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Haplotype defined by the *MLH1*-93G/A polymorphism is associated with *MLH1* promoter hypermethylation in sporadic colorectal cancers

Yasuyuki Miyakura[1,2†], Makiko Tahara[1,2†], Alan T Lefor[1], Yoshikazu Yasuda[1] and Kokichi Sugano[2*]

Abstract

Background: Methylation of the *MLH1* promoter region has been suggested to be a major mechanism of gene inactivation in sporadic microsatellite instability-positive (MSI-H) colorectal cancers (CRCs). Recently, single-nucleotide polymorphism (SNP) in the *MLH1* promoter region (*MLH1*-93G/A; rs1800734) has been proposed to be associated with *MLH1* promoter methylation, loss of MLH1 protein expression and MSI-H tumors. We examined the association of *MLH1*-93G/A and six other SNPs surrounding *MLH1*-93G/A with the methylation status in 210 consecutive sporadic CRCs in Japanese patients.

Methods: Methylation of the *MLH1* promoter region was evaluated by Na-bisulfite polymerase chain reaction (PCR)/single-strand conformation polymorphism (SSCP) analysis. The genotype frequencies of SNPs located in the 54-kb region surrounding the *MLH1*-93G/A SNP were examined by SSCP analysis.

Results: Methylation of the *MLH1* promoter region was observed in 28.6% (60/210) of sporadic CRCs. The proportions of *MLH1*-93G/A genotypes A/A, A/G and G/G were 26% (n = 54), 51% (n = 108) and 23% (n = 48), respectively, and they were significantly associated with the methylation status (p = 0.01). There were no significant associations between genotype frequency of the six other SNPs and methylation status. The A-allele of *MLH1*-93G/A was more common in cases with methylation than the G-allele (p = 0.0094), especially in females (p = 0.0067). In logistic regression, the A/A genotype of the *MLH1*-93G/A SNP was shown to be the most significant risk factor for methylation of the *MLH1* promoter region (odds ratio 2.82, p = 0.003). Furthermore, a haplotype of the A-allele of rs2276807 located −47 kb upstream from the *MLH1*-93G/A SNP and the A-allele of *MLH1*-93G/A SNP was significantly associated with *MLH1* promoter methylation.

Conclusions: These results indicate that individuals, and particularly females, carrying the A-allele at the *MLH1*-93G/A SNP, especially in association with the A-allele of rs2276807, may harbor an increased risk of methylation of the *MLH1* promoter region.

Keywords: MSI, SNP, *MLH1*, Methylation, Colorectal cancer, Haplotype

Background

Microsatellite instability (MSI) is a form of genomic instability that can be detected as changes in the length of repetitive microsatellite sequences. MSI occurs in the majority of tumors from patients with Lynch syndrome carrying germline mutations in the DNA mismatch repair (*MMR*) genes [1]. MSI also occurs in approximately 15-20% of sporadic colorectal cancers (CRCs) [1,2]. Methylation of the *MLH1* promoter region has been suggested to be a major mechanism of gene inactivation in sporadic MSI-positive CRCs [3]. Bi-allelic methylation of the *MLH1* promoter region induced transcriptional silencing in cell lines showing MSI and this epigenetic mechanism of gene inactivation is analogous to Knudson's two-hit hypothesis [4,5].

We previously reported that all CpG sites in a 1-kb region encompassing the *MLH1* promoter were methylated (designated as full methylation) in CRCs showing

* Correspondence: ksugano@tcc.pref.tochigi.lg.jp
†Equal contributors
[2]Oncogene Research Unit/Cancer Prevention Unit, Tochigi Cancer Center Research Institute, 4-9-13, Yohnan, Utsunomiya, Tochigi 320-0834, Japan
Full list of author information is available at the end of the article

high-frequency MSI (MSI-H) [6]. Full methylation was particularly observed in proximal colon cancers in females older than 70 years old and led to the transcriptional silencing of the *MLH1* gene and the MSI-H phenotype [7]. Methylation of the *MLH1* promoter region was also observed in 20% of MSI-negative CRCs, although all of these cases displayed partial methylation (limited to the most upstream region of the *MLH1* promoter); MLH1 protein expression was maintained in such cases showing partial methylation. Thus, there is an important correlation between the methylation status of the *MLH1* promoter and the development of sporadic MSI-positive CRCs.

Single-nucleotide polymorphisms (SNPs) are the most common type of human genetic variation and occur at about every 1000 bases in the human genome. Numerous studies are now ongoing to assess their possible associations with human diseases or phenotypes [8-10]. SNPs in the promoter region have been shown to influence gene transcription [11]. G/A SNP −93 bp upstream of the translation start site was identified in the *MLH1* gene promoter region [*MLH1*-93G/A SNP (rs1800734)] [12]. The *MLH1*-93G/A SNP has recently been proposed to have an association with CRCs, ovarian and endometrial cancer [13-16]. In particular, it was shown to be associated with *MLH1* promoter methylation, loss of MLH1 protein expression and MSI-H tumors [14,16-21]. However, these results are based largely on analyses of cancers in Caucasian populations. Allelic frequencies of the *MLH1*-93G/A SNP differ between Caucasians and Japanese, and the frequency of the A-allele in Caucasians (20-23%) is lower than that in Japanese (46%) [12,16,20].

The purpose of this study was to address the association between the *MLH1*-93G/A SNP and methylation status in the *MLH1* promoter region in a series of sporadic CRCs in a Japanese population. Furthermore, we also examined the association between six other SNPs located in the 54-kb region surrounding the *MLH1*-93G/A SNP and methylation status in the *MLH1* promoter region. We report here that the *MLH1*-93G/A SNP was significantly associated with *MLH1* promoter methylation in a Japanese population. Furthermore, a haplotype comprising the A-allele of rs2276807 and the A-allele of *MLH1*-93G/A SNP showed a significant association with *MLH1* promoter methylation. This haplotype may be associated with an increased risk for methylation-positive CRCs, especially in females.

Methods

Tissue samples

Tumor tissues and corresponding normal mucosa were obtained from 210 consecutive CRC patients who underwent surgery from 1996 through 1998 at Jichi Medical University Hospital. Genetic analyses were carried out in the Oncogene Research Unit/Cancer Prevention Unit, Tochigi Cancer Center Research Institute. As all samples were derived from archived tissue samples, they were coded anonymously, prior to the analysis of methylation status and genotyping of the vicinity of the *MLH1* promoter regions, according to the Ethical Guidelines for Human Genome/Gene Analysis Research (Ministry of Education, Culture, Sports, Science and Technology, Ministry of Health, Labour and Welfare and Ministry of Economy, Trade and Industry, March 29, 2001) and the study protocol was approved by the institutional review board of each institution. Normal mucosa was obtained from the surgical margin of the resected specimen before sampling the tumor tissue to avoid contamination by tumor cells. Kindred in whom the Lynch syndrome was suspected were excluded from this study, since patients with at least one CRC among first-degree relatives were not included. Tumors were staged according to a modified version of Dukes classification [22]. DNA was extracted from fresh tumor material by a standard procedure using proteinase K digestion and subsequent phenol-chloroform extraction. Methylation status and the genotype of the *MLH1* promoter region were also examined in peripheral blood lymphocytes (PBLs) from 100 anonymous samples obtained from normal healthy donors over 50 years of age undergoing routine health checkups.

Analysis of MSI

Genomic DNA was subjected to PCR amplification at two mononucleotide microsatellite repeat loci, BAT26 and BAT25. The BAT26 locus contains a 26-repeat adenine tract and is located in intron 5 of the *MSH2* gene, whereas the BAT25 locus contains a 25-repeat thymine tract located in intron 16 of the *c-kit* oncogene. Both loci have been shown to be sensitive markers of MSI, which manifests as alteration in the size of the respective mononucleotide repeats in tumor DNA. PCR reactions were performed as described previously [6]. When either BAT26 or BAT25 showed MSI, we examined 7 microsatellite repeat loci, D2S123, D5S346, D17S250, MSH3, MSH6, TGFBR2 and BAX, according to the recommendations of the Bethesda guidelines [23]. Tumors were classified as MSI-H when ≥30% of the 9 markers showed MSI. Low-frequency MSI (MSI-L) is classified as MSI-negative.

Methylation analysis of the *MLH1* promoter region

Na-bisulfite PCR/single-strand conformation polymorphism (SSCP) (BiPS) analysis was performed as described previously [6,24]. With the adenine residue at the initiation codon numbered as +1 nt, the *MLH1* promoter (−755 to +86) was divided into five regions [region A (from −755

to −574, containing 23 CpG sites), B (from −597 to −393, 12 CpG sites), C (from −420 to −188, 16 CpG sites), D (from −286 to −53, 13 CpG sites) and E (from −73 to +86, 13 CpG sites)] and amplified with 5 sets of PCR primers. Sequences of PCR primers were as reported previously [6]. Each primer set was designed to anneal to both methylated and unmethylated DNA sequences and the amplicons could be separated by SSCP analysis depending on their methylation status (Figure 1). Amplified DNA fragments were visualized using SYBR® Gold nucleic acid gel stain (Cosmo Bio Co., Tokyo, Japan) and scanned with a Fluorescent Image Analyzer Model FLA-3000G (Fuji Photo Film Co., Tokyo, Japan). When the bands showed mobility shifts, they were cut from the gel, reamplified and directly sequenced using an ABI 310 PRISM™ sequencer (Perkin-Elmer Co., Branchburg, NJ) with a Big-Dye Terminator Cycle Sequencing Ready Reaction Kit™ (Perkin-Elmer Co., Branchburg, NJ). Methylation profiles were classified as follows: full methylation if all CpG sites in regions A to E showed methylation, partial methylation if some CpG sites, in any region, showed methylation, and no methylation if all CpG sites in any region did not show methylation. Methylation status of the *MLH1* promoter region D was also analyzed by methylation-specific PCR (MSP) and the allelic status of methylation was examined by direct sequencing of the *MLH1*-93G/A SNP in region D (Figure 1) [7].

Analysis of the genotype frequencies of the *MLH1* promoter region

The genotype frequencies of the *MLH1*-93G/A SNP were examined by SSCP analysis using an ALFexpress DNA sequencer (Pharmacia, Tokyo, Japan). Briefly, primer sequences were 5′Cy5-gacgaagagacccagcaaccc3′ (forward) and 5′tagatgctcaacggaagtgc 3′ (reverse). The 5′-terminus of the forward primer was labeled with indodicarbocyanine (Cy5) fluorescent dye. PCR reactions were performed as described previously [7]. The data were analyzed using the software package Fragment Manager™ (Pharmacia, Tokyo, Japan).

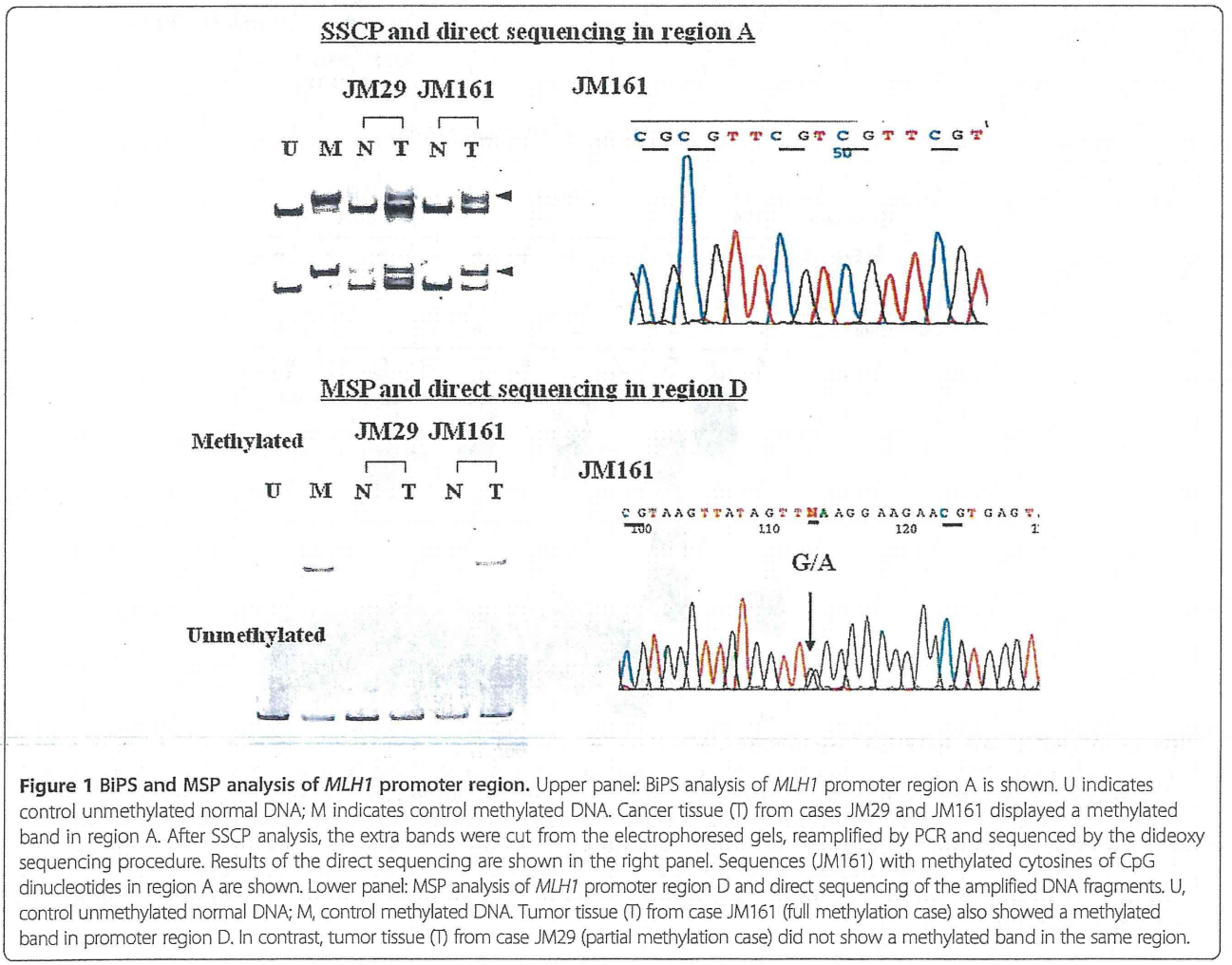

Figure 1 BiPS and MSP analysis of *MLH1* promoter region. Upper panel: BiPS analysis of *MLH1* promoter region A is shown. U indicates control unmethylated normal DNA; M indicates control methylated DNA. Cancer tissue (T) from cases JM29 and JM161 displayed a methylated band in region A. After SSCP analysis, the extra bands were cut from the electrophoresed gels, reamplified by PCR and sequenced by the dideoxy sequencing procedure. Results of the direct sequencing are shown in the right panel. Sequences (JM161) with methylated cytosines of CpG dinucleotides in region A are shown. Lower panel: MSP analysis of *MLH1* promoter region D and direct sequencing of the amplified DNA fragments. U, control unmethylated normal DNA; M, control methylated DNA. Tumor tissue (T) from case JM161 (full methylation case) also showed a methylated band in promoter region D. In contrast, tumor tissue (T) from case JM29 (partial methylation case) did not show a methylated band in the same region.

Analysis of six SNPs surrounding the *MLH1*-93G/A SNP

The genotype frequencies of the following six SNPs, rs2276807 (C/A), rs4678922 (A/T), rs6789043 (T/C), rs1046512 (C/A), rs3774343 (G/A) and rs4647215 (C/A) (Figure 2a), located in the 54-kb region surrounding the *MLH1*-93G/A SNP, were examined by SSCP analysis. The locations of the SNPs and the PCR primer sequences are described in Additional file 1: Table S1. Each PCR was carried out using 0.1 μg of genomic DNA as a template, 10×PCR buffer, 1.25 mM dNTP, 10 μM each primer and 0.625 units of *Taq* DNA polymerase in a total volume of 25 μL. The PCR conditions were as follows: heat denaturation at 95°C for 12 min, 30 cycles of PCR comprising 95°C for 30 sec, an annealing step with different temperatures, namely, 55°C (rs4678922, rs6789043, rs1046512, rs3774343), 63°C (rs2276807) or 68°C (rs4647215), for 30 sec, and an extension step at 72°C for 30 sec, followed by a final extension at 72°C for 10 min. Conditions of the SSCP analysis are described in Additional file 1: Table S1. The data were analyzed using the software package Fragment Manager™ (Pharmacia, Tokyo, Japan).

Electrophoretic mobility shift assay (EMSA)

EMSA was performed using the Gelshift™ Kit (Active Motif, Carlsbad, CA) (Figure 2b). The sequences of ^{32}P-labeled complementary oligonucleotide pairs and complementary competitor oligonucleotide pairs corresponding to the *MLH1* promoter sequence were as follows: MLH-184 to −132: 5′-ACCCACAGAGTTGA GAAATTTGACTGGCATTCAAGCTGTCCAATCAATA GCTG-3′ [12], *MLH1*-93G: 5′-AGCTACAGCTGAAGG AAGAA-3′, and *MLH1*-93A: 5′-AGCTACAGCTAAAGG AAGAA-3′. After the reaction mixtures with and without

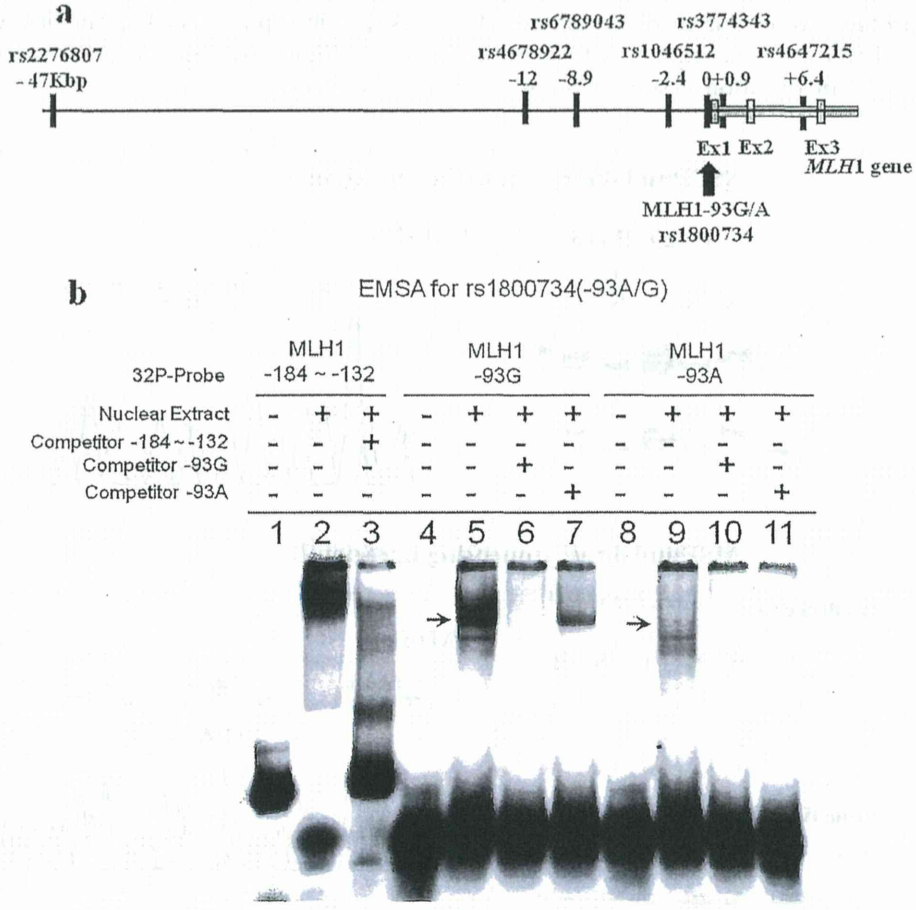

Figure 2 Map of six SNPs and EMSA for rs1800734. a. Map of six SNPs, rs2276807 (C/A), rs4678922 (A/T), rs6789043 (T/C), rs1046512 (C/A), rs3774343 (G/A) and rs4647215 (C/A), located in the 54-kb region surrounding the *MLH1*-93G/A SNP. **b**. EMSA using nuclear extracts from HeLa cells. The competition assay was performed with ^{32}P-labeled MLH1-184 to −132 and unlabeled MLH1-184 to −132 oligomer (lanes 1–3). A shifted band was observed in the presence of HeLa nuclear extract, which was blocked in the presence of excess unlabeled competitor (lanes 2 and 3). The competition assay was performed with matched sets of DNA oligomers homologous to each genotype of the *MLH1*-93G/A SNP (lanes 5–7, 9–11). When a ^{32}P-labeled MLH-93G probe was mixed with nuclear extract from HeLa cells, a shifted band was blocked by the competitor oligomer of MLH1-93G, but not MLH1-A (lanes 5–7). When ^{32}P-labeled MLH-93A probe was mixed with the nuclear extract from HeLa cells, a shifted band was not detected (lanes 9–11).

an excess of unlabeled competitor and HeLa cell nuclear extract (HeLa Nuclear Extract™; Activemotif, Carlsbad, CA) were incubated for 20 min on ice, ^{32}P-labeled oligonucleotides were added as a probe. The binding reactions were carried out according to the manufacturer's instruction manual. After the binding reaction, the DNA protein complexes were resolved by electrophoresis in a 5% non-denaturing acrylamide gel chilled at 4°C using a circulating water bath. After electrophoresis, the gel was dried and scanned with a Fluorescent Image Analyzer Model FLA-3000G (Fuji Photo Film Co., Tokyo, Japan).

Statistical analysis

Statistical analysis was carried out using Pearson's chi-square (X^2) test or Student's t-test. Multivariate logistic regression analysis was performed using Stat View 5.0 statistical package (SAS Institute Inc., Cary, NC) to identify independent variables associated with the presence of *MLH1* promoter methylation. The included variables were *MLH1*-93G/A genotype (A/A vs. A/G + G/G), tumor location (right vs. left), gender (female vs. male) and age at onset (more than 70 vs. less than 70). Absence of departure from the Hardy-Weinberg equilibrium was calculated by the asymptotic X^2 goodness of fit test. The haplotypes of the seven SNPs were analyzed using SNPAlyze software ver. 5.0 (Dynacom, Chiba, Japan) and a case–control study was performed to examine the relationship between methylation-positive and methylation-negative subjects. Permutation analysis was used to determine the empirical significance and to calculate the probability (p) values based on 10,000 replications. The global p-values represent the overall significance using the X^2-test when the observed versus expected frequencies of all haplotypes are considered together.

The individual haplotypes were tested for association by grouping all other haplotypes together and applying the X^2-test with one degree of freedom. P-values <0.05 were considered statistically significant.

Results

Comparison of clinicopathological and molecular features with methylation status of the *MLH1* promoter region

The clinicopathological background, MSI status and the association of these variables with methylation status are summarized in Table 1. The category of methylation-positive includes both full methylation (n = 13) and partial

Table 1 Association between clinicopathological features and MSI status and methylation status of the *MLH1* promoter region in sporadic colorectal cancers

	Methylation-positive				Methylation-negative	p values[4]
	Full methylation	Partial methylation	p values[3]	Total (Full + Partial methylation)	(No methylation)	
Numbers of cases	13	47		60	150	
Age at onset	72.8 ± 10.6	64.5 ± 10.1	0.012	66.3 ± 10.7	63.9 ± 11.1	NS
Gender						
Male	3	25	NS(0.054)	28	100	0.007
Female	10	22		32	50	
Tumor location[1]						
Right	13	15	<0.0001	28	39	0.004
Left	0	32		32	110	
Histological type[2]						
well	6	24	NS	30	105	0.04
mod	3	19		22	36	
muc	2	3		5	5	
por	2	1		3	4	
Dukes						
A/B	1/10	2/27	NS	3/37	8/75	NS
C/D	1/1	14/4		15/5	51/16	
Tumor size (mm)	66.4 ± 35.5	58.2 ± 26.9	NS	60.0 ± 28.9	52.2 ± 22.4	0.04
MSI-H	13	2	<0.0001	15	4	<0.0001

[1]right: cecum, ascending colon and transverse colon, left: descending colon, sigmoid colon and rectum.
[2]well: well-differentiated adenocarcinoma, mod: moderately differentiated adenocarcinoma, por: poorly differentiated adenocarcinoma, muc: mucinous adenocarcinoma.
[3]P values were analyzed using Pearson's chi-square test or Student's t-test between cases with full methylation and cases with partial methylation. NS: not significant. P values of <0.05 were statistically significant.
[4]P values were analyzed using Pearson's chi-square test or Student's t-test between methylation-positive cases (full methylation + partial methylation) and methylation-negative cases. NS: not significant. P values of <0.05 were statistically significant.

methylation (n = 47). There were significant differences between methylation-positive (n = 60) and -negative groups (n = 150) with respect to gender, tumor location, histologic type and tumor size (Table 1). Methylation-positive tumors showed a marked preponderance in females (p = 0.007) and the proximal colon (p = 0.004). The proportion of well-differentiated adenocarcinomas was lower in the methylation-positive group (p = 0.04). The average tumor size was significantly larger in methylation-positive tumors (60.0 ± 28.9 mm) than in methylation-negative ones (52.2 ± 22.4 mm) (p = 0.04). Regarding MSI status, the frequency of MSI-H was significantly higher in the methylation-positive group (p < 0.0001).

In the methylation-positive group, there were significant differences between patients showing full methylation (n = 13) and partial methylation (n = 47) with regard to age at onset, tumor location and MSI status. The average age at onset was significantly higher in patients with full methylation than in those with partial methylation (72.8 ± 10.6 y/o vs. 64.5 ± 10.1 y/o, p = 0.012). All tumors with full methylation developed in the proximal colon and showed MSI-H (13/13, 100%), while those with partial methylation were more prevalent in the distal colon (32/47, 68.1%) and MSI-H was observed less frequently than in those with full methylation (2/47, 4.3% vs. 13/13, 100%, p < 0.0001).

Comparison of *MLH1* genotypes with methylation status of the *MLH1* promoter region

Genotypes and allelic frequencies of the *MLH1*-93G/A SNP were examined in 210 sporadic CRC patients and 100 PBL samples from normal donors, and the results were compared with previous studies carried out in cohorts of different populations. The allelic frequency for each allele was nearly 50% in the normal donors, other Japanese and Korean cohorts, while the frequency of the G-allele (78–80%) was higher than that of the A-allele (20–22%) in Caucasians [12,16,20,25]. In each study, observed genotype frequencies were consistent with the expected frequencies according to the Hardy-Weinberg equilibrium.

In the 210 sporadic CRCs, the proportions of genotypes A/A, A/G and G/G were 26% (n = 54), 51% (n = 108) and 23% (n = 48), respectively (Table 2). There were no significant associations between genotypes and clinicopathological parameters such as age at onset, sex, tumor location, Dukes classification and histologic type.

Table 2 Association between methylation status of the *MLH1* promoter region and genotypes of the *MLH1*-93G/A SNP in sporadic colorectal cancers

<Total cases>	Genotype				Allelic frequency			
	A/A (n = 54)	A/G (n = 108)	G/G (n = 48)	p values	A	G	RR	p values
Methylation-positive	24	26	10	0.0103[1]	74	46	1.303	0.0094[1]
Full methylation	4	8	1		24	10		
Partial methylation	20	18	9	0.0229[2]	58	36		0.0044[2]
Methylation-negative (No methylation)	30	82	38		142	158		
<Female cases>	Genotype	Allelic frequency						
	A/A (n = 23)	A/G (n = 37)	G/G (n = 22)	p values	A	G	RR	p values
Methylation-positive	14	13	5	0.0259[1]	41	23	1.525	0.0067[1]
Full methylation	4	5	1		13	7		
Partial methylation	10	8	4	NS[2]	28	16		0.0223[2]
Methylation-negative (No methylation)	9	24	17		42	58		
<Male cases>	Genotype	Allelic frequency						
	A/A (n = 31)	A/G (n = 71)	G/G (n = 26)	p values	A	G	RR	p values
Methylation-positive	10	13	5	NS[1]	33	23	1.179	NS[1]
Full methylation	0	3	0		3	3		
Partial methylation	10	10	5	NS[2)]	30	20		NS[2)]
Methylation-negative (No methylation)	21	58	21		100	100		

[1]P values were analyzed using Pearson's chi-square test between methylation-positive (full + partial) and methylation-negative cases (no methylation). NS: not significant. P values of <0.05 were statistically significant.
[2]P values were analyzed using Pearson's chi-square test between full, partial and methylation-negative cases (no methylation). NS: not significant. P values of <0.05 were statistically significant.

The proportions of the *MLH1* genotypes were compared with methylation-positive and methylation-negative cases or cases of full methylation, partial methylation and no methylation of the *MLH1* promoter region (Table 2), and were significantly associated with methylation status (methylation-positive vs. methylation-negative, p = 0.0103; full methylation vs. partial methylation vs. no methylation, p = 0.0229). Allelic frequencies of the *MLH1*-93G/A SNP were also compared with methylation status of the *MLH1* promoter region. The A-allele was more common in methylation-positive cases (RR 1.303, p = 0.0094) and was also more common in subjects with full methylation and partial methylation than the G-allele (p = 0.0044). In an analysis of cases subdivided by gender, the proportions of the *MLH1* genotypes were significantly associated with methylation status in females (methylation-positive vs. methylation-negative, p = 0.0259), but not in males. Furthermore, allelic frequencies of the A-allele were also significantly associated with methylation status in females (RR 1.525, p = 0.0067).

The clinical characteristics, pathological features and MSI status based on methylation status (full, partial or none) were compared according to three genotypes of the *MLH1*-93G/A SNP (Additional file 1: Table S2). Patients who had tumors with full methylation were older and included a marked preponderance of females (compared to no methylation), right-sided lesions and MSI-H compared to those with partial and no methylation in genotype A/A. In contrast, patients who had tumors with full methylation were significantly different regarding tumor location, pathological type (compared to no methylation) and MSI status compared to those with partial and no methylation in genotype A/G. The distribution of mucinous and poorly differentiated adenocarcinomas is significantly higher in patients with full methylation compared to those with no methylation. In genotype G/G, there was no difference among the three methylation types except for MSI-H.

MLH1 genotypes and other risk factors contributing to *MLH1* promoter methylation in CRCs

In logistic regression analysis using the genotype of the *MLH1*-93G/A SNP (A/A vs. A/G + G/G), tumor location (right vs. left), gender (female vs. male) and age at onset (more than 70 vs. less than 70) as the independent variables, genotype was shown to be the most significant risk factor for hypermethylation of the *MLH1* promoter region (Table 3). The odds ratio (OR) in a multivariate analysis for genotype A/A was 2.82 (95% CI 1.42–5.62, p = 0.003), followed by tumor location (OR 2.4, 95% CI 1.23–4.70, p = 0.011) and gender (OR 2.13, 95% CI 1.08–3.92, p = 0.027), while age at onset was not a significant factor contributing to methylation status.

Table 3 Multivariate-adjusted odds ratio for *MLH1* promoter methylation with genotypes and other variables

Factors	OR[1]	95% CI[2]	p values[3]
Genotype of the *MLH1* (A/A vs. A/G, G/G)	2.82	1.42-5.62	0.003
Tumor location (right vs. left)	2.40	1.23-4.70	0.011
Gender (female vs. male)	2.06	1.08-3.92	0.027
Age of onset (more than 70 vs. less than 70)	1.05	0.53-2.07	0.885

[1]*OR*: Odds ratio, Odds ratio adjusted for other variables listed in the table.
[2]*CI*: Confidence interval.
[3]P values of <0.05 were statistically significant.

Analysis of genotype frequencies and haplotype of the SNPs surrounding the *MLH1*-93G/A SNP and their association with methylation status

We analyzed the genotype frequencies of six SNPs located −47 kb upstream to 6.4 kb downstream of the MLH1 translation start site, namely, rs2276807, rs4678922, rs6789043, rs1046512, rs3774343 and rs4647215, surrounding the *MLH1*-93G/A SNP (rs1800734) (Figure 2a), and their association with *MLH1* methylation status (methylation-positive vs. methylation-negative). The observed frequency of each genotype was consistent with the expected frequency according to the Hardy-Weinberg equilibrium. There were no significant associations between the frequency of each genotype and the methylation status in these SNPs, except for rs1800734. Furthermore, we analyzed the haplotypes of these seven SNPs and their association with *MLH1* methylation status (methylation-positive vs. methylation-negative). As a result, only the haplotype A-A-T-A-A-A-C (rs2276807-rs4678922-rs6789043-rs1046512-rs1800734-rs3774343-rs4647215) had a significant association with *MLH1* promoter hypermethylation in the analysis of all cases (p = 0.012), as well as in the female cases (p = 0.00038), but this was not significant in the male cases (Table 4).

EMSA

To elucidate whether the genotype of the *MLH1*-93G/A SNP affects the binding activity of nuclear transcription factors, each synthetic double-stranded DNA oligomer of the *MLH1*-93G/A SNP was subjected to EMSA (Figure 2b). First, in order to confirm the accuracy of this assay, a competition assay was performed using ^{32}P-labeled MLH-184 to −132 and unlabeled MLH1-184 to −132 oligomers as described previously [12] (Figure 2b, lanes 1–3). A shifted band was observed with HeLa nuclear extract, which was blocked completely in the presence of an excess of unlabeled competitor sequence, as reported previously. HeLa cell nuclear extract was then incubated with 20-bp DNA oligomers homologous to each genotype of the *MLH1*-93G/A SNP (Figure 2b, lanes 4–7, 8–11). When the ^{32}P-labeled MLH1-93G

Table 4 Association between haplotype of seven SNPs including *MLH1*-93G/A SNP and the methylation status of the *MLH1* promoter region

<Total cases > Haplotype[1]	Haplotype frequencies[2]			χ^2-value	p-value[3]
	Total	M-negative	M-positive		
C-A-T-A-**A**-A-C	0.3141	0.3031	0.3431	0.6274	0.4283
A-A-T-A-**G**-A-C	0.3116	0.3366	0.2499	2.9665	0.085
A-A-T-A-**A**-A-C	**0.198**	**0.1667**	**0.2755**	**6.3116**	**0.012**
C-T-C-C-**G**-G-A	0.149	0.1644	0.1102	1.9578	0.1618
C-A-T-A-**G**-A-C	0.0273	0.0291	0.0213	0.1968	0.6573
<Female cases > Haplotype[1)]		Haplotype frequencies[2]		χ^2-value	p-value[3]
	Total	M-negative	M-positive		
C-A-T-A-**A**-A-C	0.2983	0.3046	0.2955	0.0154	0.9014
A-A-T-A-**G**-A-C	0.2801	0.3346	0.2017	3.3986	0.0653
A-A-T-A-**A**-A-C	**0.2077**	**0.1154**	**0.3452**	**12.6416**	**0.00038**
C-T-C-C-**G**-G-A	0.1829	0.21	0.1406	1.2578	0.2621
C-A-T-A-**G**-A-C	0.0309	0.0354	0.017	0.4818	0.4876
<Male cases > Haplotype[1]		Haplotype frequencies[2]		χ^2-value	p-value[3]
	Total	M-negative	M-positive		
C-A-T-A-**A**-A-C	0.3323	0.3381	0.3105	0.1457	0.7027
A-A-T-A-**G**-A-C	0.3243	0.3028	0.4031	1.9442	0.1632
A-A-T-A-**A**-A-C	0.1916	0.1922	0.1895	2.00E-03	0.9643
C-T-C-C-**G**-G-A	0.127	0.1414	0.0741	1.7339	0.1879
C-A-T-A-**G**-A-C	0.0249	0.0255	0.0229	0.0117	0.9138

[1]Loci of SNPs examined were as follows: rs2276807 - rs4678922 - rs6789043 -rs1046512- rs1800734 (bold letter) - rs3774343 - rs4647215.
[2]Total cases, methylation-negative (M-negative) cases and methylation-positive (M-positive) cases of haplotype frequencies.
[3]P values of <0.05 were statistically significant.

probe was mixed with the nuclear extract, we detected a shifted band, which was blocked by the unlabeled MLH1-93G competitor (Figure 2b, lanes 5 and 6), but not by the unlabeled MLH1-93A competitor (Figure 2b, lane 7). However, a shifted band was not detected when ^{32}P-labeled MLH1-93A probe was mixed with the HeLa cell nuclear extract (Figure 2b, lanes 9–11).

Discussion

Methylation of the *MLH1* promoter region and subsequent transcriptional silencing have been shown to play a critical role in the development of MSI-positive CRCs [3]. In a previous study, we reported two types of methylation profile in the *MLH1* promoter region, namely, full methylation and partial methylation [6]. Only the former was associated with *MLH1* gene silencing followed by the MSI-H phenotype. Partial methylation was observed in CRCs that developed in both proximal and distal colon, while the majority of cases showing full methylation developed in the former. The average age at onset was 10 years earlier in CRCs with partial methylation than in cases with full methylation [7]. Partial methylation of the *MLH1* promoter region implies initiation of the methylation process, but only a subset of cases with partial methylation may eventually progress to full methylation and develop MSI-positive CRCs. It is therefore important to elucidate factors contributing to methylation of the *MLH1* promoter region in CRC tumorigenesis.

Recent studies have reported such a factor. The *MLH1*-93G/A SNP located in the promoter region is significantly associated with *MLH1* promoter methylation followed by loss of MLH1 protein expression and plays an important role in MSI-H colorectal tumorigenesis [14,16-21]. However, these results are derived mostly from Caucasian populations, in which the frequencies of the A-allele and A/A homozygosity are low, at 20–22% and 4–5%, compared with those in East Asians including the Japanese [12,16,20,25]. The allelic frequency of *MLH1*-93A in a Japanese cohort is as much as 50%; therefore, study on the Japanese would be important to validate the results previously reported for Caucasians. The present study confirms the association between the genotype of *MLH1*-93G/A and methylation status for sporadic CRCs in a Japanese population. The frequency of methylation of the *MLH1* promoter region in CRCs is significantly higher in those carrying the A-allele in

Japanese. The *MLH1*-93G/A SNP genotype is associated with the methylation status of the *MLH1* promoter region, with either full or partial methylation.

Previous studies reported a different affinity of the DNA binding proteins to the *MLH1*-93G/A SNP, suggesting that some transcription factors bind preferentially to the sequence of MLH1-93G but not to MLH1-93A [26,27]. In EMSA using HeLa cell nuclear extract, the band showing a mobility shift of the ^{32}P-labeled MLH1-93G probe had greater intensity than that of the MLH1-93A probe, suggesting that the affinity of DNA binding proteins to the MLH1-93A sequence is less than that to MLH1-93G (Figure 2b). These results suggest that individuals carrying the *MLH1*-93A allele are prone to transcriptional silencing due to the decreased affinity to allele-specific DNA binding proteins. However, the definitive mechanism of developing *MLH1* promoter methylation based on the different affinity of DNA binding proteins to the *MLH1*-93G/A SNP has not been elucidated yet. Furthermore, the frequencies of MSI-positive CRC were reported to be as high as 10–15% in Caucasians, compared with 9.05% (19/210) in this series and 13% in another Japanese cohort [28]. Assuming that the frequency of MSI in the Japanese is the same as that in Caucasians, carrying the A-allele at the *MLH1*-93G/A SNP is not the only risk factor for developing MSI-positive CRCs. Methylation of the *MLH1* promoter region was found in 28.6% (60/210) of patients and 78.3% (47/60) showed partial methylation, among which methylation was limited to the most upstream region of the *MLH1* promoter sequences that is distant from the *MLH1*-93G/A SNP. As shown in Table 2, the frequency of A/A homozygosity was significantly higher in cases with partial methylation (42.5%, 20/47) than in those with full methylation (30.8%, 4/13) or no methylation (20.0%, 30/150) ($p = 0.0229$). These data suggest that the *MLH1*-93G/A genotype was not the only determinant of the MSI phenotype, which was mostly associated with full methylation.

We further examined the association between the genotypes of the six other SNPs surrounding the *MLH1*-93G/A SNP (rs1800734) and methylation status in the *MLH1* promoter region. Rs1800734 was the only SNP showing a significant association with methylation. A haplotype-based case–control study showed a significant association of the haplotype comprising A-A-T-A-A-A-C alleles with *MLH1* promoter methylation (Table 4). The A allele of rs1800734 had only 2 haplotypes comprising either C-A-T-A-A-A-C or A-A-T-A-A-A-C, and the latter showed a significant association with *MLH1* promoter hypermethylation; that is, rs2276807 located in the most upstream region spanning −47 kb of rs1800734 was a determinant of the haplotype associated with *MLH1* promoter hypermethylation. These findings suggest that additional genetic and/or environmental factors may contribute to the progression of methylation status from partial to full methylation, eventually associated with the MSI phenotype. To our knowledge, this is the first report of an association between this haplotype and methylation status in the *MLH1* promoter region.

In an analysis of cases subdivided by gender, the frequency of the A-allele *MLH1*-93G/A SNP was significantly higher in females (RR 1.525, $p = 0.0067$), while this was not significant in males (RR 1.179) (Table 2). Subjects carrying the A-allele, particularly females, may harbor an increased risk of methylation of the *MLH1* promoter region. Furthermore, a haplotype associated with A-alleles of both rs2276807 and *MLH1*-93G/A (rs1800734) also had a significant association with *MLH1* promoter methylation in female subjects (Table 4). Slattery et al. suggested that estrogen exposure in women protects against MSI, whereas the lack of estrogen in older women increases the risk of MSI, as shown in a population-based case–control study [29]. In this series, the clinical characteristics of methylation-positive tumors, such as female predominance and late age at onset, are compatible with this epidemiological observation for MSI-positive tumors. Individuals carrying the A-allele of *MLH1*-93G/A (rs1800734), especially in association with the A-allele of rs2276807, may be susceptible to methylation, but hormonal status or other genetic factors may modify the age of onset of the cancer. As the present study size is relatively small, further studies are needed to elucidate the mechanism of methylation susceptibility of the *MLH1* promoter region defined by the genotype of *MLH1*-93G/A SNP, along with the relevant haplotype.

Conclusions

The *MLH1*-93G/A SNP (rs1800734) was significantly associated with methylation of the *MLH1* promoter region in a Japanese population. Furthermore, a haplotype comprising the A-allele of rs2276807 and the A-allele of *MLH1*-93G/A SNP showed a significant association with methylation of the *MLH1* promoter region. Individuals, particularly females, carrying the A-allele at the *MLH1*-93G/A SNP, especially in association with the A-allele of rs2276807, may harbor an increased risk of methylation of the *MLH1* promoter region.

Additional file

Additional file 1: Haplotype defined by the MLH1-93G/A polymorphism. Table S1. PCR primer sequences and PCR conditions of the six SNPs. **Table S2.** Association between clinicopathological features and methylation status according to the genotype of the *MLH1* promoter region.

Abbreviations

BiPS: Na-bisulfite PCR/single-strand conformation polymorphism; CRC: Colorectal cancer; EMSA: Electrophoretic mobility shift assay;

HNPCC: Hereditary nonpolyposis colorectal cancer; *MMR* gene: mismatch repair gene; MSI: Microsatellite instability; MSI-H: high-frequency MSI; MSI-L: low-frequency MSI; MSP: Methylation-specific PCR; PBL: Peripheral blood lymphocyte; SNP: Single-nucleotide polymorphism; SSCP: Single-strand conformation polymorphism.

Competing interests
The authors declare that they have no competing interests.

Authors' contributions
M.Y. designed the study, performed genetic analysis and wrote the manuscript; T.M. performed genetic analysis and revised the manuscript; S.K. designed the study, performed genetic analysis, revised the manuscript and gave final approval of the manuscript; L.A. performed the English editing and revised the manuscript; Y.Y. designed the study and revised the manuscript. All authors read and approved the final manuscript.

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Author details
[1]Department of Surgery, Jichi Medical University, 3311-1, Shimotsuke, Tochigi 329-0498, Japan. [2]Oncogene Research Unit/Cancer Prevention Unit, Tochigi Cancer Center Research Institute, 4-9-13, Yohnan, Utsunomiya, Tochigi 320-0834, Japan.

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References
1. Aaltonen LA, Peltomaki P, Leach FS, Sistonen P, Pylkkanen L, Mecklin JP, Javinen H, Powell SM, Jen J, Hamilton SR, Petersen GM, Kinzler KW, Vogelstein B, de la Chapelle A: **Clues to the pathogenesis of familial colorectal cancer.** *Science* 1993, **260**(5109):812–816.
2. Thibodeau SN, Bren G, Schaid D: **Microsatellite instability in cancer of the proximal colon.** *Science* 1993, **260**(5109):816–819.
3. Herman JG, Umar A, Polyak K, Graff JR, Ahuja N, Issa JP, Markowitz S, Willson JK, Hamilton SR, Kinzler KW, Kane MF, Kolodner RD, Vogelstein B, Kunkel TA, Baylin SB: **Incidence and functional consequences of hMLH1 promoter hypermethylation in colorectal carcinoma.** *Proc Natl Acad Sci U S A* 1998, **95**(12):6870–6875.
4. Veigl ML, Kasturi L, Olechnowicz J, Ma A, Lutterbaugh JD, Periyasamy S, Li G-M, Drummond J, Modrich PL, Sedwick WD, Markowitz SD: **Biallelic inactivation of hMLH1 by epigenetic gene silencing, a novel mechanism causing human MSI cancers.** *Proc Natl Acad Sci U S A* 1998, **95**(15):8698–8702.
5. Jones PA, Laird PW: **Cancer epigenetics comes of age.** *Nat Genet* 1999, **21**(2):163–167.
6. Miyakura Y, Sugano K, Konishi F, Ichikawa A, Maekawa M, Shitoh K, Igarashi S, Kotake K, Koyama Y, Nagai H: **Extensive methylation of hMLH1 promoter region predominates in proximal colon cancer with microsatellite instability.** *Gastroenterology* 2001, 121(6):1300–1309.
7. Miyakura Y, Sugano K, Konishi F, Fukayama N, Igarashi S, Kotake K, Matsui T, Koyama Y, Maekawa M, Nagai H: **Methylation profile of the MLH1 promoter region and their relationship to colorectal carcinogenesis.** *Genes Chromosom Canc* 2003, **36**(1):17–25.
8. Wang DG, Fan JB, Siao CJ, Berno A, Young P, Sapolsky R, Ghandour G, Perkins N, Winchester E, Spencer J, Kruglyak L, Stein L, Hsie L, Topaloglou T, Hubbell E, Robinson E, Mittmann M, Morris MS, Shen N, Kilburn D, Rioux J, Nusbaum C, Rozen S, Hudson TJ, Lipshutz R, Chee M, Lander ES: **Large-scale identification, mapping, and genotyping of single-nucleotide polymorphisms in the human genome.** *Science* 1998, 280(5366):1077–1082.
9. Cargill M, Altshuler D, Ireland J, Sklar P, Ardlie K, Patil N, Shaw N, Lane CR, Lim EP, Kalyanaraman N, Nemesh J, Ziaugra L, Friedland L, Rolfe A, Warrington J, Lipshutz R, Daley GQ, Lander ES: **Characterization of single-nucleotide polymorphisms in coding regions of human genes.** *Nat Genet* 1999, 22(3):231–238.
10. Chung CC, Chanock SJ: **Current status of genome-wide association studies in cancer.** *Hum Genet* 2011, 130(1):59–78.
11. Buckland PR: **The importance and identification of regulatory polymorphisms and their mechanisms of action.** *Biochim Biophys Acta* 2006, **1762**(1):17–28.
12. Ito E, Yanagisawa Y, Iwahashi Y, Suzuki Y, Nagasaki H, Akiyama Y, Sugano S, Yuasa Y, Maruyama K: **A core promoter and a frequent single-nucleotide polymorphism of the mismatch repair gene hMLH1.** *Biochem Biophys Res Comm* 1999, **256**(3):488–494.
13. Beiner ME, Rosen B, Fyles A, Harley I, Pal T, Siminovitch K, Zhang S, Sun P, Narod SA: **Endometrial cancer risk is associated with variants of the mismatch repair genes MLH1 and MSH2.** *Cancer Epidemiol Biomarkers Prev* 2006, 15(9):1636–1640.
14. Chen H, Taylor NP, Sotamaa KM, Mutch DG, Powell MA, Schmidt AP, Feng S, Hampel HL, de la Chapelle A, Goodfellow PJ: **Evidence for heritable predisposition to epigenetic silencing of MLH1.** *Int J Cancer* 2007, 120(8):1684–1688.
15. Harley I, Rosen B, Risch HA, Siminovitch K, Beiner ME, McLaughlin J, Sun P, Narod SA: **Ovarian cancer risk is associated with a common variant in the promoter sequence of the mismatch repair gene MLH1.** *Gynecol Oncol* 2008, 109(3):384–387.
16. Whiffin N, Broderick P, Lubbe SJ, Pittman AM, Penegar S, Chandler I, Houlston RS: **MLH1-93G > A is a risk factor for MSI colorectal cancer.** *Carcinogenesis* 2011, 32(8):1157–1161.
17. Raptis S, Mrkonjic M, Green RC, Pethe VV, Monga N, Chan YM, Daftary D, Dicks E, Younghusband BH, Parfrey PS, Gallinger SS, McLaughlin JR, Knight JA, Bapat B: **MLH1–93G > A promoter polymorphism and the risk of microsatellite-unstable colorectal cancer.** *J Natl Cancer Inst* 2007, 99(6):463–474.
18. Allan JM, Shorto J, Adlard J, Bury J, Coggins R, George R, Katory M, Quirke P, Richman S, Scott D, Scott K, Seymour M, Travis LB, Worrillow LJ, Bishop DT, Cox A, UK NCRI Colorectal Clinical Studies Group; Colorectal Cancer Study Group: **MLH1–93G > A promoter polymorphism and risk of mismatch repair deficient colorectal cancer.** *Int J Cancer* 2008, 123(10):2456–2459.
19. Samowitz WS, Curtin K, Wolff RK, Albertsen H, Sweeney C, Caan BJ, Ulrich CM, Potter JD, Slattery ML: **The MLH1–93 G > A promoter polymorphism and genetic and epigenetic alterations in colon cancer.** *Gene Chromosom Canc* 2008, 47(10):835–844.
20. Campbell PT, Curtin K, Ulrich CM, Samowitz WS, Bigler J, Velicer CM, Caan B, Potter JD, Slattery ML: **Mismatch repair polymorphisms and risk of colon cancer, tumour microsatellite instability and interactions with lifestyle factors.** *Gut* 2009, 58(5):661–667.
21. Mrkonjic M, Roslin NM, Greenwood CM, Raptis S, Pollett A, Laird PW, Pethe VV, Chiang T, Daftary D, Dicks E, Thibodeau SN, Gallinger S, Parfrey PS, Younghusband HB, Potter JD, Hudson TJ, McLaughlin JR, Green RC, Zanke BW, Newcomb PA, Paterson AD, Bapat B: **Specific variants in the MLH1 gene region may drive DNA methylation, loss of protein expression, and MSI-H colorectal cancer.** *PLoS One* 2010, 5(10):e13314.
22. Turnbull RB Jr, Kyle K, Watson FR, Spratt J: **Cancer of the colon: the influence of the no-touch isolation technic on survival rates.** *Ann Surg* 1967, 166(3):420–427.
23. Boland CR, Thibodeau SN, Hamilton SR, Sidransky D, Eshleman JR, Burt RW, Meltzer SJ, Rodriguez-Bigas MA, Fodde R, Ranzani GN, Srivastava S: **A National cancer institute workshop on microsatellite instability for cancer detection and familial predisposition: development of international criteria for the determination of microsatellite instability in colorectal cancer.** *Cancer Res* 1998, 58(22):5248–5257.
24. Maekawa M, Sugano K, Kashiwabara H, Ushiama M, Fujita S, Yoshimori M, Kakizoe T: **DNA methylation analysis using bisulfite treatment and PCR-single-strand conformation polymorphism in colorectal cancer showing microsatellite instability.** *Biochem Biophys Res Comm* 1999, 262(3):671–676.
25. Shin KH, Shin JH, Kim JH, Park JG: **Mutational analysis of promoters of mismatch repair genes hMSH2 and hMLH1 in hereditary nonpolyposis colorectal cancer and early onset colorectal cancer patients: identification of three novel germ-line mutations in promoter of the hMSH2 gene.** *Cancer Res* 2002, 62(1):38–42.

26. Perera S, Mrkonjic M, Rawson JB, Bapat B: **Functional effects of the MLH1-93G.A polymorphism on MLH1/EPM2AIP1 promoter activity.** *Oncol Rep* 2010, **25**(3):809–815.
27. Mei M, Liu D, Dong S, Ingvarsson S, Goodfellow PJ, Chen H: **The MLH1–93 promoter variant influences gene expression.** *Cancer Epidemiol* 2010, **34**(1):93–95.
28. Ishikubo T, Nishimura Y, Yamaguchi K, Khansuwan U, Arai Y, Kobayashi T, Ohkura Y, Hashiguchi Y, Tanaka Y, Akagi K: **The clinical features of rectal cancers with high-frequency microsatellite instability (MSI-H) in Japanese males.** *Cancer Lett* 2004, **216**(1):55–62.
29. Slattery ML, Potter JD, Curtin K, Edwards S, Ma KN, Anderson K, Schaffer D, Samowitz WS: **Estrogens reduce and withdrawal of estrogens increase risk of microsatellite instability-positive colon cancer.** *Cancer Res* 2001, **61**(1):126–130.

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Original Article

Comparison of clinical features between suspected familial colorectal cancer type X and Lynch syndrome in Japanese patients with colorectal cancer: a cross-sectional study conducted by the Japanese Society for Cancer of the Colon and Rectum

Tatsuro Yamaguchi[1], Yoichi Furukawa[2], Yusuke Nakamura[3], Nagahide Matsubara[4], Hideki Ishikawa[5], Masami Arai[6], Naohiro Tomita[4], Kazuo Tamura[7], Kokichi Sugano[8], Chikashi Ishioka[9], Teruhiko Yoshida[10], Yoshihiro Moriya[11], Hideyuki Ishida[12,*], Toshiaki Watanabe[13], and Kenichi Sugihara[14] for HNPCC Registry and Genetic Testing Project of the Japanese Society for Cancer of the Colon and Rectum

[1]Department of Surgery, Tokyo Metropolitan Cancer and Infectious Diseases Center Komagome Hospital, Tokyo, [2]Division of Clinical Genome Research, Advanced Clinical Research Center, Institute of Medical Science, The University of Tokyo, Tokyo, [3]Laboratory of Molecular Medicine, Human Genome Center, Institute of Medical Science, The University of Tokyo, Tokyo, [4]Department of Surgery, Hyogo College of Medicine, Nishinomiya, [5]Department of Molecular-Targeting Cancer Prevention, Kyoto Prefectural University of Medicine, Kyoto, [6]Clinical Genetic Oncology, Cancer Institute Hospital of Japanese Foundation for Cancer Research, Tokyo, [7]Major in Science, Graduate School of Science and Engineering Research, Kinki University, Higashiosaka, [8]Oncogene Research Unit/Cancer Prevention Unit, Tochigi Cancer Center Research Institute, Utsunomiya, [9]Department of Clinical Oncology, Institute of Development, Aging and Cancer, Tohoku University, Sendai, [10]Genetics Division, National Cancer Center Research Institute, Tokyo, [11]Department of Surgery, National Cancer Center Hospital, Tokyo, [12]Department of Digestive Tract and General Surgery, Saitama Medical Center, Saitama Medical University, Kawagoe, [13]Department of Surgical Oncology, The University of Tokyo, Tokyo, and [14]Department of Surgical Oncology, Graduate School, Tokyo Medical and Dental University, Tokyo, Japan

*For reprints and all correspondence: Hideyuki Ishida, Department of Digestive Tract and General Surgery, Saitama Medical Center, Saitama Medical University, Kawagoe, Japan. E-mail: 05hishi@saitama-med.ac.jp

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Abstract

Objective: The characteristics of familial colorectal cancer type X are poorly defined. Here we aimed to clarify the differences in clinical features between suspected familial colorectal cancer type X and Lynch syndrome in Japanese patients.

Methods: We performed germline mutation analyses of mismatch repair genes in 125 patients. Patients who met the Amsterdam Criteria I but lacked mismatch repair gene mutations were diagnosed with suspected familial colorectal cancer type X.

Results: We identified 69 patients with Lynch syndrome and 25 with suspected familial colorectal cancer type X. The frequencies of gastric and extracolonic Lynch syndrome-associated cancers were lower

with suspected familial colorectal cancer type X than with Lynch syndrome. The number of organs with Lynch syndrome-associated cancer was significantly lower with suspected familial colorectal cancer type X than with Lynch syndrome. The cumulative incidence of extracolonic Lynch syndrome-associated cancer was significantly lower with suspected familial colorectal cancer type X than with Lynch syndrome. We estimated that the median cancer risk in 60-year-old patients with Lynch syndrome was 89, 36 and 24% for colorectal, endometrial and gastric cancers, respectively. Analyses of family members, including probands, revealed that the median age at diagnosis of extracolonic Lynch syndrome-associated cancer was significantly older with suspected familial colorectal cancer type X than with Lynch syndrome. The frequency of extracolonic Lynch syndrome-associated cancer was significantly lower with suspected familial colorectal cancer type X than with Lynch syndrome.
Conclusion: A significant difference in extracolonic Lynch syndrome-associated cancer was evident between suspected familial colorectal cancer type X and Lynch syndrome.

Key words: colorectal cancer, familial colorectal cancer type X, Lynch syndrome

Introduction

A family history of colorectal cancer is found in ~15% of all patients with the disease (1). Lynch syndrome (LS), formerly termed hereditary nonpolyposis colorectal cancer (HNPCC), is the most common familial colorectal cancer, and accounts for 1–3% of all colorectal cancer (2). LS with autosomal dominant inheritance is caused by germline mutations in mismatch repair (MMR) genes, including the *MSH2* (3), *MLH1* (4) and *MSH6* (5) genes. Clinically, LS is characterized by high incidences of endometrial, small intestinal and urinary tract cancers, as well as an early-onset of colorectal cancer. Inactivation of MMR genes by germline and somatic mutations triggers LS-associated tumors. Consequently, a high frequency of replication errors results at both microsatellite regions and repetitive sequences in the coding regions of various growth-related target genes (6), creating a growth advantage for LS-associated tumors. However, some patients lack deficient mismatch repair (dMMR), regardless of a familial history of colorectal cancer. Recently, patients meeting the Amsterdam Criteria I (7) but lacking dMMR and/or microsatellite instability (MSI) in the tumor tissue were classified as having familial colorectal cancer type X (FCCTX), the cancer risk of which is lower than that of LS (8). Thus, the carcinogenesis of FCCTX is considered different from that of LS, because of the lack of dMMR. Even though the definition of FCCTX has not strictly been defined, but patients with dMMR in the germline but have no information about dMMR in the tumor tissue could be called 'suspected FCCTX'. To date, neither FCCTX nor suspected FCCTX (s-FCCTX) cases have been reported in Japanese patients. To clarify the characteristics of s-FCCTX in Japanese patients, we compared the clinical features of s-FCCTX with those of LS.

Patients and methods

Study design

This nationwide cross-sectional study was conducted by the HNPCC Registry and Genetic Testing Project of the Japanese Society for Cancer of the Colon and Rectum (JSCCR) between September 2002 and July 2010. In this study, we aimed to clarify the following characteristics of Japanese patients with LS:

(i) the organ(s) in which the cancer developed;
(ii) the penetration rate of the cancer;
(iii) the prognosis of the cancer;
(iv) the relationship between genotype and phenotype; and
(v) the causative genes.

Despite mutation analyses, we were unable to detect MMR gene mutations in some patients. Therefore, we defined patients meeting the Amsterdam Criteria I but lacking MMR gene mutations as having s-FCCTX, and planned this study to clarify the differences in clinical features, particularly in incidence, between s-FCCTX and LS in Japanese patients with colorectal cancer.

The inclusion criteria were: age ≥16 years; histologically confirmed adenocarcinoma of the colon and rectum; invasion of the submucosa or deeper; and fulfillment of the modified Amsterdam Criteria II, which includes gastric cancer, because gastric cancer is common in Asian patients with LS (9). We also included first-degree relatives of the patient with germline MMR gene mutations. The modified criteria did not require pathological confirmation of a family history of cancer. The exclusion criteria were: familial adenomatous polyposis to be included in the Amsterdam Criteria II (10) as well as another polyposis syndrome: Cowden disease, Peutz–Jeghers syndrome and Juvenile polyposis syndrome.

After genetic counseling and the provision of written informed consent, the patients were enrolled in this study and given an anonymous identifier. Blood samples and clinical information were collected either from medical records or directly from patients using a case report form. Clinical information included: sex; date of birth; histological type; location of colorectal cancer; occurrence of extracolonic cancer; date at diagnosis of cancer, including extracolonic cancer; final confirmed surviving date; distinction between life and death; date of death; and family history. The study protocol and informed consent form were approved by the institutional review board at each institution.

Follow-up survey

In the follow-up survey, a case report form was sent annually to the data manager of each institution, requesting the anonymous identifier, occurrence of cancer, date at diagnosis of cancer; distinction between life and death, final confirmed surviving date and date of death of patients and their relatives.

Mutation analysis

Genomic DNA was extracted from peripheral blood samples using the standard phenol extraction/purification procedure. Mutation analysis was performed by direct sequencing of the entire coding region of *MLH1*, *MSH2* and *MSH6*. The polymerase chain reaction (PCR) mixture (25 μl) contained 50 ng of genomic DNA, 0.4 μM of each

primer, 1.5 mM $MgCl_2$, 0.2 mM of each NTP, 1× PCR buffer and 0.5 μl of KOD Plus DNA Polymerase (Toyobo Co., Ltd, Osaka, Japan). PCR comprised: initial denaturation at 95°C for 10 min; 35 cycles of denaturation at 95°C for 10 s; annealing at 57°C for 30 s; extension at 68°C for 1 min; and final extension at 68°C for 5 min. The PCR products were purified with ExoSAP-IT (Affymetrix Inc., Santa Clara, CA, USA) and underwent capillary sequencing using a BigDye® Terminator v1.1 Cycle Sequencing Kit (Applied Biosystems Inc., Foster City, CA, USA) according to the manufacturer's recommendations. The list of primer sequences used for PCR and sequencing are listed in Supplementary Table S1. The products were purified using a BigDye XTerminator Purification Kit (Applied Biosystems Inc.,) and loaded into a 3730xl Genetic Analyzer (Applied Biosystems Inc.).

For samples without deleterious mutations in the three genes, multiplex ligation of probe amplification was performed using a SALSA MLPA MLH1/MSH2 Kit (MRC-Holland, Amsterdam, The Netherlands) according to the supplier's protocol (**11**). Because tumor tissue samples were not collected in this study, microsatellite instability was not analyzed.

Statistical analysis

The right colon comprises the cecum, ascending colon and transverse colon. We endeavored to collect clinical information from all patients; however, the pathological type of eight of 94 patients remains unknown.

Data are presented as totals, *medians* (range), *means* (*95% confidence intervals*) or percentages (*95%* CIs). Statistical analysis was performed using Fisher's exact test and the Mann–Whitney *U*-test. Cumulative cancer risks were calculated using the Kaplan–Meier method, and the log-rank test was used to compare risks between s-FCCTX and LS. Statistical significance was defined as $P < 0.05$. All statistical analyses were performed with EZR (Saitama Medical Center, Jichi Medical University, Saitama, Japan; **http://www.jichi.ac.jp/saitama-sct/SaitamaHP.files/statmedEN.html**), a graphical user interface for R version 3.1.0 (The R Foundation for Statistical Computing, Vienna, Austria) (**12**). This interface is a modified version of R Commander version 2.0–4, which was designed to add statistical functions frequently used in biostatistics.

Results

Patients

Between September 2002 and July 2010, 142 patients were registered to the HNPCC Registry and Genetic Testing Project of the JSCCR with suspected LS. Of them, 123 were eligible for inclusion in this study, and 19 did not meet the inclusion criteria. However, we performed MMR gene mutation analyses on patients who did not meet the eligibility criteria: seven patients with a germline MMR gene mutation were included with the patients with LS. Among 142 patients, 69 met the Amsterdam Criteria I and 73 did not meet the Amsterdam Criteria I. Mutation analyses on the 137 patient's enrolled detected 69 patients with germline MMR gene mutations. Of them, 36 had *MLH1* mutations, 31 had *MSH2* mutations and 2 had *MSH6* mutations. Of the 142 patients, 25 were classified as having s-FCCTX, because they fulfilled the Amsterdam Criteria I without dMMR. We compared the 25 patients with s-FCCTX with the 69 patients with LS (Fig. **1**).

Differences in characteristics between patients with s-FCCTX and patients with LS patients (proband)

Clinical characteristics are summarized in Table **1**. The analyses of probands identified no significant difference in age at diagnosis of

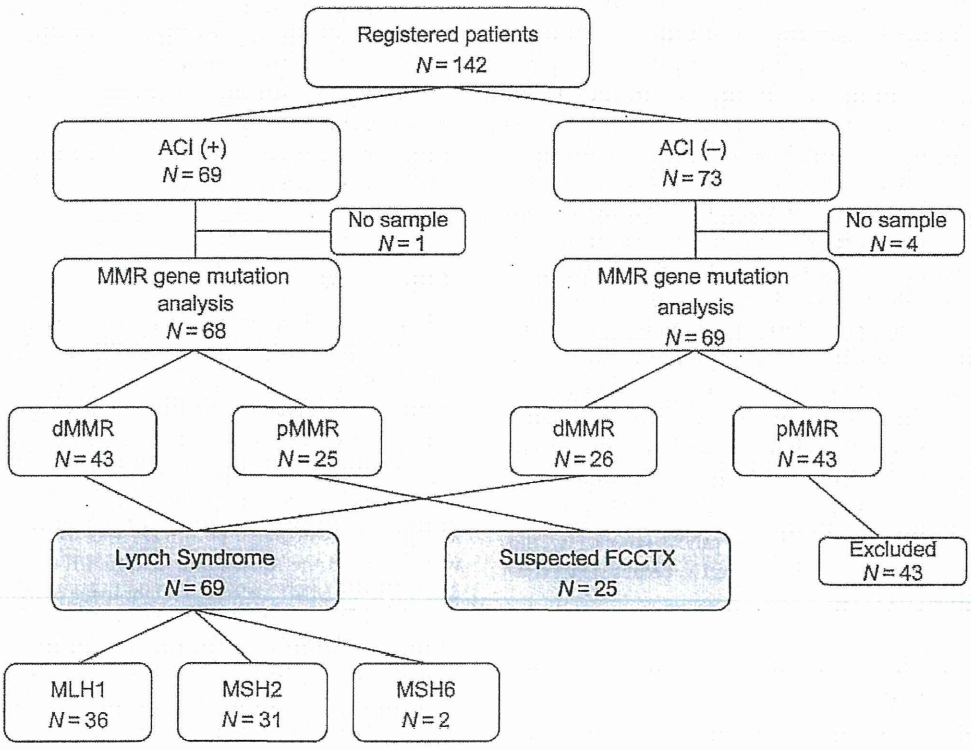

Figure 1. Consolidated standards of reporting trials diagram. MMR, mismatch repair; dMMR, deficient mismatch repair; pMMR, proficient mismatch repair; ACI, Amsterdam Criteria I.

Table 1. Characteristics of suspected familial colorectal cancer type X and Lynch syndrome

	s-FCCTX ($n = 25$)	LS ($n = 69$)	P value
Patients (proband) analysis			
Male	16/25	33/69	0.24
Median age at diagnosis of colorectal cancer (range)	48 (21–74)	45 (24–70)	0.39
Median age at diagnosis of LS-associated cancer (range)	48 (21–74)	44 (24–70)	0.27
Median age at diagnosis of extracolonic LS-associated cancer (range)	54 (24–83)	52 (23–82)	0.36
Median number of colorectal cancer (range)	1 (1–3)	1 (1–4)	0.78
Right colon cancer	14/25	43/69	0.64
Poorly differentiated adenocarcinoma or mucinous carcinoma	6/24	15/62	>0.99
Endometrial cancer	0/9	12/36	0.086
Small intestine cancer	1/25	4/69	>0.99
Urinary tract cancer	0/25	7/69	0.18
Gastric cancer	0/25	11/69	0.033
Median number of LS-associated cancer organ (range)	1 (1–2)	1 (1–4)	0.003
Extracolonic LS-associated cancer	1/25	26/69	0.001
Familial member analysis			
Median number of first-degree relatives (range)	4 (2–13)	5 (2–12)	0.96
Median number of second-degree relatives (range)	1 (0–17)	1 (0–11)	0.31
Median age at diagnosis of colorectal cancer (range)	42 (21–55)	37 (22–60)	0.11
Median age at diagnosis of LS-associated cancer (range)	42 (21–55)	36 (20–60)	0.043
Median age at diagnosis of extracolonic LS-associated cancer (range)	67 (44–86)	49 (20–80)	0.007
Colorectal cancer	25/25	64/69	0.32
Endometrial cancer	1/25	28/69	<0.001
Small intestine cancer	1/25	5/69	>0.99
Urinary tract cancer	0/25	7/69	0.18
Gastric cancer	7/25	43/69	0.005
Extracolonic LS-associated cancer	8/25	51/69	<0.001

s-FCCTX, suspected familial colorectal cancer type X; LS, Lynch syndrome.

colorectal cancer and LS-associated cancer between patients with s-FCCTX and patients with LS.

The frequency of gastric cancer in patients with s-FCCTX was significantly lower than that in patients with LS ($P = 0.033$), and the frequency of endometrial cancer in patients with s-FCCTX tended to be lower than that in patients with LS ($P = 0.086$). The frequency of extracolonic LS-associated cancer in patients with s-FCCTX was significantly lower than that in patients with LS ($P = 0.001$). Whereas the median number of organs with LS-associated cancer was one for both patients with s-FCCTX and patients with LS, there was a significant difference between patients with s-FCCTX and patients with LS ($P = 0.003$). The mean numbers of organs with LS-associated cancer were 1.04 (0.96–1.12) in patients with s-FCCTX and 1.43 (1.27–1.60) in patients with LS ($P = 0.003$; Mann–Whitney U-test).

The cumulative extracolonic LS-associated cancer and colorectal cancer risks in patients with s-FCCTX were similar to those in patients with LS; however, the cumulative extracolonic LS-associated, endometrial and gastric cancer risks were significantly lower in patients with s-FCCTX than in patients with LS (Fig. 2). In this study, we estimated that the median cancer risk of 60-year-old patients with LS was 86% (77–93%) for colorectal cancer, 36% (20–59%) for endometrial cancer and 28% (16–46%) for gastric cancer; however, we did not estimate cancer risk in patients with s-FCCTX, because few extracolonic cancers occur.

Differences in characteristics between family members with s-FCCTX and LS

In the analyses of family members, including probands, the median age at diagnosis of LS-associated cancer was significantly greater in family members of patients with s-FCCTX than in family members of patients with LS ($P = 0.043$). When colon cancer was excluded, the tendency was stronger ($P = 0.007$): median age at diagnosis of colorectal cancer in family members of patients with s-FCCTX was similar to that in family members of patients with LS.

The frequencies of gastric cancer ($P = 0.005$) and endometrial cancer ($P < 0.001$) in family members of patients with s-FCCTX were significantly lower than those in family members of patients with LS. Moreover, the frequency of extracolonic LS-associated cancer in family members of patients with s-FCCTX was significantly lower than that in family members of patients with LS ($P < 0.001$).

Discussion

We defined patients meeting the Amsterdam Criteria I but lacking MMR gene mutations as having s-FCCTX. To date, the definition of FCCTX is still controversial. Originally, FCCTX collectively describes cases of colorectal cancer that meet clinical Amsterdam Criteria I, but whose tumors are DNA MMR proficient as assessed by MSI testing (8), however, some studies of FCCTX have also included Amsterdam Criteria II families with MMR-stable tumors (13–16). The study by Nieminen et al. (17) was based on FCCX families, which fulfilled the Amsterdam Criteria I/II or the Bethesda criteria without DNA MMR defects in tumor tissue or in the germline. Moreover, there is the problem with MSI testing. It has been reported that frequency of MSI-H is 69% in LS with *MSH6* mutation (18). Therefore, LS with *MSH6* mutation may be included in the patients with Amsterdam Criteria who does not show MSI. In addition, the term 'Lynch-like syndrome' has recently been proposed (19). This indicates that dMMR (without hypermethylation of *MLH1* promotor) without germline mutation of the MMR genes, a part of which may be

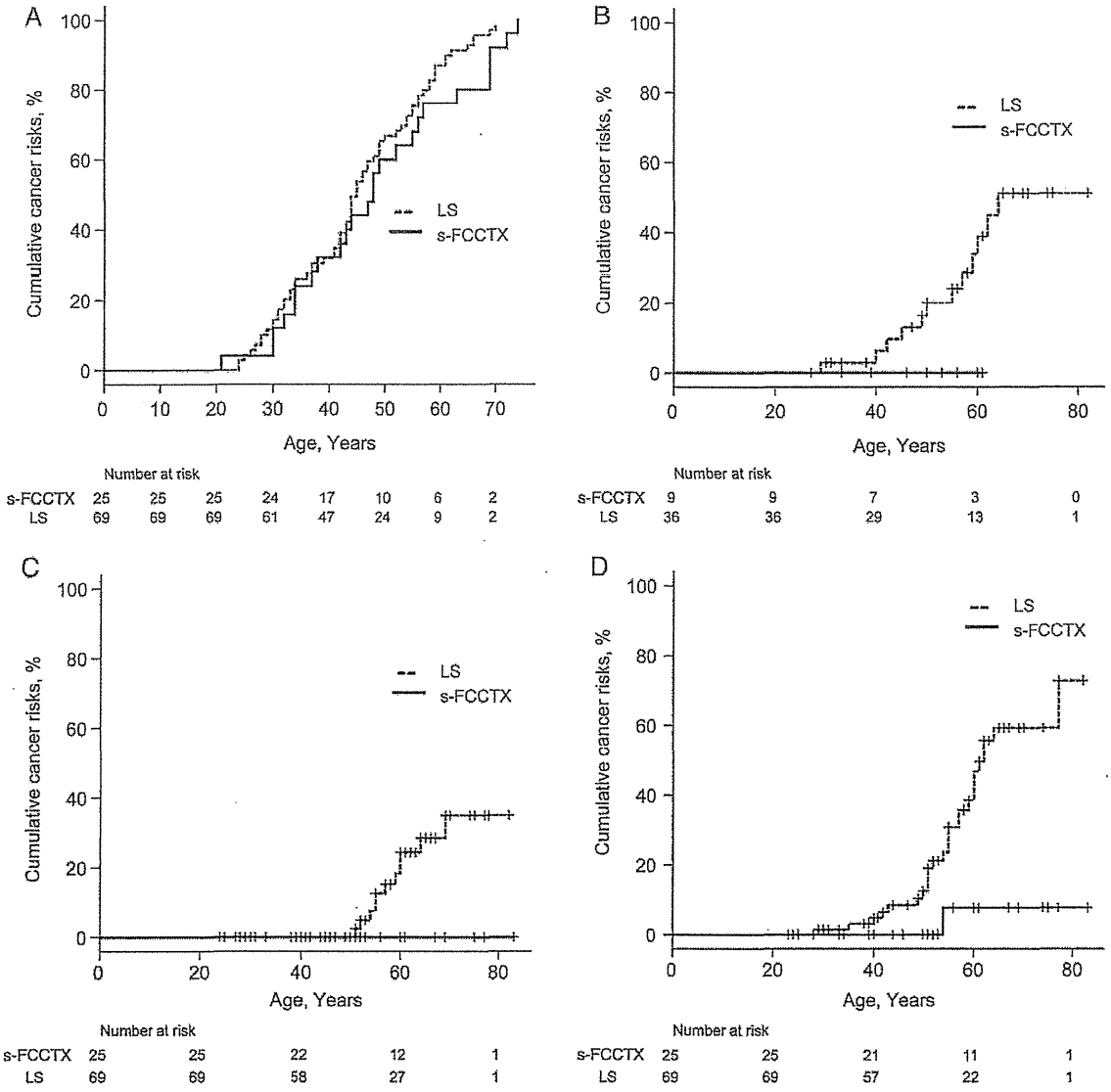

Figure 2. Comparison of the cumulative cancer risk between patients with suspected familial colorectal cancer type X (s-FCCTX) and patients with Lynch syndrome (LS) according to cancer type. (A) colorectal cancer; (B) endometrial cancer; (C) gastric cancer; (D) extracolonic LS-associated cancer.

included in the category of 'FCCTX' because of a lack in examination of the tumor tissues. Therefore, we used 'suspected FCCTX' in this study.

The cancer risk of patients with LS was 40–80% for colorectal cancer, 25–60% for endometrial cancer and 1–4% for urinary tract cancer (20). However, whether gastric cancer is an LS-associated cancer remains controversial. In East Asia, it is believed that gastric cancer is common in patients with LS (10). Reportedly, European patients with LS lack the MMR protein corresponding to the germline mutation, and exhibit microsatellite instability (21). Our data demonstrated that gastric cancer is significantly more frequent with LS than with s-FCCTX. This finding suggests that gastric cancer is an LS-associated cancer.

With respect to cancer incidence, it was reported that only the incidence of colorectal cancer is higher, whereas the incidence of LS-associated cancer is lower, in patients with FCCTX than in patients with LS (8). This study showed that the frequencies of LS-associated cancers, including gastric cancer, were lower in patients with s-FCCTX than in patients with LS. These results are consistent with reports from Western countries. Moreover, the number of organs with LS-associated cancer was lower in patients with s-FCCTX than in patients with LS. These data support the theory that s-FCCTX is a completely different syndrome from LS.

The median age at diagnosis of cancer is reportedly 43–45 years in patients with LS (22). A difference in median age at diagnosis between patients with s-FCCTX and patients with LS is evident for every organ. For example, the median age at diagnosis of colorectal cancer was 47–50 years and that of endometrial cancer was 54 years (23), and the median age at diagnosis of colorectal cancer is lower in men than in women (24). Patients meeting the Amsterdam Criteria I with dMMR tend to develop colorectal cancer at a younger age than those meeting the Amsterdam Criteria I without dMMR (8). In our study, we demonstrated a later onset of LS-associated cancer in patients with s-FCCTX compared with that in patients with LS. However, the median age at diagnosis of cancer remained young with s-FCCTX compared with sporadic cases. These findings suggest that s-FCCTX is a hereditary syndrome. Gene alterations and expressions were different in FCCTX than in LS (13,25). Recently, studies to

identify the causative genes of FCCTX have been conducted, and some candidate genes have been proposed, such as *CENPE*, *CDH18*, *GREM1*, *BCR*, *KIF24*, *GALNT12*, *ZNF367*, *HABP4*, *GABBR2* and *BMP4* (26). However, the causative genes of FCCTX have yet to be identified. In this study, additional investigation to detect causative gene of FCCTX was not performed yet. Further study is warranted.

This is first report of Japanese s-FCCTX patients. It is difficult to compare Japanese s-FCCTX patients to Western FCCTX patients directly. As mentioned above, however, both cancer incidence and median age at diagnosis of colorectal cancer in Japanese s-FCCTX patients were very similar to those in Western FCCTX patients.

The limitations of this study include low statistical power due to the limited number of cases of s-FCCTX ($n = 25$) and LS ($n = 69$), and the lack of data on *PMS2* mutation. In this study, we did not analyze *PMS2* mutation, because of the low frequency of *PMS2* mutation and the number of pseudogenes of *PMS2* (27). However, we consider the influence of this on the overall results to be small. Nonetheless, considering that there are only a few publications on FCCTX and s-FCCTX, and none from Asia, we believe that our findings will help researchers and physicians clarify the nature of s-FCCTX.

In conclusion, our study indicated that, among Japanese patients with colorectal cancer, extracolonic LS-associated cancer occurred less frequently in patients with s-FCCTX than in patients with LS, the median age at diagnosis of extracolonic LS-associated cancer was greater in patients with s-FCCTX than in patients with LS, the number of organs with LS-associated cancer was lower in patients with s-FCCTX than in patients with LS, and the cumulative incidence of extracolonic LS-associated cancer was lower in patients with s-FCCTX than in patients with LS. A significant difference in extracolonic LS-associated cancer was evident between s-FCCTX and LS.

Authors' contributions

The Japanese Society for Cancer of the Colon and Rectum contributed collectively to this study. All authors contributed to this work: Conception and design of this study, Y.M., N.T., K.T., C.I., N.M., T.W., K.S., H.I., M.A., T.Y., H.I. and K.S.; Genetic analysis, Y.F., Y.N., K.T., C.I., N.M. and K.S.; Collection and assembly of data, N.T., K.T., C.I., N.M., K.S. and M.A.; Statistical analysis, T.Y. and H.I.; Drafting of the article, T.Y. and H.I.

Supplementary data

Supplementary data are available at http://www.jjco.oxfordjournals.org.

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Conflict of interest statement

None declared.

References

1. Lynch HT, Smyrk TC, Watson P, et al. Genetic, natural history, tumor spectrum, and pathology of hereditary nonpolyposis colorectal cancer: an updated review. *Gastroenterology* 1993;104:1535–49.
2. Hampel H, Frankel WL, Martin E, et al. Screening for the Lynch syndrome (hereditary nonpolyposis colorectal cancer). *N Engl J Med* 2005;352:1851–60.
3. Fishel R, Lescoe MK, Rao MR, et al. The human mutator gene homolog MSH2 and its association with hereditary nonpolyposis colorectal cancer. *Cell* 1993;75:1027–38.
4. Bronner CE, Baker SM, Morrison PT, et al. Mutation in the DNA mismatch repair gene homolog hMLH1 is associated with hereditary nonpolyposis colorectal cancer. *Nature* 1994;368:258–61.
5. Miyaki M, Konishi M, Tanaka K, et al. Germline mutation of MSH6 as the cause of hereditary nonpolyposis colorectal cancer. *Nat Genet* 1997;17:271–2.
6. Yamaguchi T, Iijima T, Mori T, et al. Accumulation profile of frameshift mutations during development and progression of colorectal cancer from patients with hereditary nonpolyposis colorectal cancer. *Dis Colon Rectum* 2006;49:399–406.
7. Vasen HF, Mecklin JP, Khan PM, Lynch HT. The International Collaborative Group on Hereditary Non-Polyposis Colorectal Cancer (ICG-HNPCC). *Dis Colon Rectum* 1991;34:424–5.
8. Lindor NM, Rabe K, Petersen GM, et al. Lower cancer incidence in Amsterdam-I criteria families without mismatch repair deficiency: familial colorectal cancer type X. *JAMA* 2005;293:1979–85.
9. Park YJ, Shin KH, Park JG. Risk of gastric cancer in hereditary nonpolyposis colorectal cancer in Korea. *Clin Cancer Res* 2000;6:2994–8.
10. Vasen HF, Watson P, Mecklin JP, Lynch HT. New clinical criteria for hereditary nonpolyposis colorectal cancer (HNPCC, Lynch syndrome) proposed by the International Collaborative group on HNPCC. *Gastroenterology* 1999;116:1453–6.
11. Schouten JP, McElgunn CJ, Waaijer R, et al. Relative quantification of 40 nucleic acid sequences by multiplex ligation-dependent probe amplification. *Nucleic Acids Res* 2002;30:e57.
12. Kanda Y. Investigation of the freely available easy-to-use software 'EZR' for medical statistics. *Bone Marrow Transplant* 2013;48:452–8.
13. Francisco I, Albuquerque C, Lage P, et al. Familial colorectal cancer type X syndrome: two distinct molecular entities? *Fam Cancer* 2011;10:623–31.
14. Segui N, Pineda M, Navarro M, et al. GALNT12 is not a major contributor of familial colorectal cancer type X. *Hum Mutat* 2014;35:50–2.
15. Therkildsen C, Jonsson G, Dominguez-Valentin M, et al. Gain of chromosomal region 20q and loss of 18 discriminates between Lynch syndrome and familial colorectal cancer. *Eur J Cancer* 2013;49:1226–35.
16. Dominguez-Valentin M, Therkildsen C, Veerla S, et al. Distinct gene expression signatures in lynch syndrome and familial colorectal cancer type x. *PLoS One* 2013;8:e71755.
17. Nieminen TT, O'Donohue MF, Wu Y, et al. Germline mutation of RPS20, encoding a ribosomal protein, causes predisposition to hereditary nonpolyposis colorectal carcinoma without DNA mismatch repair deficiency. *Gastroenterology* 2014;147:595–8.
18. Palomaki GE, McClain MR, Melillo S, et al. EGAPP supplementary evidence review: DNA testing strategies aimed at reducing morbidity and mortality from Lynch syndrome. *Genet Med* 2009;11:42–65.
19. Boland CR. The mystery of mismatch repair deficiency: lynch or lynch-like? *Gastroenterology* 2013;144:868–70.
20. NCCN—National Comprehensive Cancer Network: Clinical Practice Guidelines in Oncology. Genetic/familial high-risk assessment: colorectal. Version1; 2014. Available: **http://www.nccn.org/professionals/physician_gls/pdf/genetics_colon.pdf** (23 April 2014, date last accessed).
21. Gylling A, Abdel-Rahman WM, Juhola M, et al. Is gastric cancer part of the tumour spectrum of hereditary non-polyposis colorectal cancer? A molecular genetic study. *Gut* 2007;56:926–33.

22. Hampel H, Stephens JA, Pukkala E, et al. Cancer risk in hereditary nonpolyposis colorectal cancer syndrome: later age of onset. *Gastroenterology* 2005;129:415–21.
23. Dunlop MG, Farrington SM, Carothers AD, et al. Cancer risk associated with germline DNA mismatch repair gene mutations. *Hum Mol Genet* 1997;6:105–10.
24. Bonadona V, Bonaïti B, Olschwang S, et al. Cancer risks associated with germline mutations in MLH1, MSH2, and MSH6 genes in Lynch syndrome. *JAMA* 2011;305:2304–10.
25. Dominguez-Valentin M, Therkildsen C, et al. Distinct gene expression signatures in lynch syndrome and familial colorectal cancer type x. *PLoS One* 2013;8:e71755.
26. Dominguez-Valentin M, Therkildsen C, Da Silva S, Nilbert M. Familial colorectal cancer type X: genetic profiles and phenotypic features. *Mod Pathol* 2014; doi: 10.1038/modpathol.2014.49. Apr 18.
27. Nicolaides NC, Carter KC, Shell BK, Papadopoulos N, Vogelstein B, Kinzler KW. Genomic organization of the human PMS2 gene family. *Genomics* 1995;30:195–206.

8. 遺伝カウンセリング・遺伝子検査

1 遺伝カウンセリング

1. 遺伝カウンセリングとは[1]

遺伝カウンセリングは遺伝的素因が原因で発症した癌が疑われるか，あるいその不安を持つ来談者（クライエント）に対して行われる．

◎**遺伝カウンセリング**は，疾患に対する遺伝的リスク評価を通じて，クライエントが自身と家族の発症リスクと対処可能な選択肢を理解し，最良の選択を行うための一連のプロセスを示す．クライエントは患者本人以外に，家族が来院する場合もある．

◎**遺伝子検査**は，遺伝カウンセリングでクライエントに提示される選択肢の一つであり，最終的に遺伝子検査を受けるかどうかはクライエントの自己決定による．

1) Ad Hoc Committee on Genetic Counseling : Am J Hum Genet, 27 (2) : 240-242, 1975.

2. 遺伝カウンセリング外来の受診を勧める場合

◎**本人が乳癌 and/or 卵巣癌を発症している場合**

遺伝性乳癌卵巣癌 hereditary breast and orarian cancer（HBOC）等の遺伝性腫瘍の可能性を疑う目安を示す．

・原因遺伝子変異が父方由来で，かつ女性の血縁者が少ないと乳癌，卵巣癌等の家族歴が認められないことがある．そのような場合，個人の発症年齢や既往歴，乳癌の臨床病理学的特徴（エストロゲン受容体，プロゲステロン受容体，HER2）等が参考になる．

・遺伝カウンセリングでは1時間から1時間半かけて，家族歴調査，家系図作成と遺伝的リスク評価が行われるので，受診前の詳しい家族歴聴取は不要．

・クライエントの病歴と家族歴から各種遺伝子検査を受けた場合に予測される陽性率を表Ⅱ-7に示す．遺伝カウンセリングの適応として，遺伝子検査の陽性率が10％以上を示すと予測される場合を挙げている．

・卵管癌，腹膜癌等の Muller 氏管由来腫瘍は，卵巣癌と同様に考えて対応する．

・表Ⅱ-7はクライエントが浸潤性乳癌を発症している場合に予測される遺伝子検査の陽性率を示している．本人が DCIS の場合，*BRCA1/2* 遺伝子検査の陽性率はこれよりも低く，*BRCA1* よりも *BRCA2* が陽性となる場合が多い．本人が DCIS であり，家族歴で卵巣癌を2名以上認める場合，卵巣癌を認めない場合に比して *BRCA1/2* 陽性となる確率がオッズ比で8.81倍高率であったとする報告がある[2]．

2) Bayraktar S, et al : Cancer, 118 (6) : 1515-1522, 2012.

◎**本人もしくは家族が乳癌の遺伝について不安を持っている場合**

・上記の「本人が乳癌 and/or 卵巣癌を発症している場合（表Ⅱ-7）」に該当しない場合でも，本人あるいは血縁者に乳癌，卵巣癌，その他の癌の既往があり，遺伝について心配している場合は受診を勧める．

◎発端者の遺伝子検査で原因遺伝子の病的変異が認められた場合の成人の血縁者

・発端者に病的変異が認められた場合，血縁者がキャリアであるリスク，第1度近親（親子姉妹）では50％，第2度近親（おば，祖母，孫，姪）では25％，第3度近親（従姉妹）では12.5％となる．このリスクは男性でも変わらないので注意が必要である．

表Ⅱ-7　遺伝相談外来の受診を勧めるケース

本人罹患歴	家族歴	遺伝子変異頻度	文献
50歳以上浸潤性乳癌	50歳未満乳癌あるいは卵巣癌(+)	*BRCA1/2*：10～22.9%	Frank TS, et al：J Clin Oncol, 20 (6)：1480-1490, 2002.
50歳未満浸潤性乳癌	50歳未満乳癌あるいは卵巣癌(+)	*BRCA1/2*：19.6～48.3% *BRCA1/2*：36.4～60%(日本人)	Sugano K, et al：Cancer Sci, 99 (10)：1967-1976, 2008.
40歳未満浸潤性乳癌	50歳未満乳癌あるいは卵巣癌(−)	*BRCA1/2*：13.2%	Frank TS, et al：J Clin Oncol, 20 (6)：1480-1490, 2002.
	50歳未満乳癌あるいは卵巣癌(+)	*BRCA1/2*：23.5～56.3%	
triple negative乳癌	50歳未満乳癌あるいは卵巣癌(+)	*BRCA1/2*：28.3% (13/46)	Hartman AR, et al：Cancer, 118 (11)：2787-2795, 2012.
35歳以下triple negative乳癌	50歳未満乳癌あるいは卵巣癌(−)	*BRCA1/2*：10%以上	
	50歳未満乳癌あるいは卵巣癌(+)	*BRCA1/2*：45%以上	
対側乳癌(同時性あるいは異時性)	異時性対側乳癌	*BRCA1/2*：35.9% (28/78)	Rogozińska-Szczepka J, et al：Ann Oncol, 15 (9)：1373-1376, 2004.
	同時性対側乳癌	*BRCA1/2*：13.3% (4/30)	
浸潤性乳癌および卵巣癌	50歳未満乳癌あるいは卵巣癌(−)	*BRCA1/2*：18.5%(5/27)～20% (5/25)	Frank TS, et al：J Clin Oncol, 20 (6)：1480-1490, 2002.
	50歳未満乳癌あるいは卵巣癌(+)	*BRCA1/2*：28.6(10/35)～64.6%(31/48)	
乳癌卵巣癌家系(卵巣癌組織型：漿液性卵巣癌が80～90%を占める)		*BRCA1/2*：77.8%(21/27)(日本人)	Sekine M, et al：Clin Cancer Res, 7 (10)：3144-3150, 2001.
30歳未満発症乳癌	家族歴を問わず	*TP53*：4%(2/52) *BRCA1/2*：17.3%(9/52) *CHEK2*：4%(2/52)	Mouchawar J, et al：Cancer Res, 70 (12)：4795-4800, 2010.
40歳未満発症乳癌	第2度近親内に乳癌，卵巣癌2名以上	*TP53*：7%(3/42) *BRCA1/2*：23.8% (10/42) *ATM*：2.4%(1/42)	
浸潤性小葉癌あるいは乳管癌と小葉癌の混合型	第2度近親(父方の場合は第3度近親)内に乳癌2名以上．発端者が45歳未満の場合は家族歴を問わない．スキルス胃癌の多発が認められる場合もある．	*CDH1*：1.3%(4/318) *BRCA1/2*：陰性例の1.6%(4/246)	Schrader KA, et al：J Med Genet, 48 (1)：64-68, 2011.
乳癌，口腔粘膜および指趾尖部に色素斑と爪甲部の色素線条	消化管ポリポーシス，小児腸重積症，消化器癌，乳癌，子宮癌，卵巣癌，膵癌，肺癌，	*STK11/LKB1*：70%(297/419)	Hearle N, et al：Clin Cancer Res,12 (10)：3209-3215, 2006.
乳癌，甲状腺癌(髄様癌を除く)，甲状腺腫瘍，消化管過誤腫，腎癌，子宮癌，大腸癌，甲状腺腫，自閉症，皮膚腫瘍，血管腫，脂肪腫等		*PTEN*：25～85%	Gene Reviews® (URL：http://www.ncbi.nlm.nih.gov/books/NBK1488/)

〔菅野康吉〕