Transmission of Hepatitis C Virus by Transfer of an Infected Individual to a New Dialysis Unit

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Table 1. Deduced amino acid sequence of the HCV-E2 HVR in consecutive serum samples isolated from patient D and in serum from a newly onset HCV-infected individual (AA) at the dialysis unit to which D was transferred

<table>
<thead>
<tr>
<th>Patient/date</th>
<th>E2 HVR sequence</th>
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<tbody>
<tr>
<td>D/Nov. 1991</td>
<td>AHTT VGAAAHAVSGFVGGFAPPKQNVQLI</td>
</tr>
<tr>
<td>D/June 1992</td>
<td>AHTT VGAAAHAVSGFVGLFASPGPKQNVQLI</td>
</tr>
<tr>
<td>D/March 1993</td>
<td>AHTT VGAAAHAVSGFVGLFASPGPKQDVQLI</td>
</tr>
<tr>
<td>AA/Sept. 1993</td>
<td>AHTT VGAAAHAVSGFVGVFSFASPGPKQDVQLI</td>
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Mutated residues are underlined; all amino acid mutations were due to single-base mutations at the nucleic acid level. Two strains of equal dominance detected.

Dear Sir,

Infection with hepatitis C virus in dialysis patients remains a significant clinical problem although the spread of this virus has been made accessible for control with modern detection assays [1]. Recently, we described non-transfusion-associated transmission between patients treated in a dialysis unit [2]. Apparently, one viral strain had been transmitted between 5 patients who had been treated in the same room on repeated occasions but not sharing hemodialysis machines. For this group of patients on maintenance hemodialysis, blood transfusions must be considered the most reasonable cause for the HCV transmission. When our molecular analyses contradicted this, it raised the possibility that non-transfusion-associated transmission may go unnoticed particularly among immunosuppressed multitransfused patients. Also, as a speculation, one may discuss whether certain HCV isolates carry properties that may facilitate transmission, in particular in hospital settings and between immunosuppressed patients.
We have now analysed consecutive serum samples (Nov. 1991-March 1993) from one of the dialysis patients (D) in the cluster of five by sequencing PCR products of the gene segment for the HCV-E2 hypervariable region, resulting in a ‘finger print’ of the predominant HCV isolate carried by the patient at each time of sampling [2]. The data show, as expected, single mutations appearing over time; in March 1993 six amino acid mutations distinct from the originally isolated virus can be seen (table 1). In January 1992, D was transferred to a different dialysis unit located several kilometers from the one where the cluster of 5 infected patients was 
detected. Surprisingly, in September 1993 another patient (AA) treated at the new dialysis unit had become infected with the HCV variant found most recently in patient D (table 1). Thus, this family of HCV has been shown to be shared by 6 patients and we can follow the transmission from one unit to another through the transferral of one HCV-infected patient.

Whether the HCV strain detected is more prone to transmission than others awaits the development of reliable ways to cultivate HCV. At present, we would again like to draw the attention to the possibility that non-transfusion-associated transmission of HCV, most reliably detected by nucleic acid sequencing, may go unnoticed and be quite prevalent in hospital settings where immunosuppressed patients are being subject to repeated parenteral diagnostic and therapeutic measures.

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References