A variant form of hMTH1, a human homologue of the E coli mutT gene, correlates with somatic mutation in the p53 tumour suppressor gene in gastric cancer patients

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Oxidative damage to diverse physiological molecules, including proteins, lipids, and nucleic acids, is an inevitable outcome of various cellular activities in living organisms. In particular, some oxidised forms of nucleotides cause miscoding of genetic information, and have therefore been present as a major threat for cells. Multigene systems to counteract such oxidative damage have evolved in diverse organisms. In E coli, several mutants designated ‘mutator’ have been isolated, and in these cells the mutation rate is significantly elevated, due to disruption of genes regulating the spontaneous mutation rate on the genome. Previous studies using these mutators have identified three genes that function in the system to counteract mutagenic oxidative damage. The mutT strain is one of the mutators that exhibit the highest spontaneous mutation rate. Maki H et al have shown that the product of the mutT gene hydrolyses an oxidised form of guanine nucleotides, 8-oxo-2′-deoxyguanosine 5′-triphosphate (8-oxo-dGTP), 1 8-oxo-dGTP incorporated into the genome stably pairs with adenine as well as cytosine in the template strand, accumulation of this oxidised form of guanine nucleotides leads to an increase in base substitution mutations—that is, A:T to G:C and G:C to T:A transversions. In the mutT strain, the rate for A:T to C:G transversion is indeed elevated 1000 fold over the wild type level. 2 The other two genes that function in cooperation with mutT are mutM (fpg) and mutY, both of which encode a DNA glycosylase to excise deleterious bases on the genome. 3 The former excises 8-oxo-guanine in the opposite site of cytosine on the genome, the latter removing adenine that pairs with 8-oxo-guanine. Thus, even in cells lacking MTH, G:C to T:A transversions are suppressed low. 4 Multiplicity of cellular anti-mutagenic systems guarantees the spontaneous mutation rate on the genome at an extremely low level.

Several mammalian counterparts of these E coli genes are now known. MTH1 is the first identified mammalian homologue of E coli mutT. 5 The human MTH1 gene, hMTH1, has been described in detail. 6 Altered function of hMTH1 and consequent elevation of the mutation rate may be an attractive hypothesis for various human diseases, particularly cancer. In several human diseases, including some common malignancies, the nucleotide sequence of hMTH1 has been exploited. 7 However, no apparent mutations were found. Instead, a single nucleotide polymorphism (SNP) at the first nucleotide of codon 83, which results in amino acid change from valine (V83: GTG) to methionin (M83: ATG), has been found, and the incidence of the M83 allele is relatively frequent in healthy controls (allele frequency = 0.09). 7 In mice, an mutT homologue has been identified and designated Mth1. MTH1-null mice, in which Mth1 is homozygously disrupted, have been reported. 8 Although the estimated increase in the mutation rate was only twice that in wild type counterparts, relatively frequent tumourigenesis was observed in the liver, lung, and stomach of the animals. 9 In patients with liver and lung cancer, sequence of hMTH1 has been determined. 1 However, no relevant sequence alterations were found, and the M83 allele is not also frequent in healthy controls, and correlates with mutation in the p53 tumour suppressor gene.

We show here that this polymorphic variation (V83M) is significantly more frequent in gastric cancer patients than in healthy controls, and correlates with mutation in the p53 tumour suppressor gene.

V83M variation of hMTH1 correlated with mutation in p53 suppressor gene. The frequency of p53 mutation is significantly higher in tumours harbouring the M83: ATG allele (6/14, 42.9%) than those without this variant allele (9/58, 15.5%).

Connection between variant hMTH1 and mutation in a common tumour suppressor gene may suggest a possible mechanism for a mutator phenotype underlying the pathogenesis of tumours.

Key points

- hMTH1 is a human homologue of the E coli mutT gene, which encodes a polypeptide that hydrolyses a potent mutagenic substrate for DNA replication, 8-oxo-dGTP. Altered function of hMTH1 has been suspected in various pathological states.
- In some common malignancies, the nucleotide sequence of hMTH1 has been explored. However, no mutations have been found. Instead, G:C to A:T transition at the first nucleotide of codon 83, GTG(Val) to ATG(Met), has been reported as a polymorphism.
- We show here that this polymorphic variation (V83M) is significantly more frequent in gastric cancer patients than in healthy controls, and correlates with mutation in the p53 tumour suppressor gene.

Patients and tissue specimens

Samples were collected from 72 gastric cancer patients who underwent surgery in our department from January 1990 to December 1997. Men and women numbered 47 and 25,
respectively; age ranged from 35 to 66 years, with a mean of 64 years. Written informed consent for studies using the tissues was obtained from each patient. Ethical approval was obtained from the IRB of Kyushu University. Specimens were taken immediately after resection and placed in liquid nitrogen.

Reverse transcription-polymerase chain reaction (RT-PCR) for hMTH1 gene
Total RNA was extracted from cancerous and corresponding normal tissue specimens using ISOGEN (Nippon Gene, Toyama, Japan), according to the manufacturer’s instructions. The first strand of cDNA was synthesised using 2 μg of total RNA, random hexadeoxynucleotide primer (TaKaRa, Tokyo, Japan), and RAV-2 reverse transcriptase (TaKaRa). After the first strand synthesis, PCR was performed using a GeneAmp 9600 thermal cycler (Applied Biosystems, Foster City, CA, USA). A 50 μl reaction mixture contained 0.2 μM oligonucleotide primer, 25 ng cDNA, 1 X PCR buffer (TaKaRa), 250 μM dNTP, and 2.5 U ExTaq polymerase (TaKaRa). The oligonucleotide primers used to amplify the hMTH1 sequence were 5’-ACCTGCCCCCACCAATTACA-3’ (forward), and 5’-GGCTCTGTGAAAGACTGTGTTT-3’ (reverse) (fig 1). The thermal conditions were as follows: 35 cycles at 95˚C for three seconds, 55˚C for 35 seconds, and 72˚C for 60 seconds; and one cycle at 72˚C for five minutes. The PCR products were purified using a microcon-100 microconcentrator (Amicon, Beverly, MA, USA).

Genomic PCR for p53 gene
Genomic DNA was extracted from tumour specimens. Tissue was ground in liquid nitrogen and lysed in digestion buffer (10 mM Tris.Cl, pH 8.0; 0.1 M EDTA, pH 8.0; 0.5% SDS; and 20 μg/ml pancreatic RNase). After treatment with proteinase K and extraction with phenol, DNA was precipitated with ethanol, and then dissolved in 1 X TE (10 mM Tris-Cl, pH 7.5; and 1 mM EDTA). To amplify the sequences corresponding to p53 exon 5 to exon 9, PCR was carried out using a GeneAmp 2400 thermal cycler (Applied Biosystems). A 100 μl reaction mixture contained 100 ng genomic DNA, 10 μM of each primer, 200 μM dNTP, and 2.5 U Taq DNA polymerase (TaKaRa). The primer sequences were for exon 5: 5’-TCTGTTCACTTGTGCCCTGAC-3’ (forward), and 5’-ATCACTGAGAATCAGAGCCGCTTGTA-3’ (reverse); for exon 6: 5’-GCGCTGTGGATTGATAGCATG-3’ (forward), and 5’-GGAGGGCCAATGTGAACCCATGGAGCTGAACC-3’ (reverse); for exon 7: 5’-TGACCACACGCTTCACCCACAGGGGCTTGTA-3’ (forward), and 5’-GCACACGGAGCCGTGGCA-3’ (reverse); for exons 8 and 9: 5’-TTGGGAGTAAGTGTGTAAGTGGGACTTCG-3’ (forward), and 5’-AGTGTTAGACTGGAAAAAGTTTT-3’ (reverse). The thermal conditions were as follows: one cycle at 95˚C for 10 minutes; 35 cycles at 95˚C for 30 seconds, 62˚C for 30 seconds, and 72˚C for 45 seconds. PCR products were purified using a microcon-100 microconcentrator (Amicon).

DNA sequencing
Labelled dideoxynucleotide terminator cycle sequencing reactions were performed using ABI Prism Dye Terminator Sequencing Kits (Applied Biosystems) and an ABI Prism 310 Genetic Analyser (Applied Biosystems). For each of PCR products, the same primers were used as a sequencing primer. Data were analysed using the ABI sequence software, DNA Sequencing Analysis, ver. 3.0 (Applied Biosystems). In each analysis, electropherograms were checked visually, not to misread minute sequence alterations. Sequence alterations were designated by comparison with the data deposited in the NCBI database sequence alterations found in one PCR product were verified by reverse sequencing and finally confirmed in more than two independently amplified PCR products.

RESULTS
A variant form of hMTH1 (M83) is more frequent in gastric cancer patients
In a panel of 72 gastric cancer patients, the nucleotide sequence of the hMTH1 gene was determined using reverse transcript-polymerase chain reaction (RT-PCR) products. The 333-bp cDNA fragment that encompasses a region coding the ‘phosphohydrolase module’, the catalytic domain of oxidised purine nucleoside triphosphatase, was amplified and sequenced (fig 1). In agreement with previous reports, the minor M83 allele that encodes methionin (ATG), instead of valine (GTG), at codon 83 was found in several patients. According to the sequence data, the subject population was divided into three allelotypes, V83: GTG/V83: GTG, V83: GTG/M83, M83: GTG/M83 (ATG) (table 1). In gastric cancer patients, the M83 allele appeared more frequent than that in healthy controls (X2 test, p = 0.007). Among 72 gastric cancer patients, 14 (19.5%) carried the M83 allele. Four patients (5.6%) were homozygous for this variant allele. The subject population was next divided into two subgroups, one homozygous for this variant allele and the other. Another X2 test revealed that the allelotype homozygous for the variant hMTH1 allele (M83) was significantly more frequent in gastric cancer patients than in healthy controls (p = 0.01) (table 1). Thus, we conclude that the variant form of hMTH1 (M83) is more frequent in gastric cancer patients. These sequence alterations were also confirmed by sequencing PCR products of genomic DNA extracted from tumour specimens and corresponding normal tissues (data not shown). No other sequence alterations were found within the region examined.

We statistically tested whether this V83M variation of hMTH1 correlates with clinicopathological features of the patients. However, no statistically significant correlation was found between the presence of this variant allele and any of the common clinicopathological features of patients (data not shown).

V83M variation of hMTH1 correlates with mutation in p53 gene
hMTH1 encodes an enzyme that hydrolyses mutagenic oxidised purine nucleoside triphosphates such as 8-oxo-dGTP. Variation of a cellular component functioning in the
anti-mutagenic systems may affect the sequence stability maintained throughout the genome. Carcinogenesis is thought to comprise stepwise alterations in proto-oncogenes or tumour suppressor genes. We therefore examined the relationship between \textit{hMTH1} variation and mutation in \textit{p53} gene, a tumour suppressor gene most commonly mutated in various human malignancies. In our panel of 72 patients with gastric cancer, \textit{p53} mutations resulting in an amino acid substitution were detected in 15 tumours (20.8%). The mutations were predominantly G:C to A:T transitions in codons, including the acknowledged hot spots (data not shown). Intriguingly, \textit{p53} mutation correlated with the variant form of \textit{hMTH1} (table 2). The frequency of \textit{p53} mutation was significantly higher in tumours harbouring at least one M83 allele than in those without M83 allele (Fisher’s exact test, \(p = 0.034\)). However, in a comparison between tumours homozygous for M83 allele and others, difference in the incidence of \textit{p53} mutation was not statistically confirmed, probably due to a paucity of M83-homozygous tumours. Among nine \textit{p53}-mutant tumours without the M83 allele, G:C to A:T and A:T to G:C transitions were noted in three (3/9, 33.3%) and two (2/9, 22.2%), respectively. G:C to T:A transversion was also shown in three tumours (3/9, 33.3%) (table 3). On the other hand, among six tumours with \textit{p53} mutations that possessed at least the M83 allele, G:C to A:T transitions were observed in four (66.7%) (table 3). However, this partiality of mutation to G:C to A:T transition in tumours harbouring a M83 allele was not statistically confirmed. A:T to C:G transversion was not found in neither.

**DISCUSSION**

Altered function of \textit{hMTH1} has been suspected in various pathological states, particularly in tumourigenesis, in human bodies. However, in spite of efforts to explore \textit{hMTH1} gene in various human diseases, no mutations have been found. Single nucleotide polymorphism (SNP) at codon 83, V83: GTG to M83: ATG, was not clearly associated with lung or liver cancers. However, in the present study, we have shown that in gastric cancer patients this polymorphic variation of \textit{hMTH1} is significantly more frequent than in healthy controls. In this context, this is the first report that has shown a connection between V83M variation of \textit{hMTH1} and human malignancies.

Mutations are found in various genes in tumours. One may presume a state with an elevated mutation rate in some steps of tumourigenesis. However, it still remains controversial whether a state with an elevated mutation rate plays an important role in tumourigenesis. Bodmer and colleagues\(^\text{11,12}\) pointed out that tumour cells that harbour mutations in tumour suppressor genes or proto-oncogenes can be selected merely by phenotypical advantage, without an elevated mutation rate. On the other hand, a line of evidences suggests an existence of a state with an elevated mutation rate in tumours, and this state is now referred to as ‘mutator phenotype’. The critical role of mutator phenotype in tumourigenesis has been emphasised by Loeb and colleagues\(^\text{13,14}\). Spontaneous mutation rate on the genome is invariably regulated. Previous studies using \textit{E.coli} mutators suggest that there are several cellular systems, the failure of which will lead to a significant increase in the mutation rate.

The first example of mutator phenotype derived from a disruption of such cellular systems is defective DNA mismatch repair in a cancer prone syndrome, hereditary non-polypsis colorectal cancer (HNPPCC).\(^\text{15,16}\) Deficiency in mismatch repair is also associated with other human malignancies.\(^\text{17}\) One may expect that the spontaneous mutation rate is elevated in mismatch repair defective cells. Indeed, in mismatch repair gene knock out mouse cells, the mutation rate was 15-fold higher than in wild type cells.\(^\text{18}\) However, mutations in representative tumourigenic genes, such as \textit{p53} and \textit{ras}, were not found in mismatch repair defective human tumours. Instead, insertion/deletion mutation in repetitive sequences such as microsatellites was observed. This phenomenon is now referred to as ‘microsatellite instability’ (MSI), and the cellular phenotype with MSI has been designated ‘microsatellite mutator phenotype’ (MMP).\(^\text{19,20}\) The discrepancy between knock out animals and

| Table 1 | The frequency of single nucleotide polymorphism at codon 83 in the \textit{hMTH1} gene: a comparison between gastric cancer patients and healthy controls |
|---|---|---|
| \textit{hMTH1} allelotype | Gastric cancer (\(n = 72\)) | Controls (\(n = 400\)) |
| V83: GTG/V83: GTG | 58(80.5%) | 330(83.5%) |
| V83: GTG/M83: ATG | 10(13.9%) | 67(16.8%) |
| M83: ATG/M83: ATG | 4(5.6%) | 3(0.8%) |

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| Table 2 | Relationship between \textit{p53} gene status and V83M variation of \textit{hMTH1} |
|---|---|---|
| \textit{hMTH1} allelotype | \textit{p53} gene status | |
| | wt (\(n = 57\)) | m (\(n = 15\)) |
| V83: GTG/V83: GTG | 49(84.5%) | 9(15.5%) |
| V83: GTG/M83: ATG | 10(17.5%) | 47(82.5%) |
| M83: ATG/M83: ATG | 8(57.1%) | 6(42.9%) |

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human tumours may suggest an oversimplification in our discussions.

The second example is failure in the systems countering mutagenic oxidative damage in cells. In *E. coli*, MutT, MutY, and MutM cooperatively function to minimise the effects of an oxidised form of guanine nucleotides, 8-oxo-dGTP, in the pool and on the genome. Mammalian homologues of these proteins and mice in which their genes are homozygously disrupted have been reported. As mentioned above, the failure in this system that is clearly associated with human diseases has not been found. However, in *MTTH1*-null ES cells, the mutation rate is elevated twofold higher, compared with the wild type counterparts. Altered function of *hMTTH1* may also lead to accumulated mutations in various genes in human cells.

Connection between V83M variation and mutation in other genes, particularly proto-oncogenes or tumour suppressor genes, has not thus far been addressed. This is the first report of a connection between the variant *hMTTH1* and p53 mutation.

*E coli* MutT hydrolyses an oxidised nucleotide, 8-oxo-dGTP, into its monophosphate form. 8-oxo-dGTP incorporated in the genome pairs with adenine, as well as cytosine, which results in G:C to T:A or A:T to C:G transversions. In an *E coli* strain lacking MutT, the spontaneous occurrence of A:T to C:G transversion increases 1000-fold higher than in wild type strains. In the *mutT* strain, G:C to T:A transversions are suppressed low by compensatory activities of MutM and MutY glycosylases.

Frequent variation of *hMTTH1* in gastric cancer may suggest a biased spectrum in observed mutations. However, the majority of mutations found in p53 was G:C to A:T transitions, albeit this bias has not been statistically confirmed (table 3). No A:T to C:G transversions were found. In fact, the biological significance of V83M variation has not been addressed in this study, a tight linkage between *M83* allele and another molecular variety with different biological function. This study was partly supported by a grant from the Ministry of Education, Science, Sports, and Culture of Japan.

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