Kinetic analysis of the nucleic acid chaperone activity of the Hepatitis C virus core protein

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ABSTRACT

The multifunctional HCV core protein consists of a hydrophilic RNA interacting D1 domain and a hydrophobic D2 domain interacting with membranes and lipid droplets. The core D1 domain was found to possess nucleic acid annealing and strand transfer properties. To further understand these chaperone properties, we investigated how the D1 domain and two peptides encompassing the D1 basic clusters chaperoned the annealing of complementary canonical nucleic acids that correspond to the DNA sequences of the HIV-1 transactivation response element TAR and its complementary cTAR. The core peptides were found to augment cTAR-dTAR annealing kinetics by at least three orders of magnitude. The annealing rate was not affected by modifications of the dTAR loop but was strongly reduced by stabilization of the cTAR stem ends, suggesting that the core-directed annealing reaction is initiated through the terminal bases of cTAR and dTAR. Two kinetic pathways were identified with a fast pre-equilibrium intermediate that then slowly converts into the final extended duplex. The fast and slow pathways differed by the number of base pairs, which should be melted to nucleate the intermediates. The three peptides operate similarly, confirming that the core chaperone properties are mostly supported by its basic clusters.

INTRODUCTION

Hepatitis C virus (HCV) (1) is an important human pathogen transmitted mainly through blood contacts and affecting ~170 million people worldwide (2). Chronic infections are frequent and a major cause of liver cirrhosis and cancer (3). HCV is an enveloped virus of the Flaviviridae family, which has a positive-sense, single-stranded RNA genome with an open-reading frame encoding a polyprotein of 3010 amino acids or so (4). The 5′- and 3′-ends of the viral RNA correspond to non translated, highly structured and conserved regions (5′ UTR and 3′ UTR) of 340 and 230 nucleotides, respectively. The 5′ UTR consists of five stem–loops (5) and includes an internal ribosome entry site (IRES) that directs translation of the HCV genome in a cap-independent manner. The 3′ UTR is composed of three distinct parts: (i) a variable part with the VSL1 and VSL2 stem–loops, (ii) a poly (U/UC) tract and (iii) a sequence X of 98 nucleotides (6,7). Deletion of the U-rich and X sequence results in a loss of virus replication and infectivity (8).

The polyprotein precursor is co- and post-translationally processed by cellular and viral proteases at the endoplasmic reticulum (ER) membrane to yield the mature structural and nonstructural proteins. The structural proteins include the core and the envelope glycoproteins E1 and E2 (9). The N-terminal end of the polyprotein, which is a major HCV antigen (10,11), is cleaved by a cellular signal peptidase, generating the core of 191 residues which binds the ER membrane (12). This protein is then processed by a signal peptide peptidase (13,14), giving a mature protein of 179 residues or so, which is targeted to the lipid droplets (LDs) (15–17). Apart from LDs, the protein can be retained at the ER membrane and localized on mitochondria (15,18). The mature protein is a dimeric, alpha-helical protein exhibiting features that are consistent with those of a membrane protein (19). It consists of a basic N-terminal RNA binding domain D1 (aa 2–117)

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with three highly basic amino acid clusters (BD1–BD3) (20), and a hydrophobic C-terminal domain D2 (aa 118–179 or so) involved in targeting the protein to LDs (21). Core attachment to LDs is critical for assembly and release of infectious HCV particles (HCVcc) (22).

The core exerts multiple roles in infected cells and virus replication. The core notably interacts with a number of cellular proteins which impacts on cell proliferation and differentiation (10,23) and also on the lipid metabolism with a possible influence on hepatocellular carcinomas (24). As a major viral component tightly binding to genomic RNA sequences, the core is also thought to drive genomic RNA packaging and nucleocapsid formation (25–27). Moreover, the core has potent nucleic acid chaperoning activities (20,28), similar to retroviral nucleocapsid (NC) proteins (29–35). Through this activity, the core can resolve RNA misfolding and promote annealing of complementary sequences and strand exchanges (28).

This activity appears to be mediated by the three basic clusters (BD1–BD3) of the D1 domain (20,28).

To further characterize the core RNA chaperone properties, we investigated how the D1 domain and peptides encompassing the basic clusters direct the annealing of complementary DNA sequences represented by the canonical model of the HIV-1 transactivation response (TAR) (36) element in a DNA form (dTAR) and the complementary sequence cTAR. The extremely slow annealing of these two sequences is drastically accelerated by addition of a retroviral NC protein (30,32,34) or the HCV core (28). The nucleocapsid protein NCp7 of HIV-1 activates the transient opening of the cTAR terminal base-pairs (29,37) causing a partial melting of the stem (33,38). These partly melted TAR DNAs anneal then through their termini to form an intermediate complex which is further converted into the final extended duplex (ED) (30,33,35). To determine whether the HCV core promotes cTAR/dTAR annealing through a similar molecular mechanism, we monitored the real-time annealing kinetics of fluorescently labelled cTAR with the extremely slow annealing (TAR) element in a DNA form (dTAR) and the complementary sequence cTAR. The fluorescence intensities were corrected for buffer emission and Lamp fluctuations.

Kinetic measurements were performed in pseudo first-order conditions by using concentrations of unlabelled TAR and dTAR at least 10-fold higher than the concentration of the labeled complementary sequence. Excitation and emission wavelengths were 520 and 550 nm, respectively, to monitor the Rh6G fluorescence. The corresponding wavelengths were 480 and 520 nm, respectively to monitor the Fl fluorescence. All reported concentrations correspond to those after mixing. To avoid high local concentrations during mixing, both reactant mixtures were prepared of the same volume. Peptides were added to each reactant separately, and then the reaction was initiated by mixing the peptide-coated ODNs together. The kinetics was fast enough to monitor the fluorescence intensities continuously without photo-bleaching. The apparent rate constants kobs and the amplitudes were determined from the kinetic traces by including a dead-time correction t0 to take into account the delay between the mixing of reactants and the start of the measurements. All fitting procedures were carried out with Origin™ 7.5 software based on nonlinear, least-square methods and the Levenberg-Marquardt algorithm.

The temperature dependence of the annealing kinetics was carried out with 10 nM doubly labeled cTAR derivatives and 300-nM nonlabeled dTAR derivatives at different temperatures (10°C, 20°C, 25°C, 30°C, 35°C and 40°C) in the presence of either peptide E, peptide F and Domain D1, added at a peptide to oligonucleotide ratio of 1:4:1.

Fluorescence correlation spectroscopy setup and data analysis

Fluorescence correlation spectroscopy (FCS) measurements were performed on a two-photon platform.
including an Olympus IX70 inverted microscope, as described previously (37,39). Two-photon excitation at 850 nm is provided by a mode-locked Tsunami Ti:sapphire laser pumped by a Millenia V solid-state laser (Spectra Physics, USA). The experiments were performed in an eight-well lab-Tek II coverglass system, using a 400-μl volume per well. The focal spot was set about 20 μm above the coverslip. Peptide E was added to the labeled cTAR sequences at different nucleotide to peptide ratios. To avoid high local concentrations during mixing, both reactants were of the same volume. Assuming that peptide E diffuses freely in a Gaussian excitation volume, the normalized autocorrelation function, \( G(t) \), calculated from the fluorescence fluctuations was fitted according to (40):

\[
G(t) = \frac{1}{N} \left( 1 + \frac{\tau_d}{\tau_0} \right)^{-1} \left( 1 + \frac{\tau}{S^2 \tau_d} \right)^{-1/2}
\]

where \( \tau_d \) is the diffusion time, \( N \) is the mean number of molecules within the excitation volume and \( S \) is the ratio between the axial and lateral radii of the excitation volume. The point spread function of the set-up was determined from a z-scan on one fluorescent bead (20 nm in diameter). The measured lateral and axial resolutions were respectively 0.3 and 1 μm. Typical data recording times were 10 min. Twenty autocorrelation curves were recorded for each sample. When spikes of high fluorescence intensity, most likely associated to aggregates, were observed in the fluorescence fluctuation profiles, the corresponding autocorrelation curves were discarded. In these conditions, the average autocorrelation curve calculated from the sum of the remaining autocorrelation curves could be adequately fitted by a single population model with a diffusion time close to that of cTAR alone.

**RESULTS**

**Investigating the interaction of cTAR DNA with the core peptides by FCS**

To characterize in depth the nucleic acid chaperone properties of the core protein, we first had to find experimental conditions where the core peptides did not cause DNA aggregation in a manner similar to other nucleic acid chaperones (32,34,41,42). Indeed, molecular aggregation can cause strong bias when using fluorescence-based techniques (30,32). Since destabilization of nucleic acid secondary structures is a feature of the chaperone protein activity (29,32,37,41,44), we characterized the nucleic acid destabilizing activity of the core peptides, using cTAR labeled at its 3' and 5' ends by Rh6G and Dabcyl, respectively. In the absence of peptide, the proximity of cTAR ends induces a strong fluorescence quenching of Rh6G by the Dabcyl group (37), while the melting of the lower half of the cTAR stem increases the distance between the two dyes and thus, restores Rh6G fluorescence. Thus, the destabilizing activity of the core peptides can be evaluated from the ratio of the fluorescence intensity with or without the peptide. Addition of core peptides E and F at a peptide/cTAR molar ratio of 1.4:1 led to a 1.5-fold increased fluorescence intensity for Rh6G-5'-cTAR-3'-Dabcyl, while no change was observed with the D1 domain (Figure 2). Since full melting of cTAR would lead to a 20- to 25-fold increase of the Rh6G fluorescence, <10% of the Rh6G fluorescence was restored upon binding of the core peptides. No further increase was observed with either peptide at higher ratios (data not shown), possibly due to the fluorescence quenching related to formation of aggregates. Thus, in contrast to retroviral NC proteins (30–32,37), the core peptides can only slightly destabilize the secondary structure of cTAR, in the present experimental conditions.

**Kinetics of cTAR/dTAR annealing in the presence of peptide E**

To characterize the mechanism by which the core protein can activate the annealing of the complementary cTAR and dTAR sequences, we first used the peptide E, which was easy to synthesize in large quantities and was previously shown to mimic the core chaperone properties (20,28). The real-time annealing kinetics of cTAR to dTAR was monitored by mixing Rh6G-5'-cTAR-3'-Dabcyl with an excess of non-labeled dTAR, in the presence of peptide E added at a peptide/ODN molar ratio of 1.4:1. Formation of the 55-bp ED strongly increases the

Experiments were performed at two different ODN concentrations (100 and 300 nM). In the absence of peptide, the number of fluorescent TAR molecules in the excitation volume was fully consistent with the theoretical number of molecules expected from their concentration. By adding increasing concentrations of either core peptide, we found no change in the number of fluorescent species up to a peptide/ODN molar ratio of 1.4:1, indicating that no aggregation occurred under these conditions (Figure 1). In contrast, aggregation took place at higher ratios (2.8:1 and 5.6:1) as evidenced by the sharp drop in the number of fluorescent species. Changes in the diffusion constant were also observed at these higher ratios but were less prominent (data not shown), due to the dependence of the diffusion constant on the cubic root of the molecular mass of the diffusing species. As a consequence, we selected a peptide/ODN molar ratio of 1.4:1 to characterize the chaperone properties of the core peptides.

**Estabilization of cTAR secondary structure by the core peptides**

Since destabilization of nucleic acid secondary structures is a feature of the chaperone protein activity (29,32,37,41,44), we characterized the nucleic acid destabilizing activity of the core peptides, using cTAR labeled at its 5' and 3' ends by Rh6G and Dabcyl, respectively. In the absence of peptide, the proximity of cTAR ends induces a strong fluorescence quenching of Rh6G by the Dabcyl group (37), while the melting of the lower half of the cTAR stem increases the distance between the two dyes and thus, restores Rh6G fluorescence. Thus, the destabilizing activity of the core peptides can be evaluated from the ratio of the fluorescence intensity with or without the peptide. Addition of core peptides E and F at a peptide/cTAR molar ratio of 1.4:1 led to a 1.5-fold increased fluorescence intensity for Rh6G-5'-cTAR-3'-Dabcyl, while no change was observed with the D1 domain (Figure 2). Since full melting of cTAR would lead to a 20- to 25-fold increase of the Rh6G fluorescence, <10% of the Rh6G fluorescence was restored upon binding of the core peptides. No further increase was observed with either peptide at higher ratios (data not shown), possibly due to the fluorescence quenching related to formation of aggregates. Thus, in contrast to retroviral NC proteins (30–32,37), the core peptides can only slightly destabilize the secondary structure of cTAR, in the present experimental conditions.
interchromophore distance, leading to a full recovery of Rh6G emission (29). The same fluorescence plateau was obtained as in the absence of peptide, indicating that ED formation went to completion (Figure 3A). Peptide E strongly accelerated the annealing reaction, since it was complete in <30 min, while it needed more than 24 h in the absence of peptide (30). As shown by the nearly random distribution of residuals around the zero value (Figure 3B), the annealing kinetic traces could be adequately fitted using a biexponential function:

\[
I(t) = I_f - (I_f - I_0)(a e^{-k_{obs1}(t-t_0)} - (1-a) e^{-k_{obs2}(t-t_0)})
\]

(2)

where, \(t_0\) being the dead time, \(k_{obs1,2}\) are the observed kinetic rate constants, \(a\) is the amplitude of the fast component, and \(I_0\) and \(I_f\) are the fluorescence intensities of the stem–loop and the ED, respectively.

The dTAR concentration dependence indicates a saturation behavior for both \(k_{obs1}\) and \(k_{obs2}\) values (Figure 4), consistent with a two-step reaction, where a rate-limiting interconversion step is coupled to a much faster, preceding binding step, considered as a pre-equilibrium:

\[
cTAR + dTAR \rightleftharpoons IC \rightleftharpoons ED
\]

(3)

where IC corresponds to the intermediate complex. The dTAR concentration dependence of both \(k_{obs}\) values was fitted using (45):

\[
k_{obs} = \frac{k_f K_m[dTAR]}{1 + K_m[dTAR]} + k_b
\]

(4)

Values of 4 (±2) \(10^6\) M\(^{-1}\) and 1.4 (±0.7) \(10^6\) M\(^{-1}\) were obtained for \(K_{M1}\) and \(K_{M2}\), the equilibrium binding constants of the intermediate complexes associated with the fast and slow kinetic component, respectively. Moreover, values of 0.045 (±0.008) s\(^{-1}\) and 0.016 (±0.002) s\(^{-1}\) were obtained for the sum of the forward \((k_{f1}, k_{f2})\) and backward \((k_{b1}, k_{b2})\) interconversion rate constants associated to the two kinetic components. The values of \(k_{b1}\) and \(k_{b2}\) given by the intercept, were very low (<0.001 s\(^{-1}\)) and could not be determined from the experimental data, indicating that peptide E is unable to dissociate the ED, and that the 0.045 s\(^{-1}\) and 0.016 s\(^{-1}\) values mainly correspond to \(k_{f1}\) and \(k_{f2}\), respectively.

Noticeably, substitution of the Rh6G and Dabcyl dyes at the 5’- and 3’-ends of cTAR by TMR and Fl, respectively, had a marginal influence on the kinetic parameters (Table 1), indicating that the peptide E-promoted cTAR/dTAR annealing kinetics does not depend on the nature of the dyes.

In contrast to the \(k_{obs}\) values, the amplitudes of the two components (Table 1) were independent of dTAR concentration (data not shown), suggesting that peptide E-promoted annealing reaction involves two parallel pathways. To confirm this, we repeated the annealing reaction at a peptide/ODN molar ratio of 1:1. At this lower ratio, the amplitudes of the two components were also independent of dTAR concentration, but with a decreased value for the fast component as compared to the 1.4:1 ratio, in line with the hypothesis of two parallel pathways. Moreover, while the \(K_{M1}\) and \(K_{M2}\) values were three to four times lower than at the higher ratio, the interconversion rate constants were similar (Table 1), suggesting that peptide E mainly affects the pre-equilibrium step.

On the basis of our kinetic data, a reaction mechanism with two parallel kinetic pathways involving two different
cTAR/peptide E complexes (cTAR1 and cTAR2) can be proposed:

\[
\text{Scheme 1}
\]

\[
cTAR_1 + dTAR \xrightleftharpoons[{K_{M1}}]{{k_{f1}}} IC_1 \xrightarrow[k_{f1}]{K_{M2}} IC_2 \xrightarrow[K_{M2}]{{k_{f1}}} ED
\]

where IC1 and IC2 are the intermediate complexes of the fast and slow pathways, respectively, and \( k_{f1} \) and \( k_{f2} \) are the corresponding interconversion rate constants. Further insights into nature of the two pathways were obtained from the temperature dependence of the \( k_{obs} \) values, using the Arrhenius equation:

\[
k_i = A_i \exp\left(\frac{E_a}{RT}\right) \quad (5)
\]

where the rate constant \( k_i \) is given by \( k_{obsi}/[dTAR] \), \( A_i \) is the pre-exponential Arrhenius factor, \( E_{a,i} \) is the activation energy, \( R \) is the universal gas constant and \( T \) is the temperature (in Kelvin).

Both reaction rates as well as the amplitude of the fast pathway increased with temperature (Figure 5). Positive enthalpy values for the transition state of 9.5(±0.6) kcal/mol and 24(±1) kcal/mol for the fast and slow pathways, respectively, were obtained. These values indicate that cTAR/dTAR annealing promoted by the core peptide involves pre-melting of ~2 and 5bp, for the fast and slow pathways, respectively (46,47). Moreover, since the fast pathway represents 100% at 40°C (Figure 5), it is necessarily associated with ED formation and thus differs from the unproductive fast pathway observed for the cTAR/dTAR annealing reaction promoted by the HIV-1 NC (11-55) mutant (30).

Effects of oligonucleotide sequence and stability on the annealing kinetics promoted by the core peptide E

To further characterize how the core peptide influenced the annealing kinetics, we investigated the impact of the oligonucleotide sequence and stability on the reaction. First, dTAR was substituted by the dTAR T-L mutant where the 6nt of the loop were changed to T residues (Figure 6), thus preventing base-pairing with the cTAR loop. These nucleotide substitutions did not significantly change the kinetic parameters of the two pathways (Table 1) and ED formation (Figure 7), indicating that loop–loop interactions do not play a significant role in peptide E-promoted cTAR/dTAR annealing reaction.

To investigate the role of the cTAR stem in the annealing reaction, we used the cTAR1,2 derivative where bases complementary to the bulged bases at positions 49 and 52 have been introduced in order to stabilize the lower half of the stem (Figure 6). This mutant was previously shown to be about four times more stable than cTAR (44). Peptide E did not cause a fluorescence change of the doubly labeled cTAR1,2 (data not shown), indicating that peptide E was unable to destabilize the mutated stem. Moreover, the annealing of this mutant to dTAR in the presence of peptide E was extremely slow (Figure 7) with one kinetic pathway and a 10-fold decrease in the values of the pre-equilibrium constant, \( K_M \), and the interconversion rate constant, \( k_f \) (Table 1). Thus, in a manner similar to NCP7 (30,35,48), peptide E nucleates cTAR/dTAR annealing probably through the cTAR and dTAR ends. This is confirmed by the increased value of the transition state enthalpy (30(±2) kcal/mol), indicating that the rate-limiting step of the peptide-promoted cTAR1,2/dTAR annealing involves melting of the stabilized cTAR1,2 stem (46). Moreover, the decreased...
stability of the cTAR1.2/dTAR intermediate as compared with the cTAR/dTAR one, most probably results from the base pair mismatches in the intermediate due to the addition of bases in cTAR1.2 stem, further supporting the notion that the annealing reaction is nucleated through the stem ends.

Substitution of dTAR by TAR RNA also caused a significant decrease of the annealing reaction promoted by peptide E (Figure 7), due to a decrease in the amplitude of the fast component together with a 10-fold decrease of the interconversion rate, $k_{f2}$ of the slow pathway (Table 1). This reduced annealing rate is likely caused by the higher stability of the TAR stem (29), suggesting that as with HIV-1 NCp7 (30,33,35), the cTAR/TAR annealing reaction promoted by peptide E is probably starting from the stem. This conclusion is further supported by the similar values of the transition state enthalpies (data not shown) and the equilibrium binding constants of the reaction intermediates (Table 1) in the cTAR/dTAR, cTAR/dTAR T-L and cTAR/TAR annealing reactions, indicating that the ICs in all these systems are stabilized by a similar number of base pairs.

To further confirm the critical role of the cTAR stem end, we investigated the annealing kinetics with the (14-39)cTAR derivative, also called mini-cTAR (49), in which the lower half of cTAR stem has been deleted (Figure 6). This cTAR mutant was previously shown to be about twice more stable than the entire cTAR (50). The annealing of (14-39)cTAR/dTAR in the presence of core peptide E was much slower than that of cTAR/dTAR (Figure 7), and exhibited only one kinetic pathway, confirming that the peptide E-promoted cTAR/dTAR annealing is nucleated through the cTAR ends.

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<th>Table 1. Kinetic parameters of cTAR/dTAR and cTAR/TAR annealing in the presence of core peptides</th>
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The association equilibrium constants ($K_{M1}$ for fast and $K_{M2}$ for slow components) and interconversion rate constants ($k_{f1}$ for fast and $k_{f2}$ for slow component) are calculated from Equation (4), as described in Figure 4; $k_{ass1}$ and $k_{ass2}$ are given by:

\[ k_{ass1} = \frac{K_{M1}}{C_2} \]

\[ k_{ass2} = \frac{K_{M2}}{C_2} \]

where $C_2$ corresponds to the amplitude of the fast component.

Substitution of dTAR by TAR RNA also caused a significant decrease of the annealing reaction promoted by peptide E (Figure 7), due to a decrease in the amplitude of the fast component together with a 10-fold decrease of the interconversion rate, $k_{f2}$ of the slow pathway (Table 1). This reduced annealing rate is likely caused by the higher stability of the TAR stem (29), suggesting that as with HIV-1 NCp7 (30,33,35), the cTAR/TAR annealing reaction promoted by peptide E is probably starting from the stem. This conclusion is further supported by the similar values of the transition state enthalpies (data not shown) and the equilibrium binding constants of the reaction intermediates (Table 1) in the cTAR/dTAR, cTAR/dTAR T-L and cTAR/TAR annealing reactions, indicating that the ICs in all these systems are stabilized by a similar number of base pairs.

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Substitution of (14-39)cTAR by (14-39)cTAR-TL, in which the 6 nt of the (14-39)cTAR loop were substituted with T residues (Figure 6), further decreased the annealing reaction rate (Figure 7). This suggests that as for NCp7 (51), the (14-39)cTAR/dTAR annealing reaction promoted by peptide E may partially be nucleated through kissing loop intermediates. This conclusion was further supported by the value of the transition state enthalpy 15(±5) kcal/mol, that perfectly matches the value found with the NCp7-promoted annealing of mini-cTAR (51).

Taken together, our data indicate that both kinetic pathways of the peptide E-promoted cTAR/dTAR annealing reaction are nucleated through the stems.

Promotion of cTAR/dTAR annealing by peptide F and D1 domain

Next, we investigated cTAR/dTAR annealing in the presence of peptide F and the D1 domain to determine whether they promote the annealing reaction through the same mechanism as peptide E (Figure 6B). The annealing kinetics in their presence was also biphasic with a hyperbolic dependence of $k_{\text{obs1,2}}$ values and a constant amplitude value of about 0.8, strongly suggesting that the three core peptides promote cTAR/dTAR annealing by the same mechanism. While the three peptides provide
similar values for the pre-equilibrium binding constants, they differ in the interconversion rate constants. Indeed, the interconversion rates of the intermediates to ED were about 3- to 7-fold faster with peptide F than that with peptide E and the D1 domain (Table 1).

Interestingly, the temperature dependence of the $k_{\text{obs}}$ values with peptide F and domain D1 yielded enthalpy values that were similar to those with peptide E (data not shown), confirming that the three peptides follow the same mechanism by nucleating ICs with a similar number of base pairs.

Comparison of the three peptides suggests that the third basic domain (BD3) favors the interconversion step while the additional sequences in D1, notably the tryptophan-rich domain, WD, have a counter effect.

**Comparison of HCV core peptide E and HIV-1 NCp7 in promoting cTAR/dTAR annealing**

Since both peptide E and NCp7 promote cTAR/dTAR annealing, this prompted us to compare their efficiencies in this activity. Because wild-type NCp7 strongly aggregates oligonucleotides (30,42,52,53), we used the truncated NC (11-55) peptide (Figure 6B), which mimics the activities of NCp7 without aggregation (30,38).

Comparison of peptide E with NC(11-55) at several molar ratios revealed that 1 and 1.4 molecules of peptide E provided the same annealing activity as that of 4 and 6 NC (11-55) molecules (Figure 8A), respectively. This suggests that one peptide E molecule exhibits nearly the same chaperone activity as 4 molecules of NC(11-55). Furthermore, the kinetic traces in the presence of both NC(11-55) added at a ratio of 4 peptides per oligonucleotide and peptide E added at ratios of 1 and 1.4 peptides per oligonucleotide were similar to the kinetic traces obtained with ratios of 8 and 10 NC(11-55) per oligonucleotide, respectively (Figure 8B). This confirmed that one peptide E exhibits the same chaperone activity as four NC(11-55) and favored the notion that the two peptides can chaperone in concert the annealing of the two complementary ODNs.

**DISCUSSION**

The aim of the present study was to characterize the mechanism by which the basic domain of the HCV core chaperones the annealing of two canonical complementary stem–loop sequences, namely the HIV-1 cTAR and dTAR DNA, which have been extensively used to study the chaperone properties of retroviral NC proteins (30,32–35,54–56). This study was performed with the D1 core domain and two peptides that encompass the basic clusters critical for the chaperone properties of the core (20,28).

In contrast to retroviral NCs, such as HIV-1 NCp7 and MuLV NCp10 (29,32), the core peptides exhibit only a slight destabilizing activity, suggesting that this component plays a limited role in the core-promoted annealing reaction. Nevertheless, these peptides efficiently activate the cTAR/dTAR annealing reaction as shown by the up to three orders of magnitude difference in the values of the overall kinetic constants ($k_{\text{ass}} = K_M \times k_f$) in the presence of the core peptides (Table 1) as compared to the bimolecular rate constant (85 M$^{-1}$s$^{-1}$) in their absence (30). The promotion of cTAR/dTAR annealing by the core peptides was found to start from the cTAR end and to proceed through two parallel kinetic pathways that include a fast pre-equilibrium intermediate and a rate-limiting conversion into the final ED. The fast and slow pathways likely differ by the number of base pairs ($\approx 2$ and 5, respectively) that should be melted in the original cTAR secondary structure to nucleate the ICs. Since thermally driven fraying of cTAR termini occurs spontaneously at room temperature (29,37,44), the fast pathway is probably associated with a cTAR species where the 3 bp of the terminal stem are melted, while the slow pathway may be associated with the fully structured oligonucleotide (Figure 9). Therefore, formation of IC1 in the fast pathway is thought to involve the melting of the 2 bp from the penultimate double-stranded segment while the 5 bp of both terminal and penultimate double

![Figure 8](https://academic.oup.com/nar/article-abstract/38/11/3632/3100665)
that a single pathway can probably take place at a saturating concentration of core peptide, as in the case of retroviral proteins (35, 49, 51). In the proposed model reaction (Figure 9), the amplitude of the fast component is a complex function of the fast equilibrium between cTAR1 and cTAR2 species, their stability, their initial melting by the peptides and the fluorescence intensity of the intermediates. Accordingly, the amplitude of the fast component decreased, when either of the two partners, cTAR or dTAR, was substituted by a more stable one (∼35% for cTAR/TAR and <5% cTAR1,2/dTAR) as compared to 70% for cTAR/dTAR. On the other hand, a decrease in stability of partners results in an increase of amplitude (100% at 40°C for cTAR/dTAR). Finally, the core chaperone mechanism was found to be similar for peptide E, peptide F and D1 domain, confirming that the basic clusters are the main determinants in this mechanism (20, 28).

Comparison with the truncated HIV-1 NC(11-55) peptide revealed that one core peptide molecule exhibits the same chaperone activity as four NC(11-55) molecules in cTAR/dTAR annealing (Figure 8). A similar conclusion applies for cTAR/TAR RNA annealing with the full-length NCp7, since the $K_M$ values of the ICs with peptide E (about $10^6$ M$^{-1}$) are similar to the corresponding $K_M$ value obtained with NCp7 added at a ratio of six proteins per oligonucleotide (35). This suggests that a 1.4 equivalent of peptide E could be as active as 6 NCp7 equivalents in the present experimental conditions. This is likely a consequence of the stronger 'nucleic acid aggregating' properties of the core peptides, in line with the efficient oligonucleotide aggregation observed by FCS (Figure 1). This propensity of the core peptides to neutralize the negatively charged nucleic acids and to promote their aggregation is probably related to the highly flexible nature of the core peptides (19, 57) as compared to the folded NCp7 structure with two zinc fingers (58, 59). In addition, NCp7 and the core peptides likely differ on the nature of the core peptides (19, 57) as compared to the corresponding $K_M$ value obtained with NCp7 added at a ratio of six proteins per oligonucleotide (35). For the core peptides, the corresponding values for the fast and slow pathway are respectively, two and one order of magnitude higher in the absence of any peptide is about $1.5 \times 10^{-4}$ s$^{-1}$, while it is about 3-fold higher in the presence of NCp7, at any protein/oligonucleotide ratio (35). For the core peptides, the corresponding values for the fast and slow pathway are respectively, two and one order of magnitude higher than in the absence of protein. Thus, in contrast to NCp7, the core peptides strongly favor the interconversion reaction, which is thought to be rate-limited by a conformational change involving cooperative melting of a large fragment of one or both hairpin stems. Moreover, while NCp7 also promotes cTAR/TAR annealing through kissing loop intermediates when added at sub-saturating concentrations to ODNs (35), the core peptides mainly chaperone the annealing through the stems.

Taken together, our data suggest that though at sub-saturating conditions, the core peptides only marginally destabilize the secondary structure of oligonucleotides, they are more efficient than the truncated HIV-1 NC(11-55) peptide in nucleating IC formation through their nucleic acid aggregation properties and promoting the subsequent IC conversion into ED. Moreover, in
contrast to NC(11-55) and native NCp7 (35) which requires high peptide/ODN ratios for optimal activity, the core peptides already show strong nucleic acid annealing activity at low peptide/ODN ratios, suggesting that the core protein can exert its strong chaperone activity at low fractional saturation of nucleic acids. Importantly, since the core protein and NCp7 are structurally different proteins from two different virus families, the conserved nucleic acid chaperone properties suggest that they are required in a large panel of viruses, in line with the recently demonstrated conservation of RNA chaperoning in Flaviviridae core proteins (60). The potent chaperone properties of the core peptides in the TAR oligonucleotides model used in this study further suggest that the core protein is a nucleic chaperone with broad sequence specificity. These properties may be critical for genomic RNA dimerization in HCV replication and RNA packaging, as well as for facilitating recombination between various HCV genotypes and subtypes to increase viral variability (61–63).

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