

## Replication Bypass of the Acrolein-Mediated Deoxyguanine DNA–Peptide Cross-Links by DNA Polymerases of the DinB Family

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DNA–protein cross-links (adducts) are formed in cellular DNA under a variety of conditions, particularly following exposure to an  $\alpha,\beta$ -unsaturated aldehyde, acrolein. DNA–protein cross-links are subject to repair or damage-tolerance processes. These adducts serve as substrates for proteolytic degradation, yielding DNA–peptide lesions that have been shown to be actively repaired by the nucleotide excision repair complex. Alternatively, DNA–peptide cross-links can be subjected to replication bypass. We present new evidence about the capabilities of DNA polymerases to synthesize DNA past such cross-links. DNAs were constructed with site-specific cross-links, in which either a tetrapeptide or a dodecylpeptide was covalently attached at the  $N^2$  position of guanine via an acrolein adduct, and replication bypass assays were carried out with members of the DinB family of polymerases, human polymerase (pol)  $\kappa$ , *Escherichia coli* pol IV, and various *E. coli* polymerases that do not belong to the DinB family. Pol  $\kappa$  was able to catalyze both the incorporation and the extension steps with an efficiency that was qualitatively indistinguishable from control (undamaged) substrates. Fidelity was comparable on all of these substrates, suggesting that pol  $\kappa$  would have a role in the low mutation frequency associated with replication of these adducts in mammalian cells. When the *E. coli* orthologue of pol  $\kappa$ , damage-inducible DNA polymerase, pol IV, was analyzed on the same substrates, pause sites were detected opposite and three nucleotides beyond the site of the lesion, with incorporation opposite the lesion being accurate. In contrast, neither *E. coli* replicative polymerase, pol III, nor *E. coli* damage-inducible polymerases, pol II and pol V, could efficiently incorporate a nucleotide opposite the DNA–peptide cross-links. Consistent with a role for pol IV in tolerance of these lesions, the replication efficiency of DNAs containing DNA–peptide cross-links was greatly reduced in pol IV-deficient cells. Collectively, these data indicate an important role for the DinB family of polymerases in tolerance mechanisms of  $N^2$ -guanine-linked DNA–peptide cross-links.

### Introduction

DNA–protein cross-links are formed in cells not only as a consequence of routine DNA metabolism but also from exposure to a variety of chemical toxicants and metals (1). In particular, these lesions have been detected in DNA following treatment of cultured human cells with an  $\alpha,\beta$ -unsaturated aldehyde, acrolein (2, 3). Among aldehydes that can induce DNA–protein cross-links in vitro, acrolein is one of the most potent (4). It is cytotoxic and mutagenic (5–7) and has tumor-initiating activity (8). Acrolein is ubiquitous in the environment, but more importantly, it is generated in vivo, mainly as a product of peroxidation of fatty acids (9–11). Thus, acrolein may represent a significant endogenous causative factor for induction of DNA–protein cross-links.

Being a highly reactive bifunctional electrophile, acrolein reacts with DNA to modify nucleobases at various positions,

in particular, at the exocyclic nitrogen ( $N^2$ ) of deoxyguanosine (dG)<sup>1</sup> (12–16). The major product of reaction between  $N^2$ -dG and acrolein is  $\gamma$ -hydroxypropano-deoxyguanosine ( $\gamma$ -HOPdG) (12), a mutagenic adduct (17) that has been detected in cellular DNA isolated from various tissues both following acrolein exposure and as an endogenous lesion (10, 18–20). The  $\gamma$ -HOPdG adduct undergoes spontaneous ring opening and closing (Figure 1A) with the equilibrium being shifted toward the ring-opened form in duplex DNA (21, 22). The free aldehyde of the ring-opened  $\gamma$ -HOPdG can further react with amines in peptides and proteins to yield Schiff base-mediated linkages (23, 24). Similar to the acrolein adduct,  $N^2$ -dG adducts of other biologically important  $\alpha,\beta$ -unsaturated aldehydes, crotonaldehyde and *trans*-4-hydroxynonenal, have also been shown to form Schiff base-mediated DNA–peptide cross-links (23). Therefore, elucidation of a role for acrolein and other related compounds in living organisms cannot be complete without detailed understanding of cellular processing of DNA–protein cross-links.

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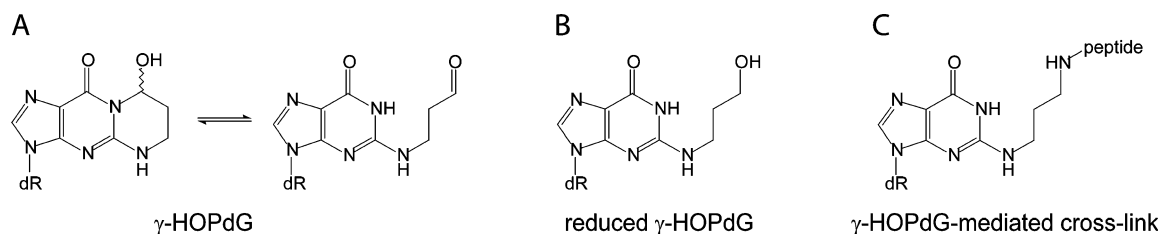
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<sup>1</sup> Abbreviations: dG, deoxyguanosine;  $\gamma$ -HOPdG,  $\gamma$ -hydroxypropano-deoxyguanosine; NER, nucleotide excision repair; pol, polymerase; *E. coli*, *Escherichia coli*.



**Figure 1.** Structure of DNA adducts used in the current study. (A)  $\gamma$ -HOPdG shown as the equilibrium between the ring-closed and the ring-opened forms, (B) reduced  $\gamma$ -HOPdG, and (C) reduced  $\gamma$ -HOPdG-mediated peptide cross-link.

Although a subset of DNA–protein cross-links can undergo spontaneous reversal, others require active removal by DNA repair machinery or are processed through damage avoidance and tolerance pathways. Prokaryotic nucleotide excision repair (NER) has been demonstrated to function on DNA–protein adducts as large as 16000 Da (25), while comparably sized cross-linked protein adducts were refractory to excision by the human NER complex (26–28). However, these data showing a lack of repair of intact proteins by human NER do not rule out a role for this pathway in the ultimate processing of these lesions, since there is a literature precedent suggesting an initial proteolytic processing of these lesions prior to excision. In this regard, data obtained from the Zhitkovich's group (29) demonstrated that repair of formaldehyde-induced DNA–protein cross-links was significantly reduced in cells treated with lactacystin, a proteasome inhibitor. It was hypothesized that the cross-linked proteins were proteolytically degraded into substrates suitable for completion of the repair process. Consistent with these results, DNA–peptide cross-links serve as much better substrates relative to DNA–protein cross-links for both prokaryotic (25, 30) and human NER (26–28). Baker et al. also demonstrated that incubation with the 26S proteasome inhibitor, MG132, resulted in a greater than 50% reduction in the intracellular repair of plasmids carrying site-specific DNA–protein cross-links (28). Collectively, these data indicate that biological processing of covalently linked protein adducts can proceed via a proteolytic degradative process, converting DNA–protein cross-links into DNA–peptide cross-links.

NER processing of DNA–peptide cross-links could be sufficiently delayed to make these lesions available for DNA replication bypass and potentially lead to mutations. Recently, we have assessed the mutagenic properties of Lys-Trp-Lys-Lys cross-links during extrachromosomal replication in mammalian cells. When this tetrapeptide was linked to the  $N^2$  position of dG via the acrolein-derived  $\gamma$ -HOPdG, lesion bypass was only moderately mutagenic (31). Previous investigations have suggested that the efficient and nonmutagenic replication bypass of bulky  $N^2$ -dG adducts can be performed by DNA polymerases (pol) of the DinB family, pol  $\kappa$  in mammalian cells, and its bacterial orthologue, pol IV, in *Escherichia coli* (*E. coli*) (32–39). Here, we hypothesized that human pol  $\kappa$  as well as pol IV also function in replication bypass of  $N^2$ -dG–peptide cross-links. To test this hypothesis, we have created site specifically modified oligodeoxynucleotides that contain either tetrapeptide (Lys-Trp-Lys-Lys) or dodecylpeptide (Lys-Phe-His-Glu-Lys-His-His-Ser-His-Arg-Gly-Tyr)  $\gamma$ -HOPdG-mediated cross-links (Figure 1) and performed replication assays in vitro. Additionally, the DNA–peptide cross-links were introduced into a single-stranded DNA vector (pMS2) (40) and the consequences of replication past these lesions were investigated in both the wild-type and the pol IV-deficient *E. coli* strains.

## Materials and Methods

**DNA Pols.** Human pol  $\kappa$  was purchased from Enzymax Inc. (Lexington, KY). The pol was full length and tagged at its N termini with the calmodulin-binding peptide. Subunits of the pol III replicase were purified as described before (41, 42). The pol III core was reconstituted by mixing  $\alpha$ ,  $\epsilon$ , and  $\theta$  subunits (1:1.5:3 molar ratio, respectively) and incubating for 30 min at 15 °C. The pol III core was resolved from unbound proteins by chromatography on MonoQ as described previously (43). The pol III replicase, containing two molecules of pol III core connected by the clamp loader, was reconstituted as follows. A mixture of  $\gamma$  and  $\tau$  (2.5:1 molar ratio, respectively) was incubated for 90 min at 15 °C, followed by the addition of  $\delta$ ,  $\delta'$ ,  $\chi$ , and  $\Psi$  (3-fold molar excess of each subunit over  $\tau$ ) followed by a further 1 h incubation. The  $\tau_2\gamma_1\delta\delta'\chi\Psi$  complex was resolved from other species ( $\tau_3\delta\delta'\chi\Psi$ ,  $\tau_1\gamma_2\delta\delta'\chi\Psi$ , and  $\gamma_3\delta\delta'\chi\Psi$ ) using a 1 mL MonoS column by elution with a 0.0–0.5 M NaCl gradient as described before (44). The  $\tau_2\gamma_1\delta\delta'\chi\Psi$  clamp loader was incubated with a 4-fold molar excess of pol III core, and pol III replicase was purified from excess pol III core by MonoQ anion exchange chromatography as reported previously (42). *E. coli* pol II (45), pol IV (46, 47), pol V (48), and RecA (49) were purified as previously described.

**Bacterial Strains.** The *E. coli* strains ZK126 (W3110 *DlacU169 tna2*) and its pol IV-deficient derivative (ZK126 *dinB::Kan*) (50) used in this study were the generous gift of Dr. Steven Finkel (University of Southern California, Los Angeles).

**DNA Substrates.** DNA oligodeoxynucleotides containing a site-specific  $\gamma$ -HOPdG (Figure 1A) were synthesized and purified as previously described (51). This 30-mer had the following sequence: GCTAGTACTCGTCGACAATTCCG-TATCCAT, where the bolded G denotes the position of the  $\gamma$ -HOPdG. Procedures to convert  $\gamma$ -HOPdG into the permanently ring-opened adduct, reduced  $\gamma$ -HOPdG (Figure 1B), were performed as previously described (31). The Lys-Trp-Lys-Lys tetrapeptide was synthesized by Sigma-Genosys. The Lys-Phe-His-Glu-Lys-His-His-Ser-His-Arg-Gly-Tyr dodecylpeptide was purchased from Sigma-Genosys. The generation of the DNA–peptide cross-links (Figure 1C) and purification of the DNA–peptide cross-link-containing oligodeoxynucleotides was carried out according to a published protocol (31). These 30-mer oligodeoxynucleotides were used as templates in replication reactions in vitro and also for preparation of site specifically modified vectors for cellular studies. All other oligodeoxynucleotides were obtained from the Molecular Microbiology and Immunology Research Core Facility, Oregon Health & Science University.

**Replication Assays in Vitro.** Preparations of primer-template DNA substrates were performed as previously described (52). Pol bypass assays with human pol  $\kappa$  and *E. coli* pol II, pol III, and pol IV were carried out using 5 nM primer-template DNA substrates in the presence of 25 mM Tris-HCl (pH 7.5), 5 mM

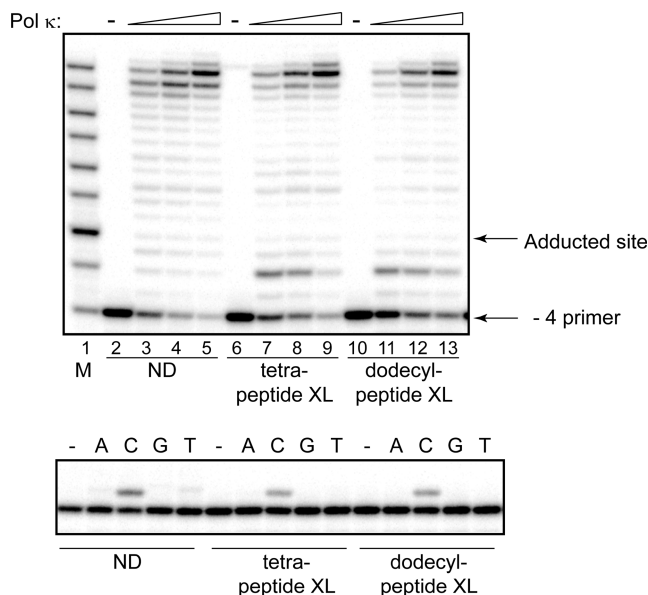
MgCl<sub>2</sub>, 10% (v/v) glycerol, 10 mM NaCl, 0.1 mg/mL bovine serum albumin, and 5 mM dithiothreitol at 37 °C. Pol bypass assays with *E. coli* pol V were carried out using 5 nM primer-template DNA substrates in the presence of 20 mM Tris-HCl (pH 7.5), 8 mM MgCl<sub>2</sub>, 4% (v/v) glycerol, 10 mM sodium glutamate, 5 mM dithiothreitol, 100  $\mu$ M EDTA, 2  $\mu$ M single-stranded 36-mer oligodeoxynucleotide, 12  $\mu$ M RecA, and 1 mM adenosine 5' [ $\gamma$ -thio]triphosphate. Prior to pol V-catalyzed reactions, single-stranded oligodeoxynucleotide and RecA were preincubated in reaction buffer in the presence of adenosine 5' [ $\gamma$ -thio]triphosphate at 37 °C for 3 min and then added to the primer-template DNA substrates. The reactions were initiated by addition of dNTPs and pol V and conducted at 37 °C. Protein concentrations, dNTPs concentrations, and incubation times are given in the figure legends. Pol reactions were terminated by the addition of an equal volume of a solution of 95% (v/v) formamide, 20 mM EDTA, 0.2% (w/v) bromophenol blue, and 0.2% (w/v) xylene cyanol. Products were resolved through a 15% (w/v) denaturing polyacrylamide gel in the presence of 8 M urea and visualized using a PhosphorImager screen (GE Healthcare).

**Replication of DNAs Containing Site-Specific DNA–Peptide Cross-Links in *E. coli*.** The pMS2 phagemid shuttle vector (40) was a gift from Dr. M. Moriya, State University of New York, Stony Brook. Single-stranded, site specifically modified pMS2 vectors were constructed as in previous studies (17, 31, 40). Transformations of *E. coli* cells with these vectors and analyses of the progeny DNAs by differential hybridization were performed as previously described (17, 31). Individual DNAs were isolated using Qiagen plasmid miniprep kits and tested by *ScaI* restriction endonuclease according to manufacturer's recommendations.

## Results

**Preparation of DNA–Peptide Cross-Links.** Although there are multiple potential sites of adduction within both DNA and protein, we have chosen to model DNA–peptide cross-links via acrolein-modified DNA at *N*<sup>2</sup>-dG. Acrolein reacts with DNA primarily at *N*<sup>2</sup>-dG, yielding  $\gamma$ -HOPdG, a lesion that undergoes spontaneous ring opening and closing (Figure 1A) (21). In the presence of NaBH<sub>4</sub>,  $\gamma$ -HOPdG can be converted to its reduced derivative (Figure 1B) that serves in our assays as a model for the permanently ring-opened form of the adduct. The free aldehyde of the natural, unreduced  $\gamma$ -HOPdG can react with primary and secondary amines in peptides and proteins (23, 24). When DNAs containing these lesions are incubated in the presence of peptides that contain both  $\alpha$  and  $\epsilon$  amino groups, the relative *pK*<sub>a</sub> of the  $\alpha$  amino group dominates the course of the cross-linking reaction, forming a carbinolamine linkage between the N-terminal  $\alpha$  amino group and the aldehyde of the  $\gamma$ -HOPdG adduct. The initial carbinolamine linkage can dehydrate to a Schiff base that can be reductively trapped in the presence of a mild reducing agent such as NaCNBH<sub>3</sub> to form an irreversible cross-link (Figure 1C) (23). Thus, DNAs incubated as described above have stable peptide cross-links that are directly amenable to replication bypass analyses. These linkages through the  $\alpha$  amino group are common intermediates for a variety of DNA glycosylase/abasic site lyases (53); thus, our DNA–peptide cross-links model biologically relevant lesions.

The 30-mer oligodeoxynucleotides containing DNA–peptide cross-links were prepared as previously described (31) and tested for purity using denaturing (8 M urea) polyacrylamide gel. No bands were detected that would suggest either the presence of



**Figure 2.** Replication bypass of DNA–peptide cross-links by human pol  $\kappa$ . Upper panel: Primer extensions by pol  $\kappa$  were carried out for 20 min in the presence of 100  $\mu$ M dNTPs at 1.25 (lanes 3, 7, and 11), 2.5 (lanes 4, 8, and 12) or 5 nM (lanes 5, 9, and 13) protein concentrations. Lower panel: Single nucleotide incorporations by pol  $\kappa$  (1 nM) were carried out for 5 min in the presence of 20  $\mu$ M individual dNTPs. M, oligodeoxynucleotide sizing markers; ND, nondamaged template; and XL, cross-link-containing template.

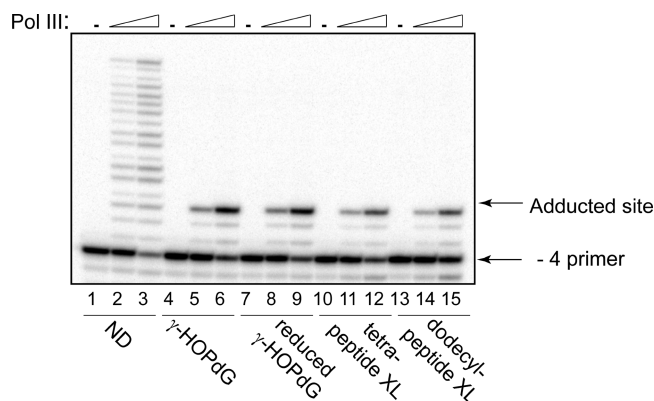
DNAs without cross-link or the decomposition of oligodeoxynucleotides (data not shown).

### Bypass of DNA–Peptide Cross-Links by Human Pol $\kappa$

Our previous studies had indicated that both the  $\gamma$ -HOPdG adduct and its reduced derivative posed a severe block to DNA synthesis by eukaryotic replicative pols, pol  $\delta$  and pol  $\epsilon$  (17, 54). On the basis of these observations, we considered it unlikely that either of them would be able to replicate past bulky  $\gamma$ -HOPdG-mediated DNA–peptide cross-links. In contrast to replicative pols, human pol  $\kappa$  could efficiently incorporate the correct nucleotide, C, opposite the ring-opened, reduced  $\gamma$ -HOPdG (54, 55). Furthermore, pol  $\kappa$  will efficiently extend a 0 primer if the correct C has been placed opposite either  $\gamma$ -HOPdG or its reduced derivative (54, 55). In the current study, we compared the ability of pol  $\kappa$  to carry out translesion synthesis past tetra- and dodecylpeptides linked to DNA via the ring-opened  $\gamma$ -HOPdG adduct vs control (unadducted) DNAs (Figure 1C).

Using a –4 primer, pol  $\kappa$  showed a significant processivity on nondamaged DNA, with a large percentage of primers being extended to near full length (Figure 2, upper panel, lanes 2–5). Surprisingly, neither of the peptide-modified  $\gamma$ -HOPdG substrates blocked the progression of pol  $\kappa$  (Figure 2, upper panel, lanes 6–13). Although there was a minor pause site, two nucleotides prior to the adducted site, there was no evidence of even a minor replication pause at the site of the lesion, and primers could be extended to full length comparable with the control DNAs.

Because pol  $\kappa$  incorporated a nucleotide opposite both lesions, the relative fidelity of the reactions was examined by carrying out single nucleotide incorporation assays using a –1 primer (Figure 2, lower panel). These assays revealed that in addition to these DNA–peptide cross-links not posing a block, pol  $\kappa$  utilized dCTP with a very strong preference over any other of the dNTPs (Figure 2, lower panel). Taken together, these data indicate that pol  $\kappa$  has the capacity to accurately bypass the complex *N*<sup>2</sup>-dG acrolein-derived peptide adducts.



**Figure 3.** Replication bypass of  $\gamma$ -HOPdG, reduced  $\gamma$ -HOPdG, and DNA–peptide cross-links by *E. coli* pol III. Primer extensions by the pol III replicase were carried out for 20 min in the presence of 200  $\mu$ M dNTPs at 0.01 (lanes 2, 5, 8, 11, and 14) or 0.05 nM (lanes 3, 6, 9, 12, and 15) protein concentrations. ND, nondamaged template; XL, cross-link-containing template.

**Replication of DNAs Containing DNA–Peptide Cross-Links by *E. coli* DNA Pols.** Whereas the blocking effect of  $\gamma$ -HOPdG and reduced  $\gamma$ -HOPdG has been shown for eukaryotic replicative pols (17, 54), the replicative pol in *E. coli* cells, pol III, has not been previously tested with any of these adducts. Here, the primer extensions by pol III were conducted with  $-4$  primers that were annealed with DNA templates containing either  $\gamma$ -HOPdG, reduced  $\gamma$ -HOPdG, or  $\gamma$ -HOPdG-derived DNA–peptide cross-links (Figure 3). The form of the multi-subunit pol III replicase employed here is the dimeric replicase that is utilized for chromosome replication; it contains two molecules of pol III core that attach to two  $\tau$  subunits of the clamp loading assembly. The observed results reveal that while the pol III replicase could efficiently catalyze DNA synthesis utilizing the nondamaged substrate (Figure 3, lanes 2 and 3), no bypass was detected in reactions containing any of the adducted templates; all primer extensions were terminated one nucleotide prior to the lesion, even at the highest enzyme concentrations (Figure 4, lanes 6, 9, 12, and 15). Previously, it has been shown that the exonuclease-deficient Klenow fragment of pol I, which is another major DNA pol in *E. coli*, catalyzed very inefficient and extremely error-prone DNA synthesis past the  $\gamma$ -HOPdG adduct (56, 57). Collectively, these data suggest that similar to mammalian cells, DNA synthesis past  $\gamma$ -HOPdG-derived lesions in bacteria is likely to utilize specialized bypass pols.

Given that human pol  $\kappa$  could readily bypass these lesions, it was hypothesized that *E. coli* pol IV, which is an orthologue of mammalian pol  $\kappa$  (58), might be capable of catalyzing translesion synthesis past these adducts. As anticipated, pol IV extended a  $-4$  primer annealed with an undamaged template to full length product (Figure 4, upper panel, lanes 2–5). In contrast, extension of the  $-4$  primer annealed to the DNA template containing  $\gamma$ -HOPdG was significantly blocked one nucleotide prior to the lesion and modestly opposite the lesion (Figure 4, upper panel, lanes 6–9). However, given a sufficient number of enzyme–DNA encounters, extension could proceed to full length. Similar reactions, but using the reduced  $\gamma$ -HOPdG, showed only a modest pause site one nucleotide prior to the lesion (Figure 3, upper panel, lanes 10–13). Thus, the permanently ring-opened analogue of the lesion affords efficient bypass.

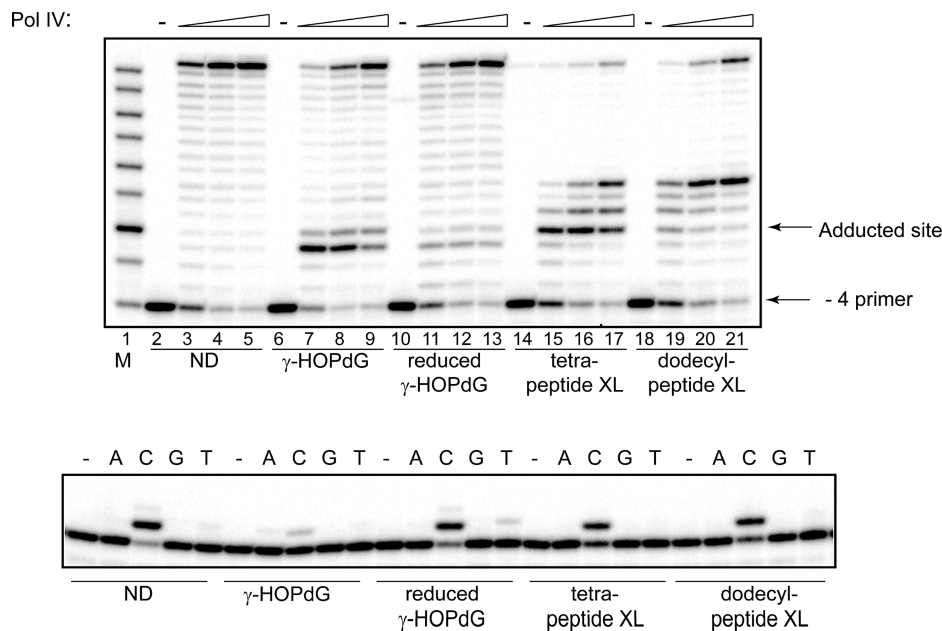
In contrast to these data, replication of the templates containing the  $\gamma$ -HOPdG adducts with tetra- and dodecylpeptide revealed different patterns of inhibition. For the DNA modified

with tetrapeptide, the dominant pause site occurred following incorporation of a nucleotide opposite the lesion (Figure 4, upper panel, lanes 14–17). However, using increasing enzyme concentrations, blockage opposite the lesion could be overcome, only to encounter replication blockage one and three nucleotides beyond the lesion (Figure 4, upper panel, lanes 16 and 17). The block at the third position beyond the lesion was very poorly extended, suggesting that there are structural impediments to the passage of the bulky adducted duplex DNA through the backside of pol IV. Comparable analyses using the dodecylpeptide-containing substrate revealed a less significant blockage opposite the lesion but an equivalent pause site at the third position beyond the lesion (Figure 4, upper panel, lanes 18–21). These data confirm that the presence of  $N^2$ -dG-linked peptide inhibits pol IV-catalyzed processive synthesis several nucleotides past the site of the lesion. However, because the magnitude and site of the pause was not affected by the increased bulk of the larger peptide, these data suggest that the impeding interactions are localized to the first few amino acids of the adducted peptides.

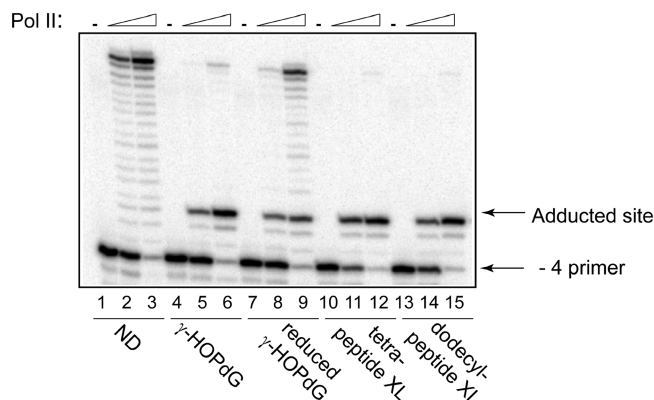
Single nucleotide incorporation analyses revealed that pol IV preferentially incorporated the correct nucleotide, C, opposite all of these lesions; however, misincorporations of A and T opposite the  $\gamma$ -HOPdG and reduced  $\gamma$ -HOPdG adducts were also observed (Figure 4, lower panel).

In addition to pol IV, *E. coli* possesses two other DNA damage-induced pols, pol II and pol V (59). Here, the abilities of pol II and pol V to synthesize DNA past  $\gamma$ -HOPdG, reduced  $\gamma$ -HOPdG, and  $\gamma$ -HOPdG-derived DNA–peptide cross-links have been tested by conducting primer extension experiments similar to those described above. The data revealed that pol II was strongly inhibited by all of these lesions one nucleotide prior to the site of modification (Figure 5). The blockage was less severe on the DNA substrate containing the ring-opened, reduced  $\gamma$ -HOPdG adduct with a significant percentage of primers being extended to the end of the template (Figure 5, lanes 8 and 9). In contrast, almost no full-length products were detected in reactions using substrates that contained either  $\gamma$ -HOPdG (Figure 5, lanes 5 and 6) or DNA–peptide cross-links (Figure 5, lanes 11, 12, 14, and 15). When pol V was examined with the same set of modified DNAs (Figure 6), patterns of inhibition of DNA synthesis appeared to be very similar to that observed for pol II, with the only exception that in pol V-catalyzed reactions, no bypass products were detected on substrates adducted with DNA–peptide cross-links (Figure 6, lanes 8 and 10). Thus, among *E. coli* DNA pols, pol IV was uniquely able to tolerate  $N^2$ -dG linked DNA–peptide cross-links in vitro.

**Replication of Plasmid DNA Containing DNA–Peptide Cross-Links in *E. coli*.** Having observed replication bypass of the  $\gamma$ -HOPdG-derived DNA–peptide cross-links by pol IV in vitro, we hypothesized that this pol may function in such a process intracellularly. To test this hypothesis, 30-mer DNA oligodeoxynucleotides adducted with either tetrapeptide or dodecylpeptide or containing no damage were individually inserted into a single-stranded pMS2 vector, and these vectors were used to transform the wild-type and pol IV-deficient *E. coli* cells. Following overnight selection on ampicillin-containing plates, colonies were counted, and the relative efficiency of transformation was calculated as the ratio of the number of clones originating from the adducted vectors to the number of clones originating from the nondamaged control. The average relative efficiencies with their standard deviations obtained from three independent experiments are given in Table 1, third

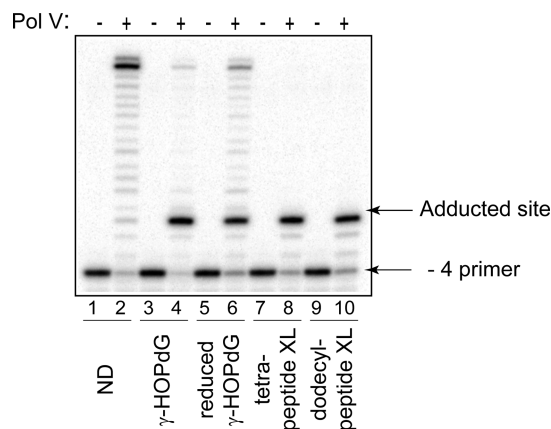


**Figure 4.** Replication bypass of  $\gamma$ -HOPdG, reduced  $\gamma$ -HOPdG, and DNA–peptide cross-links by *E. coli* pol IV. Upper panel: Primer extensions by pol IV were carried out for 20 min in the presence of 100  $\mu$ M dNTPs at 1.25 (lanes 3, 7, 11, 15, and 19), 2.5 (lanes 4, 8, 12, 16, and 20), or 5 nM (lanes 5, 9, 13, 17, and 21) protein concentrations. Lower panel: Single nucleotide incorporations by pol IV (1 nM) were carried out for 20 min in the presence of 20  $\mu$ M individual dNTPs. M, oligodeoxynucleotide sizing markers; ND, nondamaged template; and XL, cross-link-containing template.



**Figure 5.** Replication bypass of  $\gamma$ -HOPdG, reduced  $\gamma$ -HOPdG, and DNA–peptide cross-links by *E. coli* pol II. Primer extensions by pol II were carried out for 20 min in the presence of 250  $\mu$ M dNTPs at 0.5 (lanes 2, 5, 8, 11, and 14) or 5.0 nM (lanes 3, 6, 9, 12, and 15) protein concentrations. ND, nondamaged template; XL, cross-link-containing template.

column. These data suggested that DNA–peptide cross-links represented a more severe block for replication in pol IV-deficient mutant than in wild-type cells. However, on the basis of our previous experience (31), it was possible that a substantial percentage of the progeny DNAs originated from ligated pMS2 vectors that did not contain the insert sequences; therefore, they should be excluded from the analyses. To evaluate the number of progeny DNAs having specific insert sequences, the following approach was utilized. A subpopulation of clones were individually grown in the 96 well plates, transferred onto Whatman 541 paper, and subjected to differential hybridization, utilizing the 5'-radioactively labeled oligodeoxynucleotide probe G. This probe was designed to be complementary to the insert sequence, assuming no mutations were introduced. Additional 20-mer oligodeoxynucleotide probes, L and R, were designed to be complementary to the vector sequences located 60 and 52 nucleotides from the site of insertion. Hybridization with these probes allowed for the exclusion of the progeny DNAs with deletions involving the region of interest. Individual DNAs that



**Figure 6.** Replication bypass of  $\gamma$ -HOPdG, reduced  $\gamma$ -HOPdG, and DNA–peptide cross-links by *E. coli* pol V. Primer extensions by pol V (200 nM) were carried out for 20 min in the presence of 500  $\mu$ M dNTPs. ND, nondamaged template; XL, cross-link-containing template.

hybridized with a mixture of L and R probes, but did not hybridize with G probe, were isolated and analyzed further. Specifically, they were tested by cleavage with *ScaI* endonuclease. Because both the original pMS2 vector and the inserted DNAs contain *ScaI* recognition sites, cleavage of progeny DNAs containing the insert sequences can be easily identified by the generation of DNA fragments,  $\sim 1.9$  and  $\sim 3.2$  kb in length. Thus, the combination of differential hybridization and analyses of isolated plasmids by cleavage with *ScaI* facilitated the determination of the percentage of the progeny DNAs having inserted sequences (Table 1, fifth column). Subsequently, these values were used to re-evaluate the relative efficiencies of transformation, taking into account only the transformants in which vectors with inserts, but not other products of ligation and/or intracellular DNA rearrangements, were replicated. These data indicated that relative to wild-type cells, the pol IV-deficient mutant was very inefficient in replicating the adducted vectors, thus confirming the intracellular role for pol IV in bypass of  $\gamma$ -HOPdG-derived DNA–peptide cross-links.

**Table 1. Efficiency of *E. coli* Transformation Using Vector DNAs Containing DNA–Peptide Cross-Links**

<i>E. coli</i> strain	insert	relative efficiency of transformation	no. of colonies tested	colonies with inserts (%)	relative efficiency of transformation adjusted for no. of colonies with inserts	efficiency of transformation of pol IV-deficient mutant relative to wild type
wild type	nondamaged	1	106	97	1	
	tetrapeptide cross-link	0.45 ± 0.04	136	85	0.39 ± 0.035	1
	dodecylpeptide cross-link	0.39 ± 0.15	128	93	0.37 ± 0.14	1
pol IV <sup>−</sup>	nondamaged	1	136	98.5	1	
	tetrapeptide cross-link	0.05 ± 0.01	67	37	0.02 ± 0.004	0.05
	dodecylpeptide cross-link	0.12 ± 0.07	80	56	0.07 ± 0.04	0.19

**Mutagenic Properties of  $\gamma$ -HOPdG-Mediated DNA–Peptide Cross-Links in *E. coli*.** Earlier reports (17, 56, 57) indicated that translesion synthesis past the  $\gamma$ -HOPdG adduct was essentially error-free in *E. coli*. Although these studies assayed bacterial strains with various genetic backgrounds and utilized different vector systems, mutations (G to T transversions) were consistently observed at less than 1% frequencies or not detected at all. In this report, we examined the potential of the  $\gamma$ -HOPdG-mediated DNA–peptide cross-links to cause mutations during extrachromosomal replication in *E. coli*. As described above, following intracellular replication of site specifically modified pMS2 vectors, individual clones were tested by differential hybridization using a probe that hybridized only when nonmutagenic replication bypass had occurred. Using this method, the progeny DNAs containing no mutations were readily identified. To verify the accuracy of hybridization procedure, approximately 10% of such clones were analyzed by DNA sequencing using oligodeoxynucleotide R as a primer. Among these DNAs, no clone had any sequence alteration. However, a few clones were identified that did not hybridize with probe G, but according to the ScaI cleavage analyses, they contained inserts. Targeted mutations were detected in these clones by DNA sequencing, indicating that in both the wild-type and the pol IV-deficient cells, the  $\gamma$ -HOPdG-mediated DNA–peptide cross-links were only marginally miscoding. Specifically, two mutations were observed in the wild-type cells: one G to A transition (caused by the tetrapeptide cross-link) and one G to T transversion (caused by the dodecylpeptide cross-link). In pol IV-deficient mutant, the only mutation found was G to C transversion (caused by the tetrapeptide cross-link).

## Discussion

Previous investigations have provided insights into the mechanisms by which DNA–protein cross-links are processed and removed (1). Although there have been inconsistent reports in the literature on the role of NER in the removal of these adducts, these apparent contradictions may potentially be explained by differences in both the damage-inducing agents and the assays used to assess repair capacity. With the advent of technologies to create site-specific DNA–protein and DNA–peptide adducts, a much clearer picture has emerged for the role of NER in processing of these lesions. Specifically, data in both bacterial and mammalian systems indicate that relative to DNA–protein cross-links, DNA–peptide cross-links are preferable substrates for the initiation of repair by NER proteins (25–28, 30). These data are highly consistent with a role for proteolytic degradation of cross-linked proteins occurring prior to repair, since proteasomal inhibitors significantly reduce repair (29).

Because proteolytic processing of DNA–protein cross-links appears to be integral to the ultimate repair, these data raise the possibility that replication forks could encounter these intermediates prior to NER. Therefore, it is likely that replicative pols, such as pol  $\delta$  and pol  $\epsilon$  in mammalian cells and pol III in

bacteria, would be blocked. In such a scenario, specialized translesion pols could be recruited to these sites. Germane to this hypothesis, the study presented herein shows that pol  $\kappa$  was able to catalyze high-fidelity efficient bypass of DNA–peptide cross-links, where the linkage of the peptide to DNA was via an acrolein-mediated bridge to  $N^2$ -dG. These biochemical data suggest that pol  $\kappa$  contributes to the nonmutagenic bypass events during intracellular replication past  $N^2$ -dG DNA–peptide cross-links. Thus, the relatively accurate replication past the  $\gamma$ -HOPdG-mediated tetrapeptide cross-link that previously was observed in mammalian cells (31) may, at least partially, be pol  $\kappa$ . Pol  $\kappa$  has been shown to catalyze high-fidelity bypass of benzo[a]pyrene and other bulky  $N^2$ -dG adducts (32–38). Recently, we have extended the substrate repertoire of pol  $\kappa$  to include replication bypass of DNA interstrand cross-links (60). In this study, DNAs were utilized containing site specifically engineered  $N^2$ – $N^2$ -dG interstrand cross-links that model DNA repair intermediates, hypothesized to be in a repair pathway not requiring homologous recombination. We demonstrated that pol  $\kappa$  could catalyze bypass of cross-linked substrates in which nucleotides 3' to the cross-link had been removed. Data were also obtained that demonstrated that loss or even reduction in cellular levels of pol  $\kappa$  resulted in increased cytotoxicity and chromosomal damage when cells were exposed to mitomycin C, an  $N^2$ – $N^2$ -dG cross-link-inducing agent.

Collectively, these data reveal a consistent pattern of pol  $\kappa$  being an efficient and high-fidelity enzyme in the bypass of extremely bulky  $N^2$ -dG adducts. Relative to these and other catalytic bypass substrates, it is of interest that the cocrystal structure has been solved for the catalytic core of pol  $\kappa$  with a primer-template complex and an incoming nucleotide (61). This structure clearly shows pol  $\kappa$  completely encircling the duplex DNA, using an N-terminal clasp. It was hypothesized that this structure would enhance the thermodynamic stability of the core complex, thus facilitating replication bypass. Given this tight-fitting encircling of the DNA, we hypothesized that there must be considerable flexibility in the hinge domains to allow such bulky lesions to pass through the core of the complex. Thus, it is of considerable interest to determine the structures of additional complexes to reveal the conformational changes that must take place to permit these error-free reactions.

Our data also demonstrated that *E. coli* pol III, pol II, and pol V were all incapable of replicating past DNA–peptide cross-links as assayed herein but that pol IV was modestly efficient at the incorporation and extension steps; furthermore, the incorporation of the correct nucleotide opposite the lesions was highly preferred. However, unexpectedly, processive synthesis of pol IV was strongly inhibited beyond the site of the lesions. Such blocks were not observed with the  $\gamma$ -HOPdG, reduced  $\gamma$ -HOPdG (this study), or furfuryl  $N^2$ -dG adducts (34). These data suggest that the ability of pol IV to continue processive synthesis is blocked via a physical obstruction of the peptide cross-link with a portion of pol IV in a location where the newly synthesized DNA exits the pol. Such downstream blockages

have been previously observed with the HIV reverse transcriptase replicating  $N^2$ -dG styrene oxide-modified DNAs (62, 63). This blockage could be attributed directly to the interaction of  $\alpha$ -helix H and I, tracking in the minor groove of the newly synthesized duplex DNA, such that site-directed mutagenesis of selected amino acid residues in the tracking face of  $\alpha$ -helix H modulated the downstream pause sites (62, 64). We hypothesize that similar “reading heads” of pol IV may monitor the newly synthesized duplex DNA. Insights into this mechanism await crystal and cocrystal structures of pol IV.

Although DNA synthesis past the  $\gamma$ -HOPdG-mediated DNA–peptide cross-links by pol IV in vitro was partially inhibited relative to the nondamaged DNA, our cellular studies clearly implicate pol IV as a major contributor to the replication bypass of these lesions in vivo. In its absence, we observed ~5- and 20-fold reduction in recovery of plasmids when the dodecylpeptide or tetrapeptide, respectively, was site specifically linked to the single-stranded vector DNAs, and these DNAs replicated in *E. coli* cells. Surprisingly, such cross-links appeared to be only marginally miscoding in both the wild-type and pol IV-deficient strains. In wild-type *E. coli*, mutations were observed at overall frequencies of ~1%, which is significantly less than the frequency of mutations caused by the identical tetrapeptide cross-link in mammalian cells, in which ~8% of bypass events resulted in targeted mutations (31). Interestingly, the  $\gamma$ -HOPdG adduct is also less miscoding in *E. coli* relative to mammalian system (17, 56, 57). Overall, these data give strong support for the role of DinB family pols in the bypass of very bulky  $N^2$ -dG adducts.

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