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<th>MSH2 Dysregulation Is Triggered by Proinflammatory Cytokine Stimulation and Is Associated with Liver Cancer (Dissertation)</th>
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**Abstract**

Inflammation predisposes to tumorigenesis in various organs by potentiating a susceptibility to genetic aberrations. The mechanism underlying the enhanced genetic instability through chronic inflammation, however, is not clear. Here, we demonstrated that TNFα stimulation induced transcriptional downregulation of MSH2, a member of the mismatch repair family, via NF-kB-dependent miR-21 expression in hepatocytes. Liver cancers developed in ALB-MSH2<sup>−/−</sup> AID<sup>−/−</sup>, ALB-MSH2<sup>−/−</sup>, and ALB-AID<sup>−/−</sup> mice, in which MSH2 is deficient and/or activation-induced cytidine deaminase (AID) is expressed in cells with albumin-producing hepatocytes. The mutation signatures in the tumors developed in these models, especially ALB-MSH2<sup>−/−</sup> AID<sup>−/−</sup> mice, closely resembled those of human hepatocellular carcinoma. Our findings demonstrated that inflammation-mediated dysregulation of MSH2 may be a mechanism of genetic alterations during hepatocarcinogenesis. Cancer Res; 76(15); 4383-93. ©2016 AACR.

**Introduction**

It is well established that chronic inflammation predisposes to tumor development in various organs, including hepatitis virus–associated hepatocellular carcinoma (1, 2). On the other hand, cancer cells are considered to be generated by a stepwise accumulation of genetic alterations in various tumor-related genes during the process of tumorigenesis (3–5). Thus, the genetic aberrations required for malignant transformation could be accumulated in nontumorous inflamed tissues with a high risk of tumorigenesis. Indeed, whole-exome sequencing has revealed many somatic mutations in various genes in hepatitis C virus (HCV)-infected cirrhotic liver tissues (6). Accumulation of various somatic mutations in nontumorous epithelial cells has also been reported in other tissues with chronic inflammation (7, 8). These data indicate that chronic inflammation potentiates a susceptibility to gene alterations during carcinogenesis. However, the precise mechanisms underlying the generation of genetic alterations during inflammation-associated carcinogenesis remain largely unknown.

Recent advances in sequencing technology revealed the landscape of genetic aberrations in human cancers (9). The abundant information on mutation signatures in various cancers provides a clue to the molecular processes involved in genetic aberrations during carcinogenesis. Interestingly, recent studies have shown that mutation signatures detected in several human cancer tissues exhibit the conserved footprints of the activity of nucleotide-editing enzymes, the APOBEC family proteins (10, 11). Among the APOBEC family members, activation-induced cytidine deaminase (AID) is a well-defined molecule capable of inducing mutations in human DNA sequences, including immunoglobulin gene (12). We previously demonstrated that aberrant expression of AID is induced in response to inflammatory conditions and contributes to tumorigenesis through production of somatic mutations during carcinogenesis, including hepatocellular carcinoma and gastric cancers (13–17). Consistently, a strong preference for C:G to T:A transition mutations was observed, a typical footprint of AID (18). Consistently, C:G to T:A transition mutations observed in various human inflammatory conditions and in cancer cells with chronic inflammation predisposed to tumorigenesis (19).

On the other hand, DNA mismatch repair (MMR) system plays a critical role in maintaining genomic stability, and indeed, it protects the genome against the mutagenic activity of AID (18). Consistently, C:G to T:A transition mutations observed in various human inflammation-associated cancers may involve dysfunction of MMR. In this study, therefore, we examined whether inflammation induces dysregulation of MMR and, if so, its role in inflammation-associated carcinogenesis.
Materials and Methods

Cell culture and transfection

Human hepatoma-derived cell lines, HepG2, Huh-7.5, and Hep3B cells, were obtained from Institute for Virus Research, Kyoto University (Kyoto, Japan). All these cells were authenticated by short-tandem repeat analysis in January 2016 at JCRB Cell Bank, National Institute of Biomedical Innovation (Osaka, Japan). Cells were cultured in DMEM (Gibco by Life Technologies) supplemented with 10% FBS at 37°C in a humidified atmosphere with 5% CO₂. For transfection with plasmid DNA, Trans-IT LT1 Transfection Reagent (Minus Bio Corporation) was used according to the manufacturer’s protocol.

Reagents

Recombinant human TNFα was purchased from Peprotech EC. NF-κB inhibitory reagents SN50 and MG132 were purchased from Biomol International LP. Anti-MSH2/AFP antibody and anti-α-tubulin antibody were purchased from Santa Cruz Biotechnology and EMD Millipore, respectively. Anti-miR-21 inhibitor (anti-hsa-miR-21-5p miScript miRNA inhibitor) was purchased from Qiagen.

Plasmids

pCDNA3-3xRhoAN, plasmid for expression of the “super-repressor” form of the kB-α protein, was described previously (14). Expression vectors for the negative control and miR-21 were generated using BLOCK-iT Pol II miR RNAi Expression Vector Kits following the manufacturer’s protocol (Life Technologies). To create the anti-miR-21 “decoy” vector, the luciferase 3’-untranslated lesion was modified to include three tandem sequences complementary to miR-21, separated by two nucleotide spacers. The construct was analyzed using an ABI 3500 Genetic Analyzer and correctly inserted into a pLentis/VS-DTOPO vector (Life Technologies) driven by a CMV promoter to stably express genes in hepatocytes.

RNA extraction and qRT-PCR for mRNA

Total RNA was isolated and purified using Sepasol-RNA I Super (Nacalai Tesque) according to the manufacturer’s protocol. cDNA was synthesized from 1 µg total RNA using the Transcriptor High Fidelity cDNA Synthesis Kit (Roche) in accordance with the manufacturer’s instructions. Quantification of gene expression was performed by real-time RT-PCR using the LightCycler 480 Real-Time PCR System (Roche). To assess the quantity of isolated RNA as well as the efficiency of cDNA synthesis, target cDNAs were normalized to the expression level of endogenous mRNA of the “housekeeping” reference 18S rRNA (15). Each sample was tested in triplicate. Gene-specific primers are shown in Supplementary Table S1.

Quantitative PCR for miRNAs

Total RNA was isolated using Sepasol-RNA I Super (Nacalai Tesque) according to the manufacturer’s protocol. miR-21 expression levels were assessed in accordance with the TaqMan MicroRNA Assays (Life Technologies) protocol, and the products were analyzed using the LightCycler 480 Real-Time PCR System (Roche). miR-21 expression levels were normalized by U6 small nuclear RNA expression. Each sample was tested in triplicate.

Western blotting

For immunoblotting analysis, cells were lysed in RIPA buffer with protease inhibitor, and lysates were centrifuged at 12,000 rpm for 15 minutes at 4°C to remove cellular debris. Supernatants were diluted in SDS-PAGE sample buffer and boiled at 70°C for 10 minutes. Protein samples were separated using 7.5% Mini-PROTEAN TGX Precast Gels (Bio-Rad Laboratories) according to the manufacturer’s instructions and transferred to polyvinylidene difluoride membranes. The membranes were blocked with Block Ace Powder (DS Pharma Biomedical), diluted in PBS containing 0.05% Tween 20 (Sigma-Aldrich) overnight at 4°C, and incubated with primary antibody (anti-MSH2, 1:200; anti-α-tubulin, 1:200 dilution) for 1 hour. Following a washing step in PBS-0.05% Tween 20 (0.05% PBST), the membranes were incubated with secondary antibody (Bio-Rad Laboratories; anti-rabbit IgG, 1:3,000; anti-mouse IgG, 1:3,000 dilution) for 30 minutes. The membranes were then washed in 0.05% PBST and detected by Immobilon Western Chemiluminescent HRP Substrate (Millipore Corporation) using the LAS-3000 system (FujiFilm).

Lentivirus production and DNA transduction

Lentiviral stocks were produced in 293T cells in accordance with the manufacturer’s protocol (Life Technologies). In brief, virus-containing medium was collected 48 hours posttransfection and filtered through a 0.45-µm filter. One round of lentiviral infection was performed by replacing the medium with virus-containing medium, followed by centrifugation at 2,500 rpm for 30 minutes at 30°C. Cells were used for analysis 3 days after transduction.

IHC

For histologic analysis, organs were fixed overnight in 10% formalin, paraffin-embedded, and sectioned at a thickness of 6 µm. Sections were then deparaffinized in xylene and rehydrated in graded ethanol. Before incubation, sections were autoclaved for 20 minutes at 121°C in Target Retrieval Solution (Dako) and soaked in blocking solution for 30 minutes. Later, sections were incubated in anti-MSH2-antibody or anti-AFP-antibody (1:200 dilution) at 4°C overnight and washed three times with PBS, then incubated with biotinylated anti-rabbit or goat IgG antibody (1:200 dilution; Vector Laboratories) for 30 minutes at 25°C. ABC reagent (avidin-biotinylated enzyme complex; Vector Laboratories) was added, and sections were incubated with 3,3'-diaminobenzidine tetrahydrochloride substrate (Vector Laboratories) until the desired stain intensity developed.

Dual-luciferase assays

Luciferase activities were measured using the Dual-Luciferase Reporter Assay System (Promega Corp.) following the manufacturer’s protocol. The relative luciferase activity of each construct is reported as the fold induction.

Mice

The Msh2LoxP/LoxP mice (20) on a C57BL/6 background were a gift from Dr. Winfried Edelmann (Albert Einstein College of Medicine, Bronx, New York) and maintained in a specific pathogen-free facility at Kyoto University Faculty of Medicine (Kyoto, Japan). The AID cTg mice (21) were deposited at the Riken Bioresource Center (Tsukuba, Japan; no. RBRC00892). The ALB-Cre mice (22) were a gift from the Center for IPS Cell Research.
and Application, Kyoto University, and maintained by self-crossing between heterozygous mice. All mice were fed ad libitum and killed by cervical dislocation for censoring. Upon censoring, the numbers of macroscopic tumors were counted after laparotomy and thoracotomy. All animal experiments were approved by the Ethics Committee for Animal Experiments and performed under the Guidelines for Animal Experiments of Kyoto University.

Whole-exome capture and massively parallel sequencing

Fragmented DNA was used to prepare each DNA-sequencing library. The DNA libraries were prepared according to the instructions provided with the Ion Xpress Plus Fragment Library Kit (Life Technologies). Whole-exome sequence capture was then performed using SureSelect Mouse All Exon Kit (Agilent Technologies) according to the manufacturer’s instructions. The captured samples were sequenced as 130-bp paired-end reads using the Ion Proton System (Life Technologies), and the data were converted to the FASTQ format.

Using NextGENe 2nd Generation Sequence Analysis Software v2.3.4.2 (SoftGenetics), the obtained reads were aligned with the Mouse Genome UCSC mm9. We identified somatic mutations using the strict variant filtering process (Supplementary Fig. S1). Sequence reads were deposited in the DNA data bank of Japan Sequence Read Archive (http://trace.ddbj.nig.ac.jp/dra/index_e.html) under accession number of DRA003790.

Human subjects

Human liver tissues with chronic HCV infection were obtained during curative resection of primary hepatocellular carcinoma at Kyoto University Hospital (Kyoto, Japan). As a control, normal liver tissues from patients with metastatic liver cancer were also examined. All information-identifying subjects were omitted. The Ethics Committee of Kyoto University Hospital approved analyses for human subjects, and written informed consent was obtained from all patients in accordance with the Declaration of Helsinki.

Statistical analysis

Data are expressed as means ± SE. Statistical comparisons were calculated using unpaired two-tailed Student t test or χ² test and Fisher exact test. A value of less than 0.05 was considered to indicate significance.

Results

MSH2 is downregulated in response to proinflammatory cytokines via NF-κB signaling in human hepatocytes

The proinflammatory cytokine TNFα plays a central role in hepatic inflammation (23–25). Thus, we first examined the effects of TNFα on the expression of seven representative MMR-related genes in cultured human hepatocytes. Expression of all MMR-related transcripts examined was detected in quiescent HepG2 cells by quantitative real-time RT-PCR. Interestingly, among MMR-related genes, the expression of MSH2 was significantly reduced after treatment with TNFα (Fig. 1A). In contrast, TNFα treatment resulted in significant upregulation of PMS2, and no significant changes in the expression of MSH3, MSH6, MLH1, MLH3, or PMS1 (Fig. 1B). To further investigate the TNFα-mediated reduction of MSH2, we examined the time course of MSH2 expression by incubating HepG2 cells with TNFα. MSH2 expression was gradually reduced, and the lowest level was observed 6 hours after TNFα treatment (Fig. 2A). Moreover, TNFα reduced MSH2 expression in a dose-dependent manner (Fig. 2B). To examine whether TNFα generally reduces MSH2 expression in human hepatocytes, we analyzed MSH2 expression in other hepatoma-derived cell lines, Huh-7.5 and Hep3B, and confirmed that treatment with TNFα significantly reduced MSH2 expression in both types of cells (Fig. 2C). RT-PCR analysis revealed that MSH2 transcripts also decreased in response to another proinflammatory cytokine, IL1β (Fig. 2D). Immunoblotting analyses confirmed that treatment with TNFα markedly downregulated MSH2 protein expression in both HepG2 and Huh-7.5 cells (Fig. 2E).

TNFα activates NF-κB and contributes to the regulation of various genes under inflammatory conditions (26). The findings that TNFα downregulates MSH2 led us to examine whether MSH2 expression is regulated in hepatocytes in an NF-κB–dependent manner. NF-κB inhibitory reagents, SN50 and MG132,
significantly reduced TNFα-induced NF-κB activation, and pre-treatment with either drug almost completely rescued the TNFα-induced MSH2 downregulation (Fig. 2F). Furthermore, the MSH2 downregulation induced by TNFα was almost completely rescued by coproduction of the superrepressor form of IκBα, as depicted in Figure 2F. Taken together, these findings suggest that MSH2 expression is downregulated by stimulation of proinflammatory cytokines through NF-κB activation in human hepatocytes.

TNFα stimulation induces the expression of miR-21 in hepatocytes

To determine whether MSH2 downregulation induced by TNFα is due to a decrease in transcription or an increase in mRNA degradation, we inhibited de novo mRNA synthesis using actinomycin D and evaluated the effect of TNFα treatment on the expression level of MSH2 mRNA. We found that MSH2 mRNA levels were significantly reduced by TNFα administration in the presence of actinomycin D, suggesting that MSH2 downregulation in response to TNFα stimulation is due to increased mRNA degradation in hepatocytes (Fig. 3A). The absence of potential NF-κB–binding sites in the 5′ upstream region of the MSH2 gene (data not shown), along with the finding that proinflammatory cytokine stimulation increased the degradation of MSH2 mRNA, led us to hypothesize that miRNAs were involved in the regulation of MSH2 expression by NF-κB.

Using three representative miRNA target–predicting databases, microRNA.org (http://www.microrna.org), TargetScanHuman 6.2 (http://www.targetscan.org), and MicroCosm Targets Version 5 (http://www.ebi.ac.uk/enright-srv/microcosm/htdocs/targets/v5/), we identified two miRNAs, miR-21 and miR-590-5p, as putative miRNAs that potentially target MSH2 mRNA in silico (Supplementary Fig. S2A). Of the two miRNAs, we focused on miR-21, which has a higher affinity for MSH2 mRNA than miR-590-5p and is reported to be upregulated in several cancer tissues, including human hepatocellular carcinoma (Fig. 3B; refs. 27, 28).
Inflammation-Mediated MSH2 Downregulation in Hepatocytes

First, we examined miR-21 expression levels in HepG2 and Hep3B cells using TaqMan MicroRNA Assays. miR-21 expression was significantly increased after treatment with TNFα (Fig. 3C). Next, we evaluated whether the increase in miR-21 expression induced by TNFα was mediated by NF-κB activation. Pretreatment with SN50, MG132, or coproduction of the superrepressor form of IkBα almost completely abolished the TNFα–induced increase in miR-21 expression in HepG2 cells (Fig. 3D). These findings indicate that miR-21 expression is increased by TNFα stimulation through the activation of NF-κB in human hepatocytes.

To examine whether MSH2 downregulation induced by TNFα is mediated by miR-21, we transfected miR-21 in hepatocytes, expression vectors for miR-21 were transfected into HepG2 and Hep3B cells. Overexpression of miR-21 significantly reduced the expression of both MSH2 mRNA and MSH2 protein (Fig. 4A and B). To test the functional consequences of silencing endogenous miR-21 in vitro, HepG2 cells infected with a lentivirus vector were used, in which the 3′-untranslated region with three tandem miR-21–targeting sequence in the 3′-untranslated region of MSH2 mRNA. C, HepG2 and Hep3B cells were treated with TNFα (100 ng/mL) for 8 hours. The miR-21 expression level was significantly increased by TNFα stimulation (∗, P < 0.05 vs. without TNFα). D, HepG2 and Hep3B cells were treated with SN50 (50 μg/mL) or MG132 (2 μg/mL) for 2 hours, or transfected with pcDNA3-IκBα/N, and further treated with TNFα (100 ng/mL) for 8 hours. The miR-21 expression level was significantly increased by TNFα stimulation when NF-κB activity was not inhibited (∗, P < 0.05 vs. without TNFα). Total RNA was isolated from each sample, and miR-21 expression levels were measured by TaqMan MicroRNA Assays.

MSH2 is downregulated and miR-21 is upregulated in human chronic hepatitis tissues

To examine MSH2 and miR-21 expression in human hepatocytes under physiologic or pathologic conditions, we quantified the MSH2 transcripts and miR-21 expression levels in human liver tissues with chronic HCV infection and normal liver tissues (Supplementary Fig. S3A). MSH2 was transcribed in normal liver tissues, with mean MSH2/18s rRNA ratios of 3.63 ± 2.36 (± SE). On the other hand, HCV-related chronic hepatitis tissues showed significantly lower expression of MSH2 than that in normal liver tissues (1.75 ± 0.96; Supplementary Fig. S3B). In contrast, there were no significant differences in the expression level of MSH2, MSH6, MLH1, MLH3, PMS1, or PMS2 between the liver tissues with and without HCV-related hepatitis, consistent with the findings of human hepatocytes after TNFα treatment (Supplementary Fig. S3C and Fig. 1B). In addition, miR-21 expression in...
HCV-related chronic hepatitis tissues was significantly higher than that in normal liver tissues (Supplementary Fig. S3D). Taken together, these findings indicate that TNFα-induced downregulation of MSH2 transcripts is mediated by miR-21 upregulation in human hepatocytes.

Hepatocellular carcinoma develops in mice with specific disruption of MSH2 and/or AID activation in hepatocytes

Human hepatocellular carcinoma could develop in the liver with chronic inflammation, where MSH2 downregulation and AID upregulation coexist. Thus, we investigated the phenotypic effects of MSH2 inactivation and/or AID activation in hepatocytes in vivo. To disrupt MSH2 and/or express AID specifically in the liver, we crossed MSH2 conditional knockout (Msh2loxP/loxP) mice (20) and/or AID conditional transgenic (AID cTg) mice (21) with transgenic mice carrying a Cre gene under control of the albumin (ALB) promoter (ALB-Cre; ref. 22). These crosses generated cohorts of mice with various genotypes, including ALB-Cre; Msh2loxP/loxP (ALB-MSH2−/−), ALB-Cre; Msh2loxP/loxP (ALB-MSH2−/−), ALB-Cre; AID cTg (ALB-AID+), ALB-Cre; Msh2loxP/loxP; AID cTg (ALB-MSH2−/−AID+), ALB-Cre, and wild-type (WT) mice. Quantitative RT-PCR and IHC revealed the predicted deletion of MSH2 in the livers of ALB-MSH2−/− and ALB-MSH2−/−AID+ mice (Fig. 5A and B) and the predicted upregulation of AID in the livers of ALB-Cre; Msh2loxP/loxP; AID cTg (ALB-MSH2−/−AID+) mice (Fig. 5C and D).
of ALB-AID\(^+\) and ALB-MSH2\(^{-/-}\)AID\(^+\) mice (Fig. 5A). ALB-MSH2\(^{-/-}\), ALB-MSH2\(^{-/-}\)AID\(^+\), and ALB-AID\(^+\) and ALB-MSH2\(^{-/-}\)AID\(^+\) mice were born alive, appeared healthy, and had a liver weight per body weight ratio comparable with that of ALB-Cre mice (data not shown).

Most mice were viable at 90 weeks; however, we frequently observed macroscopic liver tumors in ALB-MSH2\(^{-/-}\)AID\(^+\) mice (Table 1; Fig. 5C). Macroscopic liver tumors developed in 9.1\% (1/11) of ALB-MSH2\(^{+/+}\) and 21.4\% (3/14) of ALB-MSH2\(^{-/-}\)/C0 mice at 90 weeks of age, respectively. Notably, liver tumors developed in 23.5\% (4/17) of ALB-AID\(^+\) and 50.0\% (7/14) of ALB-MSH2\(^{-/-}\)AID\(^+\) mice at 90 weeks of age, indicating that MSH2 deficiency enhanced the tumorigenesis in the mouse liver with constitutive AID expression. In contrast to these mice, no tumors were observed in ALB-Cre and WT mice examined at the same ages. Histologic examination revealed that the tumors of ALB-MSH2\(^{-/-}\)/C0 mice had the characteristics of poorly differentiated hepatocellular carcinoma, and the tumors of ALB-MSH2\(^{-/-}\)/AID\(^+\) and ALB-AID\(^+\) mice and noncancerous liver tissues of the same mice. Arrowheads, tumor nodules. D, microscopic (hematoxylin and eosin stain) images of liver tumors that developed in ALB-MSH2\(^{-/-}\)/AID\(^+\), ALB-MSH2\(^{-/-}\)/C0, and ALB-AID\(^+\) mice and noncancerous liver tissues of the same mice. Arrowheads, tumor nodules. E, IHC for \(\alpha\)-fetoprotein of nontumor and tumor tissues in ALB-Cre, ALB-MSH2\(^{-/-}\)/AID\(^+\), and ALB-AID\(^+\) mice.

Table 1. Frequencies of liver tumors observed in each mouse type

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<tr>
<th>Genotype</th>
<th>Mean age at sacrificing (weeks)</th>
<th>Frequency</th>
<th>Liver tumor(s)</th>
<th>Single/Multiple</th>
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<tr>
<td>ALB-MSH2(^{++}) (n = 11)</td>
<td>89.5</td>
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<tr>
<td>ALB-MSH2(^{-/-}) (n = 14)</td>
<td>89.1</td>
<td>21.4% (n = 3)</td>
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<tr>
<td>ALB-AID(^+) (n = 17)</td>
<td>89.7</td>
<td>23.5% (n = 4)</td>
<td>0/4</td>
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<tr>
<td>ALB-MSH2(^{-/-})AID(^+) (n = 14)</td>
<td>89.2</td>
<td>50.0% (n = 7)</td>
<td>2/5</td>
<td></td>
</tr>
<tr>
<td>ALB-Cre (n = 12)</td>
<td>88.3</td>
<td>0.0%</td>
<td>0/0</td>
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<tr>
<td>WT (n = 10)</td>
<td>90.0</td>
<td>0.0%</td>
<td>0/0</td>
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Abbreviation: n, number of mice.

Figure 5.
Liver tumors that developed in ALB-MSH2\(^{-/-}\)/AID\(^+\), ALB-MSH2\(^{-/-}\)/C0, and ALB-AID\(^+\) mice. A, total RNA was isolated from liver tissues of ALB-Cre, ALB-MSH2\(^{-/-}\)/AID\(^+\), ALB-MSH2\(^{-/-}\), and ALB-AID\(^+\) mice, and MSH2 and AID expression levels were measured by quantitative real-time RT-PCR. B, IHC for MSH2 of the ALB-Cre and ALB-MSH2\(^{-/-}\)/AID\(^+\) mouse liver. C, representative macroscopic images of multiple liver tumors that developed in an ALB-MSH2\(^{-/-}\)/AID\(^+\) mouse. Arrowheads, tumor nodules. D, microscopic (hematoxylin and eosin stain) images of liver tumors that developed in ALB-MSH2\(^{-/-}\)/AID\(^+\), ALB-MSH2\(^{-/-}\)/C0, and ALB-AID\(^+\) mice and noncancerous liver tissues of the same mice. Arrowheads, tumor nodules. E, IHC for \(\alpha\)-fetoprotein of nontumor and tumor tissues in ALB-Cre, ALB-MSH2\(^{-/-}\)/AID\(^+\), and ALB-AID\(^+\) mice.
the nontumorous regions of either mutant or control mouse liver (Fig. 5E). No histologic changes were observed in the nontumorous region of the liver tissues of any of the mutant and control mice examined.

Somatic substitution patterns in MSH2-deficient and/or AID-expressing tumors

To unveil the mutation frequency as well as mutational signature that accumulated in tumors developed in the liver with MSH2 deficiency and/or AID upregulation, we performed whole-exome sequencing of six hepatocellular carcinomas from ALB-MSH2−/−AID−, ALB-MSH2−/−, and ALB-AID+ mice. As a control, we also examined the ALB-Cre mouse liver. We targeted the whole exons of approximately 24,300 mouse genes, sequenced 1.538 Gb on average for each sample, and achieved 30.04-fold coverage per sample as the mean coverage of each base in the target regions (Supplementary Table S2). The variant filtering process is summarized in Supplementary Fig. S1. Candidate mutations were validated by repeated whole-exome sequencing using independent amplicons derived from the same samples. As a result, we identified a total of 216 single nucleotide variants, including 206 nonsynonymous mutations and 10 synonymous mutations in 121 genes of 6 hepatocellular carcinoma tissues (Supplementary Tables S3 and S4). The number of mutations suggested that MSH2 played a role in protection of AID-mediated mutagenesis in the liver tissues. Among the mutated genes identified, 5, 3, and 6 genes were recurrently mutated in two tumors from ALB-MSH2−/−AID−, ALB-MSH2−/−, and ALB-AID+ mice, respectively. Pathway analyses using the Kyoto Encyclopedia of Genes and Genomes database (http://www.genome.jp/kegg/) revealed that 6 (ALB-MSH2−/−AID−), 9 (ALB-MSH2−/−), and 6 (ALB-AID+) genes were categorized into the well-known signaling pathway, whereas the biologic functions of the remaining genes were not fully defined (Supplementary Table S5). Interestingly, several mutated genes such as Musc6 and Ing1 were also reported in human liver cancer tissues (International Cancer Genome Consortium; http://icgc.org/).

Accumulating evidence indicates that each cancer has a unique mutational signature (29). We confirmed that the most predominant substitution was C.G to T.A in the exome sequences of hepatocellular carcinomas that developed in ALB-AID+ mice (P < 0.05 by ANOVA; Fig. 6A). In contrast, hepatocellular carcinomas that developed in ALB-MSH2−/− mice had mixed mutation signatures, with a predominance of T.A to C.G, in addition to C.G to T.A transitions. The mutation signature of hepatocellular carcinomas in ALB-MSH2−/−AID− mice were enriched as C.G to T.A, followed by T.A to C.G (Fig. 6A). Of the 37 C.G to T.A transitions detected in ALB-MSH2−/−AID− mice, 23 (62.2%) were in the context of CpGpX or Ap CpX, a typical mutation pattern induced by AID (Fig. 6B). These findings indicate that mutation signatures detected in tumors developing in those models, especially in ALB-MSH2−/−AID− mice, closely resemble those of hepatitis virus-associated human hepatocellular carcinomas, which accumulate somatic mutations biased toward the T.A to C.G and C.G to T.A transition mutations (29, 30).

Discussion

Inflammation is strongly involved in carcinogenesis through various biologic processes. On the other hand, cancer is a genetic disease, and the accumulation of somatic mutations has a crucial role in malignant transformation (31). Therefore, certain mechanisms must facilitate the induction of mutations during inflammation-associated tumor development. Previously, we reported that AID, an APOBEC family protein, plays an important role in the induction of genetic alterations during inflammation-associated cancer development (2). In this study, we demonstrated for the first time that MSH2 expression is suppressed by TNFα via induction of miR-21 in hepatocytes, which predisposes the inflamed cells to acquire enhanced genetic alterations.

MSH2 is the MMR protein that protects DNA against mutation induction, and its dysfunction is strongly associated with human cancer development (32). Indeed, germline mutation in MSH2 is the most frequent cause of hereditary nonpolyposis colorectal cancer, known as Lynch syndrome (33). However, little is known about how MSH2 expression is regulated, except that it is a target gene controlled by the E2F family of transcription factors (34, 35). We showed in this study that TNFα induced downregulation of MSH2 expression in hepatocytes. The data may be in line with a previous report of the inflammation-mediated epigenetic silencing of MLH1, another MMR gene, in the inflamed colonic mucosa (36). Although PMS2 was upregulated by TNFα stimulation, the biologic implication of PMS2 upregulation is unclear at present. We also found in this study that transcription factor NF-κB mediates TNFα-induced repression of MSH2. NF-κB activation is detected in epithelial cells under inflammatory conditions and strongly involved in inflammation-associated tumorigenesis through various mechanisms, such as regulation of cell survival, proliferation and growth, and epithelial-to-mesenchymal transition (37–40). Our study adds a novel role of NF-κB in inflammation-associated carcinogenesis, namely, suppression of MMR system.

Interestingly, we found in this study that MSH2 mRNA levels were decreased by TNFα administration even in the presence of actinomycin D, suggesting that MSH2 downregulation by TNFα is not due to reduced production but is caused by increased degradation of MSH2 mRNA. These data prompted us to search putative mRNAs that potentially target MSH2 mRNA, and we identified miR-21, which appeared to have high affinity for MSH2 mRNA. Consistently, we observed that miR-21 expression was significantly induced by TNFα stimulation via NF-κB activation and that TNFα induced downregulation of MSH2 mRNA and MSH2 protein expression was restored by an miR-21 decoy or anti-miR-21 inhibitor. The data are in agreement with previous studies showing that miR-21 is transactivated by NF-κB, upregulated in hepatitis livers, and correlating with serum transaminase levels that represent hepatic inflammation activity (41–43). Collectively, our findings indicate that TNFα-induced downregulation of MSH2 in the setting of inflammation is mediated by NF-κB–induced increase of miR-21 expression. Supporting our idea, the oncogenic property of miR-21 has been demonstrated in various tumors. For example, miR-21 is upregulated in various solid tumors, and its expression levels are closely correlated with the aggressive form and poor prognosis of several tumors, such as breast and lung cancers (44, 45).

In this study, using transgenic mouse models, we observed that hepatocyte-specific loss of MSH2 results in the development of liver tumors with features of hepatocellular carcinoma. Indeed, 21.4% of ALB-MSH2−/− mice developed tumors in the liver. Notably, the incidence of tumor development in AID-expressing liver was substantially augmented by MSH2 deficiency (50.0% in ALB-MSH2−/−AID− mice vs. 23.5% in ALB-AID+ mice).
Our data are in agreement with a previous study of fl mice tumors, whole-exome sequencing revealed ALB-AID sequence context of the C:G to T:A AID is required for a AID in human chronic hepatitis tissues with HCV fl mice. The via NF-ALB-MSH2 k Cancer Res; 76(15) August 1, 2016 AID AID mice was enriched as C:G, and AID mice as compared with that in MSH2 MSH2 AID mice. The AID AID mice tumors as compared with those in fl mice. Moreover, whole-exome sequencing analyses revealed that mutation frequency was increased in the tumor tissues of ALB-MSH2+/−AID+ mice as compared with that in ALB-AID+ mice. Interestingly, somatic substitution signatures accumulated in the tumors that developed in ALB-MSH2+/−AID+ mice had predominantly C:G to T:A transitions. The preferential bias to C:G to T:A transitions at the preferred AID target sequence, that is, GpCpX or ApCpX trinucleotides enriched in the tumors of ALB-MSH2+/−AID+ mice suggest that MSH2 is required for protection of AID-mediated mutagenesis, and dysfunction of MSH2 concurrent with AID expression strongly accelerates tumorigenesis in liver tissues.

In addition to a predominance of C:G to T:A transitions in ALB-MSH2+/−AID+ mice tumor, whole-exome sequencing revealed a predominance of T:A to C:G transitions in ALB-MSH2+/− mice tumors and increase of T:A to C:G transitions in ALB-MSH2+/−AID+ mice tumors as compared with those in ALB-AID+ mice. Our data are in agreement with a previous study of MMR-deficient mice showing that the mutations accumulated in the reporter gene of epithelial cells of MSH2-deficient mice are biased toward T:A to C:G mutations (46). A recent deep sequencing analysis also revealed that a yeast strain with MSH2 dysfunction accumulates somatic mutations biased toward the transition mutations, T:A to C:G and C:G to T:A substitutions (47). Moreover, whole-genome sequencing on MMR-deficient human tumors also revealed that approximately 3 of 4 of all nucleotide substitutions represent transition mutations, including T:A to C:G and C:G to T:A (48). Importantly, T:A to C:G transitions are enriched in human hepatocellular carcinoma tissues (30). In this study, we showed the reduced expression of MSH2 in human chronic hepatitis tissues with HCV infection. Taken together, it is tempting to speculate that MSH2 dysfunction is involved in inflammation-associated carcinogenesis in human liver. The reason why MSH2 deficiency preferentially induces T:A to C:G transition remains unknown.

In conclusion, we found in this study that MSH2 expression was downregulated by TNFα via NF-kB–mediated miR-21 expression in hepatocytes and that these mechanisms may contribute to inflammation-associated hepatocarcinogenesis through enhanced susceptibility to mutagenesis. Previously, we reported an important role of AID in promoting gene mutations during inflammation-associated carcinogenesis (2). Thus, inflammation appears to enhance genetic alteration by not only accelerating gene mutation induction but also inhibiting MMR, both of which are working in concert, leading to cancer development.

Disclosure of Potential Conflicts of Interest
No potential conflicts of interest were disclosed.

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