IU per mL of plasma. The patient was subsequently lost to follow-up.

*Patient 2* was a 52-year-old woman with chronic renal failure from eastern India who had been receiving thrice-weekly hemodialysis sessions for 5 months prior to presentation at our center. On routine testing she was found to be HCV antibody positive. HCV viral load was $9 \times 10^4$ IU per mL of plasma. ALT level was 35 U/L. The patient was followed up for three years and ALT enzyme estimations performed eight times showed stable levels (mean 44.5 U/L, range 30 to 54). This patient continues to exhibit low reactivity to HCV antibody.

Both patients were negative for hepatitis B surface antigen and antibody to the human immunodeficiency virus 1 and 2.

HCV RNA testing was carried out using primers from the 5’ non-coding region of the HCV genome.4 After viremia was confirmed in both cases, nucleotide sequencing of the core region of the genome identified the infecting HCV strains as belonging to type 6. For sequencing of the core region, a nested PCR was performed using the primers and thermal cycling conditions described by Ohno et al.5 To eliminate the possibility of mixed infection with other HCV genotype strains the PCR products were cloned (Invitrogen, CA, USA) and 5 clones from each sample were sequenced *(ABI 310 Genetic Analyzer, Foster City, CA)*. The 320-base-pair sequence amplified by the primers was used for identifying the infecting genotype using the Basic Local Alignment Search Tool (BLAST) (http://www.ncbi.nlm.nih.gov, National Center for Biotechnology Information, US National

**Fig:** Phylogenetic relationship of HCV genotype 6 clones derived from two Indian patients. Clones from patient 1 are indicated by Accession numbers AY887978–82 and from patient 2 by AY887973–77 (in bold font). Other GenBank sequences are indicated by their accession numbers with genotype identity in parentheses. Strain D63946 was reported from Thailand, AB162868 from Vietnam, L38339 from Southeast Asia, and Y12083 from Hong Kong.
Library of Medicine, MD, USA). The phylogenetic tree (DNASTAR, WI, USA) showed that all clones from both samples clustered with other published genotype 6 sequences from the GenBank (Figure). The HCV clones from patient 2 (Accession number AY887973-77) showed a high degree of homology to another HCV type 6 strain from Thailand (Accession number D63946).

There was no recorded history of travel outside India in the hospital charts of both patients. The second patient had undergone her hemodialysis sessions only in India.

Discussion

Prior identification of the infecting genotype will help in planning the optimal duration of treatment for patients in a cost-effective manner. Hui et al. showed that HCV genotype 6 strains exhibit greater sustained virological response (SVR) as compared to genotype 1 when treated with interferon. Additionally, this study showed that a longer course of interferon did not increase the SVR in patients with HCV genotype 6 infection.

With increasing globalization, the geographical isolation of certain HCV genotypes may become obsolete. Indian laboratories and physicians must take into consideration the possibility of encountering HCV genotype 6 strains among their patients. Their immune response, long-term prognosis, and response to interferon remain to be seen.

References


Correspondence to: Professor Abraham, Department of Clinical Virology. Fax: (416) 223 2035. E-mail: priyaabraham@cmcvellore.ac.in
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