INTRODUCTION

Hepatitis C virus (HCV) infects nearly 2.2% of the world population and is a common cause of chronic liver disease (Alter, 2007; Lavenchay, 2009). No vaccine is available, and the only current treatment (combination therapy of pegylated interferon with ribavirin) has limited efficacy and serious side effects (Sakamoto & Watanabe, 2009; Tan et al., 2006). HCV, an enveloped positive-sense ssRNA virus (Choo et al., 1989), belongs to the genus Hepacivirus of the family Flaviviridae. The 9.6 kb HCV genome encodes a single 3000-residue precursor polyprotein cleaved by host-cellular and viral enzymes into three structural proteins (core, the envelope glycoproteins E1 and E2) and seven non-structural (NS) proteins (p7, NS2, NS3, NS4A, NS4B, NS5A and NS5B) of diverse functions (Moradpour et al., 2007). Core, the capsid protein, is essential for infectious particle assembly and release (Miyanari et al., 2007; Penin et al., 2004; Shavinskaya et al., 2007; Strosberg et al., 2010). This protein of 191 residues consists of three distinct domains: (i) D1, an N-terminal hydrophilic domain of 117 aa; (ii) D2, a more hydrophobic domain of about 60 aa; and (iii) the C-terminal D3 which contains approximately the last approximately 14 mostly hydrophobic residues cleaved off during core maturation and which serve as the signal peptide for the downstream protein E1 (Boulant et al., 2006). D1 is mostly responsible for self-association, for binding RNA and for interaction with several host cellular proteins (Angus et al., 2010; Chen et al., 2008; Yan et al., 2007), whereas D2 is responsible for coating of lipid droplets (LDs) and for the folding of the N-terminal part (Appel et al., 2008; Boulant et al., 2005; Masaki et al., 2008). Core dimers and higher-order complexes associate with the viral RNA to form the nucleocapsid and associate with E1 and E2 to form the infectious particles (Boulant et al., 2005; Klein et al., 2004; Kunkel et al., 2001; McLauchlan, 2000; McLauchlan et al., 2002). Recent studies suggest that several steps of virus assembly take place near the LDs and their associated membranes (McLauchlan, 2009a; McLauchlan et al., 2009b; Miyanari et al., 2007; Rouille et al., 2006; Strosberg et al., 2010). The interaction of NS5A with core and its recruitment to the LDs (McLauchlan et al., 2002; Shi et al., 2002) appear to be essential for virus assembly (Miyanari et al., 2007) and a prerequisite for HCV particle production (Masaki et al., 2008). In addition to the central role of core and that of NS5A, several recent studies suggest that other NS proteins,
such as p7, NS2 and NS4B as well as NS3, may also be important in viral assembly (Jones et al., 2007, 2009; Ma et al., 2008; Murray et al., 2007, 2008; Steinmann et al., 2007; Yi et al., 2007, 2009).

NS3 displays a serine protease activity at the N terminus (aa 1–166), and helicase and nucleoside triphosphatase activities in the remainder of the 631 residues of the protein (Fig. 1a) (Gallinari et al., 1998). The NS3 protease activity becomes fully active by association with NS4A. The helicase portion of NS3 (NS3h) folds and functions independently of the protease domain. Recent studies with the HCV strain 2a J6/JFH-1 in infected cells suggest the involvement of NS3h at an early step of viral assembly, independently of its essential roles in polyprotein processing and in viral replication (Ma et al., 2008). However, the physical interaction between HCV core and HCV helicase was not demonstrated and a precise role for NS3 in virus assembly and release remains unclear.

Several independent methods were used here to show that HCV core protein indeed interacts directly with NS3h. Moreover, inhibitors previously found to disrupt core oligomerization and production of infectious particles (Kota et al., 2009, 2010; Wei et al., 2009) abolish the core–NS3 interaction in vitro, suggesting that dimerization of core protein is important for the binding of helicase. Collectively, these data underline the essential role of core as a key organizer of HCV particle assembly.

**RESULTS**

**Purification of core106, core169 and NS3h**

The first N-terminal 106 residues of HCV core (core106) were chosen as the minimum domain necessary to homodimerize (Kota et al., 2009; Matsumoto et al., 1996; Nolandt et al., 1997) and to mimic the hydrophilic domain D1. The first 169 residues (core169) were selected to represent mature core composed of domains D1 + D2 (Boulant et al., 2005; Kota et al., 2009). Both core106 and core169 homo/heterodimerize in a similar fashion, at comparable concentrations. Proteins were expressed as such or as fusion proteins with glutathione S-transferase (GST) or Flag at their N terminus (Kota et al., 2009) and tagged with eight His residues at their C terminus (Fig. 1a, upper panel). GST-tagged HCV NS3 protein lacking the NS3 residues 1–166 (i.e. the protease domain) (here named NS3h or GST-NS3h), unwinds both DNA and RNA duplexes at rates comparable to those seen with the full-length NS3–NS4A complex (Frick et al., 2004). The protein was produced as an N-terminally GST-fused and a C-terminally 8-His-tagged protein (Fig. 1a, lower panel). The proteins were purified to apparent homogeneity from Escherichia coli extracts, by using immobilized metal ion affinity chromatography and followed, for GST-NS3h, by glutathione-bead purification. The identity and homogeneity of the proteins were verified by SDS-PAGE followed by Coomassie blue staining (Fig. 1b, lanes 1–3) and immunoblotting (Fig. 1b, lanes 4–6), revealing expected bands for core106, core169 (both contain a C-terminal 8-His) and GST-NS3h at 15, 20 and 80 kDa, respectively. (Of the 80 kDa for GST-NS3h, 50 kDa correspond to the helicase domain and 30 kDa are contributed by the GST protein and His-tag.)

**Core interacts directly with NS3h**

Recent studies suggest the involvement of NS3h at an early step of viral assembly (Ma et al., 2008) and describe colocalization of NS3 with core in LDs (Miyanari et al., 2007). However, the physical interaction between core and NS3 proteins was not demonstrated. An indirect sandwich ELISA was used here for the initial characterization of the interaction between affinity-purified HCV core and NS3h proteins (Fig. 2a). When GST-NS3h was included in wells coated with either core106 or core169, a strong signal was observed revealing the interaction with the capsid protein. An irrelevant GST-fusion protein (GST-IRP), used as a negative control, gave a signal similar to the background in the assay, confirming that the interaction between NS3h and either core106 or core169 was specific (Fig. 2a).

To measure the strength of the core–NS3h interaction, we adapted a previously developed Amplified Luminescent Proximity Homogeneous Assay (AlphaScreen) to follow core dimerization using GST-fused and Flag-fused core

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**Fig. 1.** (a) HCV core protein and NS3 protein constructs. (b) Analysis of purified HCV core and NS3 protein. Lanes 1 and 4: core106 (15 kDa); lanes 2 and 5: core169 (20 kDa); and lanes 3 and 6: GST-NS3h (80 kDa) were resolved by SDS-PAGE and stained with Coomassie blue (lanes M and 1–3) or detected by immunoblotting using mouse monoclonal anti-core or anti-helicase antibodies (lanes 4–6). The immunoblot revealed also minor degradation products of core106 (13 kDa), core169 (14 and 17 kDa) and GST-NS3h (60 kDa).
proteins, and core106 as a specific competitor (Kota et al., 2009). This assay, displaying a signal-to-background ratio greater than 50-fold, confirmed both the Flag-core106–GST-NS3h and the Flag-core169–GST-NS3h interactions (Fig. 2b). Several groups have previously reported that the cellular DEAD-box protein DDX3, a human helicase homologous to HCV NS3h, interacts with viral core (Angus et al., 2010; Mamiya & Worman, 1999; Owsianka & Patel, 1999; You et al., 1999): the first 40 aa residues of the N-terminal part of HCV core are important for this interaction. We evaluated the effects of five peptides spanning the 44 first residues of the N-terminal part of core (Fig. 2c) by AlphaScreen. The two most potent mostly hydrophilic peptides were able to inhibit core–NS3h interaction by about 80 %, indicating that residues localized between 1 and 24 are important for the interaction but other residues of core are also required.

Full-length NS3 from HCV-infected cells interacts with the N-terminal domain of core

First, the expression of core, NS3 and NS5A in HCV-infected Huh-7.5 cells was verified by immunoblotting revealing the expected molecular mass of the full size proteins: 20, 70 and 65 kDa, respectively (Fig. 2d). A GST pull-down assay was then used to verify that NS3 and
N55A (as a control) produced by the virus in cells could interact with core (Fig. 2e). After incubation of GST-core106 with a lysate of HCV-infected Huh-7.5 cells, the protein complexes were pulled down by glutathione-Sepharose beads and analysed by immunoblotting using mouse anti-NS3 and anti-N55A antibodies. As a negative control, the cell lysate was incubated with beads alone to exclude non-specific interactions of NS3 with the glutathione-Sepharose beads. Moreover, GST-IRP was analysed in parallel to exclude the eventual participation of the GST moiety in the interaction. The presence of protein bands of apparent molecular mass of 70 and 65 kDa, respectively, seen only with beads coated with GST-core106, confirmed specific pull-down of the full-length NS3 and N55A produced in cells (Fig. 2e). A 2 h RNase treatment of GST-core106 and of the cell lysate did not decrease the amount of pulled-down proteins, suggesting that interaction between core and NS3 is not mediated by RNA (Fig. 2f).

Core oligomerization is required for binding of NS3h

Core is known to oligomerize to form the viral particle (Klein et al., 2004; Kunkel et al., 2001). We investigated the size of the complex formed between core and NS3h by performing cross-linking experiments using dimethyl suberimidate (DMS), which reacts with amino groups, and which we previously used to characterize core oligomerization (Kota et al., 2009). While no evidence was found for cross-linking of a core106 monomer to NS3h monomer (expected molecular mass 95 kDa), trimer formation was readily apparent between core106 dimer (30 kDa) and GST-NS3h (80 kDa); the identity of the band of the expected total size of 110 kDa (Fig. 3a) was confirmed by immunoblotting with both anti-core and anti-GST antibodies (Fig. 3b). With core169, GST-NS3h formed not only trimers (120 kDa) but also tetramers (140 kDa) (Fig. 3c, d). The immunoblots confirm the presence of both core169 and NS3h in these two bands. Regarding apparent molecular masses, the trimers and tetramers may correspond to the interaction of GST-NS3h (80 kDa) with two (2 × 20 kDa) or three molecules of core169 (3 × 20 kDa), respectively. Higher molecular-mass oligomers, associated with N55h, are also visible for core106 (Fig. 3a, b) and core169 (Fig. 3c, d).

Interestingly, in the AlphaScreen experiments, the interaction between GST-NS3h and core yielded a signal superior to that seen for the core–core interaction alone, reflecting a better transfer of energy between GST-NS3h and the two molecules of dimerized Flag-core (Fig. 2b).

Disruption of HCV core–NS3h interaction by inhibitors of core dimerization confirms role of oligomerization

To verify the role of dimerization of core in the binding of NS3h, we evaluated the effects of an inhibitor (SL201) and of a competitor (core106) by AlphaScreen (Kota et al., 2010; Wei et al., 2009). Buffer only and individual protein partners in the presence of donor/acceptor beads alone provided the background value for the assay (Fig. 4a). Addition of 1% DMSO without SL201 did not reveal any effect of the solvent on the interaction. As positive control, we used the Flag-core106–GST-core106 interaction (Fig. 4a). The AlphaScreen showed the Flag-core106– and Flag-core169–GST-NS3h interactions were inhibited by core106 (10 μM) and SL201 (15 μM) (Fig. 4b). Core106 inhibited the Flag-core106–GST-NS3h interaction with an IC_{50} of 0.344 μM, i.e. four times higher than the IC_{50} of 0.089 μM for the core106 homodimer (Fig. 4c and Table 1). The higher IC_{50} could be explained by the need for two molecules of core106 to abrogate completely the interaction between Flag-core106 dimer and GST-NS3. The inhibition by one molecule of core106 only weakened the signal partially. Similarly, the IC_{50} for the Flag-core169–GST-NS3h was 0.873 μM (Fig. 4e and Table 1). SL201, a 513 Da inhibitor of core106 dimerization, was discovered when screening with a time-resolved fluorescence resonance energy transfer (TR-FRET)-based screen assay, the Center for Chemical Methodology and Library Development at Boston University library of 2240 compounds (Kota et al., 2010; Wei et al., 2009). When evaluated on the Flag-core106– or Flag-core169–GST-NS3h pairs of proteins, SL201 strongly inhibited (~90%) these interactions (Fig. 4b). In a dose–response format, SL201 displayed strikingly consistent IC_{50} values ranging from 9.3 μM for the homologous core106 self-association to 9.0 μM and 10.5 μM for Flag-core106–GST-NS3h and Flag-core169–GST-NS3h interactions, respectively (Fig. 4d, f and Table 1). These results suggest that it is most likely that SL201 acts on the same single interaction site on core, regardless of the protein interaction partner, in contrast to what is observed when the much larger core106 molecule is used as the disruptor of the interaction.

Treatment by SL201 abolishes infectious virus production

Recently developed cell-culture-based systems for production of infectious HCV from genotype 2a JFH-1 have facilitated the study of the virus life cycle (Lindenbach et al., 2005; Wakita et al., 2005; Zhong et al., 2005). SL201 was previously shown to substantially decrease HCV production by HCV-infected Huh7.5 cells, as revealed by quantitative RT-PCR (Kota et al., 2010; Wei et al., 2009). The compound was added here at various dilutions with infectious supernatant from electroporation of 2a J6/ JFH-1 RNA into naive cells and incubated for 3 days (early stage – T1). This stage corresponds to the entry and replication of the virus. T1 culture supernatant was used to infect naive cells to study infectivity (late stage – T2) (Fig. 5a). The compound was shown to be active with an effective concentration at 50% (EC_{50}) of 8.8 μM for T1 and 8.1 μM for T2 (Fig. 5b). The compound SL201 had no effect on production of a subgenomic HCV replicon which
contains only the NS proteins, confirming that the compound does not affect replication and supports the hypothesis that it blocks HCV particle assembly by acting on core or core’s interactions with other HCV proteins, including NS3 (Fig. 5c).

**DISCUSSION**

Until recently, the only known role for HCV NS3 in the viral life cycle was thought to be linked to its protease activity in HCV polyprotein processing and its helicase activity in viral replication. There is, however, growing evidence that NS3 may participate in the assembly/production of infectious viral particles (Ma et al., 2008; Murray et al., 2008; Patkar & Kuhn, 2008), as do other NS proteins such as NS5A (Appel et al., 2008; Miyanari et al., 2007; Tellinghuisen et al., 2008) and NS2 (Jirasko et al., 2008; Jones et al., 2007; Murray et al., 2007; Yi et al., 2007, 2009). With regard to NS3h, two successive spontaneous mutations were identified that restored the production of infectious virus by a strain that was otherwise quite unproductive (Ma et al., 2008). Core and NS3h were also found to be colocalized on LDs of cells transfected with HCV RNA (Ma et al., 2008; Miyanari et al., 2007).

In the present work, we demonstrate for the first time that NS3h directly interacts with core as shown by several biochemical methods. After showing the physical interaction between recombinant affinity-purified core and NS3h proteins by ELISA and AlphaScreen, we confirmed the interaction of GST-core106 with the full-length NS3 protein produced in HCV-infected hepatoma cells using a GST pull-down assay. We verified that prior treatment with RNase did not reduce the interaction, thus discarding an indirect effect due to the presence of RNA. Taken together, these experiments showed that NS3h binds to HCV core and that the N-terminal fragment core106 and the helicase domain of NS3 (167–631) are sufficient for the interaction. Using an AlphaScreen, the ability of core106 to block association of GST-NS3h with Flag-core106 confirmed the involvement of N-terminal residues in the interaction. By screening the ability of peptides spanning the N-terminal part of core known to interact with DDX3, a human homologue of HCV NS3h (You et al., 1999), two peptides, 1–18 and 7–24, were found to block binding by

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**Fig. 3.** Cross-linking of HCV core protein oligomers with HCV NS3h. (a, c) SDS-PAGE stained with Coomassie blue of core106 (C106) and core169 (C169), respectively, with or without GST-NS3h cross-linked in the presence of DMS. (b, d) Immunoblotting with an anti-core antibody (left) or anti-GST antibody (right).
80%, indicating the importance of one or several residue(s) of those N-terminal peptides in the interaction. Moreover, the C-terminal region of core may contain additional residues important for the binding since interaction between NS3h and core169 displays a higher signal than that between core106 and NS3h as shown by AlphaScreen.

We previously developed an ELISA and an AlphaScreen using core106, the region essential for self-association, and identified SL201, a small molecule that inhibits HCV core dimerization (Kota et al., 2010; Wei et al., 2009). Core106 and SL201 potently inhibit the binding with the helicase. Using a molecular beacon-based helicase assay (Belon & Frick, 2008), no effect of SL201 was observed on DNA
indicating lack of effect on viral replication. These results
pound did not modify HCV replicon propagation,
cells (S. Valente, personal communication). The com-
HCV production by infected hepatoma cells (Kota
2010; Tellinghuisen 
trimer in the complex formed with NS3. '*' Indicates data previously
Indicates that core106 or core169 is actually present as a dimer or
IC


unwinding (D.N. Frick, unpublished observations). The
strong inhibition by core106 and SL201 suggests that NS3h
recognizes and interacts preferentially with dimers or
oligomers of core. This observation is strengthened by
the cross-linking experiments, which show that NS3h
interacts with core106 dimers and core169 dimers and
trimers, but not monomers. The presence of cross-linked
tetramers containing core169 trimers and NS3h but not
core106 trimers suggests that NS3h better stabilizes
oligomeric forms of core169 than of core106.

The NS3 protein of yellow fever virus (YFV), the prototype
flavivirus, which like HCV is a member of the family
Flaviridae, also plays an essential role in virus assembly
as shown by trans-complementation of a mutation
(Trp349Ala) by expression of the wild-type NS3 protein
(Patkar & Kuhn, 2008). Since domains 1 and 2 of the HCV
helicase show a high degree of similarity with the
corresponding domains in YFV helicase, and the sequence
alignment reveals 21 % similarity including the presence of
a conserved aromatic residue (Tyr350) in HCV at the
position corresponding to 349 in YFV (Wu et al., 2005),
they may also share mechanistic features in the process of
virus assembly and release. The interaction observed
between core and NS3h might be equally important for
HCV assembly. We propose the following sequence of
events: initially, HCV core is processed by signal peptide
and recruits NS5A and NS3 to the LDs, a prerequisite for
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to differentiate between an effect on assembly and entry,
time-of-addition intracellular and extracellular infectivity
assays were performed. To analyse the results, we used both
real-time RT-PCR and HCV-limiting-dilution (TCID50)
assays. These data confirm that SL201 appears at least 10-
fold less effective when added before viral infection than
during or after infection (see Supplementary Figs S1 and S2
and Supplementary Table S1, available in JGV Online).

The colocalization and interaction of core with NS proteins
on LDs confirms core as a key organizer of virus assembly
and suggests that it acts by recruiting the replication complex
near the site of assembly to facilitate the packaging and integration of the newly synthesized RNA.
Whether core actually modulates the HCV RNA unwinding
activity of the viral helicase, and thus actually affects
replication and translation, remains an open question.

In conclusion, the present studies establish that HCV helicase physically interacts with the oligomerized HCV
core protein, and that this interaction involves the first 106 residues from core and residues 166–631 from NS3.
Binding is stronger when domain D2 of core, up to residue 169, is present, and is inhibited by small molecule
SL201, a disruptor of core dimerization and of infectious
HCV production.

**METHODS**

**Materials.** Anti-GST (Sigma-Aldrich), anti-core (MA1-080)
(Thermo Scientific), anti-NS3 [H23] (Abcam), anti-NS5A [9E10] (gift
from Dr T. Tellinghuisen, Scripps-Florida, USA) were purchased.
HRP-conjugated secondary antibodies were obtained from Jackson
ImmunoResearch. Infectious HCV 2a strains J6/JFH-1 and JC1 were
produced using previously published protocols (Lindenbach et al.,
2005; Pietschmann et al., 2006; Wakita et al., 2005; Zhong et al.,
2005). Cells were cultured in Dulbecco’s modified Eagle’s medium
(Invitrogen) supplemented with 10 % heat-inactivated FBS (Akron
Biotech), 1X Pen-Strep-Gln and 1 × non-essential amino
acids (Invitrogen) at 37 °C in a humidified atmosphere with 5 % CO2.

**Cloning, expression and purification of proteins.** A vector
encoding GST-NS3h (from HCV HC-16CH genotype 2a;
AF177036) was generated by excising the HCV helicase-encoding
region from p24Hel-2a (Lam et al., 2003) and inserting it into vector
pET41a. Recombinant protein was expressed in transformed E. coli
BL21(DE3) cells and purified by Hi-Trap nickel-nitritotriacetic acid
(Ni-NTA) column and affinity-capture of GST-NS3h with glutathione-Sepharose beads as described previously (Lam et al., 2003).

The cloning, expression and purification of the recombinant HCV
core106, Flag-core106 and GST-core106 were done as described
previously (Kota et al., 2009). Core106 was further purified for the
cross-linking assays by reverse-phase HPLC on a semi-preparative
column Agilent Zorbax Extend C18 using an isocratic (0–5 min, 22 %)
followed by linear gradients (5–55 min, 32 %; 55–60 min, 100 %) of
buffer B (acetonitrile, 0.01 % trifluoracetic acid) at 2 ml min
flow rate and at room temperature. Core106 fractions were dialysed
overnight at 4 °C against 20 mM Tris (pH 8.0), 0.5 M NaCl and
stored at −80 °C.

The sequences of core covering the first 169 residues were amplified
by PCR from HCV H77 genotype 1a (NC-004102) plasmid pCV-
H77C and inserted into pET42b. For expression, this plasmid or

<table>
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<tr>
<th>Partners</th>
<th>Disrupters</th>
<th>IC50 [μM]</th>
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<tr>
<td>GST-fusion protein</td>
<td>Flag-fusion protein</td>
<td>Core106</td>
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<tr>
<td>Core106†</td>
<td>Core106†</td>
<td>0.09 ± 0.10*</td>
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<tr>
<td>Core106†</td>
<td>NS3h</td>
<td>0.22 ± 0.15</td>
</tr>
<tr>
<td>Core169†</td>
<td>NS3h</td>
<td>0.87 ± 0.53</td>
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Table 1. IC50s of core106 and SL201 to block GST-NS3h
and core interactions

IC50s were calculated from Fig. 4 using Graphpad Prism software.
IC50s were calculated using an ‘n of 2’ with duplicate data points. ‘+’
Indicates that core106 or core169 is actually present as a dimer or
trimer in the complex formed with NS3. ‘*’ indicates data previously
published (Kota et al., 2009; Wei et al., 2009) included here as a
control.
Fig. 5. Effect of SL201 on HCV 2a J6/JFH-1 virus and PSGR-JFH1 replicon. (a) Scheme of infection of naïve Huh-7.5 cells by HCV. Infectious supernatants were obtained from cells electroporated with RNA from HCV (Kota et al., 2009). (b) Inhibition assay of SL201 was performed on HCV 2a J6/JFH-1 virus by adding serially diluted SL201 and virus onto naïve Huh-7.5 cells and then incubating for 3 days (T1). Culture supernatant from T1 was transferred onto naïve Huh-7.5 cells and the cells were incubated for an additional 3 days (T2). RNA was purified from lysed cells from both T1 and T2 and analysed by real-time RT-PCR. EC50 values for this new batch of SL201 were 8.8 μM and 8.1 μM, respectively. (c) Effect of SL201 on PSGR-JFH1 replicon cells. Inhibition assay of SL201 was performed on PSGR-JFH1 replicon cells by adding serially diluted SL201 onto cells and incubating for 3 days. RNA was purified from cell lysates and analysed by real-time RT-PCR. RNA production from cells in the presence of various concentrations of SL201 was compared with the cell-only control. Data points are presented in terms of percentage inhibition, which was calculated using the uninhibited control as 0 % reference. These are representations of one experiment with triplicate data points.
pT7Flag plasmid containing Flag-core169 were transformed into E. coli BL21(DE3) cells using standard expression procedure (Boulant et al., 2005). Core169 (containing only an 8-His tag) or Flag-core169-containing pellets were solubilized using lysis buffer containing 6 M urea (Thermo Fisher Scientific) and the clarified lysate was applied to Ni-NTA affinity columns pre-equilibrated with 20 mM Tris/ HCl buffer (pH 8.0), 0.5 M NaCl, 6 M urea and 0.1 % dodecyl β-maltoside (DM; Sigma-Aldrich). Recombinant proteins were eluted with 50, 100 and 150 mM imidazole (Thermo Fisher Scientific) and dialysed overnight at 4 °C. The presence of the purified proteins was determined by SDS-PAGE and confirmed by immunoblotting using mouse monoclonal anti-core antibodies.

**Indirect sandwich ELISA.** The assay was performed similarly as described previously (Kota et al., 2009). Core106 and core169 (500 pmol) were coated to high-binding 96-well plates and GST-fusion proteins were tested at 1 pmol per well. Rabbit anti-GST antibodies were used at a dilution of 1: 1000 and anti-rabbit IgG-HRP antibodies were added at a dilution of 1: 10,000. Colour development was assessed by using the Ultra 3,3’-5,5’-tetramethylbenzidine (Thermo Fisher Scientific). The colour reaction was stopped by adding 1 N H2SO4 and absorbance measured at 450 nm.

**GST pull-down.** Huh-7.5 cells were grown for 24 h before electroporation with infectious HCV 2a strain J6/JFH-1. At day 4 post-electroporation, the supernatant was removed and cells were lysed in 400 μl lysis buffer (PBS with 1 % Triton X-100, 1 mM PMSF, protease-inhibitor cocktail) and stored at −20 °C. The presence of HCV proteins core, NS3 and NS5A in cell lysate was verified by immunoblotting using anti-core, anti-NS3 and anti-NS5A antibodies. For GST pull-down, GST-core106 or GST-IRP (kindly provided by Dr N. Ayad, Scripps-Florida) immobilized on glutathione-Sepharose 4B beads (GE Healthcare Biosciences) was incubated with 80 μl of cell lysate in incubation buffer [20 mM Tris (pH 8.0), 150 mM NaCl, 10 % glycerol, 0.05 % Triton X-100] for 4 h at room temperature under end-over-end agitation. As control, GST-core106 and the cell lysate were alternatively treated with 10 U of RNase A (New England Biolabs) at 37 °C for 2 h. The beads were washed three times and centrifuged at 5000 g for 1 min using a SigmaPrep spin column and boiled in the SDS loading buffer for 5 min, and the pulled-down proteins were detected by immunoblotting.

**Cross-linking analysis.** For cross-linking experiments, core106 and NS3h were dialysed against cross-linking buffer (200 mM phosphate buffer, pH 8.0), and core169 in cross-linking buffer containing 0.01 % CHAPS, and stored at −80 °C. Cross-linking analysis was performed by incubating 8 μM of core106 or core169 proteins with or without 2.5 μM of NS3h in cross-linking buffer followed by the addition of 200 molar equivalents of DMS for 1 h at room temperature. The reaction was stopped by adding an equal volume of SDS loading buffer and sample was boiled for 10 min. The products were resolved by SDS-PAGE and analysed by Coomassie blue staining or by immunoblotting using anti-core and anti-GST antibodies to detect core and GST-NS3h, respectively.

**AlphaScreen.** This method was developed as described previously (Kota et al., 2009). In brief, the GST-fusion proteins and Flag-fusion proteins at a concentration of 208 and 250 nM, respectively, were used. GST-core106 and Flag-core169 at 150 nM each were included as a positive control. Alternatively, in order to evaluate the possible role of RNA in the core–NS3h interaction, proteins were treated with 10 U of RNase A for 2 h at 37 °C. The untagged core106 domain (10 μM) or compound SL201 (15 μM) (previously published as compound #15) (Wei et al., 2009) were added to the proteins as reference competitors. Core-derived peptides were evaluated as potential inhibitors on core–NS3h interaction and/or core–core interaction at 40 μM concentration. Anti-Flag acceptor beads and glutathione donor beads were added to the proteins at a final concentration of 20 μg ml−1. The data of the uninhibited control compared with the inhibition by either core106 or SL201 were analysed using unpaired Student’s t-test.

**Inhibition of HCV 2a J6/JFH-1 in Huh-7.5 cells.** The addition of SL201 to infected cells was done as per previously published protocols (Kota et al., 2009) for an initial 72 h period (T1) and an additional 72 h (T2). The compound was dosed from 200 μM, 100 μM, and then 1:3 serial dilutions down to 0.015 μM. For time-of-addition experiments, naive Huh-7.5 cells were treated with serial dilutions of compound from 1 to 100 μM before (for 6 h), during and after (24 h) infection with HCV 2a JCI. Supernatants from cells were removed and titrated at 10−6 dilution for HCVcc-limiting-dilution assay to determine TCID50 values (Lindenbach et al., 2005). Infected cells were lysed by three freeze–thaw cycles and titrated in medium to 10−6 dilution for HCVcc-limiting-dilution assay to obtain TCID50 values. Cells in a duplicate plate were lysed for RNA analysis by real-time RT-PCR.

**PSGR-JFH1 replicon cell assay.** PSGR-JFH1 replicon cells (Tellinghuijzen et al., 2008) were maintained in G418 selection and taken out of selection for assay. Cells were plated into 24-well plates and incubated with 0.195–200 μM final concentration of SL201 for 3 days, along with a cells-only control. Cells were then lysed for RNA purification with Qiagen RNaseasy kit. Real-time RT-PCR was performed on RNA samples, using Roche’s LightCycler RNA amplification kit HybProbe, for analysis.

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