Multifaceted Recognition of Vertebrate Rev1 by Translesion Polymerases $\zeta$ and $\kappa^*$

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Jessica Wojtaszek $^{3,1}$, Jiangxin Liu $^{3,1}$, Sanjay D’Souza $^{3,1}$, Su Wang $^3$, Yaohua Xue $^3$, Graham C. Walker $^3$, and Pei Zhou $^{1,2}$

From the $^3$Department of Biochemistry, Duke University, Medical Center, Durham, North Carolina 27710, the $^5$Department of Biology, Massachusetts Institute of Technology, Cambridge, Massachusetts 02139, and the $^6$Trinity College of Arts & Sciences, Duke University, Durham, North Carolina 27708

**Background:** Translesion synthesis requires the scaffolding function of the Rev1 CTD.

**Results:** We determined the structures of the Rev1 CTD and its complex with Pol $\kappa$ and mapped its Rev7-binding surface.

**Conclusion:** Distinct surfaces of the Rev1 CTD separately mediate the assembly of extension and insertion translesion polymerase complexes.

**Significance:** Cancer therapeutics could be developed by inhibiting Rev1 CTD-mediated translesion synthesis.

Translesion synthesis is a fundamental biological process that enables DNA replication across lesion sites to ensure timely duplication of genetic information at the cost of replication fidelity, and it is implicated in development of cancer drug resistance after chemotherapy. The eukaryotic Y-family polymerase Rev1 is an essential scaffolding protein in translesion synthesis. Its C-terminal domain (CTD), which interacts with merase Rev1 is an essential scaffolding protein in translesion resistance after chemotherapy. The eukaryotic Y-family poly- fidelity, and it is implicated in development of cancer drug duplication of genetic information at the cost of replication deviation; PCNA, proliferating cell nuclear antigen.

An alarming number of DNA lesions are generated continually in living cells from endogenous cellular processes and from exposure to exogenous genotoxic agents (1, 2). DNA lesions that have escaped from sophisticated DNA repair mechanisms such as nucleotide and base excision repair cannot be utilized as a template by high-fidelity replicative DNA polymerases, resulting in blockage of the replication fork and formation of replication gaps. To promote cell survival and complete DNA replication before mitosis, cells employ specialized DNA poly- merases to bypass lesions in a damage tolerance process known as translesion synthesis at the cost of replication fidelity (3, 4).

Translesion synthesis in mammalian cells is carried out by four Y-family polymerases, Pol$\zeta$, Pol $\kappa$, Pol $\iota$, Pol $\eta$, and Rev1, and one heterodimeric B-family polymerase Pol $\zeta$ that consists of the Rev3 catalytic subunit and the Rev7 accessory subunit. Accumulating evidence suggests that translesion synthesis is often achieved in a two-step fashion, with one set of poly- merases carrying out insertion opposite the lesion followed by a second set of polymerases carrying out the extension (5). The insertion step is achieved by one of the Y-family polymerases $\kappa$, $\iota$, $\eta$, or Rev1, with each specialized at bypassing distinct lesions (cognate lesions) for optimal replication accuracy (4). In addition to cognate lesions, these insertion polymerases can also bypass a variety of other lesions, often redundantly, though with elevated mutagenic rates. In contrast, many of the translesion synthesis events require the action of the Rev1-Pol $\zeta$ complex for efficient primer extension regardless of lesion types (5). Accordingly, deletions of REV1 and genes encoding the sub- units of Pol $\zeta$, REV3, and REV7, exhibit reduced spontaneous mutation rates and are severely defective for mutations induced by a wide variety of DNA-damaging agents (6–8). Recently, translesion synthesis has also been shown to function in replication-coupled DNA interstrand cross-link repair in a Pol $\zeta$-dependent manner (9), and monoubiquitinated Rev1 has been found to interact with the Fanconi anemia core complex, providing a critical link between the Fanconi anemia pathway and
translesion synthesis activity (10). These results have further expanded the function of translesion synthesis and highlight the fundamental roles of Rev1 and Pol ζ in this biologically important process.

The overlapping phenotype of rev1 and rev3 mutants in yeast has long implied a functional connection between Rev1 and Pol ζ, although their physical interaction has only been established recently (11–14). The binding between Rev1 and Pol ζ has been mapped to the C-terminal domain (CTD) of ~100 residues of Rev1 and the Rev7 subunit of Pol ζ. Accordingly, the Rev1 CTD has been shown to play an essential role in cell survival following UV irradiation and exposure to DNA-damaging agents such as methyl methanesulfonate or cisplatin in yeast and vertebrate cells (14, 15).

In vertebrates, but not in lower eukaryotes such as Saccharomyces cerevisiae, the Rev1 CTD has also been shown to interact with disordered Rev1-interacting regions (RIRs) of Y-family polymerases κ, λ, and η (12, 13, 16, 17). Such interactions are functionally important for Pol κ and Pol η activity in translesion synthesis. For example, the protective effect of Pol κ against benzo[a]pyrene in mammalian cells requires the binding of the Pol κ RIR and Rev1 (18, 19); in addition, the Rev1-Pol η RIR interaction promotes nuclear accumulation of Rev1 at sites of UV irradiation and helps suppress spontaneous mutations in human cells (20).

Despite its essential role in translesion synthesis, there has been no structural information about the Rev1 CTD or its complex with other translesion polymerases. As a first step toward understanding the molecular basis of the Rev1-mediated assembly of translesion polymerase complexes, we have determined the solution structures of the mouse Rev1 (mRev1) CTD and its complex with the RIR of mouse Pol κ (mPol κ), and have mapped its binding interface toward the Rev7 subunit of Pol ζ using yeast two-hybrid assays. Our structural and biochemical studies reveal two distinct but adjacent binding surfaces of the mRev1 CTD that separately interact with Pol ζ and the RIRs of insertion polymerases in translesion synthesis.

**EXPERIMENTAL PROCEDURES**

**Molecular Cloning and Protein Purification**—The NMR constructs contain the mRev1 CTD of 100 residues (1150–1249) or 115 residues (1135–1249) cloned into a modified pMAL-C2 vector (New England Biolabs) to yield a His10-MBP-tagged protein with a TEV site between MBP and the Rev1 CTD. The mPol κ RIR constructs of 546–616 and 560–582 were cloned into a modified pET15b vector (EMD Biosciences) to produce His6-MBP-tagged protein with a TEV site between MBP and the Rev1 CTD. The mPol κ RIR tag, the Rev1 CTD was further purified by size-exclusion chromatography. The mPol κ RIR was overexpressed in BL21(DE3)STAR E. coli cells, induced with 1 mM isopropyl 1-thio-β-d-galactopyranoside at 37 °C for 6 h, and purified following a similar procedure as the mRev1 CTD. The mRev1 CTD-Pol κ RIR complex was prepared by co-purification. Isotopically enriched proteins were overexpressed in M9 media using 15N-NH4Cl and 13C-glucose as the sole nitrogen and carbon sources (Cambridge Isotope Laboratories). NMR buffers contain 25 mm sodium phosphate, 100 mM KCl, and 10% D2O or 100% D2O (pH 7.0).

**NMR Spectroscopy**—NMR experiments were conducted using Agilent INOVA 600 or 800 MHz spectrometers at 25 °C and 37 °C for the mRev1 CTD and the mRev1 CTD-Pol κ RIR complex, respectively. Backbone resonances were assigned based on standard three-dimensional triple-resonance experiments (21), and side chain resonances were assigned using sparsely sampled high-resolution four-dimensional HCCH-TOCSY and four-dimensional HCCONH TOCSY experiments (22). Distance constraints were derived from high-resolution three-dimensional 15N- or 13C-separated NOESY-HSQC experiments and from sparsely sampled four-dimensional 13C-HMQC-NOESY-15N-HSQC and four-dimensional 13C-HMQC-NOESY-13C-HSQC experiments. NMR data were processed by NMRpipe (23) and analyzed with Sparky (24). NOE cross-peaks were analyzed with a combination of manual and automated assignments and converted into distance constraints using the calibration module in CYANA (25). Dihedral angles were derived by TALOS+ analysis of chemical shift information (26) and from analysis of local NOE patterns. Structural ensembles were generated with CYANA (25). The final structural ensembles (20 structures) of the mRev1 CTD and the mRev1 CTD-Pol κ RIR complex display with no NOE violations >0.5 Å and no dihedral angle violations >5°. The quality of these structures can be evaluated in Tables 1 and 2.

**Yeast Two-hybrid Analysis**—Protein-protein interactions in the yeast two-hybrid system were performed in the PJ69–4A strain of yeast (27). The mRev1 CTD(1150–1249) and mRev7 harboring the previously described R124A substitution (28) were cloned into the pGAD-C1 (GAL4 activation domain) and pGBD-C1 (GAL4 DNA-binding domain) plasmids marked with leucine and tryptophan, respectively. The assay was performed by growing strains harboring the two plasmids in 3 ml of media lacking leucine and tryptophan for 2 days at 30 °C and spotting 5 μl of cells on selective medium plates lacking leucine and tryptophan (−LW) and on medium also lacking adenine and histidine (−AHLW) to score positive interactions. Interactions were scored after 3 days of growth at 30 °C. Site-directed mutations were generated using the QuikChange protocol (Stratagene) and verified by sequencing.

**RESULTS**

**Rev1 CTD Adopts Atypical Four-helix Bundle**—After extensive screening for Rev1 CTD constructs, we have identified the mRev1 CTD(1150–1249) with a cleavable His10-MBP tag as the optimal construct for structural characterization by NMR. With the exception of disordered residues at the N terminus, the mRev1 CTD is well structured, with mean pairwise r.m.s.d. of 0.47 and 0.94 Å for the backbone and heavy atoms, respectively (Fig. 1A). The detailed statistics on the structural ensemble are given in Table 1.

The structure of the mRev1 CTD contains an atypical four-helix bundle consisting of mixed parallel and anti-parallel helices (Fig. 1B). Starting from α1 (Phe1163–Thr1175) in a down-
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![Image](https://example.com/figure1.png)

**FIGURE 1. Structure of the mRev1 CTD.** A, stereo view of backbone traces from the structural ensemble of the mRev1 CTD, with helices colored in red and loops in blue. B, ribbon diagram. Conserved hydrophobic residues are shown in the stick model (left panel). The + sign indicates helices pointing away, whereas the − sign indicates helices pointing inward (right panel). C, sequence alignment of the Rev1 CTD. Listed species include Mus musculus (Mm), Homo sapiens (Hs), Bos taurus (Bt), Gallus gallus (Gg), Drosophila melanogaster (Dm), S. pombe (Sp), and S. cerevisiae (Sc). Conserved hydrophobic residues are colored in yellow. Disordered mRev1 CTD residues that undergo RIR binding-induced folding are boxed in blue. Residues important for Rev7 binding are denoted by asterisks. C, C-terminal; N, N-terminal.

### TABLE 1

| NOE distance restraints (total) | 2262 |
|--------------------------------|------|
| Intra-residue                   | 610  |
| Sequential                     | 545  |
| Medium range (1 < j − i ≤ 4)   | 666  |
| Long range (l − j ≥ 5)          | 441  |

| Dihedral angle constraints*    | 160  |
| Target function value          | 0.46 ± 0.11 |
| Ramachandran plot              |      |
| Favored region (98%)           | 97.2 |
| Allowed region (99.8%)         | 99.9 |

| Mean pairwise r.m.s.d. (residues 1163–1249) |
|---------------------------------------------|
| Backbone Heavy atoms                        |
| 0.47 ± 0.10 Å                              |
| 0.94 ± 0.09 Å                              |

* Dihedral angle constraints were generated by TALOS + based on backbone atom chemical shifts and by analysis of NOE patterns (26).

Four-helix bundle, the residues C-terminal to 4 form an extended β-loop, with the side chains of Leu1246 and Val1248 juxtaposed to interact with the exposed hydrophobic surface between 3 and 4. The vast majority of these hydrophobic residues are highly conserved from yeast to human (Fig. 1C), supporting the existence of a stable protein module in the Rev1 CTD across different species.

Intriguingly, compared with typical four-helix bundle proteins containing equally spaced helices, the location of α1 in the mRev1 CTD is much closer to α3 than to α2. This creates an extended, solvent exposed hydrophobic surface that is optimal for interaction with other proteins. Query of the Dali Server (29) did not reveal a similar fold of isolated four-helix bundles with r.m.s.d. <4 Å or Z-score >5. However, a similar topology can be found as part of seven-helix bundle proteins (e.g. CID of PCF11, Protein Data Bank code 2BF0) to interact with other structural elements, reinforcing the notion that the Rev1 CTD is ideally suited as a scaffolding protein.

**Rev7 Recognition Surface Centers at α2-α3 Loop and α3 Helix of Rev1 CTD**—Having elucidated the structure of the mRev1 CTD, we next probed its interaction with the Rev7 subunit of Pol ζ using yeast two-hybrid assays. The mRev1 CTD and mouse Rev7 (mRev7) containing a R124A substitution, thought to stabilize its closed conformation (28), were fused to either the activation domain or the DNA-binding domain of the Gal4 transcription factor, respectively. Reciprocally, we also appended the mRev1 CTD to the DNA-binding domain and mRev7 to the activation domain of Gal4. The presence of the constructs after transformation into the P69-4A strain of yeast was verified by growth on selective medium plates lacking leucine and tryptophan (~LW). Interactions between the two proteins activate the expression of the HIS3 and ADE2 reporter genes, both driven by promoters responsive to the Gal4 transcription factor. These interactions were scored by growth on selective medium plates additionally lacking adenine and histidine.
dine (−AHLW). Consistent with published data (12), the interaction between the mRev1 CTD and mRev7 resulted in robust growth of strains in selective media lacking AHLW when either protein was fused to the activation domain or DNA-binding domain of Gal4; in contrast, no growth was observed in strains expressing the mRev1 CTD and empty expression plasmids, verifying that the Rev1 CTD-Rev7 interaction is specific (Fig. 2A).

After establishing a strong interaction between the mRev1 CTD and mRev7, in an effort to identify “hot spot” residues that contribute prominently to the binding energy, we mutated pairs of residues of the mRev1 CTD and evaluated their interactions with mRev7 in yeast two-hybrid assays using the mRev1 CTD fused to the DNA-binding domain and mRev7 appended to the activation domain of Gal4.

We first evaluated the effect of mutating pairs of highly conserved hydrophobic residues of individual helices of the mRev1 CTD (Fig. 2B). Double mutations of V1166A/L1170A with K1167A/K1171A, I1185A/V1189A, R1190A/D1194A, V1207A/M1211A, K1209A/R1213A, W1223A/F1227A, D1228A/D1232A abrogated the mRev1 CTD interaction with mRev7. Because these residues form the hydrophobic core of the mRev1 CTD, their substitutions by alanine likely disrupted the proper folding of the mRev1 CTD and thus its interaction with mRev7.

We next evaluated the contribution of surface exposed hydrophilic residues of individual helices toward Rev7 binding, using double alanine substitutions or mutations that result in single- or double-charge reversion (Fig. 2, B–D). None of the double-alanine substitutions (K1167E/K1171E, R1190E/D1194E, K1209E/R1213E, D1228R/D1232R) disrupted the mRev1 CTD-Rev7 binding. Although single- or double-charge reversion mutants on α1 (K1167E, K1171E), α2 (R1190E, D1194E, R1190E/D1194E) or α4 (D1228R, D1232R, D1228R/D1232R) of the mRev1 CTD
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FIGURE 3. mRev7 binds to the mRev1 CTD primarily through a surface centered at the α2–α3 loop and the N-terminal part of α3. A, interactions of the GAL4 DNA-binding domain-fused mRev1 CTD harboring indicated mutations with GAL4 activation domain-mRev7 probed by yeast two-hybrid assays as described in Fig. 2A. The — indicates control reactions in which GAL4 DNA-binding domain-fused mRev1 CTD plasmids were transformed into strains harboring the GAL4 activation domain empty expression vector. AD denotes the GAL4 activation domain, and BD denotes the GAL4 DNA-binding domain. B, surface mapping of the mRev1 CTD residues important for mRev7 interaction.

had little effect on Rev7 binding, substitutions of positively charged Lys1209/Arg1213 of α3 with negatively charged glutamate residues resulted in a significant reduction of the mRev1 CTD-Rev7 binding (Fig. 2, C and D). Interestingly, mutation of K1209E, but not R1213E, of α3 severely compromised the interaction in yeast two-hybrid assays, suggesting that Lys1209 in α3 of the mRev1 CTD is directly involved in Rev7 binding.

To more specifically delineate mRev1 CTD residues important for Rev7 binding, we engineered a set of mutations that span the α2–α3 loop and α3 of the mRev1 CTD and tested their ability to disrupt the Rev7 interaction (Fig. 3A). Mutations of hydrophobic residues (L1201A or L1204A) involved in packing of the four-helix bundle disrupted the mRev1 CTD-Rev7 interaction, whereas mutations of Y1210F and L1206A had no effect. Mutation of R1213D, a surface exposed hydrophilic residue at the C-terminal end of α3, also did not affect the mRev1 CTD-Rev7 interaction, suggesting that the mRev1 CTD recognition by Rev7 is mediated by the N-terminal half of α3 of the mRev1 CTD. Consistent with this notion, single amino acid substitutions of hydrophilic residues at the N-terminal part of α3 containing an opposite charge (E1202K, K1203E, or D1205R) completely abolished the Rev7 interaction. Additionally, point mutations of K1199E and D1200R located in the loop connecting α2 and α3, either significantly reduced or abolished the Rev7 interaction. No binding was observed in control experiments between the mRev1 CTD harboring these mutations and an empty expression plasmid, verifying the specificity of these interactions in our assays. Taken together, these results define the α2–α3 loop and the N-terminal half of α3 of the Rev1 CTD as the primary Rev7-binding site (Fig. 3B).

A Minimal RIR of Pol κ for Rev1 Interaction—The interactions between vertebrate Rev1 and other members of the Y-family polymerases have been mapped to the Rev1 CTD and disordered RIR fragments of ~50 residues within Pol κ, Pol λ, and Pol η (17). Because the RIR of human Pol κ has the tightest binding affinity toward the Rev1 CTD (19), its mouse counterpart was chosen for characterization by NMR. The mPol κ RIR (546–616) displays a typical 1H-15N HSQC spectrum of a disordered peptide, with amide resonances showing a narrow chemical shift distribution. By analyzing mPol κ RIR amide resonances that experience substantial perturbations upon binding to the mRev1 CTD, we have identified a 23-residue RIR peptide of mPol κ (560–582) that not only binds to the mRev1 CTD tightly but also causes identical resonance perturbations for the mRev1 CTD as the longer peptide. This 23-residue peptide was subsequently used to investigate the mRev1 CTD-Pol κ RIR interaction.

Binding-induced Folding of mRev1 CTD and Pol κ RIR—During our studies of the mRev1 CTD, we found that extending the ~100 residue mRev1 CTD construct by 15 residues at the N terminus improved the sample yield and stability. This optimized construct (mRev1(1135–1249)) was used for structural determination of the mRev1 CTD-Pol κ RIR complex. The overall structure of the mRev1 CTD-Pol κ RIR complex is well defined, with mean pairwise r.m.s.d. of 0.42 and 0.89 Å for the backbone and heavy atoms, respectively (Fig. 4A). The detailed statistics on the structural ensemble are given in Table 2.

The core helix-bundle structure of the mRev1 CTD in complex with the Pol κ RIR is similar to that of the free protein. However, the six residues N-terminal to α1 (Asn1156–Val1161) are completely disordered in the free Rev1 CTD, whereas binding of the Pol κ RIR induces folding of these residues into a β-hairpin that projects over the shallow hydrophobic surface between α1 and α2 and creates a deep hydrophobic cavity for high-affinity interaction with the essential FF motif of the Pol κ RIR (Fig. 4, B–D).

The binding of the mRev1 CTD similarly induces folding of the disordered Pol κ RIR into a three-turn α-helix, starting from Phe566 and ending at Ile575 (Fig. 4). The folding of the RIR helix is stabilized by a prototypical N-helix cap at Ser565 (30), with the side chain of Ser565 forming hydrogen bonds with amides of Phe567 and Asp568 and its backbone carbonyl oxygen atom forming another hydrogen bond with the amide of Lys566. Substitution of the corresponding serine residue in human Pol κ RIR by alanine reduced its binding affinity toward Rev1 by more than 50% in a yeast two-hybrid assay (19); however, substitution of serine with proline, another N-helix cap residue, did not
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FIGURE 4. Structure of the mRev1 CTD-Pol α RIR complex. A, stereo view of backbone traces from the structural ensemble of the mRev1 CTD-Pol α RIR complex, with helices colored in red, loops colored in gray, and a six-residue hairpin loop that undergoes a binding-induced folding transition, colored in blue. B, ribbon diagram, with mRev1 CTD colored in green and Pol α RIR colored in blue. C, interface of the Rev1 CTD-Pol α RIR complex. Side chains of conserved Pol α RIR residues and their binding partners are shown in the stick model. D, sequence alignment of RIR peptides from Y-family polymerases α, i, and η. Conserved residues are colored, with the essential FF motif highlighted. i refers to a helix cap residue that is predominantly serine but can be replaced by proline. E, representative intermolecular NOEs (indicated by arrows) between the aromatic side chains of Phe566 and Phe567 of the mPol α RIR and their interacting residues of the mRev1 CTD.

TABLE 2
Structural statistics for the mRev1 CTD-mPol α RIR (20 structures)

None of these structures exhibit distance violations >0.5 Å or dihedral angle violations >5°.

| mRev1 CTD | NOE distance restraints | 3530 |
| Pol α RIR | NOE distance restraints | 202 |
| | Intra-residue | 737 |
| | Sequential | 738 |
| | Medium range (1≤|i-j|≤4) | 1029 |
| | Long range (|i-j|>5) | 1026 |
| | Dihedral angle constraints* | 178 |
| Intermolecular NOE distance constraints | 167 |
| Target function value | 1.76 ± 0.09 |
| Ramachandran plot* | Favored region (98%) | 97.6 |
| | Allowed region (>99.8%) | 100.0 |
| Mean pairwise r.m.s.d. (mRev1 CTD 1153–1249; Pol α RIR 564–576) | Backbone | 0.42 ± 0.09 Å |
| | Heavy Atoms | 0.89 ± 0.09 Å |

* Dihedral angle constraints were generated by talos+ based on backbone atom chemical shifts, and by analysis of NOE patterns (26).

Toll-like RIR residues Lys564, Arg571, and Arg574 and mRev1 CTD residues Met1181, Ala1158, and Ala1160, respectively. Although affect Rev1 binding (19), highlighting the important contribution of an N-terminal cap to the stability of this binding-induced RIR helix.

Immediately following Ser565 are two essential phenylalanine residues Phe566 and Phe567 that emanate from the same side of the RIR helix to interact with the Rev1 CTD. The aromatic ring of Phe566 extends over a hydrophobic surface patch formed by residues Trp1173, Thr1176, and Ile1177 located at the C-terminal end of α1 and the loop immediately following it. The side chain of Phe567, with its phenyl ring located almost perpendicular to that of Phe566, wedges into and is completely immersed in a deep hydrophobic pocket of the Rev1 CTD. The base of the hydrophobic pocket is formed by Leu1170 of α1 and Val1188 of α2. At one side of the hydrophobic pocket lies the indole ring of the Trp1173 of α1, whereas the opposite side of the pocket is sealed by the side chains of Leu1157 and Ala1158 that project over from the newly forged β-hairpin in response to the binding of the Pol α RIR. These core hydrophobic interactions are additionally supported by interactions between Phe567 and the side chain methylene groups of the nearby Gln1187 of α2. Reflecting their essential role in the Rev1 CTD-RIR interaction, the FF motif is strictly conserved, their strong interactions with the Rev1 CTD are supported by the observation of numerous intermolecular NOEs (Fig. 4E), and alanine substitution of either of the FF residues abolishes the Rev1 CTD-RIR interaction (19).

The two residues after Phe567, Asp568, and Lys569 are surface-exposed and are not engaged in Rev1 CTD interaction. In contrast, the following residue, Lys570, is located on the same side of the RIR helix as the two essential phenylalanine residues, with its side chain extending over the aromatic ring of Phe566. A number of intermolecular NOEs can be observed between the side chains of Lys570 of the Pol α RIR and Glu1172 of the mRev1 CTD; additional NOEs between both residues to the aromatic ring of Phe566 in the Pol α RIR are also visible, suggesting that these two residues are located in the vicinity of Phe566 and they are engaged in a specific charge-charge interaction. Reflecting this observation, Lys570 is highly conserved among vertebrate RIRs that have been shown to interact with the Rev1 CTD.

In addition to these essential and highly conserved interactions, intermolecular NOEs have also been observed between Pol α RIR residues Lys564, Arg571, and Arg574 and mRev1 CTD residues Met1181, Ala1158, and Ala1160, respectively. Although
these interactions may provide additional support to anchor the Polκ-RIR onto the Rev1 CTD, these RIR residues are not conserved, and they are unlikely to contribute significantly to the binding affinity.

Our structure of the mRev1 CTD-Polκ-RIR complex has revealed a binding surface of the Rev1 CTD that consists of α1 and α2 helices and a newly forged N-terminal β-hairpin loop in response to RIR interaction. This structurally defined RIR-binding surface is located adjacent to, but is distinct from, the Rev7-binding surface of the Rev1 CTD centered at the α2–α3 loop and the N-terminal half of the α3-helix as revealed by our yeast two-hybrid studies.

**DISCUSSION**

Conserved and Acquired Roles of Rev1 CTD in Translesion Synthesis—Rev1 is a unique member of the eukaryotic Y-family polymerases and is conserved from yeast to human. Its gene was identified in a screen for reversion mutants of *S. cerevisiae* after UV irradiation (6), and it was the first Y-family polymerase that was characterized enzymatically (31). The limited polymerizing ability of Rev1 (31), coupled with the profound effect of the *rev1*Δ mutation, which did not affect the catalytic activity of Rev1, led to the proposal of a “second function” of Rev1 in translesion synthesis (32). This second function is now attributed to the scaffolding function of the Rev1 CTD that coordinates recruitment of Polζ (14, 33). Deletion of the Rev1 CTD completely abolishes Rev1-dependent translesion synthesis; likewise, elevated levels of the Rev1 CTD show a strong dominant-negative effect on cell viability and induced mutagenesis after DNA damage in yeast (14). Recent studies have revealed a similarly important function of the Rev1 CTD in higher eukaryotes and suggest that the vertebrate Rev1 CTD may have acquired a more prominent role in recruiting Polζ and controlling translesion synthesis in the absence of monoubiquitinated PCNA at the stalled replication fork (15, 34). Taken together, these results highlight an essential and highly conserved role of the Rev1 CTD-Polζ interaction in translesion synthesis that has now been mapped to the α2–α3 loop and the N-terminal half of the α3-helix in the Rev1 CTD.

In contrast to the Rev1-Polζ interaction that is conserved in all eukaryotes, the Rev1 interaction with the RIRs of Polκ, η, and ι has only been found in vertebrates, but not in *S. cerevisiae* or *Schizosaccharomyces pombe*, suggesting an evolutionary divergence between animals and yeast (17). Because translesion synthesis accounts for <10% of damage bypass events in yeast (35), whereas the frequency of potentially mutagenic translesion synthesis may be as high as 50% in higher eukaryotes (36), the formation of the Rev1 CTD-RIR helix has a significant impact on its binding affinity toward the Rev1 CTD. Substituting the helix cap Ser565 by alanine significantly reduced the Rev1 CTD-RIR binding (19); likewise, proline substitution of RIR residues after the FF motif (D568P, K569P, K570P, or R571P) abolished the Rev1 interaction (19), suggesting that the formation of the RIR helix requires a minimum of six residues in addition to a helix stabilizing cap. Such an observation may account for a lack of binding affinity of the Rev1 CTD toward the FF motif found in the PCNA-interacting peptides of Polκ and Polη (40). Because the PCNA-interacting peptide of Polκ contains a single residue after the FF motif, and the PCNA-interacting peptide of Polη contains a proline residue at the second position after the FF motif, neither is expected to be an effective binding partner of the Rev1 CTD.

**Targeting Rev1 CTD-mediated Translesion Synthesis for Cancer Therapy**—A hallmark of cancer cells is the accumulation of a vast number of mutations in their genomes (41–43). Cancer-specific mutations have been shown to increase the capacity of cancer cells to carry out mutagenic translesion bypass (44, 45), and extensive mutagenesis in turn contributes to the development of drug resistance in relapsed tumors after chemotherapy (46). The recent discovery that depletion of Rev1 greatly reduces the number of carcinogen-induced lung tumors in mice highlights an important role of translesion synthesis in cancer development (47). In human ovarian carcinoma cells, alteration of the Rev1 level modulates the cytotoxicity and mutagenicity of cisplatin (48, 49). Depletion of Rev1 or Rev3L, the catalytic unit of mouse Polζ, sensitizes B-cell lymphomas and chemoresistant lung adenocarcinomas to cisplatin treatment *in vivo* (50). Suppression of Rev1 limits cyclophosphamide-induced mutagenesis *in vitro* and delays the emergence of chemoresistant tumors *in vivo* (50, 51). These studies high-
light the therapeutic potential of inhibiting translesion synthesis in cancer treatment.

Given the essential function of the Rev1 CTD in translesion synthesis, compounds that transiently disrupt the Rev1 CTD–Pol ζ interaction could sensitize cancer cells to DNA damaging therapeutic agents while reducing their mutagenic consequences, suggesting that these compounds may be developed into novel adjuvants to enhance the clinical outcome of current therapies. In this regard, the elucidation of the Rev1 CTD structure and its binding surfaces toward Rev7 and the Pol ζ RIR is an important first step toward this goal. Our structural studies have revealed an atypical four-helix bundle fold of the mRev1 CTD, and our yeast genetic data have further identified a set of hot spot residues of the Rev1 CTD and have provided the first residue-specific view of the Rev7-binding interface of the Rev1 CTD, laying a molecular framework for designing novel inhibitors to disrupt the essential and evolutionary conserved Rev1 CTD–Pol ζ interaction. The discovery of multifaceted recognition of the Rev1 CTD by Rev7 and RIR has hinted at the exciting possibility of generating potent inhibitors that separately occupy the Rev7- or RIR-binding surfaces of the Rev1 CTD, which can be used individually or in combination to suppress translesion synthesis. Should these compounds display the desired effectiveness in vivo, they could become a novel class of therapeutics to sensitize cancer cells to chemotherapy and to suppress the development of cancer drug resistance.

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