The use of an artificial nucleotide for polymerase-based recognition of carcinogenic O\textsuperscript{6}-alkylguanine DNA adducts

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ABSTRACT

Enzymatic approaches for locating alkylation adducts at single-base resolution in DNA could enable new technologies for understanding carcinogenesis and supporting personalized chemotherapy. Artificial nucleotides that specifically pair with alkylated bases offer a possible strategy for recognition and amplification of adducted DNA, and adduct-templated incorporation of an artificial nucleotide has been demonstrated for a model DNA adduct O\textsuperscript{6}-benzylguanine by a DNA polymerase. In this study, DNA adducts of biological relevance, O\textsuperscript{6}-methylguanine (O\textsuperscript{6}-MeG) and O\textsuperscript{6}-carboxymethylguanine (O\textsuperscript{6}-CMG), were characterized to be effective templates for the incorporation of benzimidazole-derived 2\textsuperscript{′}-deoxynucleoside-5\textsuperscript{′}-O-triphosphates (BenziTP and BIMTP) by an engineered \textit{KlenTaq} DNA polymerase. The enzyme catalyzed specific incorporation of the artificial nucleotide Benzi opposite adducts, with up to 150-fold higher catalytic efficiency for O\textsuperscript{6}-MeG over guanine in the template. Furthermore, addition of artificial nucleotide Benzi was required for full-length DNA synthesis during bypass of O\textsuperscript{6}-CMG. Selective incorporation of the artificial nucleotide opposite an O\textsuperscript{6}-alkylguanine DNA adduct was verified using a novel 2\textsuperscript{′},3\textsuperscript{′}-dideoxy derivative of BenziTP. The strategy was used to recognize adducts in the presence of excess unmodified DNA. The specific processing of BenziTP opposite biologically relevant O\textsuperscript{6}-alkylguanine adducts is characterized herein as a basis for potential future DNA adduct sequencing technologies.

INTRODUCTION

Human genetic material is under constant attack by harmful substances. For example, exposure to alkylating agents from the diet, tobacco smoke, environment, and chemotherapeutics, as well as endogenous sources can lead to DNA damage by chemical alkylation of nucleophilic sites on DNA bases giving rise to DNA adducts (1,2). Among the types of DNA adducts that may be formed, O\textsuperscript{6}-alkylguanine (O\textsuperscript{6}-alkylG) adducts are of important biological relevance because of their high propensity for inducing mutations (3,4), including G to A transitions prevalent in cancer, for example in codon 12 or 13 of the proto-oncogene K-ras (5), and the tumor suppressor gene p53 (6). Therefore, together with an understanding of the causal relationship between adduct formation and mutagenesis, strategies for locating alkylation adducts in DNA is an important basis to establish early biomarkers of carcinogenesis (7).

Among O\textsuperscript{6}-alkylG adducts, O\textsuperscript{6}-methylguanine (O\textsuperscript{6}-MeG) and O\textsuperscript{6}-carboxymethylguanine (O\textsuperscript{6}-CMG; Figure 1A) have been found to be present in human blood DNA (8) and tissue samples from meat-eaters and cancer patients (9,10). Putative sources of O\textsuperscript{6}-MeG include methylaziridines, e.g. the tobacco specific nitrosamine 4-(methylaziridinyl)-1-(3-pyridyl)-1-butane (11), endogenous methyl donors such as S-adenosylmethionine (12), and methylation-inducing antitumor drugs like temozolomide (13). O\textsuperscript{6}-CMG is hypothesized to arise from endogenous nitrosation of glycine in the human gastrointestinal tract (14) and its occurrence has been linked to diets high in red meat (10), an established risk factor for colon cancer (15). O\textsuperscript{6}-alkylG adducts occur physiologically at extremely low levels and are therefore difficult to detect. Generally applied methods for quantifying O\textsuperscript{6}-MeG and O\textsuperscript{6}-CMG adducts are based on LC–MS/MS approaches (10,15), however, these methods do not account for DNA
inoligonucleotides acted as BIM bleDNAduplexes when paired opposite O6 pairing partners and resulted in the formation of more sta-
O6 minated with some of the artificial bases paired opposite were polymerases substrates for extending DNA primerster-
vs unmodified G (26–28). Furthermore, these analogues were probes for DNA adducts.

BIM BARTIFICIAL nucleotides Artificial nucleotides and BenziTP investigated as alternatives for enzymatic discrimination between various DNA adducts and unmodified DNA with single-base resolution has been achieved by single molecule real time (SMRT) sequencing (17). This approach has excellent potential for future biological applications, but amplification or enrichment of the target sequence is still required prior to sequencing, along with further development of quantitation algorithms. Bowers and co-workers have reported two methods for sequencing oxidative lesions that are substrates for base excision repair (BER) (18,19). Following specific excision of the adducts with BER DNA glycosylases, they either marked the site with an amplifiable unnatural base pair or they identified the adduct location by introducing a deletion mutation (18,19). However, such specific enzymes do not exist for DNA alklyation adducts, thus an alternative strategy could be valuable.

Artificial nucleosides that specifically pair with DNA alkylation adducts together with DNA polymerases with the capacity to process altered base pairs offer a basis for alklyation adduct sensing at single base resolution. Polymerase-mediated incorporation of synthetic triphosphates opposite DNA damage has been reported for abasic sites, isoguanine, 8-oxoguanine (8-oxoG), cis-platinumed guanine, and O6-alkylG adducts (20–25). For example, the synthetic nucleoside triphosphate dAdaptTP discriminates 8-oxoG from G in single nucleotide incorporation studies by the A-family DNA polymerase Klenow(exo-) (22). Artificial bases like BIM and Benzi, and related analogues in oligonucleotides acted as O6-alkylG adduct-specific base pairing partners and resulted in the formation of more stable DNA duplexes when paired opposite O6-alkylG adducts vs unmodified G (26–28). Furthermore, these analogues were polymerase substrates for extending DNA primers terminated with some of the artificial bases paired opposite O6-alkylG adducts (29,30). Artificial nucleotides BIMTP and BenziTP acted as impeding substrates for human DNA polymerase η (hPol η) in replication of the major cisplatin DNA adduct (23). Recently, we communicated specific incorporation of BenziMP opposite O6-benzylguanine (O6-BnG) adducts versus nondamaged guanine templates by a mutant KlenTag polymerase KTqM747K. Furthermore, BenziTP was required for full-length product formation in bypass of this bulky lesion and additionally was used for amplification of alkylated DNA in linear PCR by KTqM747K polymerase (25). This discovery was the first report of an artificial nucleotide being specifically incorporated opposite an O6-alkylG DNA adduct, but previous studies were carried out with the model adduct O6-BnG, which has not been observed in vivo (31).

Herein, we addressed the scope of an alkylation adduct-artificial nucleotide replication system with regards to O6-alkylG adducts of biological relevance, namely O6-MeG and O6-CMG (Figure 1A). We investigated the bypass of these adducts by a mutant KlenTag DNA polymerase using artificial nucleotides as substrates (Figure 1B). The DNA polymerase KTqM747K is a mutant of the N-terminally truncated A-family Taq polymerase. It is thermostable and can efficiently bypass various DNA lesions (25,32,33). We found that the O6-alkylG adducts template the specific incorporation of the artificial nucleotide BenziMP when DNA synthesis was carried out by KTqM747K. Furthermore, full-length products were formed following effective incorporation and extension of Benzi nucleotide. A 2′,3′-dideoxy Benzi-nucleotide was newly synthesized and allowed verification that the artificial nucleotide does not impede KTqM747K polymerase in processive DNA replication past natural templates. Furthermore, it enabled marking of the adduct site with the artificial nucleotide. Finally, we found that with BenziTP biologically relevant O6-alkylG adducts could be recognized in mixtures of damaged and non-damaged DNA. The findings demonstrated herein represent a chemical basis for enzymatic O6-alkylG adduct detection technologies at single-base resolution that are required for establishing biomarkers of cancer risk or chemotherapeutic drug efficacy.

**MATERIALS AND METHODS**

**Chemical reagents and materials**

Reagents were purchased from Sigma-Aldrich and used without further purification. Nucleoside analogues BIM and Benzi (30,34), and triphosphates BIMTP and BenziTP were synthesized as described previously (25). O6-MeG and unmodified 5′-O-dimethoxytrityl phosphoramidites were purchased from Link Technologies Ltd. The O6-CMG phosphoramidite was prepared as reported (35). Unlabeled dNTPs were obtained from Invitrogen and [γ-32P]ATP was purchased from PerkinElmer Life Sciences. KTqM747K mutant DNA polymerase was kindly provided by myPOLS Biotec GmbH. Pyrophosphatase (Inorganic, Escherichia coli) was purchased from New England Biolabs. Silica gel 60 F254 plates with aluminum backing were used for thin layer chromatography. Flash column chromatography was performed on a Biotage system with pre-packed Flash+ KP-SiO2 cartridges. 1H, 13C and 31P NMR spectra were recorded on a Bruker Biospin 400 MHz NMR instrument, and chemical shifts are reported in parts per million (ppm, δ) relative to the chemical shift of the respective NMR solvent. High resolution mass spectra were recorded on
Thermo Scientific exactive mass spectrometer with electrospray ionization.

**Oligonucleotides**

Oligonucleotides were either purchased from Eurofins, Microsynth or Eurogentec. DNA sequences are listed in Supplementary Table S1. Modified oligonucleotides containing O6-CMG were synthesized as described elsewhere (36). Oligonucleotides were purified by reverse phase HPLC on a Phenomenex Luna C-18 column (5 μm, 4.6×250 mm). The O6-CMG DNA 28mer was purified with a mobile phase gradient of 10.5–14.5% acetonitrile in 50 mM TEAA over 50 min and eluted at 31 minutes (Supplementary Figures S1 and S2). 48mer O6-CMG DNA was prepared and purified as reported elsewhere (35). Corresponding oligonucleotide fractions were collected and combined, dried on a centrifugal vacuum concentrator and stored at −20°C until further use. The ssDNA concentration was determined by UV spectrosocopy at 260 nm on a NanoDrop 1000 spectrophotometer. Theoretical molar extinction coefficients of the DNA sequences were determined using Integrated DNA technologies online at [http://eu.idtdna.com/analyzer/Applications/OligoAnalyzer/](http://eu.idtdna.com/analyzer/Applications/OligoAnalyzer/).

**Primer extension assays**

Radioactive labeling of primer strands at their 5’ end was carried out using T4 polynucleotide kinase (Promega) and [γ-32P]ATP following manufacturer protocol. Primer and templates were annealed by incubating at 95°C for 5 min and slow cooling over 12 h. Final concentrations were 1 μM primer and 1.5 μM template. Standard primer extension reactions (10 μl) contained 1x KTq reaction buffer, 5 mM enzyme, 15 nM DNA (15 nM primer and 22.5 nM template), and 10 μM dNTPs. In full-length DNA synthesis experiments, reactions contained all four natural dNTPs (10 μM total) with or without BenziTP (10 μM). Primer/template, nucleotides and DNA polymerase were incubated at 55°C for 10 min. 1x KTq reaction buffer contained 50 mM Tris–HCl (pH 9.2), 16 mM (NH4)2SO4, 2.5 mM MgCl2, 0.1% Tween 20. Reactions were quenched by adding 20 μl PAGE gel loading buffer (80% formamide, 20 mM EDTA, 0.05% bromophenol blue, 0.05% xylene cyanole FF) and the product mixtures were analyzed by 15% polyacrylamide/7M urea denaturing gels, visualized by autoradiography, and quantified with Quantity One Software (Bio-Rad). To obtain kinetic parameters v_{max}, K_M and k_{cat}, the intensities of n + 1 bands (quantified on the Quantity One Software, Bio-Rad) were fit to a Michaelis–Menten hyperbola using SigmaPlot12 Software (Systat Software). Reactions were performed in triplicate and for K_M values, means (± standard deviations) are reported.

**Linear amplification of O6-alkyIG DNA**

Reactions were incubated in a Biometra T3000 thermocycler, where 30 cycles of denaturation, annealing, and elongation were performed under the following conditions: 30 s at 95°C, 30 s at 42°C, and 30 s at 55°C. Reactions contained 0.5 ng of corresponding O6-alkyIG template DNA (28 nt), 300 nM primer (19 nt), 25 nM KTqM747K DNA polymerase, 1x KTq reaction buffer, all four dNTPs (10 μM), and 10 μM or no BenziTP. Product mixtures were separated on a 20% polyacrylamide/7M urea denaturing gel, stained with SybrGold nucleic acid gel stain (Invitrogen) and visualized on a Bio-Rad molecular imager Gel Doc XR+ Imaging System. Product bands were quantified using the software Image Lab 3.0 (Bio-Rad) and normalized to the known quantity of the 28 nt marker loaded on the same gel, indicating a yield of 14.6 ng ampiclon (theoretical yield on the basis of 30 cycles is 15 ng).

**Molecular modeling studies**

Structures were computed with the Molecular Operating Environment software suite (Chemical Computing Group). Crystal structures of a KTq mutant polymerase with incoming ddBenziTP opposite template G (PDB code: 3PY8) (33) and structures of Bst DNA polymerase with incoming dCTP opposite template G (PDB code: 1LV5) or incoming ddTP opposite template O6-MeG (PDB code: 2HHW) were used (39). For modeling studies with the KTq mutant, crystal structure (PDB code: 3PY8) was modified by attaching an O6-CMG group to the templating G and replacing incoming ddCTP by BenziTP or BIMTP (in favored syn conformation). In studies involving Bst DNA polymerase with template G incoming dCTP (PDB code: 1LV5) was replaced by syn BenziTP and for template O6-MeG, dTTP was altered to syn BenziTP (PDB code: 2HHW). For energy minimizations the potential energy of the protein was fixed and followed by applying the Amber99 force field. Visualization was performed in the PyMol software (Schrodinger).
Sensing O6-alkylG-containing DNA mixed with unmodified DNA

Mixtures of G and O6-alkylG DNA were prepared with a constant amount of template (22.5 nM template annealed to 15 nM radiolabeled primer) at varying ratios of G:O6-alkylG DNA: 1:0, 1000:1, 100:1, 10:1, 5:1, 3:1, 2:1, 1:1. Primer extension reaction mixtures (10 μl) contained 1 × KTq reaction buffer, 5 nM enzyme, 15 nM DNA, and 10 μM BenziTP. DNA mixtures were prewarmed and BenziTP/Polymerase mixture was added and allowed to react at 55°C for 10 min. Products were separated on a 15% polyacrylamide/7M urea denaturing gel and visualized by autoradiography. Intensity of n + 1 bands was quantified on the Quantity One Software (Bio-Rad). The experiment was performed in triplicate and mean values ± standard deviations are reported.

RESULTS AND DISCUSSION

Translesion DNA synthesis past O6-alkylG adducts by KTqM747K

To investigate the capacity of the mutant KlenTaq polymerase KTqM747K to replicate DNA containing O6-MeG or O6-CMG, primer extension studies were performed. Thus, a 5'-end radiolabeled 23 nucleotide (nt) primer and a 28 nt template containing either G, O6-MeG, or O6-CMG (referring to X positioned at nucleotide 24, Figure 2A) were allowed to react with KTqM747K polymerase and dNTPs, (Figure 2). Extension products were analyzed by gel shift assay on denaturing polyacrylamide gels and visualized by autoradiography. For results presented in Figure 2, the level of nucleotide incorporation is indicated as percent primer extension and was calculated as a ratio of the amount of n + 1 extension product formed to initial amount of primer.

The capacity of KTqM747K to replicate DNA containing O6-alkylG adducts in the presence of four natural dNTPs depended on adduct structure. Replication in the presence of O6-MeG gave rise to full-length product (26%, Figure 2B, X = O6-MeG, lane 4), whereas in the presence of O6-CMG significantly less full-length product was observed (7%, Figure 2B, X = O6-CMG, lane 4). In both cases, misincorporation of dTMP was favored over correct dCMP incorporation (Figure 2B). For O6-MeG, dTMP was incorporated to a large extent (92%) and dCMP was also incorporated (41%). For O6-CMG templates, natural nucleotides were incorporated less than they were for O6-MeG templates. Thus, there was 32% dTMP misincorporation and 17% correct dCMP incorporation. In a previous study concerning O6-BnG (25), the polymerase was stalled. Considering the proficiency of O6-MeG bypass, stalling in the other two cases may be attributed to the larger sizes of the adducts. For O6-BnG, dTTP misincorporation was favored over dCTP incorporation (32 vs 18%) (25). Misincorporation of dTTP has been observed in bypass of O6-MeG by bacterial Escherichia coli KF DNA polymerase (40), B. stearothermophilus Bst polymerase, Vent (exo-) (41), viral

Figure 2. (A) DNA polymerase-mediated primer extension experiments and sequences used in this study. (B) Replication by KTqM747K DNA polymerase past templates with X = G, O6-MeG, or O6-CMG for natural or artificial nucleotides. M, blank; 4, all four dNTPs; G, dGTP, A, dATP, T, dTTP; C, dCTP, BIM, BIMTP; Benzi, BenziTP; final dNTP concentrations were 10 μM or 10 μM each in case of 4, incubated at 55°C for 10 min.

T4 (42), T7 (exo-) DNA polymerase and HIV reverse transcriptase (43), or eukaryotic Drosophila melanogaster Pol α (44). Also, human Pol β and translesion Pol α had a similar preference for dTTP when replicating over O6-MeG (4,45).

Specific incorporation of an artificial nucleotide opposite O6-alkylG DNA adducts

Having established how KTqM747K polymerase bypasses O6-alkylG adducts with natural nucleotides as substrates, the incorporation of two benzimidazole-derived base-modified nucleotide analogues (BIMTP and BenziTP) was investigated in the same manner as described above, adding BIMTP or BenziTP in primer extension reactions. Both artificial nucleotides were effective substrates for KTqM747K polymerase (Figure 2B). However, BIMTP yielded little extension product in general: G (20%), O6-MeG (11%), and O6-CMG (14%; Figure 2B). On the other hand, BenziTP was a good substrate and there were high incorporation percentages for both adducts (Figure 2B, X = O6-MeG: 95%; X = O6-CMG: 87%) but, importantly, not with G (Figure 2B, X = G: 12%). This observation matched the preference for alkylated templates previously reported for O6-
due to template-independent incorporation of an additional nucleotide (46). BenziTP was required for efficient bypass of O6-CMG by overcoming the stalling of the polymerase at the adduct site to result in full-length products.

Steady-state kinetic analysis of translesion DNA synthesis

In order to quantitatively compare efficiencies of nucleotide incorporation in replication of DNA containing O6-MeG or O6-CMG, steady-state kinetic parameters for KToqM747K polymerase catalysis were determined (Table 1). In this experiment, single nucleotide incorporation (nt+1 product formation) was followed over time, and kinetic parameters \( k_M \) and \( k_{cat} \) were derived (37). In general, the presence of the O6-alkylG DNA adducts did not greatly influence the catalytic turnover \( k_{cat} \), but decreased the binding affinity (increasing \( K_M \)) compared to replication of unmodified DNA with natural dNTPs. The catalytic efficiencies \( k_{cat}/K_M \) for synthesis past O6-MeG (0.038 μM⁻¹min⁻¹), O6-CMG (0.007 μM⁻¹min⁻¹), and O6-BnG (0.021 μM⁻¹min⁻¹) (25) by KToqM747K were similar to values measured previously for incorporation of dTMP opposite O6-MeG by the A-family Bst DNA polymerase (0.075 μM⁻¹min⁻¹) (39). Compared to misincorporation of dTMP by the archaeal Sulfolobus solfataricus DNA polymerase Dpo4 (dTTP opposite O6-MeG: 0.0044 μM⁻¹min⁻¹) (47), the KToqM747K polymerase tested herein was 9-fold more efficient in replicating O6-MeG adducts. The human translesion DNA polymerase \( \eta \) on the other hand is more efficient in translesion synthesis past O6-alkylG adducts than KToqM747K: 20-fold more for O6-MeG (48), and 9-fold more in bypass of O6-CMG (35).

The \( K_M \) value for processing of BenziTP was the same order of magnitude for unmodified as well as adducted templates (Table 1). However, catalytic turnover \( k_{cat} \) was significantly higher for replication over O6-alkylG adducts versus G (17-fold for O6-CMG; 55-fold for O6-MeG). The highest catalytic efficiency \( k_{cat}/K_M \) for BenziMP incorporation was observed when O6-MeG was in the template, and was 13-fold higher than for O6-CMG or 6-fold than for O6-BnG (\( k_{cat}/M_0 \).120 μM⁻¹min⁻¹) (25). Finally, by comparing these values with catalytic efficiencies for incorporation of BenziMP opposite natural templates (25), incorporation opposite A was almost 2-fold more efficient than with templating O6-MeG. However, processing of BenziTP opposite A was 30-fold less efficient than incorporation of dTMP (25). When comparing incorporation of BenziMP vs dTMP, the difference in selectivity was 19-fold with the O6-MeG template, 8-fold for O6-CMG, and 6-fold for O6-BnG (25). We previously demonstrated that BenziMP was also incorporated by hPol \( \eta \) during replication of unmodified or platinated G templates (23). However, incorporation of BenziMP by KToqM747K opposite O6-MeG was 29-fold more efficient than its incorporation by hPol \( \eta \) opposite the major platinum intrastrand cross-link product \( cis\text{-}Pr-1,2\)-d(GpG) (\( k_{cat}/K_M \) 0.025 μM⁻¹min⁻¹) (23). In summary, kinetic data confirmed the specific incorporation of BenziMP opposite O6-alkylG adducts compared to guanine with the catalytic efficiency of incorporation opposite G being reduced 150-fold compared to O6-MeG, 24-fold for O6-BnG (25), and 12-fold for O6-CMG. Steady-state kinetic data re-

**Figure 3.** Full-length product formation in replication of O6-alkylguanine adducts by KToqM747K. (A) Setup of running start primer extension experiment. (B) PAGE analysis of 19 nt primer extension products with template X = O6-MeG or O6-CMG at position 24 nt. M19, marker for primer (19 nt); M23, marker for 23 nt (position prior to adduct site X) 4, all four dNTPs (10 μM); 4+B, all four dNTPs (10 μM) plus 10 μM BenziTP.
revealed the fastest incorporation efficiencies for Benzi were opposite \(O^6\)-MeG, and the highest selectivity for BenziTP over natural dNTPs was observed for \(O^6\)-MeG templates. Findings from primer extension and steady-state kinetic experiments indicate that \(K{TqM747K}\) polymerase can readily bypass \(O^6\)-MeG, with natural nucleotides being well incorporated. Since \(K{TqM747K}\) was significantly stalled by \(O^6\)-CMG and adding BenziTP promoted bypass of this adduct, we focused further attention on \(O^6\)-CMG.

**Molecular modeling of \(O^6\)-CMG: Benzi base pair**

Molecular modeling was performed to visualize a possible structural basis for the specific incorporation of Benzi opposite \(O^6\)-CMG. Thus, molecular mechanics simulations of base pairing interactions between BenziTP and G or \(O^6\)-CMG in the active site of a \(K{Tq}\) mutant polymerase (164K, M747K; PDB code: 3PY8 (33)) were performed. Original crystal structures containing an incoming ddCTP opposite templating G were modified by replacing ddCTP with BenziTP and adding a carboxymethyl group to the templating G. The modified nucleotides were placed in anti conformation, since in syn conformation a steric clash was evident between the substituent at position 2 on the nucleobase and the oxygen of the sugar moiety (23). Following energy minimization (Amber 99 force field, Figure 4 and SI, Figure S6) possible differences in base pair geometries were considered. For incoming BenziTP in the \(K{Tq}\) mutant active site BenziTP was computed to be flipped out when paired with G (Figure 4A). Whereas Benzi: \(O^6\)-CMG was predicted to adopt a planar Watson-Crick-like geometry and potentially form two hydrogen bonds (Figure 4B): one between the –NH donor on Benzi and the N2 of \(O^6\)-CMG (2.4 Å); the other was predicted between the carbonyl group of Benzi and the –NH2 donor on \(O^6\)-CMG (2.1 Å). Similar findings were observed with hPol \(\eta\) in replication of the major cisplatin adduct where two hydrogen bonds were possibly formed with Benzi when it was incorporated opposite the first base of a platinated GG site (23).

Additionally, we modelled BenziTP in the active site of another thermostable A-family polymerase, \(B{s}t\) DNA Pol, for which a crystal structure is available with an incoming ddTTP opposite \(O^6\)-MeG (PDB code: 2HHW (39)). Furthermore, \(B{s}t\) DNA Pol has the closest amino acid sequence homology to \(K{Tq}\) polymerase with 51% identity matches (blastp against PDB protein database, http://www.ncbi.nlm.nih.gov/, 15/01/16) They share high sequence similarities in three conserved motifs among A-family DNA polymerases (Supplementary Figure S6A). The structures were analyzed in the same manner described above, and the data indicate that BenziTP is anticipated to be extruded approaching a pairing relationship with a template G and adopt a co-planar, two hydrogen bond, configuration when paired with \(O^6\)-MeG (Supplementary Figure S6B and C). The modeling results suggest the importance of hydrogen bonding interactions within the polymerase active site in explaining the experimental data.

**Linear amplification of \(O^6\)-alkylG DNA**

With the knowledge that BenziTP specifically promotes full-length synthesis past \(O^6\)-CMG adducts, we further investigated whether adducted DNA could be linearly amplified using BenziTP, which is specifically incorporated opposite \(O^6\)-alkylG as a marker for the adduct (Supplementary Figure S7A). Thus, to a low amount of \(O^6\)-CMG DNA (28 nt, \(X = O^6\)-CMG at position 24 nt, 0.5 ng DNA) was added four dNTPs plus BenziTP and extension of a 19 nt primer to a full-length 28 nt product was monitored after 30 amplification cycles (95°C, 30 s; 42°C, 30 s; 55°C, 30 s) by

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**Table 1. Steady-state kinetic parameters for nucleotide incorporation by \(K{TqM747K}\) DNA polymerase**

<table>
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<tr>
<th>dNTP</th>
<th>(K_M) [(\mu)M]</th>
<th>(k_{cat}) [min(^{-1})]</th>
<th>(k_{cat}/K_M) [(\mu)M(^{-1})min(^{-1})]</th>
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<tr>
<td>(X = G)</td>
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<tr>
<td>dCTP</td>
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<td>190</td>
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<tr>
<td>BenziTP</td>
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<td>0.005</td>
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<tr>
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<tr>
<td>dCTP</td>
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<tr>
<td>BenziTP</td>
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<td>0.058</td>
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<tr>
<td>(X = O^6)-MeG</td>
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<td>dCTP</td>
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<td>0.038</td>
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<tr>
<td>BenziTP</td>
<td>18±4</td>
<td>13.2</td>
<td>0.730</td>
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from biologically-relevant this study, we demonstrated successful linear amplification an elongation product up to adduct site X was formed. In plate (SI, Figure S7B). However, with natural dNTPs only, a plicolin in 29-fold increased abundance relative to the tem-

ination of the catalyst and subsequent addition of pyrophos-

nating bases we performed a primer extension assay with a termi-

adducts

Verification of Benzi incorporation opposite O6-CMG adducts

In order to verify that Benzi is only incorporated op-

position of canonical bases and did not impede DNA replica-

With the newly synthesized ddBenziTP at hand, we used it to test whether Benzi is exclusively incorporated opposite O6-alkylG or if Benzi is also a substrate in replication of natural templates. Thus, templates containing G or O6-

DNA polymerase. In the presence of DNA containing

Scheme 1. Synthesis of 2′,3′-dideoxy Benzi nucleotide. (a) MsCl, Pyr, 0 °C. (b) (i) NaI, DME, 90 °C; (ii) DCA. (c) H2, 10% Pd/C, MeOH. (d) (i) (4-chlorobutyl)(methyl)phosphoramidic dichloride, HOBr, THF, Pyr; (ii) NMI, THF. (e) Br2, DMAP, THF. (f) (i) H2, 10% Pd/C, DMF; (ii) PP.

KTqM747K. Notably, with O6-CMG template DNA, the addition of BenziTP promoted formation of the 28 nt am-

900 and 2000/?H9262 M of all four natural dNTPs and 10 μM BenziTP, M19, primer 19 nt; M23, 23 nt marker; 4, all four dNTPs; 4+B, all four dNTPs plus BenziTP; 4+B+ddB, all four dNTPs, BenziTP, plus ddBenziTP; 4+B+ddG, all four dNTPs, BenziTP, plus ddGTP.

Figure 5. (A) Primer extension experiment with ddBenziTP marking the position of O6-CMG adduct in DNA by KTqM747K DNA polymerase. (B) PAGE analysis of reactions with DNA containing X = G or X = O6-CMG at 24 nt using increasing concentrations of ddBenziTP (0, 100, 500, 1000 and 2000 μM) added to 10 μM of all four natural dNTPs and 10 μM BenziTP. M19, primer 19 nt; M23, 23 nt marker; 4, all four dNTPs; 4+B, all four dNTPs plus BenziTP; 4+B+ddB, all four dNTPs, BenziTP, plus ddBenziTP; 4+B+ddG, all four dNTPs, BenziTP, plus ddGTP.

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(24 nt; Figure 5, X = O6-CMG, 4+B+ddB). An additional band is visible at 23 nt, consistent with impeded incorporation of nucleotides opposite the O6-CMG adduct due to polymerase stalling. Accordingly, this band is also observed in all other lanes. In control reactions, addition of ddG to all four dNTPs and BenziTP resulted in bands at expected sites (Figure 5, X = O6-CMG, 4+B+ddG). In reactions with template O6-CMG containing the highest ddBenziTP concentration (2000 μM), a band was visible at the adduct site X (24 nt; Figure 5B, X = O6-CMG). This observation indicates that ddBenziMP is specifically incorporated opposite O6-CMG and can be used to directly mark the adduct site. In control reactions containing the highest amount of supplemented ddG, extension ended prior to the lesion (23 nt) resulting from O6-CMG stalling KTqM747K polymerase. Thus, ddBenziTP marked the O6-CMG adduct specifically in the presence of natural dNTPs, further supporting the O6-alkylG adduct-specific incorporation of Benzi and that the presence of the artificial nucleotide analogue does not perturb DNA replication by KTqM747K polymerase.

Recognition of O6-alkylG adducts in DNA mixtures with unmodified templates

Knowing that Benzi is incorporated selectively opposite O6-alkylG adducts, we examined whether the adducts could also be sensed in a mixture with non-damaged DNA. Thus, we performed a primer extension experiment with various dilutions of O6-alkyl- and G-containing DNA (at a constant template concentration). Reactions were carried out with BenziTP and KTqM747K, and the formation of n + 1 extension products was monitored (Figure 6). Reactions contained a 23 nt primer annealed to corresponding 28 nt templates with G or O6-alkylG adducts at nucleotide 24. Concentration-dependent formation of extension products was observed that correlated with increasing fraction of O6-alkylG present in a mixture with G templates (Figure 6, Supplementary Figure S8). For a 1:1 mixture of O6-CMG:G DNA, 35% product was observed. In the absence of the O6-CMG adduct, no extension product was formed (3%; Figure 6, dashed line). The lowest visually observable product (7%) was in the case of a 1:10 ratio of O6-CMG:G. When the experiment was performed with O6-MeG, 51% extension product was formed from a 1:1 mixture of O6-MeG:G DNA, and the lowest detectable dilution was also 1:10 O6-MeG:G (9%; Supplementary Figure S8). Critical limitations for addressing DNA adducts are that they exist at much lower levels and in the presence of a far larger excess unmodified DNA, as well as the lack of suitability of phosphorimaging as a basis of an optimized detection strategy. Nonetheless, the capacity for artificial nucleotide incorporation in a mixture was achieved, and furthermore, the amount of O6-alkylG template present in the reactions, which corresponds to 0.17 ng O6-alkylG DNA mixed with 1.7 ng unmodified DNA, was 3-fold lower than was detected by linear amplification (0.5 ng O6-alkylG DNA; SI, Figure S7).

**CONCLUSIONS**

We investigated artificial nucleotides as substrates for the replication of DNA containing carcinogenic alkylation adducts O6-MeG and O6-CMG. We demonstrated that KTqM747K DNA polymerase specifically incorporated artificial nucleotide BenziMP opposite O6-MeG and O6-CMG independent of its sequence context, and was competent in further extension. The specific incorporation of BenziMP opposite O6-alkylG adducts versus G was 150-fold higher for O6-MeG, and 12-fold for O6-CMG. O6-MeG was readily bypassed by KTqM747K polymerase and full-length products were formed in the presence of natural dNTPs, whereas O6-CMG stalled the polymerase and BenziTP was required for efficient full-length DNA synthesis. A structural basis for O6-alkylG adduct-specific incorporation of Benzi may be due to favorable hydrogen bonding interactions with O6-alkylG while Benzi is extruded from the duplex when it is opposite G.

An additional advance described in this study was the preparation of the 2’,3’-dideoxynucleoside BenziTP, which was used to mark the adduct site in O6-CMG-containing DNA and confirm that Benzi is not incorporated opposite natural templates in full-length synthesis. This demonstration is the first example of an artificial dideoxynucleotide used in a sequencing experiment involving marking a DNA adduct site. The combination of artificial BenziTP and KTqM747K polymerase allowed us to demonstrate a basis whereby O6-alkylG adducts in mixtures with nondamaged G containing DNA may be sensed. While significant further adaptations for real biological applications, including enrichment strategies, sensitive analytical read-out methods, and further refinement of polymerase characteristics are needed, these findings are a chemical basis that suggest novel approaches for single-base resolution determination of mutagenic DNA adduct occurrence.
SUPPLEMENTARY DATA

Supplementary Data are available at NAR Online.

ACKNOWLEDGEMENT

We are grateful to Michael Raez (ETH Zurich, Switzerland) for preparing oligonucleotides containing O\textsuperscript{6}-CMG.

FUNDING

European Research Council [260341]; Swiss National Science Foundation [156280]; ETH research commission [ETH-43 14-1]. Funding for open access charge: ETH Zurich

Conflict of interest statement. None declared.

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