The Regulatory and Kinase Domains but Not the Interdomain Linker Determine Human Double-stranded RNA-activated Kinase (PKR) Sensitivity to Inhibition by Viral Non-coding RNAs

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Double-stranded RNA (dsRNA)-activated protein kinase (PKR) is an important component of the innate immune system that presents a crucial first line of defense against viral infection. PKR has a modular architecture comprising a regulatory N-terminal dsRNA binding domain and a C-terminal kinase domain interposed by an unstructured ~80-residue interdomain linker (IDL). Guided by sequence alignment, we created IDL deletions in human PKR (hPKR) and regulatory/kinase domain swap human-rat chimeric PKRs to assess the contributions of each domain and the IDL to regulation of the kinase activity by RNA. Using circular dichroism spectroscopy, limited proteolysis, kinase assays, and isothermal titration calorimetry, we show that each PKR protein is properly folded with similar domain boundaries and that each exhibits comparable polyinosinic-cytidylic (poly(rI:rC)) dsRNA activation profiles and binding affinities for adenoviral virus-associated RNA I (VA RNA1) and HIV-1 trans-activation response (TAR) RNA. From these results we conclude that the IDL of PKR is not required for RNA binding or mediating changes in protein conformation or domain interactions necessary for PKR regulation by RNA. In contrast, inhibition of rat PKR by VA RNA1 and TAR RNA was found to be weaker than for hPKR by 7- and >300-fold, respectively, and each human-rat chimeric domain-swapped protein showed intermediate levels of inhibition. These findings indicate that PKR sequence or structural elements in the kinase domain, present in hPKR but absent in rat PKR, are exploited by viral non-coding RNAs to accomplish efficient inhibition of PKR.

Phosphorylation of the eukaryotic translation initiation factor eIF2 is a critical regulatory mechanism for control of eukaryotic protein synthesis. Four mammalian kinases act on eIF2α in response to different stress stimuli: double-stranded RNA (dsRNA)3-activated protein kinase (PKR), heme-regulated inhibitor kinase, PKR-like endoplasmic reticulum kinase, and general control nonderepressible 2 (1). Among these, PKR plays a crucial role in the innate immune system’s primary response to cellular viral infection. PKR has a modular architecture composed of an N-terminal regulatory dsRNA binding domain (dsRBD; residues 1–169 in human PKR) containing two tandem N-terminal dsRNA binding motifs (dsRBM 1 and 2) and a C-terminal kinase domain (KD; residues 252–551). These structured domains are separated by an 82-residue interdomain linker (IDL) region (Fig. 1A). The dsRBD additionally has an ~22-amino acid unstructured linker between the two dsRBMs that is proposed to wrap around the dsRNA to allow optimal interaction of each dsRBM with the A-form RNA helix (2). The KD fold possesses two lobes connected by a small hinge region, with distinct functional roles: the smaller N-terminal lobe mediates PKR dimerization, whereas the larger C-terminal lobe interacts with the eIF2α substrate (3). The IDL separating the regulatory domain from the catalytic domain is unstructured in solution but has been speculated to play a role in mediating communication between the two structured domains during activation by dsRNA (4, 5).

How the kinase activity of PKR is controlled in the absence of activating RNA has been the subject of debate. An autoinhibition model for PKR activation was originally proposed in which direct interaction of the N-terminal dsRBD and KD inhibits the latent kinase activity before the dsRNA-mediated release of this inhibition (6, 7). However, several lines of evidence argued for

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3 The abbreviations used are: dsRNA, double-stranded RNA; Ad2, adenovirus type 2; CTD, C-terminal domain; dsRBD, double-stranded RNA binding domain; dsRBM, double-stranded RNA binding motif; IDL, interdomain linker; KD, kinase domain; NTD, N-terminal domain; PKR, double-stranded RNA-activated protein kinase; rPKR, rat PKR; hPKR, human PKR; TAR, trans-activation response (element of HIV-1); VA RNA, virus-associated RNA.
PKR Inhibition by Viral RNA Requires Both Structured Domains

The best characterized role of PKR is as a sensor of cytosolic dsRNA. dsRNA represents a potent pathogen-associated molecular pattern, present in some viral genomes or produced as a consequence of viral gene expression and replication (17). Viral dsRNA-promoted PKR homodimerization leads to subsequent autophosphorylation and kinase activation (8, 18). Activated PKR phosphorylates Ser-51 of the eukaryotic initiation factor 2 (eIF2α) (3). This kinase deletion (ΔT170-Δ251). The alignment also identified a region in the human PKR KD that is absent in the other homologs and previously deleted in the human PKR KD construct used to determine its crystal structure in complex with eIF2α (3). This kinase deletion (ΔT170-Δ251) was additionally included in some of the constructs generated in this study (those denoted with asterisks). Other than hPKR-IDLΔ1 and hPKR-IDLΔ1*, the hPKR IDL deletion variants required the use of an N-terminal SUMO tag (obtained by PCR amplification of the Smt3 domain switching in order to generate S-r/hPKR (rat dsRBD and human KD) and S-h/rPKR (human dsRBD and rat KD).

Protein Expression and Purification—E. coli Rosetta2(DE3) cells were transformed with each PKR-encoding plasmid and plated on LB-agar containing ampicillin (100 μg/ml) and chloramphenicol (34 μg/ml). For PKR constructs without an N-terminal His6-SUMO tag, soluble protein expression was accomplished using overnight autoinduction (29) at 20 °C after initial growth at 37 °C for 6 h. For N-terminal His6-SUMO-tagged proteins, cells were grown in Terrific Broth (TB) at 37 °C and induced at mid-log phase using isopropyl 1-thio-β-D-galactopyranoside (0.1 mM), and growth continued overnight at 20 °C for protein expression.

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For N-terminal His$_6$-SUMO-tagged PKR proteins, Ni$^{2+}$ affinity was used as the first step in place of heparin affinity. The column (HisTrap FF Crude 1 ml) was pre-equilibrated with 20 mM Tris HCl (pH 7.5–8.5) buffer containing 500 mM NaCl, 20 mM imidazole, and 10 mM β-mercaptoethanol. Bound proteins were eluted using an imidazole gradient (20–400 mM, over 10 column volumes) in the same buffer. PKR-containing fractions were pooled, diluted with salt-free buffer to give a final concentration of ~150 mM NaCl, and further purified using poly(rI:rC) dsRNA affinity and gel filtration chromatographies as described for the tagless proteins.

Where used, cleavage of the N-terminal His$_6$-SUMO tag was accomplished by buffer exchange into SUMO cleavage buffer (50 mM Tris HCl (pH 7.5), 2 mM DTT, 150 mM NaCl, and 10% glycerol) and treatment of the fusion protein with SUMO protease (Life Sensors) at 4 °C overnight. Cleaved PKR proteins were purified from the free His$_6$-SUMO tag and uncleaved fusion using a round gel filtration chromatography.

**RNA in Vitro Transcription and Purification**—A truncated form of human adenovirus type 2 (Ad2) VA RNA$_1$ (94 nucleotides), which retains full wild-type activity but lacks the entire terminal stem ("TSΔ21") and a short sequence in the apical stem ("A2d12") was in vitro transcribed using T7 RNA polymerase under previously established optimal conditions (31, 32). HIV-1 TAR RNA (59 nucleotides) was also prepared by T7 RNA polymerase run-off transcription using established conditions (33, 34). Transcripts were resolved by preparative denaturing (50% urea) polyacrylamide gel electrophoresis (PAGE; 10% acrylamide), excised from the gel, and recovered by electroelution using a Biorad device (Schleicher and Schuell). RNAs were annealed in 1× Tris-EDTA buffer and dialyzed overnight against the appropriate assay buffer before use. To verify the absence of dimerized RNA that would confound interpretation of PKR inhibition assays (35), purified HIV-1 TAR RNA was examined by native PAGE (10% acrylamide) and stained with SYBR Gold.

**Kinase Activity Assays Using Slot Blot or SDS-PAGE**—Slot blot assays of PKR autophosphorylation contained PKR (0.1 μg) in 50 mM Tris buffer (pH 7.8) with poly(rI:rC) dsRNA (0–100 μg/ml), 20 μM ATP, 1 μCi of $[^{32}P]ATP$ (10 mCi/ml, 6000 Ci/mmol), 50 mM KCl, 2 mM MgCl$_2$, 2.5 mM DTT, and 10% glycerol in a total reaction volume of 10 μl. SDS-PAGE assays of PKR autophosphorylation and elf2α phosphorylation were performed identically but included elf2α (0.25 μg) in the absence or presence of a single concentration of poly(rI:rC) dsRNA (0.3 μg/ml). Reactions were incubated at 25 °C for 10 min and then stopped by the addition of gel loading dye (for SDS-PAGE analysis) or 400 μl of ice-cold phosphate-buffered saline containing 200 μM ATP (for slot blot analysis). In the latter case quenched samples were applied promptly to a Bio-Dot SF (Bio-Rad) microfiltration system, and proteins were bound to a nitrocellulose membrane under vacuum. The membrane was washed to remove unreacted $[^{32}P]ATP$ and then air-dried. For both membranes and dried SDS-PAGE gels, the extent of PKR and elf2α phosphorylation was determined by exposure to a phosphor storage screen and analysis using a Typhoon FLA 7000 PhosphorImager and ImageQuant software (GE Healthcare).

PKR inhibition assays were performed in a similar manner but included a 10-min preincubation step at 25 °C with the in vitro transcribed RNA (0–100 μM) and PKR (0.1 μg) in 50 mM Tris buffer (pH 7.8) containing 50 mM KCl, 2.5 mM DTT, and 10% glycerol. Reactions (10 μl final volume) were initiated by the addition of 0.04 μg/ml poly(rI:rC) dsRNA, 20 μM ATP, 1 μCi of $[^{32}P]ATP$ (10 mCi/ml, 6000 Ci/mmol), and 2 mM MgCl$_2$. After a 10-min incubation at 25 °C, the reactions were quenched, and the products were quantified as described above for the activation assays. IC$_{50}$ values were obtained by non-linear regression analysis using the log(inhibitor) versus response equation in GraphPad Prism software.

**Circular Dichroism (CD) Spectroscopy**—CD spectra (250–190 nm) of protein (5–10 μM) in 10 mM sodium phosphate (pH 7.5) and 10% glycerol were recorded at 25 °C on a Jasco J810 spectrophotometer using a quartz cuvette with a 0.1-cm path length and instrument settings of 1-nm bandwidth, 0.2-nm step size, and 16-s averaging time. Spectra were recorded in triplicate and averaged, and background was subtracted before unit conversion to mean residue ellipticity (36).

**Limited Proteolysis**—Purified proteins were diluted to a concentration of ~0.2 mg/ml in gel filtration buffer and digested by different ratios of trypsin:PKR (1:10,000, 1:5,000, 1:1,000) at 20 °C for 45 min. The reaction products were resolved by SDS-PAGE (10% acrylamide) and visualized by staining with Coomassie Brilliant Blue.

**Isothermal Titration Calorimetry**—Binding affinities of VA RNA$_1$ or HIV-1 TAR for select PKR variants were measured using an Auto-iTC200 microcalorimeter (Malvern/MicroCal). Samples were prepared by dialyzing overnight against 50 mM Tris buffer (pH 7.5) containing 100 mM NaCl, and the experiments were performed by titrating RNA (80 μM) into the sample cell containing PKR (10–15 μM) at 25 °C in 16 × 2.5-μl injections with 150-s spacing. Titration curves were fit by a non-linear least squares method in MicroCal Origin software using the single site binding model.

**Results**

**Design and Expression of IDL Deletion PKR Variants**—hPKR is a 551-amino acid protein with an N-terminal dsRB1 (residues 1–169) and C-terminal catalytic domain (KD; residues 252–551) (Fig. 1A) separated by a highly acidic and unstructured IDL. To examine the potential role of the hPKR IDL in dsRNA-mediated activation and inhibition of its kinase activity, we used the known hPKR domain boundaries and sequence alignment with PKR homologs from rodent species as a guide to design three IDL deletion variants (Fig. 1, A and B). Specifically, hPKR-IDL$_{A1}$ and hPKR-IDL$_{A2}$ were designed to mirror the short natural IDL deletion in mouse/rat PKR (mPKR/rPKR) and the larger IDL deletion of variant 2 of the Golden Hamster protein (Mesocricetus auratus PKR), respectively. The third construct, hPKR-IDL$_{A3}$ corresponds to complete deletion of the hPKR IDL. These proteins lack a total of 16, 58, and 82 residues from the hPKR IDL, respectively (Fig. 1, A and B).

Wild-type hPKR and hPKR-IDL$_{A1}$ were expressed and purified using established protocols (10, 30), whereas the shorter IDL$_{A2}$ and IDL$_{A3}$ constructs were insoluble when expressed in *E. coli*. We found that the addition of an N-terminal SUMO
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FIGURE 1. PKR domain organization and design of PKR variants. A, domain architecture and boundaries within hPKR. The locations and boundaries of the N-terminal dsRBD consisting of two dsRNA binding motifs, the IDL, and catalytic KD are indicated. Also noted are the placement of an N-terminal SUMO tag (dashed line box and denoted S elsewhere) and KD deletion (ΔD338–N350, denoted *) used in some expression constructs (see “Experimental Procedures” for details). Residues removed in each of the IDL deletion constructs are noted below. B, alignment of human (h), mouse (m), rat (r), and hamster (ma) PKR sequences within the IDL. C, design of human-rat NTD/KD domain swap chimeric PKR proteins. The last NTD residue and first KD residue used in each of the chimeric proteins are indicated, and these positions highlighted beneath the sequence alignment of panel B.

(IDL) Deletions Do Not Change the Structure or Regulation of hPKR by RNA—Wild-type hPKR and each IDL deletion mutant was analyzed by far UV CD spectroscopy (Fig. 3A) after removal of the N-terminal SUMO tag for hPKR-IDLΔ2 and hPKR-IDLΔ3*. The spectra revealed that each protein is well folded as suggested by gel filtration chromatography. Furthermore, the spectra were essentially superimposable demonstrating that none of the IDL deletions altered the secondary structure content of the remaining two major domains. The spectra are also consistent with prior observations that the IDL region is flexible and lacks defined α-helical or β-sheet secondary structure.

The first steps in RNA-mediated PKR activation involve PKR dimerization on dsRNA and autophosphorylation. The activation of PKR follows a bell-shaped curve where the extent of activation initially increases with the concentration of dsRNA but then declines at the highest activator concentrations as PKR binds in a monomeric form to different dsRNA molecules (37, 38). Assays of PKR autophosphorylation in the presence of [γ-32P]ATP are established as a direct readout of PKR activation (32) and were used to assess the activation and inhibition of each IDL deletion mutant by poly(rI:rC) dsRNA and VA RNAi, respectively. In both cases the regulation of PKR by RNA was essentially unaffected by any of the three IDL deletions; PKR activation followed a bell-shaped curve with approximately the same maximum poly(rI:rC) dsRNA concentration, and inhibition by VA RNAi was accomplished with similar IC50 values (Fig. 2, B and C, and Table 1). We conclude from these results that the IDL deletions do not alter the structural elements responsible for recognizing and responding to activator or inhibitor RNAs, including communication between the N-terminal regulatory domain and C-terminal kinase domain. The hPKR IDL appears to play no role in control of dsRNA-mediated PKR regulation.

PKR Domain Substitutions Do Not Significantly Alter Protein Boundaries or Activation by dsRNA—In the absence of any apparent role for the IDL, we next asked whether each folded domain might influence PKR regulation by different RNAs. For example, whereas binding of dsRNA of sufficient length via the N-terminal regulatory domain might be sufficient to drive activation by promoting PKR dimerization, it is less clear whether RNA-mediated inhibition is exclusively controlled by interaction with the two N-terminal dsRNA binding motifs. To address this question, we speculated that hPKR and rPKR might exhibit differential sensitivity to a human viral inhibitor non-coding RNA that could be exploited to dissect the relative contributions of each folded domain to the process of RNA-mediated inhibition. Thus, we first compared inhibition of hPKR and rPKR by human Ad2 VA RNAi. Soluble expression and purification of rPKR required the use of an N-terminal SUMO (smt3) fusion. Therefore, although hPKR and S-hPKR were essentially indistinguishable in their responses to poly(rI:rC) dsRNA and VA RNAi, (Fig. 2) the latter human protein was used for this comparison as well as subsequent analyses. Consistent with our anticipation, the human non-coding viral transcript was a significantly weaker inhibitor of rPKR than the human homolog (Fig. 4 and Table 1).

To assess the specific contribution of each PKR domain to this differential sensitivity to VA RNAi-mediated inhibition, we generated chimeric N- and C-terminal domain swap variants of hPKR and rPKR. Again, each chimeric construct was expressed
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FIGURE 2. Regulation of human PKR by dsRNA is unaffected by an N-terminal SUMO fusion or kinase domain loop deletion (ΔD338-N350). A, comparison of poly(rI:rC) dsRNA-induced PKR autophosphorylation (activation) using human protein without (hPKR) and with (S-hPKR) an N-terminal SUMO domain. Activation follows the established bell-shaped response to poly(rI:rC) dsRNA concentration. B, as panel A but for adenovirus VA RNA1-mediated inhibition of PKR autophosphorylation in the presence of a fixed concentration of poly(rI:rC) dsRNA activator. Data in panels B and D were fit to determine the IC50 values shown in Table 1.

FIGURE 3. The IDL of human PKR plays no role in its regulation by RNA. A, CD spectra of hPKR (black), hPKR-IDLΔ1 (purple), hPKR-IDLΔ2 (orange), and hPKR-IDLΔ3* (red) demonstrate that PKR secondary structure is essentially unchanged upon deletion of the IDL. Inset shows the same spectra normalized to the minimum in CD signal at 207 nm. B, comparison of poly(rI:rC) dsRNA-induced PKR autophosphorylation (activation) of hPKR, hPKR-IDLΔ1*, S-hPKR-IDLΔ2*, and S-hPKR-IDLΔ3*. Color coding is the same as in panel A; dashed lines are used for proteins with an N-terminal SUMO tag, and solid lines indicate where the SUMO tag was cleaved or not included in the expression construct. C, as in panel B but for adenovirus VA RNA1-mediated inhibition of PKR autophosphorylation in the presence of a fixed concentration of poly(rI:rC) dsRNA activator. Data were fit to determine the IC50 values shown in Table 1.
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**TABLE 1**

<table>
<thead>
<tr>
<th>Protein construct</th>
<th>PKR inhibition, IC$_{50}$ (µM)</th>
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<tr>
<td></td>
<td>VA RNA$_1$</td>
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<tr>
<td>hPKR</td>
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<tr>
<td>hPKR-IDLΔ1</td>
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<td>hPKR-IDLΔ1*</td>
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<tr>
<td>S-hPKR-IDLΔ3*</td>
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<td>S-h/rPKR</td>
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<tr>
<td>S-r/hPKR</td>
<td>48 ± 6.0</td>
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**FIGURE 4. Human Ad2 VA RNA, is a poorer inhibitor of rat than human PKR.** Comparison of adenovirus VA RNA$_1$-mediated inhibition of PKR autophosphorylation in the presence of a fixed concentration of poly(rI:rC) dsRNA activator for S-hPKR and S-rPKR. Data were fit to determine the IC$_{50}$ values shown in Table 1.

mon, if not precisely conserved, among hPKR, rPKR, and the chimeric proteins. Trypsin cleavage of untagged hPKR largely recapitulated the prior analysis with two major cleavage sites observed within the IDL and the C-terminal kinase domain (sites A and B, respectively; Fig. 5, A and B, red and orange arrowheads). An equivalent pattern of proteolytic fragments was observed for S-hPKR with two identical bands corresponding to one fragment each from sites A and B, with the former site producing a larger N-terminal fragment (43 kDa) due to the inclusion of the SUMO tag (Fig. 5, A and B). Additionally, with the increased size of the protein N terminus, a weak band (23 kDa) was observed that corresponds to the previously noted third, minor cleavage site (site C; Fig. 5, A and B, black arrowhead).

S-rPKR showed a similar pattern of sensitivity to trypsin with a major cleavage site (denoted A’, red open arrowheads) corresponding to the main hPKR site A and a weaker site corresponding to hPKR site C between the two dsRBMs (denoted C’, black open arrowhead). Critically, both chimeric S-h/rPKR and S-r/hPKR proteins maintained this pattern of sensitivity to trypsin with major bands arising from cleavage at site A’ and a weaker band from site C’ (Fig. 5, A and B). We conclude from these analyses that the folded domains within each PKR construct are maintained and each protein possesses similar accessible unstructured regions within its truncated IDL and between the two dsRBMs.

We next tested the activation of S-rPKR and the two chimeric proteins by poly(rI:rC) dsRNA using a slot-blot assay and found a similar profile of autophosphorylation for each protein (Fig. 5C). Compared with S-hPKR, the response curves for the other proteins were shifted slightly to higher RNA activator concentration with the most pronounced effect observed for S-rPKR and S-h/rPKR, but critically, each followed the typical bell-shaped curve in response to increasing RNA concentration.

Although the correlation between autophosphorylation and downstream kinase activity on eIF2α substrate is established for hPKR, we used a second assay to directly measure the activity of rPKR and each chimeric protein on eIF2α in the absence or presence of a single concentration of poly(rI:rC) dsRNA (0.3 µg/ml). As expected, hPKR/S-hPKR showed both autophosphorylation and robust phosphorylation of eIF2α only in the presence of dsRNA, with no detectable activity in its absence (Fig. 5D, left panel). Although S-rPKR and each chimeric protein also showed strong up-regulation of autophosphorylation and eIF2α phosphorylation in the presence of dsRNA, S-rPKR and S-r/hPKR appeared to exhibit significant kinase activity even in the absence of the activator. To determine whether this activity might be an intrinsic property of these proteins and not an artifact of the expression or purification process, we first performed analytical gel filtration chromatography with purified PKR proteins. Both SUMO-tagged proteins (S-rPKR and S-r/hPKR) as well as the SUMO protease-treated r/hPKR, eluted exclusively at a volume corresponding to the monomeric protein (Fig. 5E). Although each protein was co-expressed with λ-protein phosphatase, to eliminate the possibility that the apparent constitutive activity of these proteins was due to uncontrolled phosphorylation and activation during expression in *E. coli*, the kinase assay was repeated after *in vitro* λ-protein phosphatase treatment. Again, although up-regulated by dsRNA, both S-rPKR and S-r/hPKR showed auto- and eIF2α phosphorylation activities in the absence of dsRNA (Fig. 5D, right panel). These activities were maintained in the cleaved form of the chimera, r/hPKR, indicating that the SUMO tag did not alter the protein activity. Thus, rPKR and the chimeric protein with the rat NTD appeared to possess low level, RNA-independent activity in a manner dependent upon the remaining IDL sequence and/or the N-terminal dsRBD (see “Discussion”).

In summary, the data of Fig. 5 collectively demonstrate that the two chimeric human/rat domain swap PKR proteins retain the essential structural and functional properties of the parent proteins. Each has essentially identical domain folding and boundaries and exhibits both a similar response to dsRNA activator and capacity to phosphorylate eIF2α (albeit with some constitutive, dsRNA-independent activity for r/hPKR).

Both the Regulatory and Catalytic Domains of PKR Determine the Sensitivity to Inhibition by Human Virus Non-coding RNAs—As described above, human Ad2 VA RNA$_1$ was a significantly weaker inhibitor of S-rPKR than the human homolog. We next tested the ability of this RNA to inhibit the two chimeric proteins and found, remarkably, that each was inhibited to a similar degree and between the two extremes of the human and rat proteins (Fig. 6A and Table 1). To establish that this effect is not specific to VA RNA$_1$, we tested the inhibitory activity of a second human viral non-coding RNA, HIV-1 TAR, against all four proteins. HIV-1 TAR acts as an inhibitor in its monomeric form but can activate PKR as an RNA dimer (35). Therefore,
before performing kinase inhibition assays we confirmed that our HIV-1 TAR RNA preparation was exclusively monomeric (Fig. 6, inset). We found that HIV-1 TAR RNA was a dramatically poorer inhibitor of S-rPKR compared with S-hPKR, with a substantially greater differential activity than observed with VA RNAI (7- and 300-fold differences in IC50 for VA RNAI and TAR RNA, respectively; Fig. 6 and Table 1). Furthermore, each chimeric protein again possessed a similar inhibitory activity falling between the two extremes of S-hPKR and S-rPKR.

Finally, to examine whether differences in PKR-RNA binding affinity underpin the observed differences in inhibition, we used isothermal titration calorimetry to measure S-hPKR and S-rPKR binding affinity for VA RNAI and HIV-1 TAR RNA. Remarkably, essentially the same binding affinity was determined for each protein with both non-coding RNAs, with all Kd values in the range 210–275 nM (Fig. 6, C and D). Curiously, however, the Kd for S-hPKR/VA RNAi interaction was 5-fold weaker than we previously measured for hPKR with the same RNA (32). Although performed under otherwise similar solution conditions, this difference in affinity had two obvious potential origins: the presence of the N-terminal SUMO tag or the reversal of the titrant and titrand in the current experiments (necessary due to the lower maximum concentration that we were able to achieve for S-rPKR). We, therefore, performed additional titrations with hPKR and VA RNAI to examine the effect of titration order (i.e., hPKR titrated into VA RNAI, compared with VA RNAI titrated into hPKR) using common buffer solutions and preparations of each component. Strikingly, a Kd of 290 nM was obtained with hPKR in the cell but reverting to the previously used configuration (i.e., protein in the syringe) resulted in a Kd of 50 nM comparable to the published value for hPKR (32). Thus, the titration orientation, and not the presence of the N-terminal SUMO tag, is the origin of the modestly weaker PKR-RNA affinities determined here.

In conclusion, we find that viral non-coding RNA inhibition of hPKR is dependent on features of both the N-terminal dsRNA binding regulatory domain and the C-terminal kinase domain but essentially independent of the binding affinity of the protein-RNA complex.
Discussion

The modular architecture of multidomain proteins can confer benefits such as adding cooperative functions (40), and the regions linking them (the IDLs) can couple the activities of regulatory and catalytic domains (41, 42). Additionally, alterations in the length of these IDL “hinge” regions have been shown to impact protein stability, folding rates, and domain-domain orientation in functionally diverse proteins, such as Src family kinases, polyketide synthase, and myosin (41, 43, 44). In the current work, our goal was to assess the contributions of the IDL and folded domains of the human eIF2 kinase PKR to its regulation by RNA.

The hPKR IDL has been proposed to mediate dynamic communication between its N-terminal regulatory dsRBD and C-terminal KD during activation by dsRNA as well as potentially play a role in PKR self-association and activity (4, 6, 14). To directly define the role of hPKR IDL in regulation of the kinase activity by RNA, we created three IDL deletion variants of hPKR guided by alignment of the human and rodent PKR sequences. Contrary to our initial expectation based upon the putative role(s) of the IDL, we found that deletion of the entire hPKR IDL had no effect on PKR activation by a synthetic dsRNA activator poly(rI:rC) or on its inhibition by the adenoviral non-coding transcript VA RNA. The hPKR IDL, therefore, appears to be entirely dispensable for RNA-mediated regulation and is not necessary to relay an RNA binding signal from the N-terminal regulatory domain to the C-terminal KD.

Although the IDL may not be necessary for PKR dimerization/activation or inhibition when these processes are driven by RNA binding in vitro, our results do not fully exclude a contribution to PKR function in vivo. Additionally, although our analyses show that an N-terminal SUMO fusion has no influence on RNA-mediated regulation of PKR, SUMOylation is proposed to modulate PKR antiviral activity when appended to specific lysine residues, one of which is located in the NTD near its junction with the IDL (45). Fully excluding roles for the IDL in RNA-mediated regulation or the influence of adjacent post-translational modifications on PKR activity will thus require further extensive cell-based experiments.

The IDL may also play important roles in PKR function in other contexts. In addition to acting as a cytosolic dsRNA sensor in an antiviral capacity, hPKR is involved in other key cellular processes (46, 47) that may require the IDL to promote or block activity. For example, the IDL is serine- and threonine-rich and is a potential site of post-translational modification and, thus, regulation by other cellular kinases. Regions of the
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IDL in addition to the folded domains are also targeted by viral PKR inhibitors (48), strongly implying the IDL either contributes to the control of PKR activity or may be manipulated for this purpose. Adoption of defined IDL structure and/or interactions at the PKR dimer interface may acquire functional relevance in RNA-independent activation or inhibition processes while being redundant in the context of RNA-mediated regulation.

Although the biological significance of RNA-independent hPKR self-association and activation at high protein concentrations is not clear, a role for the IDL in dimerization in the absence of RNA remains possible (4, 49). The PKR IDL varies considerably in length between species, with the longest sequence found in hPKR (~80 amino acid residues), compared with mouse/rat (~55–60 residues) and other rodents, e.g. Golden hamster (M. auratus PKR with ~20 residues). Thus, species-specific differences in the contribution of the IDL to PKR regulation are possible. We found that rPKR has detectable auto- and elf2α phosphorylation activity in the absence of RNA at much lower protein concentrations than are required for hPKR. In further support of a role for the IDL in controlling such RNA-independent dimerization, we found that the Golden hamster (M. auratus PKR) variant 2 appears to be fully constitutively active and did not bind or respond to dsRNA activator despite conservation of key residues for RNA interaction within the NTD.4 M. auratus PKR has a minimal IDL (Fig. 1B) containing only the conserved C-terminal segment proposed to promote self-association, possibly through a transition to an ordered structure in the context of the dimer interface (49).

Based on the data presented here, the contributions of the IDL and NTD to the greater propensity for RNA-independent activity in rPKR cannot be fully discerned. RNA-independent activity at the low PKR concentration used in our kinase assay was maintained in the rat NTD/human CTD domain swap but not the alternate chimeric protein. This activity might, therefore, depend on features of the rPKR NTD (common to rPKR and r/hPKR), differences in the IDL sequences between the human and rat proteins, or potentially both. Although each contains the most conserved C-terminal portion of the IDL, hPKR and rPKR differ significantly in their N-terminal IDL sequence length, and r/hPKR lacks the N-terminal 24 residues of the hPKR IDL. An intriguing possibility is that sequences within the hPKR IDL, one or more absent in rPKR, may compete to hinder or promote PKR dimerization in the absence of RNA. Indeed, alanine substitution of either Ser–242 or Thr–255 at the C-terminal end of the IDL, residues which are unique to hPKR compared with the rodent proteins, has been shown to exacerbate the impact on kinase activity conferred by substitution of the conserved Thr–258 in the KD (50). However, a simple, direct competition between N-terminal and C-terminal sequences in the hPKR IDL would be expected to result in similar retention of constitutive activity in the alternate h/rPKR chimera (containing the majority of the rPKR IDL), which we did not observe. Therefore, the possibility remains that the rPKR NTD has the major influence on the variation of PKR self-association either directly or by altering the context of the IDL sequences involved. High resolution structures of intact PKR in the absence and presence of RNA will be required to fully reveal the molecular details of control of PKR activation via RNA-driven dimerization and PKR self-association.

Our analyses of the human/rat chimeric PKR proteins also revealed an unanticipated significance for the C-terminal KD in determining the sensitivity of PKR activity to human viral non-coding RNAs. Although we found that hPKR, rPKR, and both domain swap chimeric proteins responded similarly to dsRNA activator, rPKR was much more weakly inhibited by two human viral non-coding RNAs, and each chimeric protein had a similar intermediate sensitivity. We additionally confirmed that the observed difference in sensitivity between hPKR and rPKR is independent of the protein–RNA binding affinities. Host factors must continually adapt to evade pathogen-derived inhibitors and substrate mimics; PKR in particular has undergone recent episodes of intense evolutionary adaption that resulted in changes in both domains of prime PKR sequences, including multiple protein surfaces in the C-terminal KD that control interaction with elf2 (51). Given the greater evolutionary distance between human and rat PKR, the latter protein's lower sensitivity to human viral RNAs is not unexpected. However, our finding suggests that human viral non-coding RNAs are also adapted to specifically exploit sequence or structural features of the hPKR C-terminal KD to confer their inhibitory effect.

References

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