Stoichiometry of MutS and MutL at unrepaired mismatches in vivo suggests a mechanism of repair

Marina Elez1,*, Miroslav Radman1,2 and Ivan Matic1

1Université Paris-Descartes, Sorbonne Paris Cité, Inserm Unit 1001, 75015 Paris, France and
2Mediterranean Institute for Life Sciences, 21000 Split, Croatia

Received August 4, 2011; Revised December 9, 2011; Accepted December 18, 2011

ABSTRACT

Mismatch repair (MMR) is an evolutionarily conserved DNA repair system, which corrects mismatched bases arising during DNA replication. MutS recognizes and binds base pair mismatches, while the MutL protein interacts with MutS–mismatch complex and triggers MutH endonuclease activity at a distal-strand discrimination site on the DNA. The mechanism of communication between these two distal sites on the DNA is not known. We used functional fluorescent MMR proteins, MutS and MutL, in order to investigate the formation of the fluorescent MMR protein complexes on mismatches in real-time in growing Escherichia coli cells. We found that MutS and MutL proteins co-localize on unrepaired mismatches to form fluorescent foci. MutL foci were, on average, 2.7 times more intense than the MutS foci co-localized on individual mismatches. A steric block on the DNA provided by the MutHE56A mutant protein, which binds to but does not cut the DNA at the strand discrimination site, decreased MutL foci fluorescence 3-fold. This indicates that MutL accumulates from the mismatch site toward strand discrimination site along the DNA. Our results corroborate the hypothesis postulating that MutL accumulation assures the coordination of the MMR activities between the mismatch and the strand discrimination site.

INTRODUCTION

Since the first experiment that showed a direct evidence for the existence of a strand-directed mismatch repair (MMR) in bacteria in 1976 (1), several thousand papers describing MMR in vivo and in vitro have been published (2–5). MMR is a major guardian of genomic stability that improves the fidelity of DNA replication (6), prevents genomic rearrangements (7) and acts as genetic barrier between related species (8) by abolishing recombination between non-identical DNA sequences (2,6). Key bacterial MMR proteins, MutS and MutL, are conserved in all kingdoms of life (2,6). The MutS protein, and its eukaryotic homologs, detects and binds diverse mismatches arising during DNA replication. The MutL protein, and its eukaryotic homologs, links a mismatch-bound MutS with the strand discrimination site of helicase/exonuclease activities that remove the mismatched base specifically from the newly synthesized strand.

In Escherichia coli, discrimination between template and newly synthesized strand is based on the methylation status of adenines in the GATC sequences (2,6). In newly synthesized strands, adenines in GATC sequences are transiently unmethylated thus providing a binding site for the MutH endonuclease. MutH is a MutL-binding protein that can cleave the newly synthesized strand at a proximal non-methylated GATC sequence on either side of the mismatch (2,6). DNA cleavage by MutH triggers mismatch repair involving UvrD (helicase II), single-stranded exonucleases, DNA polymerase III holoenzyme, single-strand DNA-binding protein and DNA ligase (2,6). In E. coli, GATC cleavage can occur even at kilobase or larger distances from the mismatch (6,9).

Despite the decades of research, a key mechanistic aspect of mismatch repair remained mysterious, i.e. what is the nature of molecular communication between the site of mismatch and the site of strand discrimination? Several conceptually exclusive models, which can be grouped into three categories, have been proposed to explain interaction between these two DNA sites. All models are based exclusively on in vitro biochemical studies of MMR proteins and there are yet no in vivo experiments that confirm their biological relevance. The first model postulates that DNA looping brings the stationary mismatch–MutS–MutL complex and the hemi-methylated GATC sequence in proximity (10–12). The second model proposes that MutS–MutL complex, or MutS alone,

*To whom correspondence should be addressed. Tel: +0033140615327; Fax: +0033140615321; Email: marina.elez@inserm.fr
travel along the DNA helix from the mismatch towards the proximal strand discrimination site (13,14). Finally, the third model suggests that mismatch recognition by MutS triggers polymerization of MutL along DNA between the mismatch and the strand discrimination signal (15). This model was promulgated by studies showing that MutS binding to the mismatch protects ~10 bp on either side of the mismatch against DNase I digestion, while the addition of MutL extends the footprint dramatically (11,16). Also the study of the effect of the DNA chain length on the formation of the ternary complex mismatch–MutS–MutL led to the proposal that the ternary complex formation could involve the polymerization of MutL along the helix (17). A corollary of this model is the assumption that more MutL than MutS proteins should be required for the repair of a mismatch. This was further strengthened by genetic evidence showing that the cellular level of MutL, and not of MutS, becomes limiting when MMR is saturated in the presence of numerous mismatches (18–22). Because both MutS and MutL are present in equimolar concentrations in the cell, MutL protein limitation cannot simply be due to a lower amount of MutL in the cell (23).

In this study, we looked whether more MutL than MutS proteins are present on the mismatches in vivo. We investigated individual growing *E. coli* cells carrying functional MutS and MutL proteins fused to fluorescent proteins and followed the formation of the fluorescent MMR protein complexes on individual mismatches in real-time by fluorescent microscopy. Our previously published data show that the MutL forms fluorescent foci on unrepairable mismatches and that MutL foci formation is dependent on MutS (24). However, the expected co-localization of MutS and MutL was not explored and the relative amount of MutS and MutL on these mismatches was not quantified. Here, we show that MutL and MutS fluorescent foci co-localize and that the fluorescence of MutL foci is always more intense than the fluorescence of MutS foci. Furthermore, the presence of a roadblock at the GATC sequences reduces the amount of fluorescence of MutS foci. Furthermore, the presence of a roadblock at the GATC sequences reduces the amount of fluorescence of MutS foci. Furthermore, the presence of a roadblock at the GATC sequences reduces the amount of fluorescence of MutS foci. Furthermore, the presence of a roadblock at the GATC sequences reduces the amount of fluorescence of MutS foci.

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**MATERIALS AND METHODS**

*Escherichia coli* strains expressing fluorescently tagged MutL and MutS

To assess the co-localization of MutS and MutL proteins in single *E. coli* cells, we constructed translational fusions of Yellow Fluorescent Protein (YFP) and Cyan Fluorescent Protein (CFP) to the N-termini of MutS and MutL proteins. This was done by modifying the plasmids pEGFP-MutSwt and pEGFP-MutLwt (24) in several steps. First, we replaced eGFP in the pEGFP-MutLwt and pEGFP-MutSwt by YFP and CFP. We amplified by PCR the fragment encoding YFP from the template pUC18-yfp (25) and the fragment encoding CFP from the template pUC18-cfp (26). We used primers 5’-CCCCAGATCTGGTACCCAGCAAGCAAGAAGATGGCTAGCAGAAAGGAGAAGAAGATC3’ and 5’-ATGGAATTCGCAAGATCTGGATACGGCAATCAGTGG-3’. Also the study of the effect of the DNA chain length on the formation of the ternary complex mismatch–MutS–MutL led to the proposal that the ternary complex formation could involve the polymerization of MutL along the helix (17). A corollary of this model is the assumption that more MutL than MutS proteins should be required for the repair of a mismatch. This was further strengthened by genetic evidence showing that the cellular level of MutL, and not of MutS, becomes limiting when MMR is saturated in the presence of numerous mismatches (18–22). Because both MutS and MutL are present in equimolar concentrations in the cell, MutL protein limitation cannot simply be due to a lower amount of MutL in the cell (23).

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To construct pBAD24 plasmids expressing MutHwt or MutHE56A, we amplified by PCR the fragment encoding MutHwt using pTX417 as a template, and the fragment encoding MutHE56A using as a template pWY1016 (28,29). We used for PCR amplification primers 5’-GGGCAATGCATATACAGACTCAGATTAGGGC-3’ and 5’-GGGCAATGCAGAGAGAAGAGAGATC-3’ with an EcoRI restriction site at the C-terminal. We digested the PCR-amplified fragments by EcoRI and cloned them in the peGFP-MutSwt or peGFP-MutLwt. This resulted in the plasmids pYFP-MutS, pCFP-MutS, pYFP-MutL and pCFP-MutL expressing YFP-MutS, CFP-MutS, YFP-MutL and CFP-MutL, respectively. In the second step, we cloned the compatible fluorescent versions of MutS and MutL on the same plasmid, each under control of the individual T7 RNA polymerase promoter. We used the plasmids pCFP-MutS and CFP-MutL as templates for PCR amplification of the fragments encoding CFP-MutS and CFP-MutL and including T7 RNA polymerase promoter and terminator. We used for PCR amplification primers 5’-GGGCAATGCATATACAGACTCAGATTAGGGC-3’ and 5’-GGGCAATGCAGAGAGAAGAGAGATC-3’ with an EcoRI restriction site at the N-terminal and an EcoRI restriction site at the C-terminal. We digested the PCR-amplified fragments by EcoRI and cloned them in the peGFP-MutSwt or peGFP-MutLwt. This resulted in the plasmids pYFP-MutL CFP-MutS expressing YFP-MutL and CFP-MutS, and the plasmid pYFP-MutS CFP-MutL expressing YFP-MutS and CFP-MutL. These plasmids were introduced in cells with inactivated chromosomal *mutS* and *mutL* genes. To carry out experiments in which we determine the effect of the roadblock protein MutHE56A on MutL focus fluorescence, we cloned wild-type or partial loss-of-function *mutH* (*mutHE56A*) allele on the pBAD24 plasmid under arabinose promoter (27) and expressed *yfp* tagged from *mutL* from lactose promoter on the chromosome.

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For yfp-mutL integration in the chromosome, we first modified the plasmid pYFP-MutL to include the
chloramphenicol resistance cassette (CmR), flanked by FLP recombinase recognition targets, downstream of mutL. We amplified the sequence coding for the CmR (cat) by PCR using as a template the plasmid pKD3 (30). We used for PCR amplification primers 5’-CCGCCGCCGTGAGCTGACGCTTCTC-3’ and 5’-CCGGCGCCGCCATGAAATCTCCTCTTAG-3’ including a NotI restriction site at the N- and C-termini. We digested the resulting PCR product by NotI and cloned it in NotI site of the pYFP-MutL. This resulted in the plasmid pYFP-MutL.CmR. In a second step, we used the pYFP-MutL.CmR as a template to clone the yfp-mutL-cat under lactose promoter on the chromosome using gene replacement technique (30). We amplified the yfp-mutL-cat by PCR using primers that include homologies to the chromosomal lactose region. The primer 1 (5’-TGTCGGAATTTGGCCTGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGACGCTTCTC-3’ and 5’-CCGGCGCCGCCATGAAATCTCCTCTTAG-3’) includes at 5’ 45 bp sequence homologous to lactose promoter region (from −1 to −45) and the primer 2 (5’-CACCCGACACCTGTAATGGTCGCCACCGGCTCACTGCTTGAAGCTGACGCTTCTCCTCTTAG-3’) includes at 5’ 40 bp sequence homologous to lacZ C terminal (from 3026 to 3065). The resulting PCR product was introduced by transformation in MG1655 strain using P1 transduction and transformation.

Strains, growth conditions and mutation frequency assays
Strains and plasmids are listed in Supplementary Tables S1 and S2. All strains were derived from wild-type E. coli MG1655 strain using P1 transduction and transformation. We verified strain genotypes by testing the UV resistance, capacity to generate mutations conferring resistance to rifampicin or ability to use arabinose in McConkey plates supplemented by arabinose. We grew cells in M9 medium (31) supplemented by 2mM MgSO4, 0.003% vitamin B1, 0.001% uracil, 0.2% casamino acids, 0.01% glycerol and ampicillin (100 μg/ml) (to select for plasmids expressing the fluorescently labeled derivatives of MMR proteins). We added arabinose (0.02%) to the growth medium to induce the expression of MutHE56A or MutH above their basal level of expression from the pBAD24 plasmid. To block DNA replication we used rifampicin at 150 μg/ml. We performed mutagenesis experiments as described previously (24).

Live cell microscopy
Microscopy of live cells was done as described previously (24). Briefly, we grew cells in supplemented M9 medium to early exponential phase (OD600 0.1–0.2) at 37°C. When indicated, cultures were split in two. We treated one culture with rifampicin for 30 min, while the other culture was not treated. We concentrated the aliquots of treated and untreated cells and spread them on supplemented M9 agarose medium, in a cavity slide to obtain a cell monolayer, as described previously (24). We mounted the slide on Metamorph software (Universal Imaging) driven temperature controlled (Life Imaging Services) Zeiss 200M (Zeiss) inverted microscope. Images were recorded at 100-fold (for MutS/MutL co-localization experiments and for MutL foci fluorescence experiments of rifampicin treated or untreated cells) or 63-fold magnification (for roadblock experiments) using CoolSNAP HQ camera (Princeton Instruments), in phase contrast and in fluorescence. Co-localization experiments and MutL foci fluorescence experiments of rifampicin treated or untreated cells we done using HBO 103 lamp (Zeiss) regulated to 100% power at wavelengths of 500 nm (YFP) and 420 nm (CFP) during 20 s (for YFP and eGFP) and 6 s (for CFP) of exposure time. Roadblock experiments were done with HXP 120 lamp (Zeiss) regulated to 100% power at wavelength of 500 nm (YFP) during 6 s of exposure time. We acquired, merged and analyzed images using Metamorph software (Meta Imaging Systems).

Image analysis
Images were analyzed as described previously (24). Briefly, for all foci, we defined the region delimiting each focus, and one control region in the cell, representing the cytoplasmic fluorescence, using Metamorph region tool. For the co-localization analysis, we defined two regions (focus and control) first on the fluorescent image taken with the yellow filter. That was the image that we always recorded first. We then transferred both regions to the same position on the fluorescent image taken with the blue filter and measured the fluorescence of the control and focus regions for each cell, and for each image. We also recorded the fluorescence background of the agarose for each image. We calculated focus fluorescence by subtracting the maximal pixel intensity of focus region from the average fluorescence of control region. The cytoplasmic fluorescence was determined by subtracting from the average fluorescence of the control region the average fluorescence of the background. All presented data are the cumulative from at least three independent experiments, which always showed similar results.

RESULTS
Fluorescently tagged MutS and MutL are functional
Using GFP-MutL fusion, we and Walker’s group showed previously that MutL forms MutS-dependent fluorescent foci on mismatches in growing E. coli and Bacillus subtilis cells (24,32). While the B. subtilis fluorescent MutL was non-functional, the E. coli one that we constructed conserved its function completely. For this study, we constructed YFP- and CFP-tagged MutL and MutS. To determine whether these fluorescent protein fusions are functional, we examined their ability to complement the deletions of mutS and mutL genes (Figure 1A and Supplementary Table S3). The strains deleted for mutL and mutS carrying the plasmid expressing YFP-MutL and CFP-MutS, or carrying the plasmid expressing CFP-MutL and YFP-MutL, exhibited the spontaneous mutagenesis levels of the wild-type strain (Figure 1A). On the other hand, the frequency of mutations of same...
**Relative stoichiometry of MutL and MutS**

When the number of mismatches increases in the cell, MutL but not MutS becomes limiting (18–22). MutL could become limiting during MMR if the stoichiometry of the mismatch repair reaction is such that more MutL than MutS proteins are needed in the repair of a mismatch. This hypothesis predicts that the MutS and MutL foci co-localized on the mismatches should contain a greater amount of MutL than MutS protein. To compare the relative amount of MutS and MutL proteins per mismatch, we analyzed the fluorescence intensity of the co-localized MutS and MutL foci. First, we identified a MutL focus and the coincident MutS focus, and then we measured their respective fluorescence intensities. We performed these experiments with the combinations of YFP-MutL and CFP-MutS as well as with CFP-MutL and YFP-MutS protein fusions (Figure 1B and C). In both cases, the fluorescence intensity of MutL foci was higher compared to the intensity of MutS foci (Figure 2A). The average ratio of MutL foci fluorescence to co-localized MutS foci fluorescence was 2.7 (Figure 2B). These differences are not due to differences in the cytoplasmic fluorescence that varies very little among cells carrying differently labeled MutS and MutL proteins (Figure 2A).

For the YFP-MutL CFP-MutS pairs, the mean YFP-MutL and CFP-MutS foci fluorescence (±SEM) was 230 (±17.6) and 73 (±2.7), respectively. For the YFP-MutS CFP-MutL pairs, the mean YFP-MutS and CFP-MutL foci fluorescence was 76 (±3.8) and 162 (±7.4), respectively. Observed differences between fluorescence intensity of MutL and MutS foci are statistically significant ($P < 0.0001$, Wilcoxon test).

To examine the possible stoichiometric relationships of MutS and MutL co-assembled on mismatches, we examined the correlation between the intensity of fluorescence of the co-localized MutL and MutS in single foci. We detected no correlation between the MutL and MutS fluorescent intensities. For the YFP-MutL CFP-MutS pair, the $R^2$ was 0.09 (Figure 2C) and for the YFP-MutS CFP-MutL pair $R^2$ was 0.08 (Figure 2D). The absence of correlation demonstrates that, beyond the greater number of MutL than MutS molecules on mismatches noted above, there is no regularity in the stoichiometric relationship between MutS and MutL on mismatches.

**Number of MutL molecules on mismatches is independent of the intracellular concentration of MutL**

Since, we established that MutL assembles in greater numbers on mismatches than MutS, we wondered if this was determined by the intracellular concentration of MutL. To examine this possibility, we quantified the cytoplasmic fluorescence of eGFP-MutL and examined its correlation with the fluorescence intensity of MutL foci. No correlation between these fluorescence intensities was seen (Figure 3A). We conclude that the cytoplasmic concentration of MutL does not determine its amount assembled on mismatches.

The absence of such correlation could result also from a limited life-time of the MutL foci (24). The disassembly of the MutL foci could affect the detection of any correlation...
between the amount of MutL in the cytoplasm and on mismatches. The disassembly of MutL foci depends on DNA replication (24). When replication initiation is blocked with rifampicin, the life-time of MutL foci is greatly increased, but their fluorescence does not increase (24). To test the possible effect of the disassembly of MutL foci on the correlation between the amount of MutL in the cytoplasm and on mismatches, we treated the cells with rifampicin in order to block the initiation of chromosome replication. There was also no correlation between the fluorescence intensity of the MutL foci and the cytoplasmic fluorescence in cells treated with rifampicin (Figure 3B).

Together, these results confirm that the fluorescence of MutL foci depends on the number of MutL molecules in the focus and not on its intracellular concentration or on the life-time of the focus.

Roadblocks on DNA reduce the number of MutL molecules assembled on mismatches

There are two possibilities as to why the mismatches lead to the accumulation of MutL. MutL could assemble along the DNA or it could form a complex that is not in contact with the DNA. These two possibilities can be distinguished by placing roadblocks on the DNA. If MutL assembles along the DNA, then such roadblocks would limit the number of MutL molecules in the focus. The decreased number of MutL molecules in the foci would decrease the MutL focus fluorescence, or the frequency of foci, when the number of MutL molecules becomes insufficient for focus detection. If MutL forms a complex that does not make contact along the DNA, then such roadblocks would have no effect on the focus fluorescence or on the foci frequency.

The mutHE56A codes for a MutH protein that efficiently binds to GATC sequences in vitro without cleaving them (29). Due to this property, MutHE56A can be used as a roadblock on the GATC sequence proximal to a mismatch.

We first tested how the expression of MutHE56A affects the frequency of MutL foci in wild-type and in mutH cells. We showed previously that the frequency of fluorescent MutL foci corresponds closely to the mutation frequency of different strains examined (24). We found that the production of MutHE56A increases significantly the frequency of MutL foci in the wild-type cells compared to controls (Figure 4A). We confirmed this result by a classical mutagenesis assay, i.e. we measured the frequency of appearance of spontaneous mutations conferring resistance to rifampicin in strains expressing MutHE56A and in the control wild-type strains (Figure 4B). The results show that expression of MutHE56A increased spontaneous mutagenesis.

We interpret this result to be a consequence of a dominant negative effect of the mutant over the wild-type protein expressed from its native chromosomal site.

Figure 2. The stoichiometry of MutL and MutS on DNA mismatches. (A) The mean cytoplasmic fluorescence and the mean fluorescence of foci for 108 cells with YFP-MutL and CFP-MutS foci from 1B and 95 cells with YFP-MutS and CFP-MutL foci from 1C. (B) The histogram of the ratio of MutL focus fluorescence to co-localized MutS focus fluorescence for 203 pairs of co-localized MutL and MutS foci from A. (C) No correlation between the fluorescence intensity of co-localized foci of YFP-MutL and CFP-MutS ($R^2 = 0.09$) and (D) YFP-MutS and CFP-MutL ($R^2 = 0.08$). Error bars in A indicate standard error of the mean, $N$ in B stands for number, a.u. in A, C and D stands for arbitrary units and fluo in C and D stands for fluorescence.
The binding of MutHE56A to GATC sequences likely competes with MutHwt rendering mismatch repair inefficient and explaining the increase in mutation frequency. In vivo dominant negative effect of MutHE56A is consistent with previous in vitro studies showing that MutHE56A binds GATC sequences as efficiently as MutHwt but is completely defective for the DNA incision (29).

The expression of MutHE56A had no effect on the frequency of MutL foci in mutH cells compared to control cells (Figure 5A), arguing that these cells were still MMR deficient. On the other hand, the expression of MutHwt from a plasmid completely restored the MMR proficiency of the mutH cells. This was determined by measuring the frequency of YFP-MutL foci and the frequency of appearance of rifampicin resistant mutants (data not shown). These results are consistent with previous studies of mutation frequencies of mutH cells expressing MutHE56A or MutHwt (29).

Finally, we examined the effect of MutHE56A expression on the amount of MutL associated with mismatches. We performed this experiment in mutH cells because they provide a large number of MutL foci, which is necessary for good statistics.

The fluorescence intensity of MutL foci was significantly lower in cells expressing MutHE56A compared to control cells that did not express this mutant protein (3-fold; $P < 0.0001$, Wilcoxon test) (Figure 5B–D).

There was no difference in the intracellular concentration of MutL between the cells that expressed MutHE56A and those that did not, as judged by the fluorescence intensity of the cytoplasm (Figure 5C). This result suggests that MutL foci are less fluorescent as binding of MutHE56A to GATC prevents MutL from accumulating further along DNA. However, the decrease in MutL foci fluorescence and the increase in mutation frequency observed in the presence of MutHE56A could also be due to occluding the binding sites on MutL by overproducing one of its binding partners, in our case MutH. If this is so, we expect that the overproduction per se of wild-type or mutant MutH should have the same effect. However, our data with overproduction of wild-type MutH eliminate this hypothesis (Supplementary Figure S1).

Taken together, our results suggest that MutL assembles along the DNA from the mismatch site toward a proximal unmethylated GATC sequences.

**DISCUSSION**

MutL is a molecular matchmaker protein, which interacts with MutS, MutH and UvrD (2,6). MutL interaction with...
the MutS–mismatch complex triggers MutH endonuclease activity at a distal-strand discrimination DNA site (2,6). The nature of communication between these distal sites is not known. Several models based on cis and trans communication between these sites have been proposed (10–14). All of these models are based on in vitro studies and imply an equal stoichiometry of MutS and MutL proteins in the mismatch repair reaction. One hypothesis, that still awaits experimental evidence, suggests that the accumulation of MutL on DNA could allow the establishment of a physical interaction between the mismatch–MutS complex and the strand discrimination site (15). There are two predictions of this hypothesis that could be tested in vivo. The first is that the in vivo stoichiometry of mismatch repair involves more MutL than MutS molecules. The second is that a steric block on the DNA around a mismatch prevents the accumulation of MutL.

We used functional fluorescent MutS and MutL proteins to test these predictions. We found that MutS and MutL co-localize on mismatches in visible foci and that MutL foci are, on average, 2.7 times more intense than the co-localized MutS foci. These results indicate that the stoichiometry of the mismatch repair reaction in vivo involves more molecules of MutL than MutS. There is a caveat to this interpretation. Mismatch–MutS–MutL complexes that we are detecting are forming on mismatches that are unrepairable, due to mutH deficiency. It is possible that MutS and MutL stoichiometry on repairable mismatches is different from the one that we observe.

Our results on MutS and MutL stoichiometry on unrepairable mismatches are consistent with the in vitro DNA footprinting studies that show that MutS alone covers about 20 bp around mismatch, but that the addition of MutL increases considerably the size of the footprint (to 143 bp or more) (11,16). Our calculations, based on the resolved structure of MutS and on the model of the intact MutL (33–36), predict that one...
MutS dimer protects ~20 bp while one MutL dimer covers ~10 bp. Therefore, the extensive coverage of DNA seen in the presence of MutL is most likely due to the binding of multiple MutL proteins to the MutS-bound mismatch.

The second prediction of the model that suggests that MutL contacts the DNA while it accumulates around a mismatch is that a steric block on the GATC, proximal to the mismatch, would limit the amount of accumulated MutL. We used a mutant MutH protein, MutHE56A, which is able to bind to GATC sequences, but cannot cleave them. This protein was dominant negative when present in the cell and it reduced the amount of MutL present around mismatches. This is consistent with the idea that MutL contacts the DNA as it accumulates around a mismatch. This notion also suggests that MutL has at least two sites of where it can bind around a mismatch, to another MutL molecule and to the DNA. This predicts that the binding of MutL to the DNA could be cooperative. Indeed, it was shown that E. coli MutL, as well as its homologs, Mlh1-Pms1, bind DNA cooperatively in vitro (37,38).

On the account of the in vivo results presented here, and previous genetic and biochemical studies on MMR proteins, we propose the following model for in vivo MMR mechanism. Upon initial binding of MutS to a mismatch, MutS may diffuse and translocate along the DNA helix hence allowing additional copies of MutS to be loaded. Such repetitive MutS loading on mismatch is predicted by MMR models that involve movement of MMR proteins along the helix contour (14,17). Iterative binding of MutS to mismatches could explain the appearance of MutS foci in vivo. Binding of MutL to mismatch-bound MutS prevents MutS from sliding away as suggested by a study reporting an increased half-life of MutS–heteroduplex DNA complex upon MutL addition (10). Presumably, MutL does not affect MutS that is bound to mismatch but it interacts with MutS that slide away (14). MutL binding to DNA-bound MutS forms a ternary complex and establishes a nucleation point for further MutL accumulation on DNA surrounding the mismatch. Escherichia coli MutS tetramerization domain structure reveals that stable dimers but not tetramers are essential for DNA mismatch repair in vivo (39). A homodimeric MutS might be able to interact with two MutL dimers, which would lead to a ratio of MutL:MutS of 2 that is close to the observed values (2.1, for the combination of CFP-MutL and YFP-MutS, and 3.2 for the combination of YFP-MutS and CFP-MutL). However, our results show (data not shown) that, in all combinations, the fluorescence of MutS and MutL foci is highly variable and that the coefficient of variation of foci fluorescence is similar for differently labeled MutS and MutL. This suggests that not just one MutS and two MutL dimers accumulate on unrepaired mismatches but several MutS dimers and on average twice more dimers of MutL. We hypothesize that MutS–MutL–DNA filament-like structure is dynamic. A static filament might be inhibitory for strand discrimination as the binding of MutL to the DNA in a filament like manner could occlude the GATC sites similar as in MutS–MutL–DNA footprinting experiments (11,16).

Why may in vivo MMR require multiple MutL molecules? The average distance between two adjacent GATC sequences in E. coli genome is 256 bp. Except for runs of repeated mono-, di- and tri-nucleotides, the replicative DNA polymerase presumably makes errors randomly. Therefore, mismatches can be found anywhere in between two adjacent GATCs. So, the average distances between the mismatch and the proximal GATC are between 1 and 125 bp. Therefore, longer distances between mismatch and proximal GATC require accumulation of multiple copies of MutS and MutL proteins. In the light of our results, it would be interesting to test if the regions with low GATC abundance are more prone to mutations due to the requirement of higher numbers of the MutL protein, which appears to be in limiting quantity for replication fidelity control (40) as well as for recombination between non identical DNA sequences (41).

Our findings are also relevant for the understanding of the phenomenon of MutL saturation in vivo. MMR system has limited capacity to repair DNA mismatches: it saturates when the number of mismatches increases in the cell above a certain threshold. It was shown in several studies that MMR saturation is a result of MutL limitation, and not of limitation of MutS (18–22). However, the cause of MutL limitation was not identified. The simple possibility that MutL limitation is due to a lower amount of MutL in cell was excluded as both MutL and MutS are present in cells in equimolar concentrations (23). We found that treatments, which saturate MutL, do not lead to degradation of MutL that could lead to the deficit of functional MutL (Elez, M. and Radman, M., unpublished data). Therefore, in the light of our results, we propose that the deficit of MutL under conditions which increase the load of mismatches in cells could be due to engagement of more MutL than MutS proteins on the DNA mismatches. Unlike MutS, MutL associates with other members of the mismatch repair pathway in E. coli, the stoichiometry of which is unclear. This added involvement of MutL could also be an additional reason for MutL becoming saturating instead of MutS.

The MMR mechanism that involves more MutL accumulation relative to MutS observed in this study could be evolutionary conserved. For example, while this article was in revision, Kolodner’s group published the article demonstrating the mechanism of MMR in yeast using the same in vivo approach as we did here (42). They reported that the mismatch recognition by Msh2–Msh6 directs formation of superstoichiometric Mlh1-Pms1 foci.

SUPPLEMENTARY DATA

Supplementary Data are available at NAR Online: Supplementary Tables 1–3, Supplementary Figure 1 and Supplementary Reference 43.

ACKNOWLEDGEMENTS

The authors thank Martin Marinus and Wei Yang for kindly providing bacterial strains and plasmids as indicated. We also acknowledge Alex Dajkovic,
Lydia Robert, François Heslot and Mario Pende for critical reading of the manuscript. M.E., M.R. and I.M conceived the experiments. M.E. performed the experiments. M.E., M.R. and I.M. analyzed and interpreted the results, and wrote the paper.

FUNDING
European Commission Cordis (FP7-HEALTH-F3-2010-241476) and from the Agence Nationale de la Recherche (ANR-09-BLAN-0251); University Paris-Descartes (to M.E.) and Inserm Unit 1001 funds (to Rechearse (ANR-09-BLAN-0251); University Paris-

Conflict of interest statement. None declared.

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