A Human Cell-Based Assay to Evaluate the Effects of Alterations in the MLH1 Mismatch Repair Gene

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Abstract

We describe a new approach to investigate alterations in the human MLH1 mismatch repair (MMR) gene. This is based on complementation of the phenotype of a MLH1-defective subclone of the ovarian carcinoma A2780 cells by transfection of vectors encoding altered MLH1 proteins. Measurements of resistance (tolerance) to methylating agents, mutation rate at HRRIT, microsatellite instability (MSI), and steady-state levels of DNA 8-oxoguanine were used to define the MMR status of transfected clones. The approach was validated by transfecting cDNA of wild-type (WT) MLH1, cDNAs bearing two previously identified polymorphisms (I219V and I219L) and two with confirmed hereditary nonpolyposis colorectal cancer (HNPCC) syndrome mutations (G224D and G67R). A low-level expression of two MLH1 polymorphisms partially reversed methylation tolerance and the mutant phenotype, including MSI. Higher levels of I219V resulted in full restoration of these properties to WT. Increased expression of I292L did not fully complement the MLH1 defect, because there was a simultaneous escalation in the level of oxidative DNA damage. The findings confirmed the important relationship between deficient MMR and increased levels of oxidative DNA damage. Mutations from Italian HNPCC families (G224D and G67R, N635S, and K618A) were all ineffective at reversing the phenotype of the MLH1-defective A2780 cells. One (K618A) was identified as a low penetrance mutation based on clinical and genetic observations. (Cancer Res 2006; 66(18): 9036-44)

Introduction

Colorectal cancer remains one of the most common fatal cancers in developed countries in which it represents a significant public health problem. One approach to reducing colorectal cancer mortality is to identify individuals predisposed to the disease and to target preventive measures to this group. Familial aggregation of colorectal, uterine, and other cancers constitutes the autosomally dominant hereditary nonpolyposis colorectal cancer (HNPCC) syndrome. HNPCC is associated with defective DNA mismatch repair (MMR) that is a consequence of germ-line mutations in the MMR genes. The majority of HNPCC patients are heterozygous for a mutated MMR gene, and MMR is functional in normal somatic cells. Cancer development is thought to be the consequence of inactivation or loss of the wild-type (WT) allele.

MMR reverses replication errors that escape proofreading by replicative DNA polymerases. In MMR-defective cells, both base-to-base mismatches and insertion/deletion loops, which are precursors of missense and frameshift mutations, are left uncorrected. This results in increased spontaneous mutational rates in both expressed and nonexpressed sequences. This mutator effect is particularly marked in nonexpressed sequences comprising multiple simple repeats (microsatellites), and the characteristic microsatellite instability (MSI) is diagnostic for MMR-defective tumors (1, 2).

MMR is also involved in the processing of O6-methylguanine (O6-meGua) and 6-methylthioguanine (me6-TG), DNA adducts induced by methylating agents and thiouropurines, respectively (3). O6-meGua- or me6-TG-containing base pairs are recognized by MutSo, the MSH2/MSH6 heterodimer that comprises the major MMR recognition complex, and subsequently processed by MMR. This processing does not result in lesion repair, however. Instead, it causes cell death and MMR-defective cells are characteristically extremely resistant to killing by methylating agents, such as N-methyl-N-nitrosourea (MINU) and thiopurines. Although the precise connection between MMR processing of damaged DNA bases and cell death is not completely understood, this methylation tolerance phenotype has been consistently identified in cells with MSH2, MLH1, MSH6, or PMS2 defects. MSH3 is the single exception.

Identifying HNPCC families and defining the role of MMR gene mutations in colorectal cancer predisposition is not always easy. There are several reasons for this, including deficiencies in family information, lack of pathologic features, and incomplete gene penetrance. There is, therefore, a particular need for assays that can define the functional significance of MMR gene variants that have been identified in genetic screens. A few such assays have been established and used to examine HNPCC-related MLH1 mutations and polymorphisms. The first of these is the "dominant-negative" mutator test in Saccharomyces cerevisiae in which expression of a WT, but not of a mutant, human MLH1 cDNA induces a mutator phenotype (4). In a similar approach, analysis of the mutator phenotype conferred either by MLH1 overexpression or by homozygous or heterozygous mlh1 mutations was investigated in yeast (5). The second is a biochemical assay that measures the degree of interaction between MLH1 and PMS2 proteins in MMR-defective strains complemented with plasmids expressing MLH1 cDNAs (6–10). The activities of MLH1 variants have also been examined by looking at MMR correction using recombinant proteins or following transient transfection of MLH1 cDNA into 293T human embryonic kidney cells (11–13).
Here, we describe a new approach to determine the significance of alterations in MLH1 that are identified by genetic screens in HNPCC families. It has been validated with a WT MLH1 sequence, with MLH1 mutations described previously in Italian families, and with two known polymorphic variants. The assays have also been used to identify a previously unassigned variant as an inactivating MLH1 mutation. The approach involves stable expression of the altered cDNA in a MLH1-defective clone of A2780 human ovarian carcinoma cells that contains an epigenetically silenced MLH1 gene (14). These A2780MNU-clone1 cells manifest the pronounced mutator phenotype and extensive tolerance to methylation damage characteristic of MMR-defective cells (15). Stable transfection of WT MLH1 cDNA or cDNAs containing polymorphic variants reverts both these phenotypes, whereas mutant MLH1 cDNAs do not. In addition to classifying MLH1 changes, this new assay permits a quantitative evaluation of the consequences of the expression of variant MLH1 proteins.

Materials and Methods

Molecular characterization of HNPCC families and controls. The MLH1 mutations of this study were identified in Italian families enrolled in the Registry of Hereditary Colorectal Cancer at the Istituto Nazionale Tumori. Screening of MLH1 was done on genomic DNA purified from peripheral blood leukocytes by PCR amplification of all exons followed by either single-strand conformation polymorphism (16) or denaturing high-performance liquid chromatography (DHPLC; ref. 17). To characterize nucleotide alterations, anomalous PCR fragments were sequenced using the ABI PRISM BigDye Terminator Cycle Sequencing kit (Applied Biosystems, Foster City, CA) and examined on ABI PRISM 3100 DNA Sequencer (Applied Biosystems) using the Sequencing Analysis software. The occurrence of the identified mutations in the DNA of probands’ relatives was assessed by direct sequencing.

MSI in colorectal cancer DNA was investigated using the five-marker panel recommended by international guidelines (18). Tumor and matched peripheral blood leukocytes by PCR amplification of all exons followed by either single-strand conformation polymorphism (16) or denaturing high-performance liquid chromatography (DHPLC; ref. 17). To characterize nucleotide alterations, anomalous PCR fragments were sequenced using the ABI PRISM BigDye Terminator Cycle Sequencing kit (Applied Biosystems) and examined on ABI PRISM 3100 DNA Sequencer (Applied Biosystems) using the Sequencing Analysis software. The occurrence of the identified mutations in the DNA of probands’ relatives was assessed by direct sequencing.

Plasmid and cloning procedure. Missense mutations were introduced by site-directed mutagenesis using the Stratagene QuickChange kit (La Jolla, CA), into the vector pCMV-Bam-Neo, which contains a full-length WT MLH1 cDNA. PCRs were carried out using primers (0.1 μmol/L) containing the desired mutation, 2.5 units Taq DNA polymerase, and 3 to 15 ng plasmid DNA. The 19-kb BstXI fragments containing the desired mutation were subcloned in a new copy of the vector to avoid the risk of random mutations introduced by PCR. Digestions with EcoRI were used to verify the correctness of insertions and all the constructs were verified by direct DNA sequencing.

Cell cultures, DNA transfection, and Western blotting. Cells were grown in DMEM (Life Technologies, Gaithersburg, MD) supplemented with 10% FCS, 100 units/mL penicillin, and 100 μg/mL streptomycin (Life Technologies) at 37°C in a 5% CO₂ atmosphere. A2780MNU-clone1 cells were transfected (Lipofectamine; Life Technologies) with pCMV-Bam-Neo vectors containing WT and/or mutated MLH1 cDNA and selected for G418 (100 μg/mL) resistance (Life Technologies). Individual clones were isolated by cytosine methylation and can be partially reactivated by demethylation treatment (14). MLH1 expression in A2780MNU-clone1 is abrogated by cytosine methylation and can be partially reactivated by azadeoxyxanthidine treatment, and expression of a transfected MLH1 cDNA restores full MMR capacity to A2780MNU-clone1 (14).

A2780MNU-clone1 was transfected with a WT MLH1 cDNA and six independent transfecnts were isolated. Western blotting indicated that five of six contained MLH1 levels comparable with those of WT A2780 cells (an example is shown in Fig. 1A). In one case (MLH1-2), expression was lower than 50% of the normal level (Fig. 1A). MLH1 cDNA expression did not alter the growth rate or the cloning efficiency and was stable even in the absence of G418 selection. A2780MNU-clone1 is 100-fold more resistant to MNU than A2780 (Fig. 1B).
reversed this phenotype and their MNU sensitivity was comparable with that of A2780 (Fig. 1B). Similar results were obtained with the other clones expressing normal levels of MLH1 (data not shown). The survival of MLH1-2 after MNU treatment is similar to that of MLH1-1 (Fig. 1B), indicating that the 2-fold difference in MLH1 expression between these clones was not reflected in a differential MNU sensitivity. Thus, restoration of WT MLH1 reverses the methylation tolerance of A2780MNU-clone1 and half of the normal level of MLH1 is sufficient to restore full MNU sensitivity.

Because MLH1-1 was typical of the clones expressing a transfected WT MLH1, it was used to investigate the effect of MLH1 restoration on the mutator phenotype. The mutation rate at the BAT26 mononucleotide repeat in MLH1-1 was <0.08 \times 10^{-3} per cell per generation and we observed no changes in BAT26 allele length among 50 subclones. In contrast, the mutation rate in MLH1-defective A2780MNU-clone1 cells was 39 \times 10^{-3} per cell per generation (Fig. 1C). Among the mutations, there was a predominance of single nucleotide frameshifts, with an excess of losses over gains (Fig. 1D). Thus, the WT level of MLH1 in MLH1-1 reversed the mutator effect at BAT26 by a factor of \sim 500-fold.

The reduced BAT26 instability in MLH1-1 was paralleled by significant changes in mutation rates at other loci. Reexpression of MLH1 produced a 40-fold reduction in the spontaneous mutation rate at HPRT, which declined from a mean of 1.8 \times 10^{-8} in A2780MNU-clone1 to 4.5 \pm 2.0 \times 10^{-8} in MLH1-1 (Fig. 2A and B). The latter value is similar to the spontaneous HPRT mutation rate in A2780 cells (1.7 \pm 1.2 \times 10^{-8}). Consistent with its ability to reverse methylation tolerance, 50% of normal MLH1 in MLH1-2 was also sufficient to reverse the mutator phenotype, and the spontaneous mutation rate in MLH1-2 cells was reduced to 4.8 \pm 2.1 \times 10^{-8}, a value closely similar to that of MLH1-1 (Fig. 2B).

Thus, a full or half complement of transfected WT MLH1 efficiently reverses the methylation tolerance and genome instability of A2780MNU-clone1.

**MLH1 cDNA containing missense mutations.** We analyzed four missense mutations (199G>A, 731G>A, 1852AA>GC, and 1904A>G) that have been identified in Italian HNPCC families (Table 1). The pathologic significance of these changes is not immediately evident, although none has been observed in >200 healthy Italian controls. A causative role in familial colorectal cancer was indirectly suggested by their association with tumor MSI, which was detected in all mutation carriers analyzed, with the exception of 1904A>G that could not be tested for lack of tumor samples.

Each of the mutations was introduced by site-directed mutagenesis of the WT MLH1 cDNA and transfected into A2780MNU-clone1. The transfection efficiencies of the mutant constructs were comparable with that of the WT, although Western blotting of several clonal isolates of transfectants indicated large variations in the amount of MLH1 expressed (data not shown).
For each mutant cDNA, clones containing the highest level of MLH1 were analyzed further. In two cases (199G>A and 1904A>G), the steady-state level of mutared MLH1 was significantly lower than WT (Fig. 3A) and this was accompanied by reduced levels of PMS2, consistent with the known instability of the PMS2 protein in the absence of its partner (21–23). The clone expressing the 1852AA>GC mutation had normal levels of both MLH1 and PMS2, indicating that the mutated MLH1 was expressed at normal levels, was stable, and could interact normally with PMS2.

None of the mutant MLH1 proteins had a detectable effect on the phenotype of A2780MNU-clone1. All four mutated proteins were associated with the same degree of MNU tolerance (Fig. 3B) irrespective of their level of expression. Similarly, the mutator phenotype of the recipient cells was unaffected by any of the four mutant MLH1 proteins. HPRT mutation rates in clones expressing each of the mutated MLH1 proteins were comparable with (or even higher in 199G>A) that of A2780MNU-clone1 (Fig. 2A).

Thus, A2780MNU-clone1 cells used as recipients for transfected variants of MLH1 provide a new assay capable to identify mutated forms of this protein because of their inability to reverse the methylation tolerance of MMR-defective cells.

Expression of MLH1 polymorphisms. The effect of two reported MLH1 polymorphisms (24, 25) on the phenotype of A2780MNU-clone1 was also examined. Expression of 655A>G was detectable in 2 (of 10) transfected clones, which were designated 655A>G-1 and 655A>G-2. Their steady-state levels of MLH1 were 80% and 20% of WT, respectively (Fig. 3B). The levels of the PMS2 protein, like those of the respective MLH1 proteins, were high in 655A>G-1 cells and low in 655A>G-2.

The high-level expression of MLH1 in 655A>G-1 cells was associated with full reversion of methylation tolerance (Fig. 4A). In addition, the spontaneous HPRT mutation rate in 655A>G-1 was reduced 12-fold to $1.5 \times 10^{-7}$ (Fig. 3C). Both of these findings indicate that an almost normal level of a transfected 655A>G-1 MLH1 allele confers restoration of functional MMR.

In contrast to the effects of high-level expression of the 655A>G polymorphism, a low level of the same polymorphic MLH1 had a modest effect. There was a significant decrease in the extent of methylation tolerance in 655A>G-2 and the MNU resistance relative to MLH1-1 (in which MMR is fully corrected by expression of WT MLH1) was reduced 15-fold (Fig. 4A). The mutation rate at BAT26 was 10-fold lower in 655A>G-2 than in MLH1-clone1 ($4.1 \times 10^{-3}$

Figure 2. Spontaneous mutation rates at the HPRT gene in untransfected and MLH1-transfected A2780 clones. A, HPRT mutation rates in A2780MNU-clone1 (black column). Mutation rates of 1852AA>GC-1, 1904A>G-1, 731G>A-1, and 199G>A-1 (white columns). Columns, mean of two experiments; bars, SD.

B, spontaneous mutation rates at the HPRT locus in A2780 (dotted white column), MLH1-1 (dotted light gray column), and MLH1-2 (dotted dark gray column).

C, HPRT mutation rate in 655A>G-1 (line-patterned column), 655A>G-2 (coarse-patterned columns), 655A>C-1 (dotted white column), and 655A>C-3 (dotted black column). Number of cultures, final number of cells at time of selection, fraction of cultures with no mutants, and mutation rates at the HPRT gene in untransfected and MLH1-expressing A2780MNU-clone1 clones. The mutation rate was calculated as $\mu = MC^{-1/n_2}$ as indicated in Materials and Methods.
versus \(39 \times 10^{-3}\) per cell per generation). Nevertheless, it remained 50-fold higher than that of MMR-proficient MLH1-1 (Figs. 2A and 4C). In accordance with this moderate effect on the mutator phenotype, the spontaneous HPRT mutation rate was also 15-fold higher in 655A>G-2 than in MLH1-1 cells (a mean of \(7 \times 10^{-7}\) versus \(4.5 \times 10^{-8}\) per cell per generation, respectively; Fig. 2C).

We conclude that, when expressed at high level, the 655A>G MLH1 polymorphism behaves like WT and reverts the methylation tolerance and mutator phenotype associated with defective MMR. At \(20\%\) of expression, the same protein only partially reverses the phenotype and is associated with significant residual genetic instability.

<table>
<thead>
<tr>
<th>Mutation</th>
<th>Exon</th>
<th>Codon</th>
<th>DNA change</th>
<th>Protein change</th>
<th>No. families</th>
<th>Frequency in healthy controls</th>
<th>Tumor phenotype</th>
</tr>
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<tbody>
<tr>
<td>199G&gt;A G67R</td>
<td>2</td>
<td>67</td>
<td>GGG&gt;AAG</td>
<td>Gly-to-Arg</td>
<td>1</td>
<td>0/220</td>
<td>1 MSI-H</td>
</tr>
<tr>
<td>731G&gt;A G244D</td>
<td>9</td>
<td>244</td>
<td>GGT&gt;GAT</td>
<td>Gly-to-Asp</td>
<td>3</td>
<td>0/220</td>
<td>2 MSI-H</td>
</tr>
<tr>
<td>1852-3AA&gt;GC K618A</td>
<td>16</td>
<td>618</td>
<td>AAG&gt;GCG</td>
<td>Lys-to-Ala</td>
<td>2</td>
<td>0/220</td>
<td>1 MSI-H</td>
</tr>
<tr>
<td>1904A&gt;G N635S</td>
<td>17</td>
<td>635</td>
<td>A4C&gt;AGC</td>
<td>Asn-to-Ser</td>
<td>1</td>
<td>0/220</td>
<td>0 NI</td>
</tr>
</tbody>
</table>

Polymorphism
655A>G I219V 8 219 ATC>GTC Ile-to-Val
655A>C I219L 8 219 ATC>CTC Ile-to-Leu

NOTE: NI, no information available.
Two clones expressing a second putative polymorphism (25), 655A>C, were also compared. MLH1 was present in 655A>C-1 at 100% of the WT level, whereas it was expressed at 10% of WT in 655A>C-3 (Fig. 4B). The levels of PMS2 paralleled MLH1 expression and were high in 655A>C-1 and low in 655A>C-3 (Fig. 4B), indicating that this altered MLH1 can stably interact with PMS2. Consistent with its designation as a polymorphism, a high MLH1 level in 655A>C-1 was accompanied by full reversion of methylation tolerance (Fig. 4A). As expected, the low level of MLH1 in 655A>C-3 was associated with an unaltered MNU resistance (Fig. 4A) and these cells retained a strong mutator phenotype (Fig. 2C).

Unexpectedly, the 655A>G MLH1 in 655A>G-1 had a similar effect on DNA 8-oxoG, indicating that these cells are functionally WT for MMR. The low level of the same protein in 655A>G-2 cells was not associated with a significant reduction in DNA 8-oxoG (Fig. 5A).

The findings for the 655A>C polymorphism were in stark contrast. The DNA 8-oxoG content of 655A>C-1 remained high. At ~5 x 10^-7 per cell per generation, this rate was only slightly lower than that of the parental MMR-defective cells (Fig. 2C). Thus, although the 655A>C MLH1 protein behaves as expected for a harmless polymorphism and fully reverses the methylation-tolerant phenotype, it does not have a significant effect on the mutator phenotype even when highly expressed. Because this behavior is unexpected, we confirmed that MMR was fully active in 655A>C-1 by analyzing their sensitivity to 6-TG. High-level 655A>C MLH1 expression restored full 6-TG sensitivity and 655A>C-1 cells were as sensitive as MLH1-1 cells to the thiopurine (data not shown). The anomalous behavior of 655A>C with regard to spontaneous mutation rates was investigated in more detail.

**Steady-state levels of DNA 8-oxoG.** The mutator phenotype of MMR-defective cells is influenced by oxidative stress (20). MMR prevents the accumulation of the promutagenic base 8-oxoG in DNA, and MMR-defective A2780MNU-clone1 cells accumulate 8-oxoG in their DNA (26). Consistent with our previous observations, restoration of MMR by a transfected WT MLH1 (MLH1-1) reduced the level of DNA 8-oxoG to approximately half (Fig. 5A). A high level of the 655A>G MLH1 in 655A>G-1 had a similar effect on DNA 8-oxoG, indicating that these cells are functionally WT for MMR. The low level of the same protein in 655A>G-2 cells was not associated with a significant reduction in DNA 8-oxoG (Fig. 5A).
with which their restored MMR is unable to cope. To examine this possibility, we compared the levels of endogenous reactive oxygen species (ROS) in 655A>C-1 and A2780MNU-clone1 cells. Cytosfluorimetric analysis by dichlorofluorescein staining indicated that 655A>C-1 cells contained 30% more ROS in comparison with their parental cells (data not shown). These data indicate that the anomalous properties of the 655A>C-1 transfectant reflect the unexpectedly high levels of oxidative damage in the recipient cells rather than the properties of the encoded MLH1 itself.

Consistent with expectation and with their failure to restore active MMR, there was no reduction in DNA 8-oxoG in any of the clones expressing a mutated MLH1 (Fig. 5B).

These data confirm the relationship between defective MMR and buildup of DNA 8-oxoG. They also indicate that variations in the endogenous levels of oxidative damage among clonal isolates of a transfected population might subtly influence their mutator phenotype.

Discussion

Restoration of MMR in human tumor cell lines is generally accomplished by introducing an extra copy of the relevant human chromosome (chromosomes 2 and 3 for MSH2/MSH6 and MLH1, respectively; refs. 27, 28). The MLH1-defective clone 1 variant of the A2780 ovarian carcinoma cell line provides one of a very few examples of cell lines in which MMR deficiency is fully corrected by a transfected cDNA (14, 29). We have suggested that stable expression of MLH1 cDNA in clone 1 might be related to its dominant-negative p53 mutation that distinguishes it from most MMR-defective human tumor cell lines (15). Another example is the MMR-defective mouse cell complemented with human cDNAs (30). We show here that stable expression of WT MLH1 cDNA in A2780MNU-clone1 reverts several aspects of the phenotype associated with inactive MMR. In particular, MLH1 expression restores WT levels of methylating agent sensitivity and reverses the mutator phenotype.

A relatively low level (~50% of normal) of MLH1 was sufficient to restore a WT phenotype. This reversed the mutator phenotype and MSI, indicating efficient correction of replication errors. It also promoted efficient processing of MNU-induced O-hexGua-containing base pairs and restored MutLo-mediated sensitivity to a methylating agent. These data are consistent with the properties of 293T cells expressing variable levels of WT MLH1 (29).

Measurements of MNU sensitivity, mutator phenotype, and DNA oxidation levels in transfected A2780MNU-clone1 cells correctly differentiated a series of known MLH1 mutations and polymorphisms. For four of four presumptive mutations, there was no reversion of methylation tolerance and the transfected cells retained their strong mutator phenotype. Expression of these mutant MLH1 proteins in clone 1 cells was also associated (with a single exception) with low levels of PMS2 and with high steady-state levels of DNA 8-oxoG. These findings are consistent with the involvement of these mutations in the pathogenesis of colorectal cancer. For the G67R (199G>A) variant, our data agree with findings from other approaches to mutation identification. The G67R amino acid change introduces a positive charge in the conserved ATP-binding motif of the gene. This variant is not found in the general population and is detected in HNPCC families (31). G67R was previously designated mutant in a yeast-based assay in which overexpression of the WT MLH1 induces a dominant-negative phenotype (4, 5). The same variant MLH1 was unable to interact with PMS2 and EXOI in a yeast two-hybrid assay (7, 8). In vitro MMR assays also showed that this mutation inactivates hMutLo (13). Although we have no information about the segregation of the G67R allele in the Italian family in which it was identified, the only tumor from this family that could be examined have high MSI levels. This is consistent with our identification of this variant MLH1 as mutant.

The second mutation G244D (731G>A) has been found in three Italian families. In one of these families, three affected individuals could be tested and segregation of the mutation with the disease was observed. The mutation was not found in healthy controls, and colorectal cancers from two affected carriers were MSI-H. The altered MLH1 was associated with a mutator phenotype in yeast (5), the interaction with its partner was defective in the two-hybrid assay (7), and human 293T cell extracts expressing the mutated protein were defective in MMR (12). Together with these observations, our data confirm the probable pathogenicity of this mutation.

The third mutation, K618A (1852-3AA>G) conferred only a partial defect in its interaction with MLH1 partners in the yeast two-hybrid assay (7). Unusually, MLH1 and PMS2 levels in A2780MNU-clone1 cells expressing the K618A mutation were
comparable with WT, and in vitro MMR assays indicate that the K618A variant MLH1 retains some function (13). Expression of K618A was unable to reverse either methylation tolerance or the mutator phenotype of A2780MNU-clone1, indicating that, despite a high level of hMutLα, this variant MLH1 is unable to participate in MMR in vivo. The K618A variant has been suggested to be associated with an increased risk of multiple adenomas (32) and has been identified in early-onset Scottish colorectal cancer patients (33). In our genetic survey, the variant was never detected in healthy controls and was observed in two unrelated HNPPC patients both affected with colorectal cancer. In one case, the tumor DNA was available and tested positive for MSI. However, the K618A variant was not present in two other affected members of the same family. The other patient inherited the variant from the unaffected father and, in addition, carried a second MLH1 mutation in trans, an in-frame deletion (1852-1854delAAAG) leading to the loss of a lysine residue (K618del). This mutation (also called MLH1 del616) has been shown previously to be clearly deleterious (34). Biallelic HNPPC-related MLH1 mutations are associated with a very severe phenotype, characterized by early-onset gastrointestinal cancers, childhood hematologic malignancies, and signs of neurofibromatosis type 1 (35–37). Although our patient had neither leukemia nor neurofibromatosis type 1 symptoms, it is noteworthy that he was diagnosed with a colorectal cancer at a very young age (28 years). These observations suggest that the K618A variant has a significant pathogenic involvement and are consistent with the results of the in vitro assays that unequivocally identify K618A as nonfunctional. In addition, its absence in unaffected controls is consistent with its being a cancer-predisposing allele. The carrier father is, however, unaffected, suggesting that K618A might be a low penetrance mutation. The lack of segregation with the disease in the second family is also consistent with a low penetrance HNPPC mutation (38). Levels of expression of the WT MLH1 allele should therefore be monitored with care in the carriers of the K618A mutation because their variation might have major consequences for the stability of the genome.

The N635S (1904A>G) variant has never been reported previously in familial colorectal cancer (http://www.insight-group.org). The effect of the MLH1 alteration on the genetic stability of colorectal cancer in this family is currently unknown. In our assays, 1904A>G expression was associated with retention of methylation tolerance and a strong mutator phenotype, indicating that this variant allele encodes an inactive protein. We conclude that the N635S MLH1 is most likely a pathogenic variant that is associated with the development of colorectal cancer.

The incidence of the I219V (655A>G) MLH1 variant ranges from 3% to 34% in different geographic regions (24, 31, 39, 40). When expressed in A2780MNU-clone1, I219V restored MNU sensitivity and genetic stability. It also reduced the steady-state level of DNA 8-oxoG. These observations, together with similar findings in yeast (4, 7, 8) and in vitro assay of MMRI by human cell extracts (12, 13), are all consistent with full retention of MMR activity and a designation of I219V as a silent polymorphism. Low levels of I219V MLH1 are apparently associated with a partial defect in MMR as indicated by incomplete restoration of MNU sensitivity, accumulation of DNA 8-oxoG, and intermediate genetic instability. The partial phenotype of these cells suggests that these biological end points constitute very sensitive indicators of inefficient MMR.

Although the I219V polymorphism is not associated with an increased risk of colorectal cancer (39) and behaves as WT in our assays, it may not be completely without effect. When combined with genotypes known to influence childhood acute lymphoblastic leukemia susceptibility (GSTM1-null and CYP2A1*2A or CYP2E1*5), homozygosity causes a significant additional risk (41). Homozygosity for the I219V polymorphism is also associated with ulcerative colitis refractory to treatment with 6-mercaptopurine or azathioprine (42), suggesting that MMR capacity is compromised (3).

The I219L (655A>C) variant (25) was also confirmed as a polymorphism. This was also inferred from the yeast two-hybrid system (7). In the transfectant (655A>C1) that expressed a normal level of the I219L protein, we observed the high level of spontaneous mutagenesis typical of inefficient MMR despite a full reversion of methylation tolerance. A large part of the mutator phenotype in MMR-defective human and mouse cells depends on oxidized DNA purines (20). In that particular transfectant, we noted a significant accumulation of DNA 8-oxoG to a level even greater than that of parental A2780MNU-clone1 cells. This was accompanied by an abnormally high level of cellular ROS. It seems that this particular clone of transfected A2780MNU-clone1 cells had an altered oxidative metabolism that exacerbated its mutator effect despite the presence of sufficient MMR activity to confer methylation sensitivity.

In conclusion, this approach provides a new tool with which to investigate the effect of alterations in the MLH1 gene. These assays also provided further evidence for the importance of oxidative DNA damage in MMR-defective cells and correctly classified four missense MLH1 substitutions, including two previously reported pathogenic mutations (G67R and G244D) and two neutral polymorphisms (I219V and I216L). The in vitro assays unequivocally identified the K618A change as an inactivating mutation. The segregation of this mutation in the two Italian families is, however, inconsistent with a simple causative role in HNPPC. Our findings illustrate the importance of combining genetic and clinical observations with data from in vitro assays.

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References

8. Ellson AR, Leung J, Bitter GA. Functional analysis of human MLH1 and MSH2 missense variants and hybrid
A Human Cell-Based Assay to Evaluate the Effects of Alterations in the MLH1 Mismatch Repair Gene

Monica Francesca Blasi, Ilenia Ventura, Gabriele Aquilina, et al.


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