Integrative Array-Based Approach Identifies MZB1 as a Frequently Methylated Putative Tumor Suppressor in Hepatocellular Carcinoma

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Abstract

Purpose: The aim of this study was the identification of novel tumor suppressor genes (TSG) silenced by DNA hypermethylation in hepatocellular carcinoma (HCC).

Experimental Design: We conducted integrative array-based approach for genome-wide screening of methylation targets using a methylated DNA immunoprecipitation-CpG island microarray and expression array in three universal hepatoma cell lines and normal liver tissue. Through detailed expression and functional analyses using hepatoma cell lines and primary HCC samples, we isolated novel TSGs for HCC.

Results: A total of 642 genes were identified as methylated in three hepatoma cell lines but unmethylated in normal liver tissue, whereas 204 genes on autosomes were identified as genes unexpressed but restored after treatment with 5-aza-2'-deoxycytidine in these cell lines and expressed in normal tissue. Through the integration of results of the two-array analyses and further validation analyses of expression and methylation status in 17 cell lines and 30 primary tumors of hepatoma, we identified MZB1, marginal zone B and B1 cell-specific protein, encoding an endoplasmic reticulum protein, as a putative TSG frequently methylated within its CpG island in hepatoma. Among 162 patients with primary HCC, silencing of MZB1 protein was significantly and independently associated with a worse outcome. Restoration of MZB1 expression in hepatoma cells reduced cell proliferation in vitro and in vivo through G1-arrest.

Conclusions: These results suggest that methylation-mediated silencing of MZB1 expression leads to loss of its tumor-suppressive activity, which may be a factor in the hepatocarcinogenesis, and is a useful prognosticator in HCC. Clin Cancer Res; 18(13): 3541–51. ©2012 AACR.

Introduction

Hepatocellular carcinoma (HCC), one of the most common malignancies worldwide, is associated with hepatitis virus infections, dietary aflatoxin, chronic alcohol/tobacco consumption, and cirrhosis. Genomic alterations, such as the gain or loss of chromosomal regions and specific gene mutations, have been frequently noted in hepatocarcinogenesis (1). Furthermore, epigenetic abnormalities, such as DNA methylation and chromosome remodeling, may also promote tumorigenesis (2, 3). DNA hypermethylation of promoter CpG islands leads to the inactivation of tumor suppressor genes (TSG) and critical cancer-related genes in human cancers including HCC (4, 5). DNA methylation changes have been reported to be specific to the cancerous tissue making it possible to distinguish HCC and surrounding nontumorous tissues (6). Indeed, abnormal DNA methylation of several TSGs, such as RASSF1A, CDKN2A, CRABP1, GSTP1, CHRNA3, DOK1, SFRP1, GAAD45a, and CDKN2B, is reported to be associated with HCC, and hypermethylation of specific genes, such as CHFR and SYK is detected in advanced stages of HCC (6). However, the number of reported methylation-target genes is far fewer for HCC than for colon cancer or gastric cancer (7). Therefore, further identification of remaining targets for methylation may clarify the specific molecular events involved in HCC progression, enabling the prevention, diagnosis, and treatment of HCC to be approached as potential clinical applications of DNA methylation signature at a molecular level. To discover novel methylation-target sequences with high specificity and sensitivity in a genome-wide manner, large-scale screening methods, which have the potential to

Note: Supplementary data for this article are available at Clinical Cancer Research Online (http://clincancerres.aacrjournals.org/).

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doi: 10.1158/1078-0432.CCR-11-1007
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Cell-specific protein (MZB1), also known as proapoptotic

obtained candidates, we identified marginal zone B and B1

approaches. Through further examination of a subset of

(5-aza-dCyd), and (iii) a combination of data from both

and reactivated upon treatment with 5-aza-2

frequently involved in HCC, we applied the following

methylation and to concentrate those genes most

find novel methylation targets in a whole range of cancers,

have been developed. A combination of 3 types of pretreat-

ments, such as enzyme digestion, affinity enrichment, or

sodium bisulfitet, was followed by different analytical steps,

such as gel-, array-, or next-generation sequencing-based

analysis (8). Among them, methylated-DNA immunoprecipita-

tion (MeDIP, ref. 9) in combination with an oligonucleotide array

or next-generation sequencing allows for rapid and efficient genome-wide assessment of DNA methylation, although these methodologies generally result in a list of several hundred candidate genes. Although an analysis of possible promoters or dense CpG islands is used to narrow down the number of candidate genes, the list is still too long. Pharmacologic unmasking expression microarray approaches are also used widely to identify methylation targets (10), although they are also prone to give false-positive genes that are indirect methylation targets themselves and not considered to be a reliable gauge of DNA methylation at a given locus.

To identify genes that are downregulated because of DNA hypermethylation and to concentrate those genes most frequently involved in HCC, we applied the following integrative array-based approach to 3 hepatoma cell lines: (i) MeDIP in combination with CpG island-array (MeDIP-chip) analysis to identify genes methylated in a cancer-specific manner, (ii) expression microarray analysis to identify genes downregulated in a cancer-specific manner and reactivated upon treatment with 5-aza-2′deoxycytidine (5-aza-dCyd), and (iii) a combination of data from both approaches. Through further examination of a subset of obtained candidates, we identified marginal zone B and B1 cell-specific protein (MZB1), also known as prosapoptotic caspase adaptor protein (PACAP), pERp1, or MGC29506 (11), whose inactivation is related with a worse prognosis in primary tumors as a possible TSG for HCC.

Materials and Methods

Cell lines and primary tumor samples

A total of 17 hepatoma cell lines including 15 HCC lines (cHc4, Hep3B, Hep-Kano, Hep-TABATA, HLE, HLF, huH-1, HuH-4, JHH-1, JHH-4, JHH-5, JHH-7, Li-7, PLC/PRF/5, and SK-Hep-1) and 2 hepatoblastoma lines (HepG2 and HuH-6) were used (12). All 162 primary HCC samples were obtained during surgery from patients with HCCs treated at Tokyo Medical and Dental University (Tokyo, Japan) between 2000 and 2005. Relevant clinical and survival data were available for all patients (Table 1). The median follow-up period for the surviving patients was 19 months (ranging from 1 to 103 months). Samples from 17 of these patients with HCC were immediately frozen in liquid nitrogen and stored at −80°C until required for DNA and RNA analyses. Normal liver tissues were obtained from surgical samples in 2 patients (cases C20 and C40) with colon cancer metastasis. Written consent was obtained after approval by the local ethics committee.

MeDIP-chip analysis

The DNA methylation profiles were analyzed by MeDIP using anti-5-methylcytidine antibody (Eurogenerics) followed by the Human 244K CpG island microarray (Agilent), which consists of 237,220 probes, covering 27,800 CpG islands (97.5% of UCSC annotated CpG islands), according to the manufacturer’s instructions. Image analysis with data extraction was done using Feature Extraction Software, version 9.0 (Agilent Technologies). The analytic procedure used for the results of the MeDIP-chip assay was described in the Supplementary Experimental Procedure.1

Gene expression array

Gene expression was profiled using a 4 × 44K Human Whole Genome Ver. 2.0 gene expression array (Agilent Technologies) according to the manufacturer’s instructions. Total RNAs extracted from hepatoma cell lines and from these cells treated with 10 μmol/L 5-aza-dCyd for 5 days were used for conventional and pharmacologic unmasking analyses, respectively. Two normal livers (C20 and C40) were used as controls. All samples were analyzed twice. Image analysis with data extraction and the data analysis were conducted using Feature Extraction Software, version 9.0 and GeneSpring GX10 software (Agilent Technologies), respectively.1

Real-time reverse transcription PCR

To analyze the restored expression of genes, the cell lines were cultured with 1 to 10 μmol/L 5-aza-dCyd for 5 days. Levels of mRNA expression were measured with ABI PRISM

1The entire microarray data set is available at http://www.ncbi.nlm.nih.gov/geo/info/linking.html under the data series accession no. GSE35313.
Table 1. Association between clinicopathologic characteristics and MZB1 expression

<table>
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<th>MZB1 immunoreactivity</th>
<th>n</th>
<th>Negative (%)</th>
<th>Positive (%)</th>
<th>P</th>
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<tr>
<td>Total</td>
<td>162</td>
<td>84 (51.9)</td>
<td>78 (48.1)</td>
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<td>Gender</td>
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<tr>
<td>Male</td>
<td>122</td>
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<td>Female</td>
<td>40</td>
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<td>22 (55.0)</td>
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<td>Age, y</td>
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<tr>
<td>Mean</td>
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<td>65.7</td>
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<tr>
<td>&gt;65</td>
<td>98</td>
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<td>&lt;65</td>
<td>64</td>
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<td>Virus</td>
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<td>HCV(+)</td>
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<td>HCV(–), HBV(–)</td>
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<td>20 (44.4)</td>
<td>25 (55.6)</td>
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<td>AFP, ng/mLb</td>
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<td>5,390 ± 22,968</td>
<td>2,819 ± 13,373</td>
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<td>PIVKA-II, mAU/mLb</td>
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<td>7,252 ± 43,097</td>
<td>6,767 ± 25,669</td>
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<td>Aspartate aminotransferase, IU/Lb</td>
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<td>48.6 ± 25.3</td>
<td>54.7 ± 34.2</td>
<td>0.1982</td>
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<td>Alanine aminotransferase, IU/Lb</td>
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<td>53.7 ± 34.8</td>
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<td>Platelet (%)b</td>
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<td>84.1 ± 13.1</td>
<td>85.9 ± 13.6</td>
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<td>Total bilirubin, mg/dLb</td>
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<td>0.86 ± 0.44</td>
<td>0.86 ± 0.40</td>
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<td>Albumin, g/dLb</td>
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<td>3.9 ± 0.5</td>
<td>3.9 ± 0.4</td>
<td>0.6972</td>
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<td>Child–Pugh scoreb</td>
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<tr>
<td>5.4 ± 0.6</td>
<td>5.3 ± 0.7</td>
<td>0.8199</td>
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<td>Tumor size, cmb</td>
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<td>4.6 ± 2.8</td>
<td>4.5 ± 3.1</td>
<td>0.8411</td>
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<tr>
<td>Tumor number</td>
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<tr>
<td>Single</td>
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<td>50 (47.6)</td>
<td>55 (52.4)</td>
<td>0.1940</td>
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<tr>
<td>Multiple</td>
<td>57</td>
<td>34 (59.6)</td>
<td>23 (40.4)</td>
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<td>Histopathologic grading</td>
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<td>Well-differentiated</td>
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<tr>
<td>Moderately differentiated</td>
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<td>43 (47.8)</td>
<td>47 (52.2)</td>
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<tr>
<td>Poorly differentiated</td>
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<td>17 (58.6)</td>
<td>12 (41.4)</td>
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<td>Portal vein invasion</td>
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<tr>
<td>Absent</td>
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<td>40 (43.5)</td>
<td>52 (56.5)</td>
<td>0.0222</td>
</tr>
<tr>
<td>Present</td>
<td>70</td>
<td>44 (62.9)</td>
<td>26 (37.1)</td>
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<tr>
<td>Surgical margin</td>
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<tr>
<td>Absent</td>
<td>139</td>
<td>73 (52.5)</td>
<td>66 (47.5)</td>
<td>0.8478</td>
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<tr>
<td>Present</td>
<td>23</td>
<td>11 (47.8)</td>
<td>12 (52.2)</td>
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<tr>
<td>Background liver parenchyma</td>
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<tr>
<td>Normal liver</td>
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<td>8 (80.0)</td>
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<td>Chronic hepatitis</td>
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<td>39 (50.0)</td>
<td>39 (50.0)</td>
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<tr>
<td>Liver cirrhosis</td>
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<td>43 (58.1)</td>
<td>31 (41.9)</td>
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<tr>
<td>Tumor stage</td>
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</tr>
<tr>
<td>I</td>
<td>13</td>
<td>3 (23.1)</td>
<td>10 (76.9)</td>
<td>0.0207</td>
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<tr>
<td>II</td>
<td>57</td>
<td>25 (43.9)</td>
<td>32 (56.1)</td>
<td></td>
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<tr>
<td>III</td>
<td>58</td>
<td>33 (56.9)</td>
<td>25 (43.1)</td>
<td></td>
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<td>IVA</td>
<td>34</td>
<td>23 (67.6)</td>
<td>11 (32.4)</td>
<td></td>
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</table>

NOTE: Statistically significant values are in boldface type.
Abbreviations: HBV, hepatitis B virus; HCV, hepatitis C virus.

*P values are from χ², Fisher exact, or Student t test and were statistically significant at <0.05.

bMean ± SD.
according to the manufacturer’s instructions. Gene expression values are given as ratios between the genes of interest and an internal reference gene (Hs99999903_m1 for ACTB; Applied Biosystems) that provides an internal normalization factor, and subsequently normalized with the value in the controls (relative expression level). The assay was conducted twice for each sample.

**Methylation analysis**

Sodium bisulfite-treated genomic DNA was subjected to PCR using primer sets to amplify regions of interest (Supplementary Table S1). For the combined bisulfite restriction analysis (COBRA), PCR products were digested with *Bst*UI, *Taq*I, or *Hha*I and electrophoresed (13). The intensity of methylated alleles as a percentage on the ethidium bromide-stained gels was calculated, and a methylation density cutoff point of 20% was considered significant as described elsewhere (14). For bisulfite genomic sequencing (BGS), PCR products were subcloned and sequenced.

**Immunohistochemistry**

Indirect immunohistochemistry was conducted with formalin-fixed, paraffin-embedded tissue sections using an automated immunostainer (Benchmark XI; Ventana Medical Systems) with heat-induced epitope retrieval, anti-MZB1 (1:50; 11454-1-AP; Protein Tech), anti-PCNA (1:1,000; #2586; Cell Signaling Technology), or anti-Ki-67 antibodies (1:100; M7240; Dako). The slides were counterstained with Mayer’s hematoxylin, and analyzed under a light microscope by 2 pathologists blinded to clinical characteristics and outcomes. Twenty representative fields per slide were examined, and the percentage of the total cell population that expressed MZB1 was evaluated for each case at ×200 magnification. Expression of MZB1 protein was graded as either positive (≥10% of tumor cells showing immunopositivity) or negative (≤10% of tumor cells showing immunopositivity or no staining). Plasma cells and bile duct epithelial cells were used as positive and negative controls, respectively.

**Western blotting**

Western blotting was conducted as described elsewhere (12). Anti-FLAG-tag and anti-β-actin antibodies were purchased from Sigma-Aldrich, and the anti-cleaved caspase-3 antibody (#9661) was purchased from Cell Signaling Technology.

**Fluorescent immunocytochemistry**

The plasmid expressing C-terminally FLAG-tagged MZB1 (pCMV-3Tag3A-MZB1) was obtained by cloning the full coding sequence of MZB1 in-frame along with the 3xFLAG-epitope into the pCMV-3Tag3A vector (Stratagene). Cells were fixed in 10% trichloroacetic acid, permeabilized with 0.2% Triton X-100, and treated with blocking solution (1% bovine serum albumin in PBS). After incubation with the primary antibodies (anti-MZB1, 1:100 and/or anti-Calnexin, 1:100) for 1 hour, the bound antibody was visualized using a Cy3-conjugated or fluorescein isothiocyanate (FITC)-conjugated secondary antibody (1:1,000). After being mounted with DAPI (4’,6’-diamidino-2-phenylindole) to stain nuclei, the cells were observed under a fluorescence microscope (BZ-8100; Keyence).

**In vitro and in vivo growth assay**

Colony formation assays using cells transiently introduced with pCMV-3Tag3A-MZB1 or the empty vector (pCMV-3Tag3A-mock) was conducted as described elsewhere (15). The expression of MZB1 protein was confirmed 48 hours after transfection by Western blotting and fluorescent immunocytochemistry.

Stable MZB1 transfecteds and control counterparts were obtained by introducing pCMV-3Tag3A-MZB1 or pCMV-3Tag3A-mock into cells with G418 selection, and 2.5 × 10⁵ cells were seeded in 24-well plates. The numbers of viable cells were assessed 24 to 72 hours after seeding by the water-soluble tetrazolium salt assay. The cell cycle was evaluated 48 hours after seeding by a fluorescence-activated cell sorting (FACS) as described elsewhere (15).

The in vivo tumor-suppressive ability of MZB1 was investigated by conducting tumor xenograft experiments. Six-week-old female severe combined immunodeficient (SCID) mice were injected subcutaneously in the lower back with MZB1-expressing or control mock-transfected cells (4 × 10⁶). All procedures involving animals were approved by and conformed to the guidelines of our Institutional Animal Care and Use Committee. Tumor formation in SCID mice was monitored daily and the recipient mice were sacrificed for tumor weight evaluation and protein expression analyses 5 weeks postinjection.

**Statistical analysis**

The χ² or Fisher’s exact test was used to test for differences between groups. Kaplan–Meier method and log-rank test were used for the survival analyses. Univariate and multivariate survival analyses were conducted using the likelihood ratio test of the stratified Cox proportional-hazards model. Differences between subgroups were tested with the Student *t* test. For multiple group comparisons, ANOVA followed by Scheffé post-hoc test was used. Differences were assessed with a 2-sided test, and considered significant at the *P* < 0.05 level.

**Results**

**Screening in the MeDIP-chip analysis**

For the screening of aberrantly methylated genes by MeDIP-chip analysis, we used a CpG island microarray, in which 11,229 genes harbor CpG islands upstream or within, with the algorithm shown in the Supplementary Experimental Procedure and Supplementary Fig. S1. Among 11,229 genes, CpG islands of 2,476 genes were unmethylated in normal liver tissue (case C20) but methylated in at least 1 of 3 hepatoma cell lines (Hep3B,
HepG2, and HuH-7). Because CpG islands of 642 of those 2,476 genes were methylated in all 3 cell lines (Fig. 1A), we selected them as candidates consistently hypermethylated in hepatomas.

**Screening in the expression array analysis**

In expression array analysis done in a duplicate manner, we used only reproducible probes (the coefficient of variation, CV <50%) in each set of experiments to evaluate obtained values. We focused on genes satisfying 2 criteria: (a) genes whose expression was observed in normal liver tissue but repressed in hepatoma cells, and (b) genes whose expression was restored after treatment with 5-aza-dCyd in hepatoma cells. Among genes expressed in normal liver tissue (C20 and C40), the expression of 1,730, 1,158, and 1,521 genes was silenced but restored by 5-aza-dCyd in Hep3B, HepG2, and HuH-7 cells, respectively. Among them, 204 genes on autosomes commonly satisfied criteria in all 3 lines (Fig. 1A), indicating 204 genes to be candidates consistently silenced through methylation in hepatocarcinogenesis.

**Integration and validation of results in two microarray-based analyses**

On the basis of the MeDIP-chip and expression array analyses, 11 genes were selected as overlapping genes in 2 different genome-wide array-based screening methods, suggesting them to be pharmaco logically unmasked, tumor-specific methylation targets in 3 hepatoma cell lines (Fig. 1A and Supplementary Table S2). Because these genes seem to be silenced in a tumor-specific manner, they are also candidates for TSG in hepatocarcinogenesis.
We then determined the status of methylation and expression for all 11 candidates through COBRA and real-time reverse transcription PCR (RT-PCR), respectively, in a panel of 17 hepatoma cell lines and 2 normal liver tissues (Fig. 1B). Among them, ANGPT2 was highly methylated in both the hepatoma cells and normal liver tissue. Among the other 10 genes, 8 genes (LITD1, MZB1, PBX4, FAR1, RADIL, DERR1, SFRP1, and CCK) harbored at least 1 hypermethylated region in >50% of hepatoma cell lines compared with normal liver tissue, whereas OCIAD2 and KCNK6 were infrequently methylated in the hepatoma lines. Among those 8 genes, only MZB1 and FAR1 were downregulated (<0.1 relative to normal liver) in all cell lines with their hypermethylation, whereas the other 6 genes were expressed even in cell lines with their hypermethylation, suggesting MZB1 and FAR1 to be possible methylation targets for gene silencing in hepatoma cells, although the expression of all 11 genes was more or less restored by 1 to 10 μmol/L of 5-aza-dCyd treatment in each of the 3 cell lines (Supplementary Fig. S2).

**MZB1 is frequently silenced through CpG island methylation in primary tumors**

We next determined the methylation and expression status of MZB1 and FAR1 in 17 paired tumorous and nontumorous tissues from primary HCCs (cases L81-L104; Fig. 2A and Supplementary Fig. S3). Tumor-specific MZB1 (region 8) and FAR1 (region 3) hypermethylation was observed in 9 (52.9%) and 8 (47.1%) cases, respectively. In those cases with hypermethylation, tumor-specific downregulation of MZB1 and FAR1 expression was observed in 9/9 (100%) and 5/8 (62.5%) cases, respectively, suggesting MZB1 to be the most probable candidate for a gene silenced through tumor-specific methylation. In additional 13 cases (Fig. 2A, cases L77-L29), tumor-specific MZB1 hypermethylation was observed in 6 (46.2%) cases.
cells showed much higher MZB1 expression level compared with C20 (Fig. 1B), suggesting that 5-aza-dCyd treatment indirectly activates transcription of MZB1 through demethylation of transcription factors/cofactors for MZB1, which might downregulated in normal hepatocytes or other mechanisms.

**Immunohistochemical staining of MZB1 in primary HCCs**

To determine clinicopathologic significance of the MZB1 downregulation in primary HCCs, we conducted an immunohistochemical analysis of the MZB1 in 162 primary cases (Fig. 3 and Table 1). In the tumors regions, 78 (48.1%) showed immunoreactivity to MZB1 (positive in Table 1), whereas 84 (51.9%) did not (negative in Table 1). In the nontumorous regions, on the other hand, 135 (83.3%) showed immunoreactivity to MZB1, whereas 27 (16.7%) did not. Negative MZB1 immunoreactivity was more frequent in cases with portal invasion (P = 0.0222) and in higher tumor stages (P = 0.0207). However, the MZB1 protein expression in each tumor was not associated with other characteristics.

In Kaplan–Meier survival curves, univariate analyses of overall and nonrecurrent survival with log-rank tests showed a significant association between negative MZB1 immunoreactivity and a poor survival rate of patients (P = 0.0031 and 0.0044, respectively; Fig. 3B). In the Cox proportional hazard regression model (Table 2), univariate analyses showed that negative MZB1 immunoreactivity, α-fetoprotein (AFP), tumor size, tumor number, portal vein invasion, background liver parenchyma, and tumor stage were significantly associated with overall survival. Multivariate analysis using a stepwise

Figure 3. A, representative results of immunohistochemical staining of MZB1 protein in normal liver tissue, nontumorous liver tissue, and tumorous tissues in HCCs. Both normal and nontumorous hepatocytes showed MZB1 immunopositivity, whereas tumor cells showed either negative or positive immunoreactivity. Bars, 25 μm. Magnifications are ×200. B, Kaplan–Meier curves for overall survival (left) and recurrence-free survival (right) rates of 162 patients with primary HCCs. Negative MZB1 immunoreactivity of tumor cells was significantly associated with worse overall and recurrence-free survivals (P = 0.0031 and 0.0044, respectively; log-rank test).
Cox regression procedure revealed that MZB1 immuno-reactivity, tumor size, and tumor stage were independently selected as predictive factors for overall survival in both forward and backward procedures ($P = 0.0234$, 0.0319, and 0.0301, respectively).

### MZB1 reexpression suppresses proliferation and tumor formation of cancer cells in vitro and in vivo

To investigate the biologic significance of MZB1 in hepatocarcinogenesis, MZB1 expression was transiently or stably restored in hepatoma cells lacking MZB1 expression. We then measured the proliferation and tumor formation of those cells in comparison with the control counterparts transduced with an empty vector in vitro and in vivo.

In colony-formation assays using transiently transfected cells, the occupancy of the stained area of colonies produced by MZB1-transfected HLE cells (Fig. 4A), which show MZB1 hypermethylation pattern (Supplementary Fig. S4), and other hepatoma cells (data not shown) decreased compared with those of control counterparts.

In an in vitro proliferation assay using stably transfected cells, cells expressing MZB1 protein, which was predominantly colocalized with an endoplasmic reticulum (ER) marker in the cytoplasm, grew slightly but significantly slower than the control cells (Fig. 4B). In a FACS analysis to examine the mode of action of MZB1 in the cell cycle, an accumulation of cells in G0–G1 phase and a decrease in S and G2–M phase cells but no increase in sub-G1 phase cells was observed among MZB1-transfected cells compared with mock-transfected counterparts (Fig. 4C), suggesting that MZB1 contributes to the arrest of hepatoma cells at the G1-S checkpoint without inducing apoptosis.

Indeed, a similar expression pattern of cleaved caspase 3, one of markers of apoptosis, was observed between stable MZB1 transfectants and control counterparts even after treatment with CDDP for induction of apoptosis (Fig. 4C). Subcutaneous tumor growth experiments using stably transfected and resected tumors, no induction of apoptosis detected by

### Table 2. Cox proportional hazard regression analysis for overall survival

<table>
<thead>
<tr>
<th>Factor</th>
<th>Univariate HR (95% CI)</th>
<th>Univariate $P$</th>
<th>Multivariate $P$</th>
</tr>
</thead>
<tbody>
<tr>
<td>Gender Male vs. female</td>
<td>0.990 (0.509–1.925)</td>
<td>0.9764</td>
<td>X</td>
</tr>
<tr>
<td>Age, y &gt;65 vs. &lt;65</td>
<td>0.957 (0.527–1.738)</td>
<td>0.8859</td>
<td>X</td>
</tr>
<tr>
<td>AFP &gt;200 vs. &lt;200 ng/mL</td>
<td>2.202 (1.214–3.995)</td>
<td>0.0094</td>
<td>X</td>
</tr>
<tr>
<td>Tumor size &gt;3 vs. &lt;3 cm</td>
<td>3.548 (1.498–8.401)</td>
<td>0.0040</td>
<td>0.0319</td>
</tr>
<tr>
<td>Tumor number Multiple vs. single</td>
<td>2.531 (1.406–4.554)</td>
<td>0.0019</td>
<td>X</td>
</tr>
<tr>
<td>Histopathologic grading Poor-moderate vs. well</td>
<td>2.312 (1.074–4.975)</td>
<td>0.0321</td>
<td>X</td>
</tr>
<tr>
<td>Portal vein invasion Present vs. absent</td>
<td>2.309 (1.136–3.716)</td>
<td>0.0173</td>
<td>X</td>
</tr>
<tr>
<td>Surgical margin Present vs. absent</td>
<td>1.948 (0.963–3.940)</td>
<td>0.0637</td>
<td>X</td>
</tr>
<tr>
<td>Background liver parenchyma LC vs. CH + NL</td>
<td>1.825 (1.009–3.300)</td>
<td>0.0468</td>
<td>X</td>
</tr>
<tr>
<td>Stage III + IVA vs. I + II</td>
<td>3.466 (1.710–7.024)</td>
<td>0.0006</td>
<td>0.0301</td>
</tr>
<tr>
<td>MZB1 expressionc Negative vs. positive</td>
<td>2.532 (1.338–4.791)</td>
<td>0.0043</td>
<td>0.0234</td>
</tr>
</tbody>
</table>

NOTE: Statistically significant values are in boldface type.
Abbreviations: CH, chronic hepatitis; LC, liver cirrhosis; NL, normal liver.

*Forward and backward stepwise analyses were used for multivariate analysis.

*P* values are from 2-sided tests and were statistically significant at $<0.05$.

*MZB1 expression was evaluated by immunohistochemical analysis as described in Materials and Methods.
cleaved caspase 3 expression in MZB1-transfected cells was observed compared with mock-transfected counterparts in vivo (Fig. 4D).

Discussion

Epigenetic silencing of TSGs plays an important role in the carcinogenesis (16), including hepatomagenesis (5–7). Although many studies have reported aberrant hypermethylation of genes in HCC, e.g. CDH1, RASSF1A, GSTP, SOCS1, SFRP1, and PTEN identified as TSGs silenced by hypermethylation, most of these studies were limited to the analysis of a single or a few genes (5–7, 17). Because the number of methylation-target TSGs identified to date is far fewer for HCC than for other cancers possibly because of fewer attempts to conduct genome-wide analysis (18), there remain many genes hypermethylated in HCC. With advancements in microarray technology, the number of genes found to be hypermethylated in HCC in a cancer-specific manner is...
expected to increase (8, 19). Although the functional consequence of promoter hypermethylation is transcriptional silencing of the associated gene, this assumption often goes untested, as few have concurrently investigated both methylation and expression (6, 7). On the basis of these hypotheses and background, we conducted genome-wide screening of methylation-target TSGs using a combination of 2 microarray-based approaches: MeDIP-chip analysis in hepatoma cell lines and expression array analysis for genes pharmacologically unmasked in the same lines. As a result of this approach, several genes were newly identified as candidate methylation targets, and among them MZB1 was showed to be the most possible TSG, which is silenced through methylation and contributes to the hepatocarcinogenesis.

Among 11 genes we identified through genome-global screening of methylation-mediated silenced genes in hepatoma cells, 10 were newly identified candidates and only SFRP1 was known as possible methylation-target TSG in HCC (20, 21). The remarkable reduction in the number of candidate genes and lack of various known HCC-related methylation targets within candidates may be because of a small number of commonly methylated and/or silenced genes among the 3 cell lines used in this study. Indeed, several frequently methylated genes, such as SLIT2, PIGS2 (COX2), and HHIP, for which methylation data are available in all 3 hepatoma cell lines, showed different methylation patterns among the cell lines (22–24). These variations may come from the different backgrounds of the 3 cell lines, such as hepatitis B virus infection in Hep3B and no hepatitis virus infection in the other 2 lines, because hypermethylated genes in HCC tumors are known to exhibit remarkably distinct patterns depending on associated risk factors (25, 26). Therefore, it is suggested that the candidate genes identified and validated in the present study may contribute to functional pathways shared among different subtypes of HCC regardless of associated risk factors, and this might be the reason why MZB1 protein expression status was not statistically associated with the status of hepatitis virus infection and background liver parenchyma in our analysis.

One of striking findings of our immunohistochemical analysis of MZB1 using a panel of primary tumor samples of HCC was that immunoreactivity to the MZB1 protein in each sample was significantly associated with a worse clinical outcome even after stratification with other clinicopathologic characteristics. This result indicates that MZB1 might be useful as an independent prognosticator in patients with HCC, although MZB1 immunoreactivity in each case was significantly associated with portal invasion and in tumor stages. Because MZB1 seems to be downregulated in a cancer-specific manner in HCC and its expression is observed in most normal human tissues (11), it will be interesting whether MZB1 works as a TSG in specific tissues including liver or in various tissues.

MZB1 was first identified as a caspase-2–binding molecule through a yeast 2–hybrid system using a human B lymphocyte cDNA library, which was conducted to determine the mechanism of activation of caspase-2 in apoptosis of B cells triggered by ligation of the antigen receptor (11). Although MZB1 was shown to bind caspase-2 and -9 in vitro and in vivo and be triggered upon the transient transfection of human kidney cells and Rat-1 fibroblasts and stable transfection of human B cell lines (11), the precise mechanisms by which it exerts proapoptotic activity remain unclear because of the absence of structural hallmarks besides a CXXC thioredoxin motif and no homology with other molecules in apoptotic pathways. Recently, it was shown that MZB1 occurs in the luminal ER and affects multiple cellular processes, such as (a) the oxidative folding and assembly and secretion of immunoglobulin in plasma cells (27, 28) and (b) the regulation of Ca2+ homeostasis and ER Ca2+ stores, integrin-mediated adhesion, and antibody secretion in marginal zone B cells of the spleen and innate-like B cells (B1 cells, ref. 29). Because those processes are associated with the functional differentiation of B cells, it is possible that the MZB1-induced assembly of several target proteins including integrin may contribute to the antiproliferative effect of MZB1 on hepatoma cells without induction of apoptosis observed in this study. The expression of this gene is observed not only in the B-cell lineage including plasma cells, marginal zone B cells, or B1 cells (27–29), but also in most normal human tissues except the placenta constituteively in the absence of an apoptotic stimulus (11), suggesting MZB1 to affect various biologic processes in different tissues possibly through interaction with various proteins and/or the targeting of various molecules. Indeed, MZB1 protein was reported to be downregulated in intestinal-type gastric cancer, although the clinicopathologic and biologic significance was not analyzed (30), suggesting MZB1 to act as a TSG at least in some tissues including stomach and liver tissue. Further examination will be required to clarify the mechanisms of the antiproliferative effect of MZB1.

Disclosure of Potential Conflicts of Interest

No potential conflicts of interest were disclosed.

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Administrative, technical, or material support: I. Imoto, T. Muramatsu, M. Sakamoto, J. Inazawa
Study supervision: I. Imoto, T. Matsui, S. Arii, J. Inazawa

Acknowledgments

The authors thank Ayako Takahashi, Rumi Mori, and Ayumi Shioya for technical assistance.

Grant Support

This study was supported in part by Grant-in-Aid for Scientific Research (A) and (C), and Scientific Research on Priority Areas and Innovative Areas,
MZB1 Methylation in Hepatocellular Carcinoma

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Received April 28, 2011; revised April 17, 2012; accepted April 27, 2012; published OnlineFirst May 9, 2012.

References

Integrative Array-Based Approach Identifies MZB1 as a Frequently Methylated Putative Tumor Suppressor in Hepatocellular Carcinoma

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doi:10.1158/1078-0432.CCR-11-1007

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