A single amino acid change in the hypervariable region 1 of hepatitis C virus genotype 4a aids humoral immune escape

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Longitudinal analysis of chronic hepatitis C virus (HCV) infection has shown that the virus has several adaptive strategies that maintain persistence and infectivity over time. We examined four serum samples from the same chronically infected HCV genotype 4a patient for the presence of IgG antibody-associated virus. RNA was isolated from antibody-associated and antibody-free virions. Subsequent to sequence analysis, 27 aa hypervariable region 1 (HVR1) peptides were used to test the humoral immune escape. We demonstrated that differential peptide binding of Fab was associated with a single amino acid change. We provide direct evidence of natural humoral immune escape by HCV within HVR1.

Hepatitis C virus (HCV) infects 2–3 % of the world population and is a leading cause of liver disease (Freeman et al., 2001; Zhou et al., 2014). Early in infection the host immune system responds by producing neutralizing antibodies (Terilli & Cox, 2013). Although HCV infection stimulates a strong immune response, it is generally insufficient to eradicate infection, as 50–80 % of the infected individuals develop chronic liver disease (Deng et al., 2013; Freeman et al., 2001; Inchauspé et al., 2008; Kenny-Walsh, 1999). The high rate of viral persistence is thought to be a result of a complex interplay between viral diversity and suboptimal immunity. Viruses with hypervariable genomic regions evade host humoral immune response by several mechanisms (Brown et al., 2005; Quaranta et al., 2012; Thimme et al., 2006). The best understood mechanism for viral immune escape is single-point mutation which results in non-synonymous changes within the immunodominant viral envelope glycoprotein and NS3 (Cox et al., 2005; Ray et al., 2005; Thimme et al., 2006, 2012). Multiple linear epitopes within the 27 aa hypervariable region 1 (HVR1), in the N terminus of the E2 envelope protein, have been identified as the principle target of neutralizing antibodies (Ball et al., 2014; Fafi-Kremer et al., 2012; Tarr et al., 2015). Antibodies specific for epitopes within HVR1 have been reported to inhibit the binding of the E2 glycoprotein to cells and to block HCV infectivity in vitro and in vivo (Farcı et al., 1996; Haberszter et al., 1998; Owsianka et al., 2001). However, HCV pseudoparticle and cell-culture-derived HCV experiments have shown poor cross-neutralization potential of isolate-specific neutralizing antibody response to HVR1 (Brown et al., 2005; Cashman et al., 2014; Larrubia et al., 2014). Cytotoxic T-lymphocytes drive evolution of the HVR1, which can lead to the emergence of escape variants (Cox et al., 2005; Ray et al., 2005). However, there is an absence of direct in vivo evidence of humoral immune escape by host-derived antibodies and viral glycoproteins (Chung et al., 2013).

Previous research from our group has observed, over a near 10 year period, the emergence, dominance and disappearance of distinct but related lineages (L1 and L2) in a treatment-naive patient chronically infected with HCV genotype 4a (Palmer et al., 2014). L1 dominated the virome for the first 8 years of the sampling period prior to population collapse and this led to the concomitant rise to prominence of L2. During the initial dominance of L1, IgG targeting of L1 was detected in five of the first seven samples which, in part, contributed directly to the extinction of this group of variants (Palmer et al., 2012, 2014). In spite of the near total dominance of L2 sequences in later samples (96.9 and 99.9 % at T9 and T10, respectively; see Fig. 1 for details of sampling times), no IgG targeting of L2 virions was detected in this previous study (Palmer et al., 2014). Furthermore, the HVR1 of L2 variants remained predominantly under purifying selection across the 10 year period with a single principle HVR1 amino acid variant persisting during this time. Follow-up clonal analysis 1 year later (T11) revealed that a HVR1 variant with a single-point mutation had superseded the principle variant. There was no antibody-associated virus (AAV) found at T11 (Palmer et al., 2014) (Fig. 1). Fig. 1 summarizes the AAV profile of all samples analysed.
In the current follow-up study to Palmer et al. (2014) we mapped a further four serum samples T12–T15 that extended the sampling period to 13 years (Fig. 2). Serum samples were obtained from a treatment-naive patient. This study was approved by the Clinical Research Ethics Committee of the Cork Teaching Hospital and written consent from the patient was obtained. The clonal sequence analysis of these samples identify the continued dominance of L2 sequences. The constituent virions were partitioned into antibody-free virus (AFV) and AAV fractions, as described previously (Moreau et al., 2008; Palmer et al., 2014). Of these samples, only T13 contained detectable levels of AAV (GenBank accession numbers KT595222 and KT595223) (Fig. 1). The antibody–virus complex of this fraction was dissociated and disruption of the virion was achieved by treatment with proteinase K (5 mg ml\(^{-1}\)) for 2 h at 37°C with end-over-end mixing followed by overnight incubation at room temperature. Confirmation of the virus-free status of this proteinase K-treated T13 antibody (T13Ab) preparation was determined by the absence of an E1E2-specific amplicon following reverse transcription PCR; the virus-free T13Fab fragment was designated VF-T13Fab. T11 had three different HVR1 amino acid variants, i.e. H\(^{395}\)-X-X-F\(^{399}\), N\(^{395}\)-X-X-F\(^{399}\) and N\(^{395}\)-X-X-L\(^{399}\) (subscript numbering identifies specific amino acid positions within the 27 aa HVR1 with reference to GenBank accession number NC_004102). The presence of HVR1 variant H\(^{395}\)-X-X-F\(^{399}\) in the AFV fraction of T12 was confirmed by amplicon sequencing only. The subsequent AFV fraction of T13 also had the H\(^{395}\)-X-X-F\(^{399}\) amino acid profile (frequency 0.40). However, the N\(^{395}\)-X-X-L\(^{399}\) variant was now dominant in T13 (frequency 0.60). Interestingly, the predicted HVR1 sequence from AAV RNA detected at T13 indicated N\(^{395}\)-X-X-L\(^{399}\) motif targeting (Fig. 2). This Leu-containing motif was isolated in the succeeding samples, i.e. T14 and T15 (Fig. 2). AAV was not detected in samples T11, T12, T14 and T15. However, in order to exclude the possibility that the P2 variant motif containing N\(^{395}\)-X-X-L\(^{399}\) was not accessible to antibodies, we similarly tested VF-T11Fab, VF-T12Fab and VF-T15Fab for binding affinity to the HVR1 peptide variants.

A recent study by Guan et al. (2012) showed that neutralization epitopes can be between amino acid positions 16 and 24 (i.e. 399–407) in HVR1. It is interesting to note that...
In our study, amino acid variation was observed only at amino acid positions 395 and 399 within the entire HVR1. Based on the Guan et al. (2012) data, we hypothesized that the HVR1 variants with N_{395}-X-X-F_{399} (T11-AFV) and H_{395}-X-X-F_{399} (T13-AFV) motifs were potential humoral immune escape mutants which have Phe at position 399. To confirm the escape phenotype hypothesis, three N-terminally His\(_{6}\)-tagged, 27 aa HVR1 peptides were synthesized, i.e. P1 (H-HHHHHHTHTGAVASSNAQKTSFLFTFGP-QQN-OH), P2 (H-HHHHHHTHTGAVASSNAQKTLT-SLFTFGPQQN-OH) and P3 (HHHHHHTHTGAVASSH-AQKTSFLFTFGPQQN-OH) (Pepscan Presto), where underlining indicates the His\(_{6}\)-tag and bold indicates the variant amino acid at position 395 or 399. The HVR1 sequence of P1 and P3 corresponded to the dominant L2 HVR1 variant for the initial 10 years of \textit{in vivo} infection for which no AAV was detected (Palmer et al., 2014). The P2 sequence corresponded to the predicted HVR1 of AAV RNA isolated at T13. Peptides were reconstituted in 100% DMSO at a concentration of 1 mg ml\(^{-1}\) and stored at \(-20\) °C. Peptide (100 ng µl\(^{-1}\)) was used in an ELISA-based method. These peptides were incubated with VF-T11Fab, VF-T12Fab, VF-T13Fab and VF-T15Fab at 1:10 dilution for 1 h followed by incubation with anti-human IgG (H&L)–HRP conjugate secondary antibody (Promega) at 1:5000 dilution for 1 h (Fig. 3). The ELISA results confirmed that the peptide containing the N_{395}-X-X-L_{399} mutation was recognized by VF-T13Fab. The binding phenotype of VF-T13Fab had the strongest affinity to P2 (P2\(\gg\)P1\(\gg\)P3) with Leu at position 399, compared with the predicted escape variant Phe \textit{in vitro} (\(P = 0.06\), Kruskal–Wallis test using Prism 4; GraphPad) (Fig. 3). Our results prove that, in this case, a naturally occurring single amino acid change to Phe in the HVR1 alone at position 399 can drive humoral immune escape after >10 years of immune silence. Our results demonstrated that none of VF-T11Fab, VF-T12Fab and VF-T15Fab bound to the HVR1 peptide variants P1–P3.

In our current study, analysis of serum samples over a 13 year period showed two distinct periods when AAVs were present. A window period of 5 years existed between the two points during which AAVs were detectable. The antibody specificity of the latter time point, i.e. T13, targeted a different HVR1 lineage from that found previously (Palmer et al., 2012, 2014). The HVR1 variant captured by the T13Ab response was not sustained to detectable levels. The loss of neutralization antibodies is a recognized feature of the natural history of HCV infection (Shimizu et al., 1994). Additionally, it is also recognized that a sustained antibody response is likely a prerequisite for complete removal of viral variant(s). The
notable absence of a sustained and neutralizing antibody response (in T14 and T15), and likely fitness superiority, explains why the motif (N_{395}X-X-X-L_{399}) persisted in subsequent samples.

In conclusion, our proof-of-concept study has confirmed that antibodies were naturally generated against a discrete viral variant (Fig. 3). We additionally confirmed that naturally occurring amino acid variations in this epitope represent one mechanism by which HCV escapes humoral immunity.

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References


