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ABSTRACT

DNA mismatch repair (MMR) sensitizes human and *Escherichia coli dam* cells to the cytotoxic action of *N*-methyl-*N'*-nitro-*N*-nitrosoguanidine (MNNG) while abrogation of such repair results in drug resistance. In DNA methylated by MNNG, MMR action is the result of MutS recognition of O^6-methylguanine base pairs. MutS and Ada methyltransferase compete for the MNNG-induced O^6-methylguanine residues, and MMR-induced cytotoxicity is abrogated when Ada is present at higher concentrations than normal. To test the hypothesis that MMR sensitization is due to decreased recombinational repair, we used a RecA-mediated strand exchange assay between homologous phiX174 substrate molecules, one of which was methylated with MNNG. MutS inhibited strand transfer on such substrates in a concentration-dependent manner and its inhibitory effect was enhanced by MutL. There was no effect of these proteins on RecA activity with unmethylated substrates. We quantified the number of O^6-methylguanine residues in methylated DNA by HPLC-MS/MS and 5–10 of these residues in phiX174 DNA (5386 bp) were sufficient to block the RecA reaction in the presence of MutS and MutL. These results are consistent with a model in which methylated DNA is perceived by the cell as homeologous and prevented from recombining with homologous DNA by the MMR system.

INTRODUCTION

Methylating agents are found in the environment and are also used in cancer chemotherapy (1–3). These agents and laboratory versions, such as *N*-methyl-*N'*-nitro-*N*-nitrosoguanidine (MNNG), can react with DNA to create a variety lesions acted upon by different DNA repair pathways; such lesions include *N*7-methylguanine (7-meG) and O^6-methylguanine (O^6-meG), the latter being the subject of this investigation. In *Escherichia coli*, two methyltransferases can use O^6-meG as a substrate: the constitutively produced Ogt protein and the inducible Ada protein (4). In order to demethylate an O^6-meG, the Ada protein binds directly to the base, flips it out of the helix and into its substrate binding pocket, transferring the methyl group from the base to an internally located cysteine residue (5). The Ada protein also has a regulatory function to induce itself and other genes of the *ada* regulon, including *alkA*, *alkB* and *aidB* (1,3).

O^6-meG paired with cytosine or thymine is also a substrate for the MutS protein of the *E.coli* DNA mismatch repair (MMR) system (6,7). The Dam-directed MMR system of *E.coli* acts to preserve the fidelity of the genome by removing base mismatches that arise as a result of replication (mutation avoidance) (8–10). During replication, the parental DNA strand is methylated at all adenines in the sequence GATC by the product of the *dam* gene. The newly synthesized strand is not yet methylated, due to a lag between replication and methylation by Dam, which leaves a hemi-methylated DNA state behind the replication fork. The MMR system exploits the hemi-methylated state of the DNA by allowing it to distinguish the new strand from the old strand for repair. When mismatches arise in the hemi-methylated region of DNA, they are first bound by the MutS protein. MutS then recruits MutL and MutH to form a ternary complex, which activates the latent endonuclease activity of MutH. Incision by MutH occurs at a nearby GATC sequence on the unmethylated strand, followed by exonucleolytic digestion to remove the mismatch. The gap produced by exonuclease action is re-synthesized by the replicative polymerase, DNA polymerase III, which restores the correct nucleotide sequence and the remaining nick is sealed by DNA ligase. Subsequently, the repaired strand will be methylated by the Dam methyltransferase at GATC sequences, and this methylation step prevents further action by the MMR system.

In *E.coli* mutant in the *dam* locus, both strands of DNA are unmethylated and the directionality of MMR is lost, allowing MutH to incise the daughter or parental DNA strands during

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repair (11). Thus, MutH endonuclease action can occur in both replicating and non-replicating DNA, anywhere in the chromosome, unlike in wild-type cells where MMR is tightly regulated to the region trailing the replication fork. MutH action can occur either at the same GATC on opposite strands (12) or by replication fork collapse (11,13). These actions result in the formation of double-strand breaks (DSBs), which require recombination to restore genomic integrity, as mutations in genes encoding recombination proteins in combination with *dam* results in a lethal phenotype (11).

MMR also plays an important role in preventing recombination between similar but non-identical (homeologous) DNA sequences, a function termed anti-recombination (14). *Salmonella enterica* serovar Typhimurium and *E.coli* share an 83% sequence identity, and genetic crosses between them are sterile unless a mutation in the *mutS* or *mutL* genes is present in the recipient (14). Recombination is increased by at least 1000-fold in recipients where MMR is inactivated and chimeras containing DNA from both species are formed. Biochemical experiments using homeologous DNA from the closely related M13 and fd phages (3% sequence divergence) showed that the addition of MutS and MutL protein block the progression of the RecA-mediated strand exchange reaction *in vitro* (15). There was no effect of MutS and MutL when homologous M13–M13 substrates were used. The genetic and biochemical results imply that MMR impedes or actively reverses recombination intermediates with the former having experimental support (9,16).

E.coli dam mutants are more susceptible to the cytotoxic action of MNNG and other chemical agents than wild-type (17–19). Mutations inactivating MMR (*mutS*, *mutL*) in a *dam* background confer a level of resistance to MNNG similar to wild-type (17,19). This indicates that MMR can act on chemically modified substrates through MutS binding specifically to O^6-meG base pairs (6,7). MMR action at these base pairs may lead to the formation of nicks or gaps, which are converted to DSBs requiring recombination to repair them. We hypothesize that inhibition of recombinational repair by MMR would ensue because the homologous methylated DNA is perceived as homeologous DNA (20). Persistent unrepaired DSBs would eventually produce lethality. We have advanced a similar hypothesis to explain MMR sensitization of *dam* cells exposed to cisplatin in which dose- and MMR-dependent DSBs accumulate (13). MutS prevents RecA-mediated strand transfer with substrate DNAs containing platinated intrastrand crosslinks (21). In this work, we demonstrate a similar result with O^6-meG base pairs.

MATERIALS AND METHODS

Strains, media and chemicals

The *E.coli* K-12 strains used in this study are described in Table 1. Plasmid pBAR, a pEMBL derivative that contains the *ada* gene under control of an isopropyl-β-D-thiogalactopyranoside (IPTG) inducible promoter (22), was a gift from Dr Bruce Demple (Harvard School of Public Health, Boston). L medium contains 20 g tryptone (Difco), 10 g yeast extract (Difco), 0.5 g NaCl, 4 ml of 1 M NaOH per liter and solidified when required with 16 g of agar. Minimal medium was prepared as described by Davis and Mingioli

Table 1. *E.coli* strains

Strain	Genotype	Source/reference
AB1157	*thr-1 ara-14 leuB6 Δ (gpt-proA)62 lacY1 tsx-33 supE44 galK2 hisG4 rfbD1 mgl-51 rpsL31 kdgK51 xyl-5 mtl-1 argE3 thi-1*	E. A. Adelberg
GM2927	As AB1157 but *dam-13*::Tn9	Lab stock
GM3819	As AB1157 but Δ*dam-16*::Kan	Lab stock
GM7688	As GM3819 but Δ*mutL460*::Cam	Lab stock
GM7704	As GM2927 but Δ*mutS465*::Tet	Lab stock
GM7797	As GM3819 but Δ*mutS465*::Tet	Lab stock
GM8415	As AB1157 but Δ*ada*::Kan[a]	Lab stock
GM8417	As KM55 but Δ*dam-16*::Kan	Lab stock
GM8427	As GM2927 but Δ*ada*::Kan	Lab stock
GM8440	As GM7704 but Δ*ada*::Kan	Lab stock
KM55	As AB1157 but Δ*mutH461*::Cam	K. C. Murphy (36)
KT233	Δ*ada*::Kan Δ*tag*::Cam	B. Sedgwick (37)
MV1161	As AB1157 but *rfa-550*	M. Volkert
MV3855	As MV1161 but *alkA1 tagA1 zhb*::Tn5 *uvrA6*	M. Volkert

Further information about strains and markers can be found at http://users.umassmed.edu/martin.marinus/dstrains.html.
[a]Although designated as Δ*ada*::Kan, this deletion also removes the *alkB* gene.

(23). MNNG (Sigma–Aldrich) was prepared by dissolving 1 mg of MNNG in 100 μl of dimethyl sulfoxide and adding 900 μl of sterile water and aliquots were stored frozen at −20°C. Guanine, 7-methylguanine and O^6-meG were obtained from Sigma–Aldrich.

Proteins and DNA

RecA protein was purified as described previously (21). MutS and MutL proteins were a gift from F. Lopez de Saro and M. O'Donnell (The Rockefeller University). Single-stranded binding protein (Ssb) was obtained from USBiological. PhiX174 RFI (covalently closed circular) and virion (single-stranded) forms were purchased from New England Biolabs. The PhiX174 RFI DNA was digested with XhoI restriction endonuclease to produce linear double-stranded DNA for strand exchange.

Cell survival

Cells were grown in 10 ml L medium to an OD_{600} of 0.35–0.45. The logarithmic phase cells were exposed to various concentrations of MNNG for 10 or 30 min as indicated, at 37°C. Serial dilutions of MNNG-exposed cells were plated on L media and incubated overnight. Colony forming units were counted and survival calculated.

Methylation and survival of phiX174 DNA

PhiX174 RFI and linearized RFI DNA molecules were reacted with various amounts of MNNG using a protocol adapted from Sussmuth *et al*. (24). The DNA (50 μg) was added to 0.1 M citric acid phosphate buffer, pH 6, containing 0.5 μM cysteine and varying amounts of MNNG. The solution was rocked gently at 37°C for 4 h, after which the DNA was ethanol precipitated four times to remove residual MNNG. For the phage survival, aliquots of methylated or unmodified RFI were mixed with strains MV1161 (wild type) and MV3855 (*alk tag*), mixed with top agar and poured onto Luria–Bertani

plates. The plates were incubated overnight at 37°C and plaques scored.

HPLC-MS/MS

Calculation of the number of methylated purine bases in each of the DNA substrates was determined by reverse phase high-performance liquid chromatography (HPLC) with online positive ion electrospray multiple reaction monitoring MS/MS (HPLC-ESI-MRM-MS/MS). HPLC was performed using a Rheos microgradient pumping system (Leap Technologies, Inc.) with a 150 × 1 mm ID BetaBasic-18 (3 μm particle size, 150 Å pore, Keystone Scientific, Inc.) in the isocratic mode with 2% acetonitrile, 0.1% formic acid as the mobile phase at 50 μl/min. The column outlet was directly connected to the Z-Spray™ ion source on a Quattro-II triple quadrupole mass spectrometer (Waters). Optimal MS conditions for each analyte were determined by adjustment of conditions during infusion of solutions of each analyte in mobile phase with the capillary at 2.4 kV and collision cell argon pressure at 1 mBar. Guanine was measured by MRM of the transition from the m/z 136 (MH$^+$) to m/z 92 with the cone at 30 V, collision energy at 30 V and a dwell time of 0.05 s. 7-meG was measured by MRM of the transition from the m/z 166 (MH$^+$) to m/z 124 with the cone at 35 V, collision energy at 23 V and a dwell time of 0.5 s. O^6-meG was measured by MRM of the transition from the m/z 166 (MH$^+$) to m/z 134 with the cone at 35 V, collision energy at 24 V and a dwell time of 5 s. Amounts of each analyte in the samples were calculated by comparison of sample peak areas with those measured from injection of external standards. The methylated DNA was subject to formic acid hydrolysis using 65% formic acid for 30 min at 130°C.

Strand exchange assay

Reaction mixtures contained 25 mM Tris-acetate, pH 7.5, 10 mM MgOAc, 5% glycerol, 1 mM DTT, 8 mM phosphocreatine, 10 U/ml creatine kinase, 1 nM single-stranded circular DNA and 6.7 μM RecA. Reaction mixtures were pre-incubated at 37°C for 10 min, linear duplex DNA substrate was added to a concentration of 0.8 nM and incubated an additional 10 min. Strand exchange was initiated by the addition of a premixed solution containing 2 μM Ssb and 3 mM ATP. MutS and/or MutL were added 1 min prior to initiation of the reaction. Samples were taken at indicated times and strand transfer was terminated by the addition of 2 μl of buffer containing 5% SDS, 20% glycerol, 60 mM EDTA and Proteinase K to a concentration of 1 mg/ml. After incubation at 42°C for 30 min, samples were analyzed by electrophoresis in a 0.8% agarose gel with 40 mM Tris–acetate, 2 mM EDTA. Gels were processed by staining in Vistra Green (Amersham) fluorescent stain (1:10 000) for 60 min and then analyzed by Image Reader 1 Laser/1 Image at 473 nm on a Fuji FLA-5000 phosphorImager. The gels were quantified using Multi-gauge V.2.3 software.

RESULTS

Survival of *dam* strains exposed to MNNG

We have used deletion mutations in the *dam*, *mutS*, *mutL* and *mutH* genes to measure survival of strains containing them to
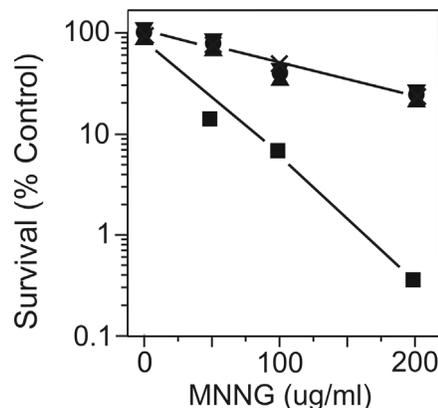
Figure 1. Cell survival after exposure to MNNG. Cells in the logarithmic phase of growth were exposed to MNNG for 10 min (to prevent substantial induction of Ada methyltransferase), diluted and portions spread on L agar to determine survival. Filled circles, wild-type (AB1157); upside down triangles, Δ*dam* Δ*mutS* (GM7797); right side up triangles, Δ*dam* Δ*mutL* (GM7688); crosses, Δ*dam* Δ*mutH* (GM8417); filled squares, Δ*dam* (GM3819).

MNNG exposure. The data in Figure 1 show that the *dam* mutant is more sensitive to MNNG than wild type. The double mutants, *dam mutS*, *dam mutL* and *dam mutH*, have a level of resistance equivalent to wild type. These results confirm previous data where inactivation of MMR by presumed base substitution mutations *mutS* and *mutL* in a *dam* background results in drug resistance. In contrast to a previous study (19), we find that the *dam mutH* strain is as resistant to MNNG as wild type.

The effect of Ada protein on cell survival

We also examined the role of the Ada protein on *dam* cell survival by using strains in which it was overproduced from a multicopy plasmid or was absent due to an *ada* gene deletion. The *dam ada* double mutant is more sensitive to MNNG than *dam* alone (Figure 2A), but overexpression of the Ada protein in both these strains results in a wild-type level of resistance (Figure 2B), indicating that Ada methyltransferase can prevent MMR-induced cytotoxicity. The survival of Ada overproducing wild-type and *dam mutS* strains was not significantly different from the Ada-oveproducing strains shown in Figure 2B (data not shown). We conclude that these results are consistent with competition between Ada and MutS for substrate, which we assume is O^6-meG base pairs.

The increased sensitivity of the *dam ada* double mutant compared with the *dam* strain alone suggests an *ada*-dependent mechanism of sensitization distinct from that caused by MMR. Further evidence for this idea is that the survival of the *dam ada mutS* triple mutant is less than that for the *dam mutS* double (Figure 2A). As expected, the *ada* derivative of the wild type also shows increased sensitivity (Figure 2A) under the same experimental conditions.

Methylation of DNA by MNNG and determination of the number of lesions by HPLC-ESI-MRM-MS

The double-stranded linear form of phiX174 DNA (5386 bp) was reacted with 0, 150, 300 and 600 μM MNNG. After formic acid hydrolysis, the levels of guanine, 7-meG and O^6-meG for each substrate were measured by HPLC-ESI-MRM-MS.
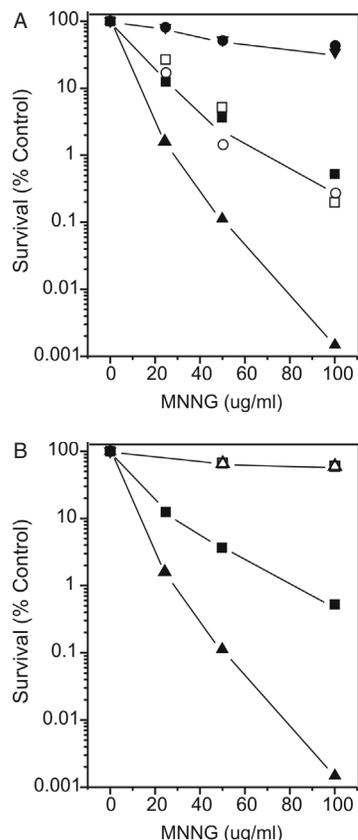
Figure 2. Effect of Ada protein on cell survival after exposure to MNNG. (**A**) Cells in the logarithmic phase of growth were exposed to MNNG for 30 min, diluted and portions spread on L agar to determine survival. Filled circles, wild-type (AB1157); open circles, Δada (GM8415); upside down triangles, Δdam ΔmutS (GM7797); filled squares, Δdam (GM3819); right side up triangles, dam ada (GM8427); open squares, Δdam ΔmutS Δada (GM8440). (**B**) Cells in the logarithmic phase of growth were exposed to MNNG for 30 min, diluted and portions spread on L agar to determine survival. Filled right side up triangles, dam ada (GM8427); filled squares, Δdam (GM3819); open right side up triangles, dam ada (GM8427)/pBAR; filled squares, Δdam (GM3819)/pBAR. The survival curves for AB1157/pBAR and Δdam ΔmutS (GM7797)/pBAR were not significantly different from the pBAR-containing strains shown. No IPTG was added to the cultures as uninduced levels of Ada protein were sufficiently high.

The tracings in the top three panels of Figure 3 show the retention times of the standards and the lower three panels from MNNG methylated phiX174 DNA. Extrapolating from linear calibration curves, there were 0, 5–10, 10–20 and 20–40 O^6-meG residues in DNA treated with 0, 150, 300 and 600 μM MNNG, respectively, in multiple trials.

Survival of methylated phiX174 DNA

We methylated phiX174 RFI (covalently closed) DNA to examine the relationship between transfection efficiency of RFI DNA methylated with 0, 150, 300 and 600 μM MNNG in wild-type and *alkA tag* bacteria. The *alk tag* strain was chosen because it is a direct measure of survival of methylated phage DNA since potentially lethal types of base methylation, such as 3-methyladenine, are not removed by the AlkA and TagA glycosylases. The data in Figure 4 show that at concentrations above 150 μM, there was a lower survival of the treated phage DNA in the *alkA tag* strain, indicating the presence of inhibitory methylated lesions.

RecA strand exchange with unmodified and methylated substrates

The strand exchange reaction is schematically represented in the top panel of Figure 5. An example of a typical assay result showing the separation of the various substrates and products using linear duplex (DS) methylated with 600 μM MNNG is shown in the bottom panel of Figure 5. We used DS methylated DNA because the types and abundance of methylated bases differ from that in single-stranded (SS) DNA and DS DNA is the probable target *in vivo*. The results of the RecA assay with unmethylated and methylated DNA and various concentrations of MutS and MutL are shown in Figure 6. The first four lanes in Figure 5 show the reaction with methylated DNA but the identical result was obtained with unmethylated DNA (data not shown), indicating that methylated bases do not interfere with RecA action at any concentration of MNNG used (Figure 6). In the absence of MutS, the reaction is complete within 45 min (Figures 5 and 6) by measuring the appearance of nicked circle (NC) product. Over time, there is also an increase in slowly migrating intermediate (I) structures, the step which precedes the formation of the NC product. Inclusion of MutS in the reaction with unmodified substrates has no significant effect on the rate or yield of the reaction up to concentrations of 250 nM (data not shown). At higher concentrations, MutS begins to bind nonspecifically to DNA, causing a slight inhibition of the reaction.

The addition of MutS to the RecA strand exchange reaction

As described above, no change in rate or yield of product is observed upon the addition of MutS to a strand transfer reaction between unmethylated substrates. In contrast, inhibition of strand transfer occurs when MutS is added to a reaction where the linear duplex substrate contains methylated bases (Figure 5, 25 μM MutS). As shown in Figure 6, addition of 25, 125 and 250 μM MutS results in a concentration-dependent inhibition of strand exchange, when the linear duplex substrate is modified by 150, 300 or 600 μM MNNG corresponding to between 5–10, 10–20 and 20–40 O^6-meG residues, respectively. At higher concentrations of MNNG, the binding of MutS to the substrate is saturated, as the percent NC formation is equal to that of the 600 μM modified substrate (data not shown). At modifying concentrations of MNNG below 150 μM, the binding of MutS has no effect on product formation and is analogous to that of the unmodified substrate as measured by product formation (data not shown). Note that phiX174 RFI DNA treated with 150 μM MNNG shows no reduction in plaque formation in transfection assays (Figure 4) but a reduction was seen at 300 and 600 μM MNNG-treated DNA.

Addition of MutL to the reaction

Previous studies with homeologous substrates (M13 and fd DNA) have shown that MutL stimulates MutS binding to mismatches during strand exchange when MutS is at suboptimal concentrations (15). The last four lanes in Figure 5 show the inhibitory effect of 50 μM MutL addition to a strand
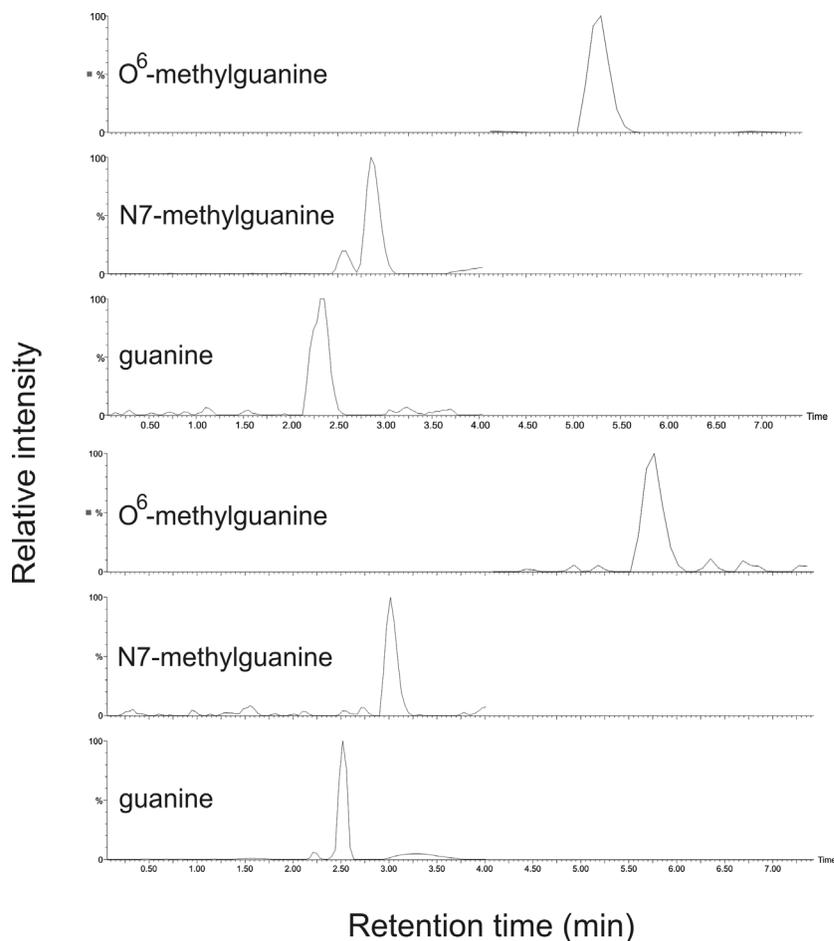
Figure 3. Detection of methylated guanines by HPLC-MS/MS. The top three panels are traces of a mixture of the indicated standard compounds while the bottom three panels are traces from formic acid hydrolyzed MNNG treated (300 µM) phiX174 RFI DNA.
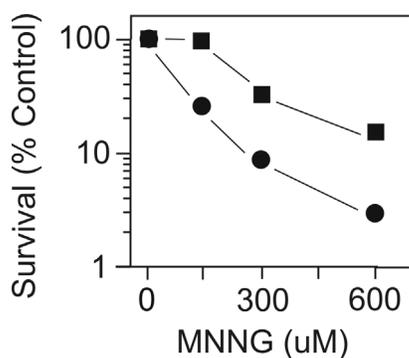

Figure 4. Phage phiX174 DNA survival after MNNG exposure. PhiX174 RFI DNA was incubated with the indicated concentrations of MNNG as described in Materials and Methods and used to transfect strains MV1161 (wild type) and MV3855 (*alkA tagA*) and survival determined by plaque formation.

exchange reaction in the presence of a lower concentration (25 µM) of MutS. Inclusion of 50 or 100 µM MutL in the reactions in the presence of MutS with methylated substrates severely reduces product formation by RecA (Figure 6). In the absence of MutS, inclusion of up to 200 µM MutL has no effect on the rate of product formation or yield of the reaction with modified or unmodified substrates (data not shown).

DISCUSSION

The cytotoxic effects of both cisplatin and MNNG are enhanced by MMR in *dam* bacteria (17–19). With cisplatin, we have shown that it promotes dose- and MMR-dependent DSB formation in *dam* cells (13). Genetic studies indicate that recombination is required for the repair of such breaks (25,26) and the initiation of recombination by RecA-mediated strand transfer is inhibited by MutS if one of the recombining partners contains platinated diguanosyl intrastrand cross-links (21). MMR anti-recombination with platinated DNA occurs because such DNA is recognized as homeologous (20) in the same manner as that formed between *E.coli* and *Salmonella typhimurium*, which are 17% divergent in sequence (14). MMR-mediated inhibition of DSB repair should lead to lethality since even a single unrepaired DSB is expected to be lethal.

The results reported in this study begin to form a unified hypothesis explaining why cisplatin and MNNG, compounds that produce damage acted upon by different repair systems, cause a similar sensitization by MMR in *dam* cells. MutS prevents RecA strand transfer when one of the substrates is either methylated or platinated. Since cisplatin has been shown to induce DSB formation in *dam* cells (13), we predict that MNNG will do so as well and experiments to test this

prediction are in progress. If, indeed, this is the case, then inhibition of DSB repair by anti-recombination underlies MMR sensitization.

The data reported here and for cisplatin (21) begin to answer how much modification in *E.coli* homologous DNA is required before it is converted to homeologous DNA. Currently, it is known that 192 mismatches, or 3% divergence, between M13 and fd (6407 nt) are sufficient for recognition as homeologous
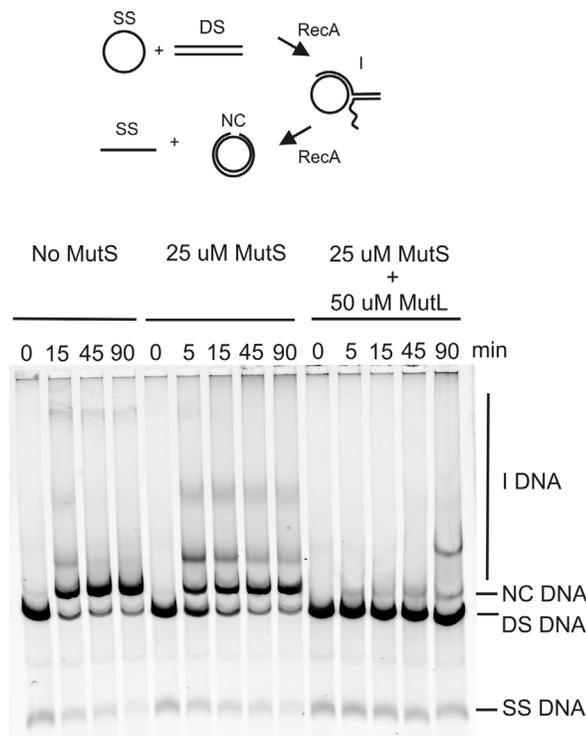

Figure 5. RecA-catalyzed strand transfer. The top of the figure shows a schematic of the reaction. Single-strand (SS) circular DNA reacts with linear duplex (DS) to form intermediate (I) structures, which are converted to nicked-circle (NC) products. The fluorograph shows the results from the RecA strand transfer assays with unmodified SS DNA and methylated DS DNA (600 μM MNNG treatment) without MutS (left four lanes), with MutS (middle four lanes) and with MutS and MutL (right four lanes). The numbers above the lanes indicate the time of the reaction.
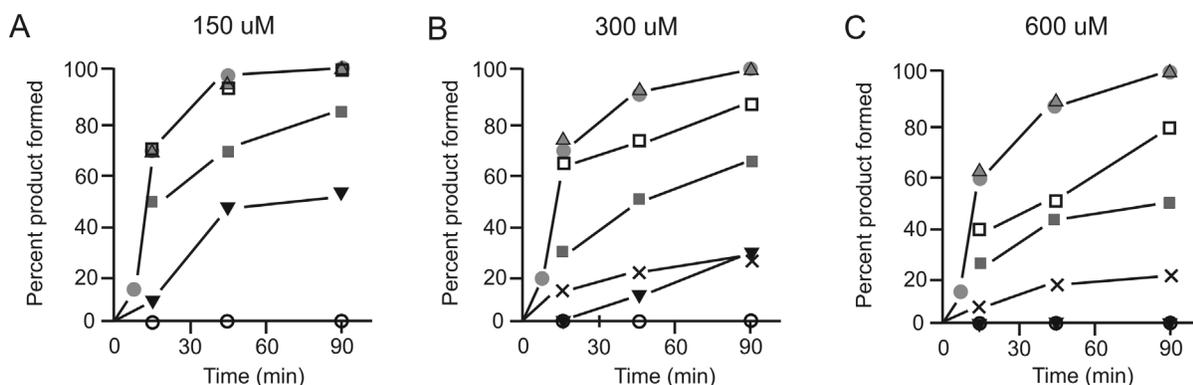
DNA (15). The data in Figure 6 show that 5–10 O^6-meG residues in the 5386 bp phiX174 molecule (1–2 modified bases per 1000 bp) are sufficient to provoke MutS and MutL inhibition of strand exchange. With cisplatin, 4–8 platinated intrastrand crosslinks in phiX174 are sufficient for a substantial MutS inhibitory effect although, unlike the case with O^6-meG mismatches (Figure 6), intrastrand crosslinks reduce the ability of RecA to perform strand transfer. With this caveat in mind, the number of lesions required to effect MutS inhibition of strand transfer is about the same (∼1–2 per 1000 bp).

The strand transfer experiments show that MutS must recognize O^6-meG paired with cytosine confirming the binding to synthetic oligonucleotides containing such a base pair (6,7). MutS affinity for O^6-meG mismatches was at least 2-fold lower than for G/T base pairs. We wish to emphasize that even though MutS has a lower affinity for DNA containing O^6-meG/C mismatches, it is sufficient to produce a striking reduction in strand transfer when a low number of such mismatches are present. This argument also holds for platinated DNA where platinated GG/CC crosslinks must be the adducts recognized by MutS and which have lower affinity for MutS than GG/CT crosslinks (7).

The *E.coli dam* mutant was shown to be more sensitive than wild type to MNNG, but not dimethylsulfate, suggesting that O^6-meG was the lesion recognized by MMR (17). Subsequently, it was shown that MutS was able to bind specifically to O^6-meG base pairs *in vitro* (6,7). Overexpression of Ada methyltransferase abrogates MMR sensitization of *dam* mutants (Figure 2B) and in its absence, the sensitization is enhanced (Figure 2A). A simple explanation for these results is that the two proteins compete for the same substrate. Given that Ada methyltransferase acts on O^6-meG residues (among others) and that MutS can also bind to O^6-meG base pairs, it is reasonable to assume that this is the modified base in question and which is recognized *in vivo*.

Mammalian cells are sensitive to the cytotoxic action of MNNG and cisplatin but MMR-deficient cell lines derived from them are resistant to the action of these agents (27–29), although this association for cisplatin has recently been questioned (30,31). The MutS protein from human cells specifically recognizes the platinated GG intrastrand crosslink

Figure 6. Kinetics of MutS inhibition of RecA-mediated strand exchange. The graphs show the effect on RecA strand transfer of varying concentrations of MutS with or without MutL on unmodified or methylated DNA. DNA was exposed to 150, 300 and 600 μM MNNG in A, B and C, respectively. Filled circles, unmodified DNA; right side up triangles, methylated DNA; open squares, 25 μM MutS; filled squares, 100 μM MutS; upside down triangles, 250 μM MutS; crosses, 25 μM MutS plus 50 μM MutL; open circles, 100 μM MutS plus 100 μM MutL.

and O^6-meG-cytosine and thymine base pairs (32). The sensitization by MMR to cisplatin or MNNG has been proposed to occur by several models, including futile repair cycles by MMR at lesions followed by DSB formation and subsequent signaling for cell cycle arrest and apoptosis (33). An alternative model posits a direct link between lesion recognition by MutS and a signal transduction cascade leading to cell death (34,35). Insofar as the work reported here with *E.coli* can be extrapolated to human cells, our results would favor the DSB model.

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Conflict of interest statement. None declared.

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