Immune evasion versus recovery after acute hepatitis C virus infection from a shared source

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Acute infection with hepatitis C virus (HCV) rarely is identified, and hence, the determinants of spontaneous resolution versus chronicity remain incompletely understood. In particular, because of the retrospective nature and unknown source of infection in most human studies, direct evidence for emergence of escape mutations in immunodominant major histocompatibility complex class I–restricted epitopes leading to immune evasion is extremely limited. In two patients infected accidentally with an identical HCV strain but who developed divergent outcomes, the total lack of HCV–specific CD4+ T cells in conjunction with vigorous CD8+ T cells that targeted a single epitope in one patient was associated with mutational escape and viral persistence. Statistical evidence for positive Darwinian selective pressure against an immunodominant epitope is presented. Wild-type cytotoxic T lymphocytes persisted even after the cognate antigen was no longer present.

Chronic hepatitis C virus (HCV) infection is common and affects 3% of the world’s population; however, the diagnosis of acute HCV rarely is made and usually is inferred based on the history of a known exposure (1, 2). Emerging data suggest that immunologic and virologic events in the early stages of infection determine the eventual outcome (3). Spontaneous resolution of acute HCV infection has been associated with robust T cell responses in chimpanzees (4, 5) and humans (6–8), and it has been suggested that a threshold frequency of CTL is required for clearance of HCV (9). Although emergence of escape mutations in class I MHC–restricted epitopes was shown to lead to immune evasion in HCV-infected chimpanzees (10, 11), direct evidence for this mechanism in humans is limited. Tsai et al. (12), by focusing on a single HLA A2–restricted HCV E1 epitope in the hypervariable region, observed variant epitope sequences with CTL antagonist activity 3 mo from onset of acute hepatitis in two patients who developed persistence. Timm et al. (13) recently described the development of CTL responses against an HLA-B8–restricted epitope (including one patient after antiviral therapy); however, mutations within this immunodominant epitope did not impact HLA class I binding or TCR recognition.

We comprehensively studied two patients who developed homologous acute HCV infection after patellar tendon transplantation from a deceased donor who was in the “window” phase of acute HCV (i.e., negative for HCV antibody but positive for HCV RNA). Antigenic and viral genetic mapping revealed striking differences in these two individuals who shared several HLA alleles but had divergent outcomes. To assess the total and specific CD4+ and CD8+ T cell response against all potential HCV epitopes in an unbiased manner, we used 750 overlapping 15-mer peptides that spanned the entire HCV polyprotein. The lack of HCV–specific CD4+ T cells, in conjunction with vigorous CD8+ T cells that targeted a single immunodominant epitope, was associated with mutational escape and viral persistence. In contrast, the patient who demonstrated vigorous and multispecific CD4+ and CD8+ T cell responses spontaneously eradicated HCV infection.
used as APCs to stimulate bead-purified CD8 T cell responses. In brief, autologous dendritic cells were lapsing by 11 amino acids, were pooled and used in an IFN-gamma and CD8 T cell responses to the whole HCV polyprotein comprehensively, 15 mer-peptides, over.

To assess CD4 T cell responses, HCV genome-wide analysis of CD4 T cells shared several HLA alleles, including HLA A2.

Two subjects with no previous history of exposure to HCV underwent elective patellar ligament (with bone) transplantation for knee reconstructive surgery in April 2002. Within 2 mo, both patients developed symptoms of fatigue and elevation in liver function tests. The first patient (PD101, a 49-yr-old white woman) became jaundiced with a peak total serum bilirubin of 8.1 mg/dl and spontaneously cleared HCV infection (Fig. 2 A). Conversely, PD102 demonstrated vigorous and multispecific CD4+ and CD8+ T cell responses (Fig. 2 B). Therefore, these results were in accord with, and extend, those reported in acute resolving HCV infection, and demonstrated an association between a strong and broad T cell response with recovery (6–8). 6 mo later, despite the fact that serum HCV RNA remained negative during that span, PD102 maintained vigorous HCV-specific CD4+ T cell responses, with 40% of the polypeptide (13 of 32 peptide pools) eliciting responses (Fig. 2 D). Because PD101 developed persistent viremia, he was treated with pegylated interferon and ribavirin starting 9.5 mo after infection. The patient’s CD8+ T cells targeted determinants limited to the NS3-5H pool throughout follow-up, including 24 mo after infection (Fig. 2 E). Of the individual peptides that made up the latter pool, only one 15-mer peptide (amino acids 1401–1415) stimulated CD8+ T cell responses. Therefore, only one of the 750 peptides screened elicited CD8+ T cell responses in PD101. Mapping identified peptide 1406–1415 as the minimal epitope, previously reported to be detectable by tetramer analysis in almost one third of HLA A2-positive, HCV-exposed individuals (14).

Tetramer frequencies for this epitope ranged from 1.43% (8 mo) to 2.24% (22 mo after infection; Table S1, available at http://www.jem.org/cgi/content/full/jem.20042284/DC1). Direct ex vivo phenotypic analysis of NS3 1406 tetramer-positive cells revealed intermediate memory cells, consistently high expression of the costimulatory molecule CD28, and decreasing levels of HLA-DR after viral clearance with therapy. Over time, CCR7 expression increased, which indicated the presence of early (central)—rather than mature—effector memory CTLs (reference 15 and Fig. S2, available at http://www.jem.org/cgi/content/full/jem.20042284/DC1). To investigate the proliferative capacity of these NS4 1406-specific CD8+ T cells at the single cell level, PBMCs were cultured short-term with HCV peptides and low-dose IL-2 and stained with carboxyfluorescein succinimidyl ester (CFSE), as described previously (14). As shown in Fig. 3, PD101 demonstrated a strikingly high frequency of proliferating NS3 1406 tetramer+ cells.

**Evidence for immune escape of a single dominant epitope**

Sequencing of a contiguous region encoding the NS3-5H pool revealed an amino acid substitution at amino acid posi-
section 4 of the epitope (A→V) at 4.5, 6, 8, and 10 mo after infection in PD101 (Fig. 4 A). Sequencing of the dominant virus from the donor and PD101 at 6 wk after infection revealed identity with the prototype sequence; this indicated that the alanine to valine change in PD101 represented a new mutation that arose after transmission from the donor organ. This de novo nonsynonymous mutation was propagated stably until antiviral therapy was initiated and was compatible with virus replication; serum viral load increased between the third and sixth month after infection (Fig. 1). Therefore, in accord with a recent HIV model, one could speculate that this rapidly emerging viral variant likely faced a low “genetic barrier” (requiring only one or a few nucleotide changes) that carried a low fitness cost to replication (16).

To determine if escape from T cell surveillance and chronic infection might have resulted from a mutation in this immunodominant NS3 1406 epitope, the mutant peptide was loaded on autologous DCs, and CD8+ T cell responses were tested directly ex vivo in an ELISPOT assay. As shown in Fig. 4 B, the mutant epitope failed to elicit IFN-γ CD8+ T cell responses; this supported the concept that virus variation which evolved in vivo outstripped the capacity of T cells to control the infection (i.e., circulating T cells did not react to the infecting sequence). Furthermore,
because peptide variants of class I–restricted epitopes potentially could antagonize naturally occurring epitopes (17), we explored this possibility by using different ratios of wild-type and mutant peptide concentrations. Mutant peptide did not inhibit IFN-γ/H9253 production after stimulation with the wild-type peptide (Fig. 4 B). These results may be due to the fact that the variant peptide bound to the HLA-A2 molecule with decreased affinity (Fig. 4 C).

To assess whether the emergence of the viral variant was the result of genetic drift or selective immune pressure, nucleotide sequences that contained the first 2741 codons of the polyprotein open reading frame were determined for the dominant quasispecies for the donor, PD101, and PD102 by directly sequencing the RT-PCR products. First, the homology between the amino acid sequence for PD101 and the peptides that we synthesized was 96.64%; thus, the peptides that were used to screen responses closely matched the infecting virus (Fig. 5). Second, the sequences from PD101 and PD102 differed by only 11 nucleotides in the open reading frame (99.9% identity) and led to 8 amino acid differences (99.7% identity). Third, the nucleotide sequences for the donor and PD102 were identical except...
for 1 nucleotide in the 5’UTR; their polyproteins from amino acid 1–2741 were identical. The amino acid differences between the sequences were (donor/PD102:PD101): F399L, A937V, V1384A, A1409V, T1474I, A2169T, P2341S, and D2597E. As shown in Fig. 5 B, these nonsynonymous mutations occurred throughout the HCV genome, including two HLA-A2–restricted epitopes. Therefore, in PD101, the rate of amino acid substitution within the immunodominant NS3 1406 CTL epitope (the only peptide that elicited CD8 responses) was 1 of 10 amino acids (10%) versus 4 of 2731 (0.15%) in the remaining flanking or non-HLA-A2–restricted regions. An exact Fisher test indicates that the number of substitutions is not independent of the amino acid position (P = 0.018). These data support a role for CD8+ T cell selective pressure as the cause of amino acid substitution because it is unlikely that this mutation arose randomly in this epitope.

The other HLA A2–restricted epitope (NS5B) demonstrated an amino acid substitution in PD101 (D2597E) that was not present in the donor or PD102. Specific stimulation with this mutant peptide (D2597E, T2600S), prototype 1a, and donor (T2600S) peptide demonstrated proliferation to the peptide derived from the initial infecting sequence (T2600S), but not the mutant peptide (Fig. S3, available at http://www.jem.org/cgi/content/full/jem.20042284/DC1).

Reports of individuals who were exposed to a single source HCV infection have been limited to subjects who acquired the infection in the remote past (18), and consequently, immunologic and virologic analyses were performed long after the outcome of infection was determined. In this study, we prospectively tracked two patients early after they acquired HCV infection from the same acutely infected, “window period” donor. Comprehensive mapping of CD4+ and CD8+ T cell responses with overlapping 15-mer peptides spanning the entire HCV polyprotein revealed statistically significant differences in the breadth and vigor of T cell responses between both individuals. These results are even more compelling when one considers that the autologous, infecting viral sequences and the peptides that were used to screen responses were nearly identical (presumably facilitating immune recognition), and that the subjects shared several HLA alleles, including the highly prevalent HLA A2 (also present in the donor).

Our results are consistent with the concept that the variant HCV carrying a substitution within an immunodominant CD8+ T cell epitope was selected by the monospecific antiviral CTL response, and the variant epitope (perhaps because of lack of HCV-specific CD4+ T cell help [11]) failed

Figure 5. Comparison of viral genetic sequence of donor, PD101, and PD102. (A) Dendrogram showing genetic relatedness of donor, PD101, and PD102 relative to other HCV isolates. Donor, PD101 (the sequence data are available from GenBank/EMBL/DDBJ under accession no. AY695436), and PD102 (the sequence data are available from GenBank/EMBL/DDBJ under accession no. AY695437) amino acid sequences were aligned against the corresponding sequences from the reference 1a isolate from which the peptides were derived (M62321), and a genotype 1b isolate [U4]. The length of the horizontal lines connecting two isolates by the shortest route (right to left and left to right) is proportional to the
to generate new variant-specific CTL populations. The only peptide region that elicited IFN-γ response in PD101 was the class I–restricted epitope region where a nonsynonymous mutation arose and was maintained. In contrast, the likelihood of CTL escape is low when the CTL response is directed against multiple viral epitopes simultaneously, as in the case of PD102. We acknowledge the possibility that T cell responses were broader at time points earlier than the 6 mo when samples first became available.

One of the most striking findings in our study was that the CTL effector response (IFN-γ production and proliferative capacity) in PD101 was maintained even when the cognate antigen that it recognizes was no longer present (after viral escape and after therapeutic viral eradication). This apparent paradox was described previously in a human study of HBV infection (19) and in HCV-infected chimpanzees (9); it could be related to recurrent stimulation from an undefined reservoir of wild-type virus (20), as suggested by the recent demonstration of low-level HCV replication in PBMCs of patients with therapy-induced or spontaneous resolution of HCV infection (20). Alternatively, mutant epitopes could stimulate expansion of the wild-type–specific CTL—a phenomenon known as “original antigenic sin”—that initially was described for antibodies, but also extended to class I HLA-restricted responses (9, 21). Direct enumeration of the frequency of mutant-specific CTL with tetramers was not possible because attempts to synthesize them failed on two occasions, possibly a reflection of the fact the mutant peptide bound to the HLA-A2 molecule with lower affinity than the wild-type peptide (which also might explain the lack of antagonistic activity of the mutant peptide; Fig. 4 B).

In summary, our findings—derived by combining viral sequence data and unbiased, functional T cell analyses that examine every potential HCV epitope after homologous challenge—indicate that the absence of CD4+ T cell help, coupled with strong selective pressure exerted by wild-type–specific CTLs, favor the emergence of immune escape (11) and indicate a patient profile associated with chronicity that might benefit from early antiviral therapy. Elucidation of the mechanisms which underlie the early failure to develop HCV–specific CD4+ T cells and their instructive signals during memory CD8+ T cell differentiation has implications for vaccine strategies that are designed to induce protective immunity to this common disease (22).

MATERIALS AND METHODS

The study protocol was approved by the Human Research Committee and Institutional Review Board of Oregon Health and Science University.

Synthetic peptides. A total of 750 overlapping (15-mers) peptides spanning the entire polyprotein (Fig. S1) of HCV-1a (accession no. M62321) was synthesized at NMI Laboratories.

ELISPOT assay. IFN-γ production was detected using an established ELISPOT protocol (23).

Flow cytometry. Flow cytometric analysis using a fluorescence activated cells sorter FACSCalibur (Becton Dickinson) was performed on the CD8+ T cell population to determine purity and on the CD4+ others to determine the percentage of CD3+CD4+ T cells in the population. Data analysis was performed using CellQuest and FlowJo software. Fluorescent-conjugated anti–human antibodies for T cell subsets, activation, memory, and differentiation markers (BD Biosciences and Caltag) were used. Soluble HLA-A2 tetramers containing core amino acids 132–140 (DLMGVIPLV), NS3 1073–1081 (CINGVWCTV), NS3 1406–1415 (KLVALGINAV), and NS5 2594–2602 (ALYDVVTKL) were synthesized (Beckman Coulter and NIH tetramer facility) and used to screen responses longitudinally.

In vitro proliferation of CFSE-labeled T cells. 10^7 cells were stained in 0.1% BSA in PBS with 1 μM CFSE (Molecular Probes); PBMCs were cultured with 10 μg/ml each of Core 131, NS3 1073, NS3 1406, and NS5 2594 epitope peptides and 0.5 ng/ml IL-2 (on days 0 and 3).

Isolation, amplification, and sequencing of HCV genomes. The plasma of both patients were collected by centrifugation in plasma preparation tubes and frozen immediately at −80°C. RNA was isolated with the QiAamp Viral RNA Mini Kit (QIAGEN) according to the manufacturer’s instructions. The RNA was reverse transcribed using random oligonucleotide primers and M-MLV Reverse Transcriptase (Fisher Scientific) for 60 min at 37°C. HCV sequences, including nt 93–8566 (reference sequence AF009606), were amplified using nested RT–PCR in four overlapping segments using the primers and conditions that are described in Table S2 (available at http://www.jem.org/cgi/content/full/jem.20042284/DC1). The sequence of the dominant quasispecies was obtained by sequencing both strands of each amplicon directly using primers averaging 300 nt apart, and the full sequence was assembled with the Vector NTI software package.

Statistical analysis. Results were graphed and analyzed using GraphPad Prism and JMP (SAS Institute) statistical package.

Online supplemental material. Figs. S1–S3 and Tables S1 and S2 demonstrate the whole genome sequencing and T cell mapping approach. Enumeration and phenotype of HCV-specific, HLA-A2 epitope responses and proliferative responses after stimulation with wild-type and mutant peptides are shown. Online supplemental material is available at http://www.jem.org/cgi/content/full/jem.20042284/DC1.

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