Establishment of a cell line constitutively expressing E2 glycoprotein of hepatitis C virus and humoral response of hepatitis C patients to the expressed protein

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A Chinese hamster ovary cell line was established which abundantly expresses the second envelope protein (E2) of hepatitis C virus under the control of an exogenous promoter. The expressed E2 protein was found to be a glycoprotein of 58 kDa by immunoprecipitation with sera from patients that had chronic hepatitis C. Using this cell line as antigen in immunofluorescence tests, as high as 93% of patients with non-A non-B hepatitis had antibodies against E2 protein. In Western blots using SDS-denatured E2 protein, however, the detectability of the antibody was drastically reduced to 30%. Immunoprecipitation assays and ELISA, using both native and denatured E2 protein, revealed that antibodies to E2 protein were present in most of the chronic hepatitis C patients and that they reacted only to the native forms.

Introduction

Hepatitis C virus (HCV) is a major causative agent of post-transfusion and sporadic non-A non-B hepatitis (NANBH) throughout the world (Alter, 1988; Choo et al., 1989; Kuo et al., 1989). HCV infection often leads to persistence, resulting in severe chronic liver diseases and, in some cases, this develops into hepatocellular carcinoma (HCC; Miyamura et al., 1990; Saito et al., 1990). However, little is known about whether or how individual HCV proteins are involved in the development of these diseases.

HCV has a positive-stranded RNA genome of 9.4 kb which encodes a precursor polyprotein of about 3000 amino acids (aa) (Kato et al., 1990; Choo et al., 1991; Takamizawa et al., 1991). From the hydropathicity profile of their deduced amino acid sequences and the extensive sequence similarity in the 5' untranslated regions, HCV has been shown to be distantly related to flaviviruses and pestiviruses (Miller & Purcell, 1990; Takeuchi et al., 1990b; Takamizawa et al., 1991). As in pestiviruses and flaviviruses, the core protein of HCV is thought to be located at the N-terminal end of the polyprotein, followed by two envelope glycoproteins, designated E1 and E2. Because no appropriate cell culture system has yet been developed to support the replication of HCV, expression of HCV genes in cultured cells is important to identify individual HCV proteins and to study their roles in the pathogenesis of HCV infection. These studies also provided information for the development of new diagnostic tests to detect antibodies to HCV antigens (Harada et al., 1991; Matsuura et al., 1992).

E1 and E2 are candidate antigens for future vaccines to hepatitis C, as the NS1 protein of flaviviruses and the E2 protein of pestiviruses, the counterparts of the HCV E2 protein, have been reported to produce neutralizing antibodies (Brandriss et al., 1990; Roehrig et al., 1990; Weiland et al., 1992; Rumenapf et al., 1993). Although several groups have described the E2 protein as a 70 kDa glycoprotein (Hijikata et al., 1991; Grakoui et al., 1993) or a 60–61 kDa glycoprotein (Tomei et al., 1993; Matsuura et al., 1994), the characterization of E2 is still limited and little is known about antibodies against the E2 protein (anti-E2 Ab) present in patients with hepatitis C. In this study, we established a mammalian cell line

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expressing the HCV E2 glycoprotein constitutively and abundantly. We found that the expressed glycoprotein had a molecular mass of 58 kDa and that about 90% of chronic NANBH patients had anti-E2 Ab when examined by an immunofluorescence assay. However, only a small portion of them showed anti-E2 Ab when examined by Western blotting. These results suggest that most of the patients’ sera reacted exclusively to the native form of the expressed E2 protein.

Methods

HCV cDNA cloning. HCV cDNA covering the C-terminal half of the E2 region was obtained by PCR (Saiki et al., 1985) after reverse transcription of RNA extracted from a serum sample of a healthy carrier, J1 (Kubo et al., 1989; Takachi et al., 1990a, b). The cDNA was synthesized from an antisense primer S254A (GGCTATCAGCGATCATCCA; nucleotides (nt) 2554-2555; nucleotide sequence and numbering according to Kato et al. (1990)) and then amplified after the addition of a sense primer J1825 (TGGCCTGCAATGTTATTGCT; nt 1836-1855). One of the cDNA clones, pc1825-3, was chosen for plasmid construction. cDNA 1325, covering the entire E2 region, was then prepared by joining cDNA from nt 1346-1906 (BanHI-SnaBI fragment) derived from pSR820x (Matsuura et al., 1992) and cDNA from nt 1907-2554 from pc1825-3.

Construction of expression vectors. Plasmid pSR1325x contains cDNA 1325 downstream of the SRα promoter (Takebe et al., 1988). The junction sequence just upstream of cDNA 1325 is derived from pSR816x (Matsuura et al., 1992). Psrl-CAGACCTGTCATCAAGGGCCGACTAGTC-nt 1346 (the underline indicates initiator codon), and the sequence just downstream is nt 2554-GGGGATCCTG-GGGAGATCTGG-TAGAGATTC-KpnI (the underline indicates terminator codon). The expected structure of the expressed protein contains an extra seven codon), and the sequence just downstream is nt 2554-GGGGATCCTG-GGGAGATCTGG-TAGAGATTC-KpnI (the underline indicates terminator codon).

Cosmid vector pChmBpneoLo (Fig. 1), a derivative of pCHD2L (Ikeda et al., 1988), contains the phage lambda cos site, the hygromycin B-resistance gene, a polynkicker and the neomycin-resistance gene derived from a 1.8 kb partial PvuII fragment of pAG60 (Colbere-Garapin et al., 1981). The neomycin-resistance gene was substituted for simian virus 40 (SV40) enhancer sequences present in pCHD2L. The cassette plasmid pSR is identical to pmoR (Ikeda et al., 1988) except that the expression unit of the SV40 early promoter is substituted by the SRα unit derived from pcDLSR296 (Takebe et al., 1988). Plasmid pSBR1325x was prepared by moving the SRα expression unit from pSBR1325x to pSR; note that in pSBR1325x the expression unit is followed by another SV40 early promoter. To construct expression cosmid pHIL6SR1325x, 16 copies of the 1.8 kb SfiI fragment of the E2 expression unit from pSBR1325x were tandemly inserted into the unique SfiI site within the SV40 early promoter of pChmBpneoLo, using a method previously described (Saito & Stark 1986; Ikeda et al., 1988). A large scale preparation of pHIL6SR1325x DNA was achieved using in vitro packaging of the cosmid (Ikeda et al., 1988).

Cell culture. Chinese hamster ovary (CHO)-K1 and COS-1 cells were obtained from the ATCC through the Japanese Cell Resources Bank (Tokyo, Japan). CHO and COS-1 cells were grown in Ham’s F-12 medium (Gibco) and Dulbecco’s modified Eagle’s medium (Nissui), respectively, supplemented with 50 µg/ml gentamicin (Gibco), 2,5 µg/ml amphotericin B (Boehringer Mannheim) and 10% heat-inactivated FCS (Filttron). To establish stable cell lines expressing the HCV E2 protein, CHO-K1 cells were transfected with the expression cosm id pHIL6SR1325x using the calcium phosphate precipitation method and cultured in the medium with 600 µg/ml G418 (Gibco). A control cell line LN4 was generated from CHO cells by transfection with the vector pChmBpneoLo. A recombinant baculovirus Ac1325, grown in Spodoptera frugiperda Sf9 cells, has been described previously (Matsuura et al., 1992, 1993).

Immunofluorescence analysis. Indirect immunofluorescence analysis was carried out as described previously (Harada & Yanagi, 1992). To define whether patients’ sera were positive for anti-E2 Ab, both E2-expressing cells and vector-transfected control cells were cultured for 16 h in parallel. Patients’ sera were diluted 10-fold with PBS and reacted with both E2-expressing and control cells, which were fixed with cold acetone-methanol (1:1). Patients’ sera were assayed as positive for anti-E2 Ab when cytoplasmic fluorescence was observed in both the E2-expressing cells but not in the control cells.

Immunoprecipitation. At 24 h after plating of the gp58-expressing 131L20 cells or 48 h after transfection into COS-1 cells, cells were kept for 1 h in methionine-free medium supplemented with 2% FCS. Cells were then labelled for 8 h with 0.1 mCi/ml of [35S]methionine (ICN). To detect expressed proteins, labelled cells were lysed with RIPA buffer consisting of 10 mm-Tris–HCl pH 7.2 containing 150 mm-NaCl, 1% sodium deoxycholate, 0.1% SDS, 1% Triton X-100 and 2 mm-PMSF, and then immunoprecipitated with the human patient serum NI as described previously (Matsuura et al., 1992). Immunocomplexes were recovered with Protein A-Sepharose CL-4B (Pharmacia) and were subsequently separated by SDS-PAGE (Laemmli, 1970). Radiolabelled bands were detected by autoradiography using Kodak X-ray film. For N-glycanase digestion, recovered immunocomplexes were treated with N-glycanase (Genzyme) according to the supplier’s instructions.

To compare lysis treatment before immunoprecipitation assays, [35S]methionine-labelled 131L20 cells were divided equally into two tubes. One was lysed with RIPA buffer (RIPA-lysate) and then divided into six aliquots. The other was lysed with SDS buffer consisting of 10 mm-Tris–HCl pH 7.2 and 2% SDS (SDS-lysate). SDS-lysates were diluted 20-fold with PBS containing 2% BSA and 2 mm-PMSF and divided into six aliquots. Each of the six patient’s sera was added to six tubes of both RIPA-lysate and SDS-lysate.

SI mapping. The procedure of SI nuclease protection mapping was described previously (Saito et al., 1986; Suzuki et al., 1989). Briefly, 0.1 mg of total cytoplasmic RNA was hybridized at 53 °C with 0.2 µg of 32P-labelled probe DNA digested with nuclease S1 (500 units/ml; Boehringer Mannheim). To prepare the 5' probe, pSBR1325x DNA was digested with Asp718I, the site being at the 5' end of cDNA 1325, and 5'-labelled using T4 polynucleotide kinase and [γ-32P]ATP. The labelled DNA was digested with XmnI, which cut within the ampicillin-resistance gene. The resulting 4.0 kb fragment was isolated and used as the 5' probe. The 3' probe was a 2.4 kb PstI-XmnI fragment. 32P-labelled at the PstI site. The PstI termini were labelled with T4 polynucleotide polymerase utilizing its 3'→5' exonuclease activity and subsequently its 3'→5' polymerase activity to add [γ-32P]ATP.

ELISA. To obtain both native and denatured antigens from insect cells, Ac1325-infected Sf9 cells were used as described previously (Matsuura et al., 1993). Infected cells were disrupted and cell extracts precipitated with 33% (w/v) ammonium sulphate. The precipitates were collected by centrifugation. The native-form antigens were prepared by suspending these precipitates in PBS at a concentration of 0.05 A280 units/ml. The denatured antigens were prepared by treating the precipitates with a solution containing 0% SDS and 2 mm-mercaptoethanol. The SDS-denatured antigen was then diluted with PBS containing 8 m-urea to a concentration of 0.05 A280 units/ml. Each well of the ELISA plates (ICN–Flow Laboratories) was coated with 50 µl of the antigen solution for 16 h at 4 °C. Human sera were
analysed for anti-E2 Ab by ELISA using the coated antigens as described (Chiba et al., 1991).

Western blotting. CHO cell lines transfected with HCV cDNAs were analysed by Western blotting using a patient's serum and an avidin-biotin detection method as described previously (Harada et al., 1991). Ac1325-infected SF9 cells (Matsuura et al., 1993) were used for antibody analysis of NANBH patients' sera by Western blotting.

Results

Establishment of CHO cell lines expressing the E2 protein of HCV

To express the E2 protein in mammalian cells, an expression plasmid pSR1325x and its derivative paSR1325x (Fig. 1a, b) were constructed. These plasmids contain HCV cDNA encoding aa 340-742 of the polyprotein and comprising the E2 region under the control of the SRα promoter. To introduce multiple copies of the expression unit into a CHO cell chromosome, we constructed a mulcos' expression cosmid, pHIL16SR1325x. This contained not only the neomycin-resistance gene but also 16 copies of a head-to-tail tandem repeat of the E2 expression unit derived from pSR1325x (Fig. 1a).

Cosmid pHIL16SR1325x was transfected into CHO cells and G418-resistant cell clones were screened for E2 expression by indirect immunofluorescence analysis with patients' serum. One of the typical cell clones, 13L20, was chosen for further analysis because it showed very
Fig. 2. Immunofluorescence analysis of the HCV E2 protein expressed in the 13L20 cell line. (a) 13L20 cells selected after transfection with pHIL16SR1325. (b) LN4, a control cell line, selected after transfection with pChmBpneoL. Fixed cells were analysed by indirect immunofluorescence analysis using patient serum NI (Matsuura et al., 1992).

intense immunostaining (Fig. 2a) compared with control cells (Fig. 2b). The immunofluorescence was detected uniformly in the cytoplasm.

Characterization of the expressed E2 protein

To identify E2 protein expressed in 13L20 cells, [35S]-methionine-labelled cell extract was immunoprecipitated with the patients’ serum. A protein with a molecular mass of 58 kDa was detected in abundance (Fig. 3a, lane 2). This protein was also detected in COS-1 cells transiently transfected with pSR1325x (Fig. 3a, lane 4) and by Western blotting in 13L20 cells, although its intensity was much lower (data not shown).

To examine whether the protein is N-glycosylated, the immunoprecipitated protein derived from 13L20 cells was digested with N-glycanase. A protein with a molecular mass of 40 kDa was detected in place of the 58 kDa protein (Fig. 3b). Moreover, the 58 kDa E2 protein was detected when 13L20 cells were labelled with [3H]glucosamine and analysed by immunoprecipitation (data not shown). These results showed that this protein was an N-glycosylated form of the expressed E2 protein and the 40 kDa protein was derived from it by losing the N-glycosylated sugar chains.

S1 mapping of HCV RNAs in CHO cells expressing the E2 protein

To examine expressed E2 mRNA species, total cytoplasmic RNA prepared from the cell line 13L20 and another typical clone 13L18 was analysed by the nuclease S1 protection technique (Fig. 4). Bands with the expected sizes of 1.42 kb and 1.35 kb were detected using the 3' labelled probe and the 5' labelled probe, respectively, and no other bands were detected. These results suggested that both cell lines expressed mRNA covering the entire 1325 cDNA region; no aberrant or abnormally spliced RNA was detected.
Cell line expressing HCV E2

Integration of the expression unit into a CHO cell chromosome

The expression cosmid pHL16SR1325x contained 16 copies of the E2 expression unit as a tandem array. To examine how many copies of the expression unit were present in 13L20 cells, the genomic DNA was analysed by Southern blotting of three different restriction digests. Using cDNA 1325 as a probe, the main band of full-length expression units was detected with an intensity of three copies per cell, although seven bands of various intensities were also observed (data not shown). This result suggests that the cell line 13L20 contained three copies of a functional expression unit integrated into its chromosomes.

Prevalence of anti-E2 Ab in sera of patients with NANBH

To investigate the prevalence of anti-E2 Ab in NANBH patients, patients’ sera were analysed by an indirect immunofluorescence assay using 13L20 cells (Table 1). Anti-E2 Ab was detected in 93% (143 out of 153) of patients with chronic NANBH. The antibody was not detected in any of the sera from 11 patients with alcoholic hepatitis or 50 normal adults. On the other hand, 65%, 93% and 93% of the same set of sera were found to be positive using the conventional HCV antibody assays for anti-C100 (Kuo et al., 1989; Miyamura et al., 1991), anti-p22 (core protein; Harada et al., 1991) and the second generation anti-HCV assay (Ortho Diagnostics), respectively. The result suggests that anti-E2 Ab is detectable in chronic NANBH patients’ sera as frequently as anti-core protein antibodies.

Anti-E2 Ab was also detected in all of the 21 sera from HCV carriers without manifestations of liver disease. The antibody was detected in only 14% (three out of 21) of patients with acute NANBH but was detected with high frequency among NANBH patients with chronic

Table 1. Detection of anti-E2 Ab present in NANBH patients’ sera using a 13L20 cell immunofluorescence assay

<table>
<thead>
<tr>
<th>Diagnosis</th>
<th>Number of patients tested</th>
<th>Number of positives</th>
<th>Percentage positives</th>
</tr>
</thead>
<tbody>
<tr>
<td>Chronic NANBH</td>
<td>153</td>
<td>143</td>
<td>93</td>
</tr>
<tr>
<td>CH</td>
<td>45</td>
<td>42</td>
<td>93</td>
</tr>
<tr>
<td>LC</td>
<td>43</td>
<td>39</td>
<td>91</td>
</tr>
<tr>
<td>HCC</td>
<td>65</td>
<td>62</td>
<td>95</td>
</tr>
<tr>
<td>Alcoholics*</td>
<td>11</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>Normal adults*†</td>
<td>50</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>Hepatitis C carriers‡</td>
<td>21</td>
<td>21</td>
<td>100</td>
</tr>
<tr>
<td>Acute NANBH</td>
<td>21</td>
<td>3</td>
<td>14</td>
</tr>
</tbody>
</table>

* All sera of these groups were found to be negative for anti-core antibodies.
† Healthy adults with a normal alanine-aminotransferase level.
‡ Healthy adults that were positive for anti-core antibodies.
Reactivity of anti-E2 Ab in patients’ sera

The antibody to E2 protein expressed in 13L20 cells was frequently detected in patients’ sera by immunofluorescence and immunoprecipitation. However, it was detected less frequently using Western blotting. One possible reason may be that the anti-E2 Ab present in sera of hepatitis C patients does not react to SDS-denatured E2 antigen. To examine this possibility, [35S]methionine-labelled 13L20 cell lysates treated with SDS (SDS-lysate) or without SDS (RIPA-lysate) as described in Methods, were immunoprecipitated using six sera from different NANBH patients, two of each from patients with HCC, CH and LC (patients A and B, C and D, E and F, respectively; Fig. 5). In good agreement with the immunofluorescence assay (shown in Table 2), E2 protein was detected with all six patients’ sera when the RIPA-lysate was used (Fig. 5). In contrast, E2 protein reacted only to three patients’ sera (patients B, D and E) when SDS-lysates were immunoprecipitated (Fig. 5, lanes 8, 10 and 11). The radioactivity of each E2 band was quantified by an image analyser and the ratios of radioactivity in RIPA-lysate:SDS-lysate were calculated (Table 2). Anti-E2 Ab present in some patients’ sera (patient A, C, D and F; ratio by immunoprecipitation > 2.9) reacted efficiently with the native form of E2 protein but very poorly with SDS-denatured E2, while other sera (B and E; ratio 1.1 and 1.0) reacted similarly to both the native and SDS-denatured form of E2 protein.

To examine further anti-E2 Ab reacting to the SDS-denatured E2 antigen, cDNA 1325 was expressed using a baculovirus expression vector (recombinant baculovirus Ac1325; Matsuura et al., 1993). The Ac1325-expressed E2 was detected in Sf9 cells much more abundantly than in 13L20 cells (Matsuura et al., 1993). Using the Ac1325-infected Sf9 cell lysates, however, three patients’ sera (A, C and F) were again negative in the Western blots (Table 2). Therefore, Western blotting using baculovirus-expressed E2 showed a result essentially identical to the one using SDS-denatured E2 derived from CHO cells, confirming that some patients’ sera react to the native form but not to the SDS-denatured form of the E2 protein. The same set of 153 chronic NANBH patients’ sera in Table 1 was tested again by Western blotting to detect antibodies reacting to SDS-denatured, Ac1325-derived E2 protein. Only

Table 2. Reactivity of six patients’ sera to E2 with or without SDS treatment

<table>
<thead>
<tr>
<th>Patient</th>
<th>Diagnosis</th>
<th>IFAt</th>
<th>RIPA-lysate:SDS-lysate radioactivity§</th>
<th>Western blotting§</th>
<th>PBS-lysate:SDS-lysate absorbance¶</th>
</tr>
</thead>
<tbody>
<tr>
<td>C</td>
<td>CH</td>
<td>++</td>
<td>3.9</td>
<td>−</td>
<td>5.3</td>
</tr>
<tr>
<td>F</td>
<td>LC</td>
<td>++</td>
<td>3.4</td>
<td>−</td>
<td>7.4</td>
</tr>
<tr>
<td>A</td>
<td>HCC</td>
<td>+++</td>
<td>3.0</td>
<td>−</td>
<td>5.3</td>
</tr>
<tr>
<td>D</td>
<td>CH</td>
<td>+</td>
<td>2.9</td>
<td>+</td>
<td>1.2</td>
</tr>
<tr>
<td>B</td>
<td>HCC</td>
<td>++</td>
<td>1.1</td>
<td>+</td>
<td>0.9</td>
</tr>
<tr>
<td>E</td>
<td>LC</td>
<td>+</td>
<td>1.0</td>
<td>+</td>
<td>0.5</td>
</tr>
</tbody>
</table>

* The six patients analysed were the same as those listed in Fig. 5. Patients’ data were listed in the order of the RIPA/SDS ratio.
† IFA, indirect immunofluorescence assay using fixed 13L20 cells.
‡ Radioactivities of CHO cell-derived gp58 bands in Fig. 4 were measured using a BioImage Analyser BAS2000 (Fuji) and the ratios of radioactivities from RIPA-lysates:SDS-lysates were calculated.
§ Using Ac1325-infected insect cell lysate.
¶ Ratio of A450 measurements from ELISA, using Ac1325-infected cell lysates as described in Methods.
33 % (51 out of 153) were found to be positive, suggesting that the majority of the patients had anti-E2 Ab reacting only to the native form of the E2 protein.

**Detecting of anti-E2 Ab by ELISA**

Because ELISA detection of anti-E2 Ab is potentially useful for new blood screening or improved diagnosis of hepatitis C, the E2 protein from Ac1325 was partially purified and two ELISA systems, with or without SDS treatment, were established. The same six sera shown in Fig. 5 were examined. The ratio of $A_{492}$ readings measured by both ELISA systems was calculated (Table 2). These ratios were consistent with those of RIPA-lysates:SDS-lysates assayed by immunoprecipitation (Table 2). The anti-E2 Ab was detected in 71 % (50 out of 70) of the chronic NANBH patients’ sera using the native lysate and in 9 % (6 out of 70) using the SDS-denatured lysate. All of the sera positive with ELISA using the native lysate were also positive in the immunofluorescence assay. All of the sera positive with ELISA using the SDS-denatured lysate were also positive by Western blotting. Therefore, these results confirm the specificity of the two ELISA systems.

**Discussion**

We have established CHO cell lines constitutively expressing the HCV E2 protein. The expressed product was identified as a 58 kDa glycoprotein. Using these cell lines, we showed that anti-E2 Ab were present in most of the chronic NANBH patients (93 %). The anti-E2 Ab present in patients’ sera reacted well to native E2 but poorly to SDS-denatured E2.

The C-terminal position of the E2 protein is not absolutely clear at present. The location of E2 in the HCV open reading frame was predicted to be from aa 384 to 729 by Takamizawa et al. (1991). Hijikata et al. (1991) reported that in an in vitro translation system the full E2 coding region does not extend past aa 740. Our recent data suggested that the N-terminal position of NS2 lies at about aa 810, although the precise C-terminal position of E2 is not known (Matsuura et al., 1994). The 1325 cDNA used in this study spanned aa residue 340 to 742 and so can be assumed to cover the entire, or at least nearly full-length, E2 region.

The 1325 cDNA also contains some sequence coding for the E1 hydrophobic region, which is necessary for signalase cleavage and subsequent glycosylation of the E2 protein (Inoue et al., 1992). An N-glycosylated 58 kDa protein was produced from cDNA 1325 and N-glycanase treatment yielded a 40 kDa product. Therefore, the 58 kDa protein is considered to be generated from a precursor protein by protease cleavage of its N-terminal region (this does not rule out the possibility that C-terminal cleavage may also occur in this system). The size of E2 protein shown in this study was similar to that found in recent reports (Tomita et al., 1993; Matsuura et al., 1994) but smaller than that seen in earlier reports (gp70; Hijikata et al., 1991; Spaete et al., 1992; Grakoui et al., 1993). This difference may simply be due to aberrant migration on SDS-polyacrylamide gels, although other proteolytic processing or different post-translational modification cannot be ruled out. The E2 protein was present predominantly in the cytoplasm and was not secreted (data not shown), probably because the C-terminal hydrophobic domain was retained in the expressed protein, allowing protein accumulation in 13L20 cells.

The prevalence of anti-E2 Ab in hepatitis C patients is much higher than previously expected (Inoue et al., 1992) and comparable to that of anti-core protein (p22) antibodies (Harada et al., 1991; Watanabe et al., 1991). Previously we reported that the N-terminal half of the E2 protein was antigenic, but the prevalence of antibody against this truncated E2 protein was low (Inoue et al., 1992). The results of the present study suggest that the E2 protein is highly antigenic and possibly useful for screening and diagnostic purposes. We found only one serum positive for anti-E2 Ab but negative for anti-core antibodies. However, this does not necessarily suggest that an anti-E2 Ab assay would improve on present HCV serodiagnosis because, unfortunately, the serum had been stored under conditions inadequate for RT-PCR analysis. Although it is not easy to find such patients, this point should be clarified in future. Recently, the high prevalence of anti-E2 Ab in hepatitis C patients has also been suggested using a limited number of patients’ sera against a baculovirus-expressed E2 protein (Lanford et al., 1993).

By Western blotting, the level of patients with chronic NANBH that were positive for anti-E2 Ab was similar to that of our previous study with a truncated E2 antigen (Inoue et al., 1992). The number of antibody-positive patients in the immunofluorescence assay was as high as 93 %. Chronic HCV patients could consequently be classified into two groups. Patients of the first group have antibodies which recognize almost exclusively a native form of the E2 protein. The patients of the other group, about one-third of the patients tested, have antibodies recognizing both native and denatured forms of the antigen. Preliminary retrospective studies have noted no apparent differences in clinical manifestations between the two groups of hepatitis C patients.

Such a phenomenon does not appear to be restricted to HCV. Monoclonal antibodies against the second envelope glycoprotein of hog cholera virus (E2; gp44/48) reacted only with its non-denatured form (Weiland et al., 1991; Spaete et al., 1992; Grakou et al., 1993). This difference may simply be due to aberrant migration on SDS-polyacrylamide gels, although other proteolytic processing or different post-translational modifications cannot be ruled out. The E2 protein was present predominantly in the cytoplasm and was not secreted (data not shown), probably because the C-terminal hydrophobic domain was retained in the expressed protein, allowing protein accumulation in 13L20 cells.

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