

Figure 1. Chromosomal distribution of HDAC targets in rat cardiomyocytes. Genomic fragments (red dots) isolated by DCS were mapped to rat chromosomes.

acetylation at these targets is also affected by HDAC activity in differentiated cardiomyocytes, we isolated cardiac myocytes from neonatal rats and incubated these cells in the absence or presence of TSA. Consistent with the results obtained with H9C2 cells (Figures 2 and 3), TSA treatment resulted in marked increases both in the acetylation level of histones associated with the genomic locus corresponding to clone H9C2T-2_D09 and in the amount of *Itp3* mRNA in neonatal rat cardiac myocytes (Figure 4A). Similarly, TSA increased both the histone acetylation level for genomic DNA corresponding to clone H9C2T-2_C06 and the abundance of *Nqo1* mRNA in the rat cardiac myocytes (Figure 4B). Furthermore, TSA increased the level of histone acetylation associated with the genomic locus corresponding to clone H9C2T-1_E03-1 in rat cardiac myocytes and, as in H9C2 cells, it increased the amount of *Jag2* mRNA without affecting that of *Mta1* mRNA (Figure 4C). Quantitation of genomic DNA corresponding to an additional 19 DCS clones in ChIP products prepared from neonatal rat cardiac myocytes revealed that the acetylation level of bound histones was increased by a factor of >5 by TSA treatment (data not shown). These data thus indicate that the genomic clones identified by DCS in H9C2 cells represent genomic regions whose associated histones are targeted by HDAC activity in differentiated cardiac myocytes. Twelve of the 23 genes that mapped to (or in the vicinity of) the DCS clones examined were also transcriptionally activated by a factor of >1.5 in the TSA-treated neonatal rat cardiac myocytes compared with nontreated cells (data not shown).

Effects of Sodium Butyrate on Histone Acetylation

Various compounds other than TSA inhibit HDAC activity with different target preferences.¹⁹ Sodium butyrate, for example, inhibits the catalytic activity of HDACs belonging to class I or IIA, whereas TSA inhibits that of HDACs belonging to class I, IIA, or IIB. We therefore examined

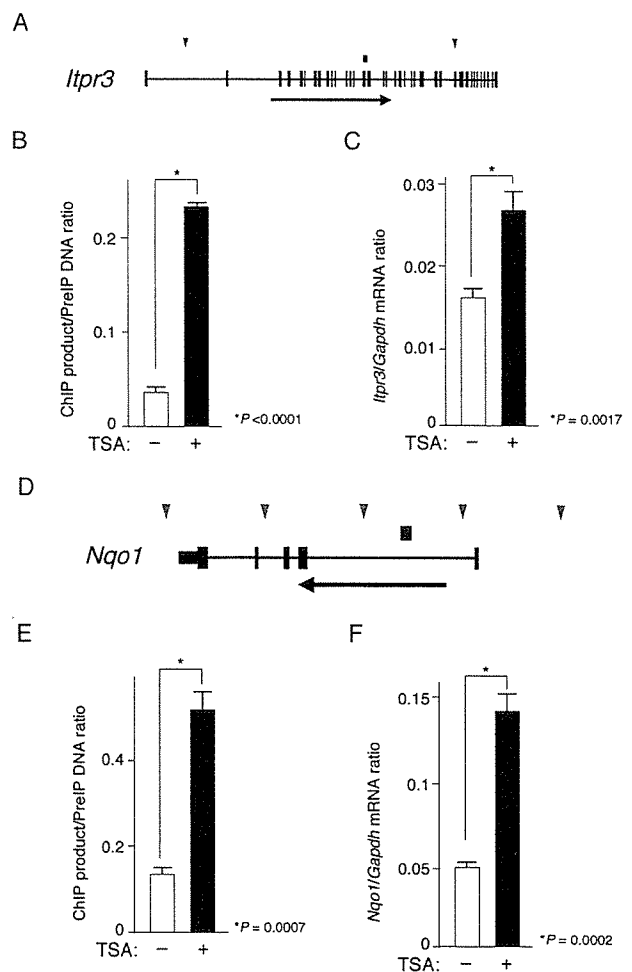


Figure 2. Identification of *Itp3* and *Nqo1* as targets of HDAC in cardiomyocytes. A, One of the DCS clones (H9C2T-2_D09; red rectangle) was mapped to chromosome 20p12, spanning intron 21 and exon 22 of *Itp3*. Exons are denoted by black boxes, the arrow indicates the direction of transcription, and blue triangles depict distance markers separated by 50 kbp. B, Chromatin immunoprecipitates were prepared from H9C2 cells treated (+) or not (-) with 300 nM TSA for 24 hours. The amount of DNA corresponding to the H9C2T-2_D09 sequence in each ChIP product relative to that in the corresponding original sample before immunoprecipitation (PreIP) was then determined by real-time PCR. C, The amount of *Itp3* mRNA relative to that of GAPDH mRNA in H9C2 cells treated or not with TSA was determined by quantitative RT-PCR. D, One of the DCS clones (H9C2T-2_C06; red rectangle) was mapped to chromosome 19q12 in the first intron of *Nqo1*. Green triangles depict distance markers separated by 5 kbp. E, The amount of genomic DNA corresponding to the H9C2T-2_C06 sequence in ChIP products relative to that in the PreIP samples was measured as in B. F, The amount of *Nqo1* mRNA relative to that of GAPDH mRNA was determined as in C. All data are mean±SD of triplicates from representative experiments that were performed at least twice. Probability values for the indicated comparisons were determined by Student *t* test.

whether sodium butyrate also affects the acetylation level of histones associated with our DCS clones.

H9C2 cells or neonatal rat cardiac myocytes were incubated for 24 hours with 0, 2, or 4 mmol/L sodium butyrate and then subjected to ChIP, and the resulting products were subjected to real-time PCR to quantitate the amount of genomic DNA corresponding to the clones

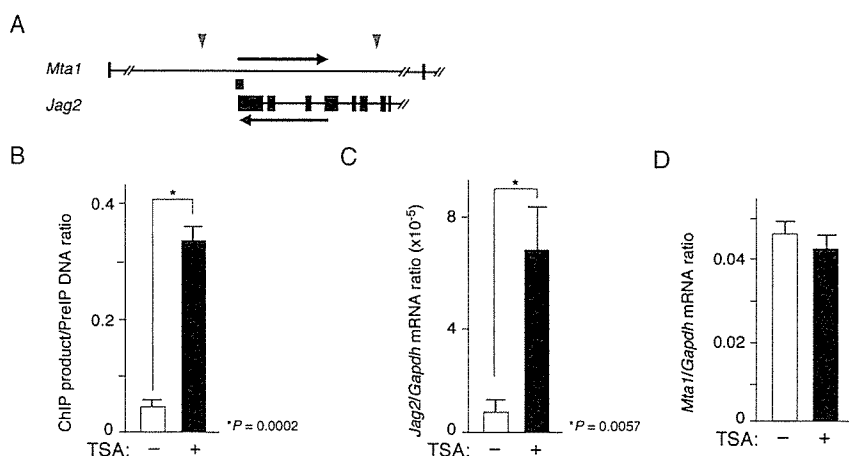


Figure 3. Identification of Mta1 and Jag2 as targets of HDAC in cardiomyocytes. A, One of the DCS clones (H9C2T-1_E03-1; red rectangle) was mapped to chromosome 6q32 in the first intron of Mta1 and the last exon of Jag2. The position of the H9C2T-1_E03-1 clone in the genome is shown schematically as in Figure 2D. B, The amount of genomic DNA corresponding to the H9C2T-1_E03-1 sequence in ChIP products relative to that in the PreIP samples was measured by real-time PCR as in Figure 2B. C and D, The amounts of Jag2 (C) and Mta1 (D) mRNAs relative to that of GAPDH mRNA were determined as in Figure 2C. All data are mean±SD of triplicates from representative experiments, and probability values for the indicated comparisons were determined by Student *t* test.

H9C2T-2_D09, H9C2T-2_C06, or H9C2T-1_E03-1. Treatment with sodium butyrate at either 2 or 4 mmol/L resulted in marked increases in the amount of DNA corresponding to each clone in the ChIP products from both H9C2 cells (Figure 5A) and neonatal rat cardiac myocytes (Figure 5B). Although the magnitudes of the

effects of 2 and 4 mmol/L sodium butyrate were similar in H9C2 cells, the effects of the higher concentration were greater than those of the lower concentration in the differentiated cardiac myocytes. The genomic regions corresponding to these 3 DCS clones were thus epigenetically regulated by both TSA and sodium butyrate.

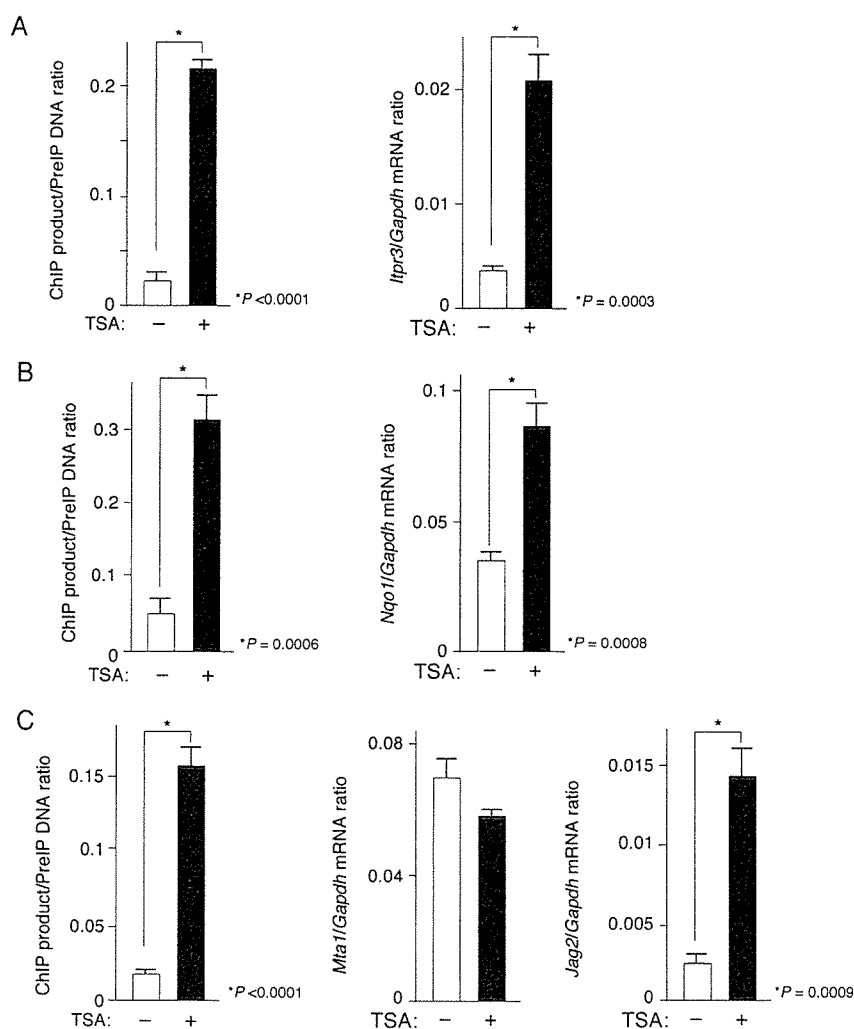


Figure 4. Histone acetylation status and gene expression in neonatal rat cardiac myocytes. Chromatin immunoprecipitates were prepared from freshly isolated cardiac myocytes treated (+) or not (-) with 300 nM TSA for 24 hours, and the amount of DNA corresponding to the H9C2T-2_D09 (A), H9C2T-2_C06 (B), or H9C2T-1_E03-1 (C) clones in each ChIP product was determined by real-time PCR. The amount of Itp3 (A), Nqo1 (B), or Mta1 and Jag2 (C) mRNAs in cells treated or not with TSA was determined by quantitative RT-PCR. All data are mean±SD of triplicates from representative experiments, and probability values for the indicated comparisons were determined by Student *t* test.

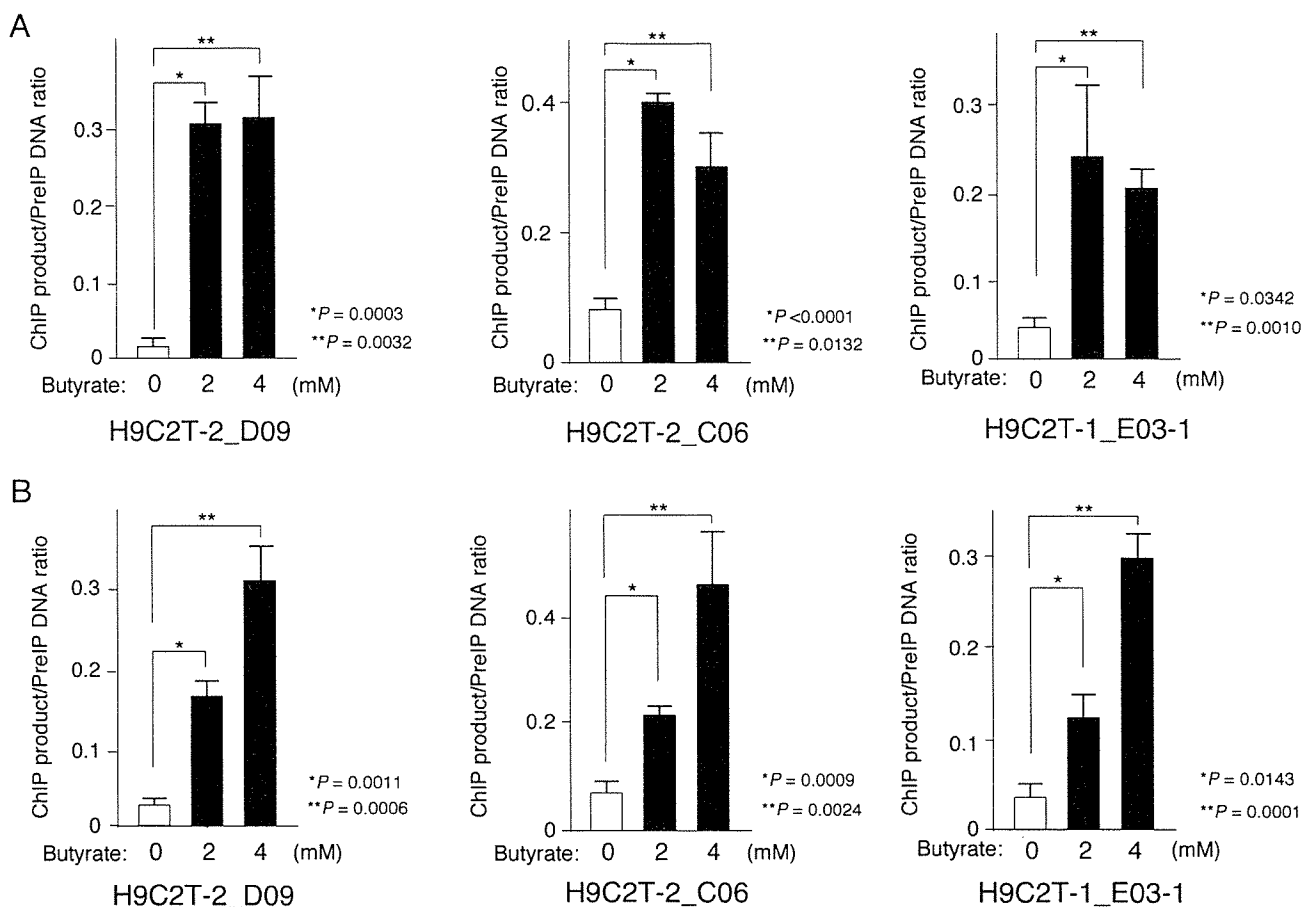


Figure 5. Regulation of histone acetylation status by sodium butyrate. Chromatin immunoprecipitates were prepared from H9C2 cells (A) or freshly isolated rat neonatal cardiac myocytes (B) after treatment with 0, 2, or 4 mmol/L sodium butyrate for 24 hours, and the amount of DNA corresponding to the H9C2T-2_D09, H9C2T-2_C06, or H9C2T-1_E03-1 clones in each ChIP product was determined. All data are mean \pm SD of triplicates from representative experiments, and probability values for the indicated comparisons were determined by Student *t* test.

Regulation of HDAC Targets by a Hypertrophic Stimulus

Given that H9C2 cells retain the ability to undergo hypertrophic changes in response to various stimuli,^{20,21} we next examined whether stimulation with a physiological hypertrophic agent, cardiotrophin-1 (CT-1), affects the extent of histone acetylation at genomic regions corresponding to DCS clones in these cells. H9C2 cells were incubated with 1 nM CT-1 for various times up to 24 hours and were then subjected to ChIP and real-time PCR analysis. Quantitation of genomic DNA revealed that the level of histone acetylation at the region corresponding to clone H9C2T-1_E03-1 was increased significantly at 6 hours and was still increasing at 24 hours (Figure 6A). Similar to the effects of TSA at this locus (Figure 3), the increase in histone acetylation induced by CT-1 was not accompanied by a change in the amount of *Mta1* mRNA (Figure 6B), but was associated with a transient activation of *Jag2* transcription apparent after stimulation for 6 hours (Figure 6C).

Finally, we analyzed a different DCS clone for epigenetic regulation by CT-1. The H9C2T-S-1-8 clone corresponds to the promoter region for the *Myocilin* (*Myoc*) gene (Figure 6D). This gene encodes a protein involved in cytoskeletal

function, and mutations in *Myoc* have been shown to cause a hereditary form of juvenile-onset open-angle glaucoma.²² We found that CT-1 induced a time-dependent increase in the extent of histone acetylation at the genomic region corresponding to this DCS clone (Figure 6E). Together, these data indicate that the histone acetylation level of genomic regions corresponding to our DCS clones is regulated not only by TSA and sodium butyrate but also by physiological stimuli.

Discussion

With the use of our recently developed screening method, DCS, we have now identified almost 200 HDAC targets in cardiomyocytes. The acetylation of histones associated with genomic regions corresponding to 37 of 38 randomly chosen DCS clones was confirmed to be induced by treatment of H9C2 cells with TSA. Genomic regions corresponding to DCS clones were also epigenetically regulated by another HDAC inhibitor, sodium butyrate. Furthermore, the histone acetylation level of genomic regions corresponding to all 22 DCS clones examined was shown to be HDAC targets also in freshly isolated cardiac myocytes. Finally, the acetylation level of histones associated with DCS clones was shown to be regulated by a physiological stimulus, CT-1. The genomic

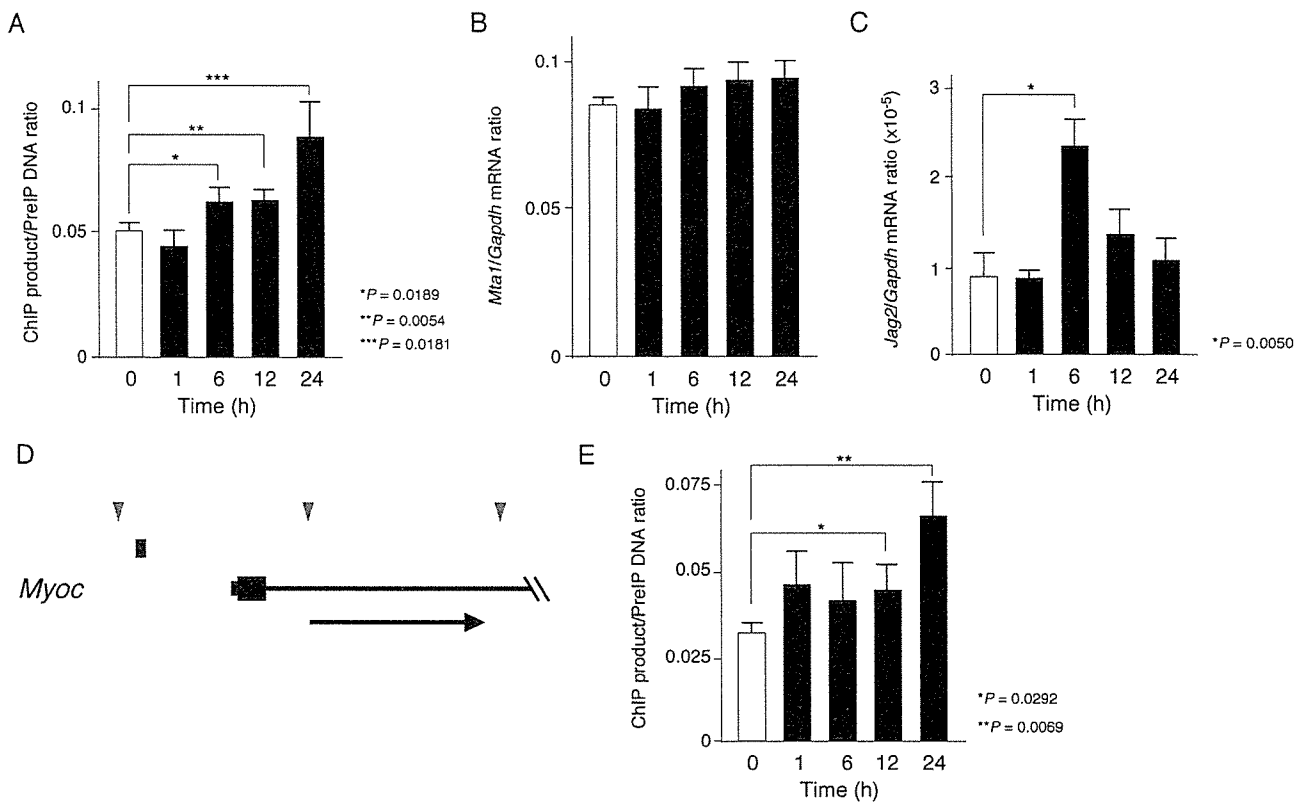


Figure 6. Effects of CT-1 on histone acetylation in H9C2 cells. A, H9C2 cells stimulated with CT-1 (1 nM) for the indicated times were subjected to ChIP, and the amount of genomic DNA corresponding to the DCS clone H9C2T-1_E03-1 was determined in ChIP products. B and C, The amounts of Mta1 (B) and Jag2 (C) mRNAs relative to that of GAPDH mRNA were determined by quantitative RT-PCR in H9C2 cells stimulated with CT-1 for the indicated times. D, The H9C2T-S-1-8 clone (red rectangle) was mapped to chromosome 13q22 in the promoter region of *Myoc*. The position of the clone in the genome is shown schematically as in Figure 2D. E, The amount of genomic DNA corresponding to the H9C2T-S-1-8 sequence was determined in ChIP products prepared from H9C2 cells treated with CT-1 for the indicated times. All data are mean \pm SD of triplicates from representative experiments, and probability values for the indicated comparisons were determined by Student *t* test.

loci identified by DCS thus include physiologically relevant targets for epigenetic modification.

The HDAC targets identified in cardiomyocytes include several genes related to cell growth or differentiation that might play an important role in heart function. In addition to *Itpr3* and *Jag2*, such genes include those for G protein-coupled receptors (*Senr*, *Gbl*), regulators of cytosolic Ca²⁺ concentration (phosphodiesterase, *Pik4cb*, *Pacsin1*), and mediators of growth signaling (*Ccnd1*, *Runx1*, *Fosl1*, *Il11*, *Oct11*, *Sox6*) (online Table SI). Our data suggest that these various genes are under epigenetic control in cardiomyocytes, a conclusion that was verified for some of them by the demonstration that the level of acetylation of associated histones was regulated by the physiological stimulus CT-1. Although CT-1 has not previously been shown to elicit intracellular signaling that affects histone acetylation, our data now indicate that this is indeed the case.

Many (42 of 178) of our DCS clones mapped to the 5'-regions of genes in the rat genome. Bernstein et al recently attempted to identify loci in the human genome whose associated histones are acetylated.²³ These researchers used the "ChIP on chip"²⁴ strategy with high-density genome-tilling microarrays for human chromosomes 21 and 22. Interestingly, consistent with our results, they found that

histone H3 acetylated on lysine-9 and lysine-14 was preferentially localized at the 5' ends of genes, with 58% of such sites of histone acetylation residing in regions encompassing -1.0 to +1.0 kbp of known genes.

Acetylation of core histones is not always associated with the regulation of gene transcription, however. Histone acetylation may thus be related to chromosome replication or to chromatin remodeling unrelated to transcriptional regulation.²⁵ In addition, various types of covalent modification, including acetylation, phosphorylation, and methylation, may exert their effects on histones in a coordinated manner, resulting in the generation of a so-called histone code.²⁶ Consistent with these considerations, only 39% and 52% of the genes corresponding to DCS clones examined showed preferential expression in TSA-treated H9C2 cells and TSA-treated neonatal rat cardiac myocytes, respectively, compared with the corresponding untreated cells.

Although DCS does not readily allow a quantitative comparison of the level of histone acetylation between samples, our method is technically straightforward and does not require any specialized apparatus such as a DNA microarray system. In conclusion, DCS enabled us to efficiently identify HDAC targets in cardiomyocytes. Our present data support the feasibility of determining genome-wide histone acetyla-

tion profiles of the cardiovascular system. They should also provide a basis for further characterization of the importance of epigenetic alterations in the development of cardiac hypertrophy or heart failure. Application of DCS to human heart specimens has the potential to highlight such information of clinical relevance.

Acknowledgments

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Screening for genomic fragments that are methylated specifically in colorectal carcinoma with a methylated *MLH1* promoter

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A subset of colorectal carcinomas (CRCs) is associated with microsatellite instability (MSI) of the genome. Although extensive methylation of CpG islands within the promoter regions of DNA mismatch repair genes such as *MLH1* is thought to play a central role in tumorigenesis for MSI-positive sporadic CRCs, it has been obscure whether such aberrant epigenetic regulation occurs more widely and affects other cancer-related genes *in vivo*. Here, by using methylated CpG island amplification coupled with representational difference analysis (MCA-RDA), we screened genomic fragments that are selectively methylated in CRCs positive for *MLH1* methylation, resulting in the identification of hundreds of CpG islands containing genomic fragments. Methylation status of such CpG islands was verified for 28 genomic clones in 8 CRC specimens positive for *MLH1* methylation and the corresponding paired normal colon tissue as well as in 8 CRC specimens negative for methylation. Many of the CpG islands were preferentially methylated in the *MLH1* methylation-positive CRC specimens, although methylation of some of them was more widespread. These data provide insights into the complex regulation of the methylation status of CpG islands in CRCs positive for MSI and *MLH1* methylation.

Introduction

Colorectal carcinoma (CRC) is one of the leading causes of cancer death in humans. Evidence indicates the existence of two major types of genomic instability in CRCs: chromosomal instability and microsatellite instability (MSI) (1). Whereas chromosomal instability is associated with an abnormal DNA content (such as aneuploidy), inactivation of the tumor suppressor gene *TP53*, and activation of oncogenes (2), MSI is associated with defects in the DNA mismatch repair (MMR)

Abbreviations: CRC, colorectal carcinoma; COBRA, combined bisulfite restriction analysis; CIMP, CpG island methylator phenotype; EGF, epidermal growth factor; GDF, growth-differentiation factor; MSI, microsatellite instability; MMR, mismatch repair; PCR, polymerase chain reaction; TGF- β , transforming growth factor- β .

system that result in frameshift mutations in microsatellite repeats, and thereby affect the structure of genes containing such repeats (3).

Although germ-line mutations of MMR genes have been detected in the genome of individuals with hereditary non-polyposis colorectal cancer (4–6), many sporadic CRCs positive for MSI are associated with epigenetic silencing of non-mutated MMR genes (7,8). MSI-positive CRCs are characterized by specific clinicopathologic features and gene mutations. Such tumors occur with a higher frequency in women than in men, develop in the right side of the colon, and manifest a mucinous or poorly differentiated histopathology. Many of the CpG dinucleotides within the promoter region of the MMR gene *MLH1* are methylated in MSI-positive CRCs (9,10), and the *BRAF* gene frequently contains activating mutations in these cancers (11–13). Some genomic fragments have been found to be methylated specifically in such CRCs (7), and an entity of CRC with a CpG island methylator phenotype (CIMP) has been proposed (14). However, the profiles of genes and genomic fragments that become methylated in CRC specimens positive for *MLH1* methylation have remained uncharacterized.

With the use of methylated CpG island amplification coupled with representational difference analysis (MCA-RDA) (15), we have now performed a global screening of pooled genomic DNA from CRC specimens positive or negative for *MLH1* methylation in order to identify differentially methylated genomic fragments. With this approach, we identified hundreds of CpG islands whose methylation was specific to CRCs with a methylated *MLH1* promoter.

Materials and methods

Tumor specimens and cell lines

Tumor specimens were obtained from patients with sporadic CRC who underwent surgical treatment in Jichi Medical School Hospital. Informed consent was obtained from each patient, and the study was approved by the ethics committee of Jichi Medical School. Normal portion of colon tissue was excised from a region >5 cm distant from the cancerous region in every case. Genomic DNA was extracted with the use of a QIAmp DNA Mini kit (Qiagen, Valencia, CA). The MSI status of each tumor was determined on the basis of analysis of nine microsatellite repeat loci as previously described (8). The methylation status of the *MLH1* promoter was also examined in each sample (11).

Colon carcinoma cell lines (Caco-2, HCT116, SW480) were obtained from American Type Culture Collection (Manassas, VA). Caco2 cells were cultured in Dulbecco's modified Eagle's medium (DMEM)-F12 (Invitrogen, Carlsbad, CA) supplemented with 10% fetal bovine serum (FBS) (Invitrogen) and 2 mM L-glutamine. HCT116 and SW480 cells were maintained in McCoy's 5A medium (Invitrogen) and Leibovitz's L-15 medium (Invitrogen), both supplemented with 10% FBS, respectively.

MCA-RDA

Genomic DNA from four tumor specimens positive for *MLH1* methylation was mixed and used as a 'tester' sample, whereas that from four specimens negative for *MLH1* methylation was used as a 'driver.' MCA-RDA was performed with the two pooled DNA samples as previously described (15). In brief, both the tester and the driver DNA samples (5 μ g of each) were digested first with the *Sma*I endonuclease (New England Biolabs, Beverly, MA) and then with

XmaI (New England Biolabs), and the resulting fragments were ligated to the RMCA adapter (15). Amplification of methylated CpG islands was achieved by polymerase chain reaction (PCR) with the RMCA24 primer. The amplified fragments of the tester-DNA and driver-DNA were digested with XmaI and SmaI, respectively. The tester amplicons were then ligated to the JMCA adapter and subjected to annealing with an excess amount of the driver amplicons. PCR with the JMCA24 primer then amplified only the tester-specific amplicons. Another round of amplification was performed with the NMCA adapter and the NMCA24 primer (15). The final products were digested with XmaI and ligated into XmaI-digested pBlueScript (Stratagene, La Jolla, CA) for nucleotide sequencing.

Combined bisulfite restriction analysis (COBRA)

The methylation status of isolated clones was tested by the COBRA method (16). The genomic DNA was denatured, incubated for 16 h at 55°C in 3.1 M sodium bisulfite, and then subjected to PCR to amplify CpG islands. The PCR products were digested with a restriction endonuclease, and the resulting fragments were fractionated by polyacrylamide gel electrophoresis (PAGE). The gel was stained with SYBR Green I (Takara Bio, Shiga, Japan) and scanned with an LAS3000 imaging system (Fuji Film, Tokyo, Japan). Genomic fragments were determined to be positive for CpG methylation if $\geq 10\%$ of the PCR products were cleaved by the restriction endonuclease. The PCR primers and endonucleases used for COBRA are shown in the Supplementary Table online.

For bisulfite sequencing of the *BMP3* promoter, genomic DNA isolated from cancer specimens or cell lines was treated with sodium bisulfite (11) and then subjected to PCR with the primers 5'-AGTTAGAGAGYGAAGAAT-TAAG-3' and 5'-ATACAACRAAATAACRACCAACC-3'. The PCR product was ligated into pGEMT-easy (Promega, Madison, WI).

Real-time reverse transcription-polymerase chain reaction (RT-PCR)

Total RNA was prepared from tester or driver samples with an RNeasy Mini column (Qiagen), treated with RNase-free DNase (Qiagen), and subjected to reverse transcription with PowerScript reverse transcriptase (BD Biosciences Clontech, San Jose, CA) and an oligo(dT) primer. Portions of the resulting cDNAs were subjected to PCR with a QuantiTect SYBR Green PCR kit (Qiagen). The amplification protocol comprised incubations at 94°C for 15 s, 63°C (64°C for *KIT* cDNA) for 30 s, and 72°C for 60 s. Incorporation of the SYBR Green dye into PCR products was monitored in real time with an ABI PRISM 7900HT sequence detection system (PE Applied Biosystems, Foster City, CA), thereby allowing determination of the threshold cycle (C_T) at which exponential amplification of PCR products begins. The C_T values for DNA molecules corresponding to the β -actin gene (*ACTB*) and to genomic fragments of interest were used to calculate the abundance of the latter relative to that of the former. The oligonucleotide primers for PCR were 5'-CCATCAT-GAAGTGTGACGTGG-3' and 5'-GTCCGCCTAGAACATTGCG-3' for *ACTB*, 5'-AAGTCAACTCCTGGCCATCTGT-3' and 5'-TGGAAAAGGT-AACCTCTCTTTGG-3' for the bone morphogenetic protein 3 gene (*BMP3*), and 5'-TGACGTCTGGTCTATGGGATT-3' and 5'-TACATTCAGCA-GGTGCGTGTTC-3' for *KIT*.

Results

MCA-RDA screening

A total of 249 cases with CRC were examined for their MSI status as well as for methylation in the promoter region of *MLH1*. The majority ($n = 213$) of the tumor specimens from these patients were negative for MSI, while the rest ($n = 36$) were MSI-positive. Also, most of them ($n = 226$) were shown to have no methylation within the *MLH1* promoter (unmethylated group), whereas the remainder ($n = 23$) had a methylated promoter (methylated group) (11). Altogether 16 patients were positive for MSI, but did not have a methylated *MLH1* promoter. On the other hand, three patients were negative for MSI despite the presence of the methylated *MLH1* promoter. The characteristics of the patients examined in the present study are summarized in Table I.

To isolate genes that were specifically methylated in the methylated group, we selected specimens from four men of each group: ID nos 2, 17, 20 and 77 (mean age, 70.0 years) from the methylated group, and ID nos 1, 8, 13 and 31 (mean age, 73.0 years) from the unmethylated group. We have

Table I. Patient characteristics

ID no.	<i>MLH1</i> methylation	MSI status	Age (years)	Sex	Dukes grade
2 ^a	Yes	MSS	70	Male	A
17 ^a	Yes	MSI	65	Male	B
20 ^a	Yes	MSI	76	Male	B
77 ^a	Yes	MSI	69	Male	A
225	Yes	MSI	83	Female	C
263	Yes	MSI	86	Female	C
280	Yes	MSI	83	Female	C
305	Yes	MSI	74	Male	B
318	Yes	MSI	76	Female	B
336	Yes	MSI	68	Male	B
413	Yes	MSI	69	Female	A
416	Yes	MSI	76	Female	B
1 ^a	No	MSS	65	Male	A
8 ^a	No	MSS	89	Male	B
13 ^a	No	MSS	74	Male	B
31 ^a	No	MSS	64	Male	B
238	No	MSS	74	Male	A
249	No	MSS	62	Male	B
255	No	MSS	69	Female	C
278	No	MSS	73	Male	C
295	No	MSS	71	Female	C
298	No	MSS	70	Male	D
307	No	MSS	80	Female	C
308	No	MSS	62	Male	B
481	No	MSS	59	Male	C

^aSpecimens used for MCA-RDA screening. MSS, microsatellite stable.

excluded female subjects from the initial screening, since an intense methylation of one X chromosome in female cells may have yielded a large number of pseudopositive clones, methylation status of which may not have linked to the clinical classes, but to lyonization.

Equal amounts of genomic DNA isolated from the four selected tumor specimens of each group were mixed and subjected to MCA-RDA analysis, with the pooled DNA of the methylated group as the tester and that of the unmethylated group as the driver. A total of 384 clones were randomly picked up from the resultant MCA-RDA products, and digestion of the purified plasmid DNA with restriction endonucleases revealed that 294 out of the 384 clones carried the insert fragments. Nucleotide sequencing of such 294 clones indicated that 209 of the clones were found to contain CpG islands. Screening of human genome databases (<http://www.ncbi.nlm.nih.gov/BLAST/> and <http://genome.ucsc.edu/cgi-bin/hgBlat>) with these sequences revealed that 186 of them were localized within or in close proximity to characterized or uncharacterized human genes (112 independent genes).

Candidate genes for differential methylation

The GenBank accession numbers and annotation information for the 112 genes identified by MCA-RDA are shown in Table II. Multiple clones were isolated for a single gene in 33 instances, whereas only one MCA-RDA product was obtained for the remaining genes. The genes listed in Table II were thus candidates for genes whose CpG islands are methylated in a manner dependent on *MLH1* methylation.

We then examined the methylation status of the isolated fragments mapped to the promoter regions. First, we tried to amplify individually by PCR all 70 fragments mapped to the promoter regions in Table II, and could successfully amplify 35 fragments from the pooled DNAs used in MCA-RDA.

Table II. Genes identified by MCA-RDA with CRCs positive or negative for *MLH1* methylation

Gene	GenBank accession no.	No. of MCA-RDA clones	Position of MCA-RDA clones	COBRA data
<i>Homo sapiens</i> , solute carrier family 38, member 3	BC042875	11	Promoter	N.D.
<i>Homo sapiens</i> hypothetical protein MGC29643 ^a	AK075487	10	Promoter	compatible
Human progesterone receptor	M15716	6	Exon 1	N.D.
<i>Homo sapiens</i> alpha-1 type XV collagen	L25286	6	Promoter	N.D.
<i>Homo sapiens</i> K-CI co-transporter KCC4	AF105365	5	Promoter	N.D.
<i>Homo sapiens</i> CGI-150 protein	AF151908	5	3' region	N.D.
<i>Homo sapiens</i> cDNA FLJ37615	AK094934	4	3' region	N.D.
Human mRNA and promoter DNA for progesterone receptor	X51730	3	Promoter	N.D.
Human arachidonate 12-lipoxygenase mRNA	M62982	3	Promoter	not compatible
<i>Homo sapiens</i> clone IMAGE:5173621	BC031660	3	Promoter	N.D.
<i>Homo sapiens</i> Ras and Rab interactor 1	BC014417	3	3' region	N.D.
<i>Homo sapiens</i> papilin (PAPLN) ^a	BC042057	3	Promoter	compatible
<i>Homo sapiens</i> F-box and leucine-rich repeat protein 7 (FBXL7) ^a	AB020647	3	Promoter	compatible
<i>Homo sapiens</i> fibronectin type 3 and ankyrin repeat domains 1	BC024189	3	Promoter	not compatible
BX444427 <i>Homo sapiens</i> ADULT BRAIN <i>Homo sapiens</i> cDNA clone	BX444427	3	Promoter	N.D.
UI-H-BW0-aju-d-09-0-UI.s1 NCI_CGAP_Sub6 <i>Homo sapiens</i> cDNA clone	AW297872	2	N.D.	N.D.
Human dystrobrevin-delta	U26742	2	Near 5' end	N.D.
<i>Homo sapiens</i> , clone IMAGE:5728979	BC035731	2	Promoter	compatible
<i>Homo sapiens</i> ras interactor (RIN1)	L36463	2	Promoter	N.D.
<i>Homo sapiens</i> partial mRNA for doublesex-mab-3 (DM) domain	AJ301580	2	Promoter	not compatible
<i>Homo sapiens</i> mRNA; cDNA DKFZp586D0619	AL834130	2	Promoter	N.D.
<i>Homo sapiens</i> mRNA for NTAK ^a	AB005060	2	Promoter	compatible
<i>Homo sapiens</i> mRNA for FLJ00396 protein	AK090474	2	3' region	N.D.
<i>Homo sapiens</i> mRNA for dihydropyrimidinase related protein-3 (DPYSL3) ^a	D78014	2	Promoter	compatible
<i>Homo sapiens</i> hypothetical protein MGC35308	BC034775	2	Exon 1	N.D.
<i>Homo sapiens</i> hypothetical protein MGC33600	BC035022	2	N.D.	N.D.
<i>Homo sapiens</i> growth differentiation factor 7 (GDF7) ^a	AF522369	2	Promoter	compatible
<i>Homo sapiens</i> gene NXN encoding nucleoredoxin	NM_022463	2	N.D.	N.D.
<i>Homo sapiens</i> clone 24649	AF070591	2	3' region	N.D.
<i>Homo sapiens</i> cDNA: FLJ21511	AK025164	2	Promoter	not compatible
<i>Homo sapiens</i> solute carrier family 30, member 10 (SLC30A10) ^a	AK090806	2	Promoter	compatible
<i>Homo sapiens</i> beta-parvin	AF237769	2	Promoter	N.D.
603031612F1 NIH_MGC_115 <i>Homo sapiens</i> cDNA clone IMAGE:5172891	BI489865	2	Promoter	N.D.
<i>Mus musculus</i> adult male spinal cord cDNA, clone:A330088B02	AK079637	1	N.D.	N.D.
<i>Mus musculus</i> 9.5 days embryo parthenogenote cDNA, clone:B130054P17	AK045275	1	N.D.	N.D.
<i>Mus musculus</i> 12 days embryo spinal ganglion cDNA, clone:D130032D18	AK051302	1	N.D.	N.D.
IL5-EN0086-281100-292-f08 EN0086 <i>Homo sapiens</i> cDNA	BF851362	1	N.D.	N.D.
Human receptor tyrosine kinase ligand LERK-7 precursor	U26403	1	Promoter	not compatible
Human solute carrier family 30, member 3 (SLC30A3) ^a	U76010	1	Promoter	compatible
Human platelet-derived growth factor receptor alpha	M21574	1	3' region	N.D.
Human pephBGT-1 betaine-GABA transporter	U27699	1	3' region	N.D.
Human oxytocin mRNA	M25650	1	Promoter	N.D.
Human mRNA for KIAA0222 gene	D86975	1	3' region	N.D.
Human c-kit proto-oncogene (KIT) ^a	X06182	1	Promoter	compatible
Human cell 12-lipoxygenase	M35418	1	Promoter	N.D.
Human bone morphogenetic protein-3 (BMP3) ^a	M22491	1	Promoter	compatible
Human (clone hST3O-1) sialyltransferase	L29555	1	Promoter	N.D.
<i>Homo sapiens</i> , Similar to parathyroid hormone receptor 1	BC031578	1	3' region	N.D.
<i>Homo sapiens</i> , potassium channel, subfamily K, member 13 (KCNK13) ^a	BC012779	1	Promoter	compatible
<i>Homo sapiens</i> , clone MGC:50339	BC043386	1	N.D.	N.D.
<i>Homo sapiens</i> , clone IMAGE:6041910	BC040712	1	Promoter	N.D.
<i>Homo sapiens</i> , clone IMAGE:5590527	BC040874	1	Promoter	N.D.
<i>Homo sapiens</i> Wilms tumor 1	BC032861	1	Promoter	not compatible
<i>Homo sapiens</i> TRALPUSH ^a	AF399708	1	Promoter	compatible
<i>Homo sapiens</i> Sry-related HMG-box protein	AF270652	1	Exon 1	N.D.
<i>Homo sapiens</i> sialyltransferase 4A, transcript variant 2 (SIAT4A) ^a	BC018357	1	Promoter	compatible
<i>Homo sapiens</i> protein tyrosine phosphatase, receptor type, N polypeptide 2	BC034040	1	3' region	N.D.
<i>Homo sapiens</i> prostaglandin E2 receptor	L25124	1	Promoter	N.D.
<i>Homo sapiens</i> polyamine modulated factor-1	AF141310	1	3' region	N.D.
<i>Homo sapiens</i> nuclear receptor subfamily 5, group A, member 1	BC032501	1	3' region	N.D.
<i>Homo sapiens</i> NEL-like 2 (NEL2) ^a	BC020544	1	Promoter	compatible
<i>Homo sapiens</i> mRNA; cDNA DKFZp667I0324	AL832828	1	N.D.	N.D.
<i>Homo sapiens</i> mRNA; cDNA DKFZp564L0472	AL080101	1	3' region	N.D.
<i>Homo sapiens</i> mRNA; cDNA DKFZp564G1482	AL136698	1	Promoter	N.D.
<i>Homo sapiens</i> mRNA, chromosome 1 specific transcript KIAA0495	AB007964	1	Promoter	N.D.
<i>Homo sapiens</i> chromosome 13 open reading frame 21 (C13orf21) ^a	BC029067	1	Promoter	compatible
<i>Homo sapiens</i> mRNA for SOX7 protein ^a	AJ409320	1	Promoter	compatible
<i>Homo sapiens</i> mRNA for nephrosis 2, idiopathic, steroid-resistant (NPHS2) ^a	AJ279254	1	Promoter	compatible
<i>Homo sapiens</i> mRNA for MDC2 alpha, MDC2 beta	AB009671	1	Promoter	N.D.
<i>Homo sapiens</i> mRNA for KIAA0641 protein	AB014541	1	N.D.	N.D.

Table II. Continued

Gene	GenBank accession no.	No. of MCA-RDA clones	Position of MCA-RDA clones	COBRA data
<i>Homo sapiens</i> mRNA for transcription factor 7-like 1 (TCF7L1) ^a	AB031046	1	Promoter	compatible
<i>Homo sapiens</i> mRNA for calmagin (CLGN) ^a	D86322	1	Promoter	compatible
<i>Homo sapiens</i> mRNA for ADAMTS19 protein ^a	AJ311904	1	Promoter	compatible
<i>Homo sapiens</i> microtubule-associated protein 1B, transcript variant 1	NM_005909	1	Promoter	N.D.
<i>Homo sapiens</i> matrix metalloproteinase-21	AF520613	1	Exon 2	N.D.
<i>Homo sapiens</i> KIAA0534 protein	BC047716	1	Promoter	N.D.
<i>Homo sapiens</i> hypothetical protein MGC49007	BC041175	1	N.D.	N.D.
<i>Homo sapiens</i> hypothetical protein LOC284801	BC036201	1	Promoter	N.D.
<i>Homo sapiens</i> hypothetical protein LOC283887 ^a	BC023651	1	Promoter	compatible
<i>Homo sapiens</i> hypothetical protein BC009980	BC009980	1	Promoter	N.D.
<i>Homo sapiens</i> GATA binding protein 2	BC051342	1	Promoter	not compatible
<i>Homo sapiens</i> forkhead-related transcription factor FREAC-9	AF042832	1	Exon 1	N.D.
<i>Homo sapiens</i> erythroblast macrophage protein EMP	AF084928	1	Promoter	N.D.
<i>Homo sapiens</i> Enah/Vasp-like (EVL) ^a	BC023997	1	Promoter	compatible
<i>Homo sapiens</i> cytokine receptor-like factor 1	BC044634	1	Promoter	N.D.
<i>Homo sapiens</i> cystathionine beta-synthase (CBS) ^a	L14577	1	Promoter	compatible
<i>Homo sapiens</i> clone DNA68818 PSST739	AY358393	1	Promoter	N.D.
<i>Homo sapiens</i> ceh-10 homeodomain containing protein	AY336059	1	Exon 1	N.D.
<i>Homo sapiens</i> cDNA FLJ42875	AK124865	1	Promoter	N.D.
<i>Homo sapiens</i> cDNA FLJ41549 ^a	AK123543	1	Promoter	compatible
<i>Homo sapiens</i> cDNA FLJ38293	AK095612	1	Promoter	N.D.
<i>Homo sapiens</i> cDNA FLJ37464 ^a	AK094783	1	Promoter	compatible
<i>Homo sapiens</i> cDNA FLJ33739	AK091058	1	3' region	N.D.
<i>Homo sapiens</i> cDNA FLJ14238	AK024300	1	Promoter	N.D.
<i>Homo sapiens</i> cDNA clone IMAGE:6025756	BC064906	1	Promoter	N.D.
<i>Homo sapiens</i> bridging integrator protein-1	U68485	1	3' region	N.D.
<i>Homo sapiens</i> brain tumor associated protein LRRRC4 ^a	AF196976	1	Promoter	compatible
<i>Homo sapiens</i> apoptosis-associated tyrosine kinase, mRNA	BC047378	1	3' region	N.D.
ho64c01.x1 Soares_NFL_T_GBC_S1 <i>Homo sapiens</i> cDNA clone	AW873619	1	Promoter	N.D.
Helix pomatia sulfatase 1 precursor	AF109924	1	Promoter	N.D.
<i>H. sapiens</i> mitogen inducible gene mig-2 (MIG2) ^a	Z24725	1	Promoter	compatible
GENCOURT_8532095 NIH_MGC_113 <i>Homo sapiens</i> cDNA clone	BU899260	1	N.D.	N.D.
EST379664 MAGE resequences, MAGJ <i>Homo sapiens</i> cDNA	AW967589	1	N.D.	N.D.
BX394700 <i>Homo sapiens</i> NEUROBLASTOMA COT 25-NORMALIZED	BX394700	1	Promoter	N.D.
AL545903 <i>Homo sapiens</i> PLACENTA COT 25-NORMALIZED	AL545903	1	Promoter	N.D.
AGENCOURT_8219616 Lupski_sympathetic_trunk <i>Homo sapiens</i> cDNA clone	BQ722471	1	N.D.	N.D.
AGENCOURT_7546470 NIH_MGC_70 <i>Homo sapiens</i> cDNA clone	BQ218409	1	Promoter	N.D.
7k34e06.x1 NCI_CGAP_Ov18 <i>Homo sapiens</i> cDNA clone IMAGE:3477227	BF058764	1	N.D.	N.D.
602695383F1 NIH_MGC_97 <i>Homo sapiens</i> cDNA clone IMAGE:4827284	BG722892	1	N.D.	N.D.
<i>Homo sapiens</i> mRNA for KIAA0711 protein	AB018254	1	3' region	N.D.
<i>Homo sapiens</i> E2F binding protein	AY152547	1	Exon 1	N.D.
<i>Homo sapiens</i> cDNA FLJ38336	AK095655	1	3' region	N.D.

N.D., not determined. COBRA data indicated that methylation level of the MCA-RDA clones in CRCs positive for *MLH1* methylation was increased (compatible) or not (not compatible) compared with that in CRCs negative for *MLH1* methylation.

^aClones analyzed in a test set of samples.

By using COBRA, their CpG methylation status was assessed among the samples used in MCR-RDA. As indicated in Table II, 28 fragments out of 35 were preferentially methylated in the tester DNA, while 7 of them were not.

The methylation status of such 28 fragments was further tested in clinical specimens that had not been used for the initial screening. This test set included eight cancer specimens positive for *MLH1* methylation and the paired normal colon tissue as well as eight cancer specimens negative for *MLH1* methylation (Table I).

The methylation status of each genomic fragment in the clinical specimens is shown color-coded in Figure 1; fragments with a methylation level of $\geq 10\%$ as determined by COBRA are indicated in red, whereas those with a methylation level of $< 10\%$ are shown in blue. Most genomic fragments were extensively methylated in most or all of the cancer specimens positive for *MLH1* methylation, but not in those negative for *MLH1* methylation. The difference in CpG

methylation for the MCA-RDA products between the methylated and unmethylated groups of patients was thus confirmed in a distinct test set of CRC specimens.

A more detailed inspection of the data in Figure 1, however, indicates that the MCA-RDA products can be separated into three subgroups on the basis of their methylation profiles. The genomic fragments in the first group (*MIG2* to *NPHS2* in Figure 1) were also methylated in $\geq 25\%$ of the paired normal colon tissue samples. The fragment corresponding to *MIG2*, for instance, was methylated in all of the *MLH1* methylation-positive cancer specimens and the respective normal tissue. Methylation of these genomic regions thus probably occurred in each patient before the development of CRC and might be related to the aging process.

The genomic fragments in the second group (*BMP3* to *DPYSL3*) were not methylated in normal colon tissue but were methylated in $\geq 25\%$ of cancer specimens that were negative for *MLH1* methylation. The methylation of these

Gene symbol	CRC specimens positive for <i>MLH1</i> methylation								Normal tissue specimens								CRC specimens negative for <i>MLH1</i> methylation							
	225	263	280	305	318	336	413	416	225	263	280	305	318	336	413	416	238	249	255	278	295	298	307	308
<i>MLH1</i>																								
<i>MIG2</i>																								
<i>SOX7</i>																								
<i>C13orf21</i>																								
<i>FLJ41549</i>																								
<i>PAPLN</i>																								
<i>ADAMTS19</i>																								
<i>FLJ37464</i>																								
<i>LRRC4</i>																								
<i>NPHS2</i>																								
<i>BMP3</i>																								
<i>TRALPUSH</i>																								
<i>SLC30A10</i>																								
<i>EVL</i>																								
<i>DPYSL3</i>																								
<i>MGC29643</i>																								
<i>KCNK13</i>																								
<i>NELL2</i>																								
<i>SLC30A3</i>																								
<i>GDF7</i>																								
<i>NTAK</i>																								
<i>CLGN</i>																								
<i>CBS</i>																								
<i>KIT</i>																								
<i>FBXL7</i>																								
<i>SIAT4A</i>																								
<i>TCF7L1</i>																								
<i>LOC283887</i>																								
<i>IMAGE5728979</i>																								

Fig. 1. Gene methylation profiles of CRC specimens. Twenty-eight clones were randomly chosen from the MCA-RDA products of the selected study specimens, and their methylation status (plus that of *MLH1*) was determined by COBRA in CRC specimens positive for the methylation of the *MLH1* promoter ($n = 8$), their paired normal colon tissue samples, and CRC specimens negative for *MLH1* methylation ($n = 8$). Each column represents a clinical specimen (ID numbers are shown), and each row indicates a gene corresponding to an MCA-RDA product. Red box, methylated gene; blue box, unmethylated gene; white box, not examined.

fragments thus appeared to be specific to the cancerous state with a slightly increased prevalence among *MLH1* methylation-positive CRC.

The fragments in the third group (*MGC29643* to *IMAGE5728979*) were methylated in <25% both of normal specimens and of cancer specimens negative for *MLH1* methylation. The methylation of these genes thus appears to be regulated in concert with that of *MLH1*.

Analysis of *BMP3*

Among the genomic clones analyzed, we first focused on that corresponding to *BMP3*. *BMP3* is a member of the transforming growth factor- β (TGF- β) superfamily of proteins that also includes TGF- β 1, TGF- β 2, TGF- β 3, Mullerian inhibitory substance, *BMP2A*, *BMP2B*, *BMP6*, growth-differentiation factor (*GDF*) 5, *GDF6* and *GDF7* (17,18). Members of this protein superfamily exert inhibitory effects on various human cancers through activation of their cognate receptors and SMAD proteins (19,20). *BMP2*, for instance, induces both the activation of the p38 isoform of mitogen-activated protein kinase and apoptosis in medulloblastoma cells (21). Although little is known of the physiological functions of *BMP3*, it is possible that this protein also possesses antitumor activity and that its expression is epigenetically regulated in cancer cells. Interestingly, Dai *et al.* (22) have recently reported that *BMP3*

promoter is methylated frequently (~50%) in non-small-cell lung carcinoma, which many imply that dysfunction of *BMP3* may be commonly involved in the carcinogenesis of a wide range of human tumors.

The COBRA assay revealed that the MCA-RDA clone corresponding to the promoter region of *BMP3* was methylated in CRC specimens that were positive or negative for *MLH1* methylation (Figures 1 and 2A). Further, as shown in Figure 2B, detailed analysis of the methylation status of the *BMP3* promoter by sequencing of DNA fragments after sodium bisulfite treatment revealed extensive hemi- or biallelic methylation of the promoter in CRC specimens positive for *MLH1* methylation (ID nos 225, 318 and 481) but not in one negative for *MLH1* methylation (ID no. 249). CpG methylation throughout the promoter fragment was also evident in CRC cell lines positive (HCT116) or negative (Caco2) for *MLH1* methylation, but not in the *MLH1* methylation-negative line SW480. Together with the COBRA data in Figure 1, these results suggest that the promoter region of *BMP3* is methylated in all clinical specimens and cell lines positive for methylation of the *MLH1* promoter as well as in some specimens and cell lines negative for *MLH1* methylation.

We then examined whether the epigenetic changes in the *BMP3* promoter affected its transcriptional activity. Quantitative real-time RT-PCR analysis revealed that *BMP3*

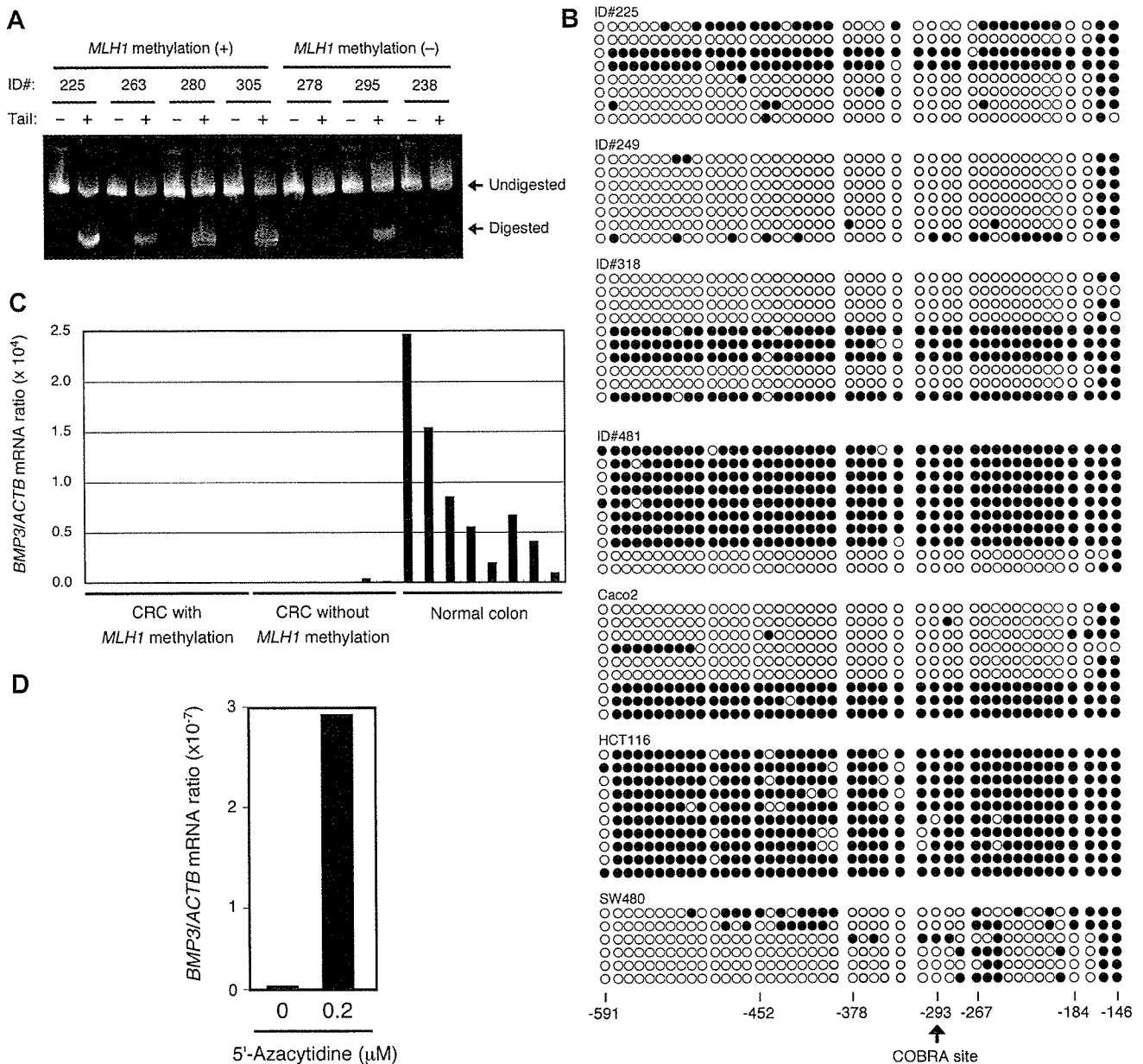


Fig. 2. Methylation status of the *BMP3* promoter and *BMP3* expression in CRC specimens. (A) The methylation status of the promoter region of *BMP3* in the indicated clinical specimens was examined by COBRA. Sensitivity of PCR products to digestion with *TaiI* is indicative of methylation of the CpG island examined. (B) Genomic DNA of the indicated clinical specimens and CRC cell lines (Caco2, HCT116 and SW480) was treated with sodium bisulfite, after which the *BMP3* promoter region was amplified by PCR and sequenced. Closed and open circles indicate methylated and unmethylated CpG islands, respectively. The nucleotide positions of the CpG islands (numbered relative to the transcriptional start site) are indicated at the bottom, and the *TaiI* digestion site for COBRA in (A) is shown by the arrow. (C) The level of expression of *BMP3* relative to that of *ACTB* in clinical specimens was determined by quantitative RT-PCR. (D) HCT116 cells were incubated for 72 h with or without 0.2 μM of 5'-azacytidine, and were then subjected to RT-PCR analysis for determination of the amount of *BMP3* mRNA relative to that of *ACTB* mRNA.

was transcriptionally silent in CRC specimens positive for *MLH1* methylation (Figure 2C), in which the *BMP3* promoter was also extensively methylated. In contrast, *BMP3* mRNA was abundant in the paired normal colon tissue samples. Although *BMP3* expression was detected in some CRC specimens negative for *MLH1* methylation, the level of expression was greatly reduced compared with that in normal colon tissue. These data thus indicate that *BMP3* transcription is suppressed in most CRCs.

In order to directly examine the relationship between promoter methylation and gene silencing of *BMP3*, HCT116 cells were incubated for 3 days with 5'-azacytidine, an inhibitor of *de novo* methylation of genomic DNA. Interestingly, treatment with 5'-azacytidine markedly induced the amount of *BMP3* mRNA in the cells (Figure 2D) and demethylation of its promoter region as well (data not shown). Therefore, extensive methylation of the *BMP3* promoter region should be directly linked to the suppression of its transcription.

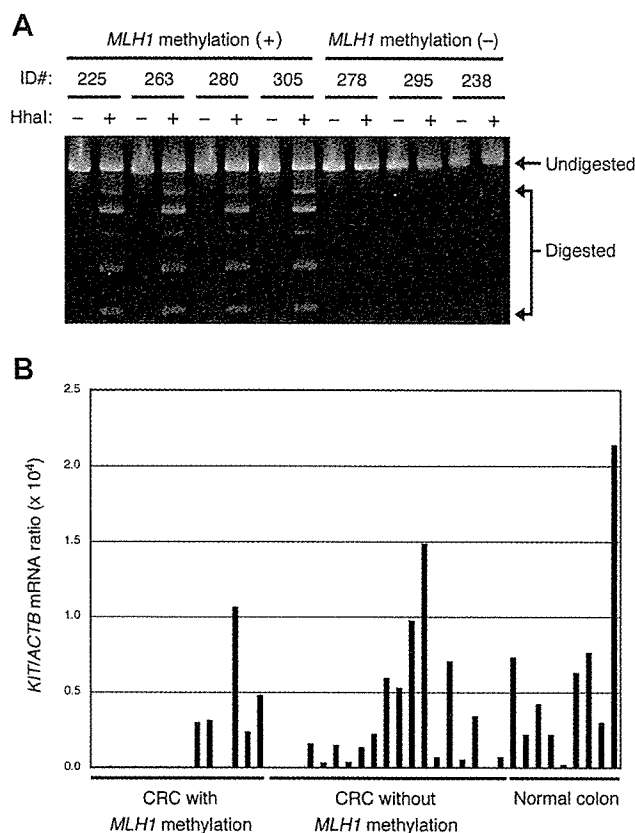


Fig. 3. Methylation status of the *KIT* promoter and *KIT* expression in CRC specimens. (A) The methylation status of the promoter region of *KIT* in the indicated clinical specimens was examined by COBRA. Sensitivity of PCR products to digestion with HhaI is indicative of methylation of the CpG island examined. (B) The level of expression of *KIT* relative to that of *ACTB* in clinical specimens was determined by quantitative RT-PCR.

Analysis of *KIT*

KIT encodes a receptor tyrosine kinase for stem cell factor. Point mutations in *KIT* that increase the kinase activity of the encoded protein have been identified in human gastrointestinal stromal tumors (23), suggestive of a causative role for *KIT* in these tumors. The expression and activation status of *KIT* in CRCs have been unclear, however (24,25). We therefore analyzed the methylation status of the *KIT* promoter region in our samples.

Methylation of the *KIT* promoter was highly restricted to CRC specimens positive for *MLH1* methylation (Figures 1 and 3A). However, the abundance of *KIT* mRNA did not necessarily match the methylation status of the *KIT* promoter. Despite extensive methylation of the promoter in one CRC sample (ID no.77), for instance, the amount of *KIT* mRNA was relatively high ($KIT/ACTB$ mRNA ratio = 4.78×10^{-5}), indicating that promoter methylation might not be a major determinant of transcriptional activity. It is possible, however, that our COBRA analysis revealed the methylation status of a CpG site that is not important for *KIT* transcription.

The mean expression level of *KIT* in the *MLH1* methylation-positive CRC specimens [$KIT/ACTB$ mRNA ratio, $1.72 \times 10^{-5} \pm 3.02 \times 10^{-5}$ (mean \pm SD)] was significantly lower than that in normal colon tissue ($6.03 \times 10^{-5} \pm 6.29 \times 10^{-5}$; $P = 0.038$, Student's *t*-test). The level of *KIT* expression

in CRCs negative for *MLH1* methylation ($2.92 \times 10^{-5} \pm 1.61 \times 10^{-5}$) was also lower than that in normal colon tissue, but this difference was not significant ($P = 0.123$). It is therefore likely that *KIT* is not overexpressed in CRCs.

Discussion

We have screened for genomic fragments whose CpG islands are selectively methylated in CRC specimens positive for methylation of the *MLH1* promoter region. We could readily identify hundreds of genomic fragments with CpG islands that were expected to be differentially methylated between CRCs with or without *MLH1* methylation. Twenty-eight such clones (Table II) were indeed proved to be preferentially methylated in the four CRC specimens positive for *MLH1* methylation compared with the four samples negative for *MLH1* methylation, both of which were used in the original MCA-RDA screening (data not shown).

To verify the selective methylation of these clones, we performed COBRA with a different set of specimens including eight CRCs with *MLH1* methylation and their paired normal tissue samples as well as eight CRCs without *MLH1* methylation. Although all the 28 clones examined were preferentially methylated in the CRC specimens positive for *MLH1* methylation, their methylation profiles among the specimens were not identical, indicating that all CpG methylation observed in MSI-positive CRCs was not specific to this subtype of tumor.

The methylation of certain genomic fragments (14 out of 28 clones examined), however, was highly specific to CRCs that manifested *MLH1* methylation. Almost 50% of the genes were thus methylated in a parallel manner to the CpG methylation of the *MLH1* gene, indicating that a subset of genes is specifically methylated in a subset of CRCs. Our data thus support the existence of CIMP-positive CRCs (14), while it would be mandatory for the better characterization of CIMP-positive tumors to further collect co-methylated genes and to define precisely the hallmark genes for the identification of CIMP (26). It would be interesting to examine whether such clearly defined CIMP is associated with certain clinical manifestations.

Genes corresponding to the co-methylated genomic fragments in our assay included those whose function relates to cell proliferation or differentiation. The predicted structure of *NELL2*, for example, contains epidermal growth factor (EGF)-like repeats (27), which are present in diverse proteins involved in regulation of the cell cycle, cell proliferation, and developmental processes. *NTAK* is a member of the EGF family of proteins and is a ligand and activator of ErbB protein tyrosine kinases (28). In addition, *GDF7* is a member of the TGF- β superfamily (18), and *TCF7L1* is highly homologous to *TCF1* which is a target gene of the Wnt- β -catenin signaling pathway (29), and which plays an important role in CRC carcinogenesis. Aberrant epigenetic regulation of these genes may thus contribute to the pathogenesis or clinical features of CRCs positive for *MLH1* methylation.

The MCA-RDA method thus proved to be highly effective for the identification of differentially methylated genes among fresh clinical specimens. Given the high fidelity of this approach, it is likely that a large number of genes (or genomic fragments) are methylated in CRCs in concert with methylation of the *MLH1* promoter. Our study provides a basis for further characterization of the molecular pathogenesis of CRCs classified as MSI. Together with the results of other

studies (7,30), it also suggests the possibility of development of a stratification scheme for CRCs based on genome methylation profile.

Supplementary material

Supplementary material can be found at: <http://www.carcin.oxfordjournals.org/>

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Retroviral expression screening of oncogenes in pancreatic ductal carcinoma

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Abstract

Pancreatic ductal carcinoma (PDC) remains one of the most intractable malignancies in humans. In order to clarify the molecular events underlying the carcinogenesis in PDC, we constructed a retroviral cDNA expression library from a PDC cell line, and used it to screen transforming genes in PDC by a focus formation assay with mouse 3T3 fibroblasts. We could obtain a total of 30 transformed cell foci in the screening, and one of the cDNA inserts harvested from such cell clones turned out to encode a wild-type human ARAF1. Unexpectedly, a long terminal repeat-driven overexpression of *ARAF1* mRNA was confirmed to induce transformed foci in fibroblasts. The oncogenic potential of ARAF1 was examined by injecting the transformed fibroblasts into athymic nude mice. Importantly, *ARAF1* mRNA was highly expressed in pancreatic ductal cell specimens purified from patients with PDC. These results have unveiled the transforming potential of ARAF1 protein, and also suggest that quantity of intracellular ARAF1 may be important in carcinogenesis of various human cancers.

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Keywords: Pancreatic ductal cell carcinoma; Retrovirus; ARAF1; cDNA library; Oncogene

1. Introduction

Pancreatic ductal carcinoma (PDC) originates from pancreatic ductal cells, and is one of the most intractable malignancies in humans [1,2]. Effective therapy for PDC is hampered by the lack of specific clinical symptoms. At the time of diagnosis, most patients are no longer candidates for surgical resection, and, even in individuals who do undergo such surgery, the 5-year survival rate is only 20–30% [1].

Vast efforts have been made to elucidate molecular events responsible for the carcinogenesis of PDC. Mutations of *TP53* gene can be, for instance, found in PDC specimens [3], and in the intraductal *in situ* regions as well [4]. Similarly, inactivation has been found for other tumour-suppressor genes, such as *DPC*, *RB1* and *p16* [5].

As for oncogenes, activating mutations in the *KRAS2* gene has been reported to be frequently associated with PDC [6]. The same *KRAS2* mutations could be, however, found in the samples for chronic pancreatitis [7], making their pathogenetic role uncertain. Additionally, an increased telomerase activity was shown to be present only in PDC, but not in nonmalignant pancreatic disorders [8]. Again, however, others could detect an elevated telomerase activity in chronic pancreatitis and normal

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pancreas [9]. Therefore, it is yet to be revealed which transforming genes truly promote a clonal growth of pancreatic ductal cells.

For an efficient isolation of tumour-promoting genes in PDC, it would be desirable to conduct functional screening based on transforming ability. Focus formation assays with mouse 3T3 fibroblasts have been highly successful for the identification of oncogenes in human cancer [10]. In such screening, genomic DNA is isolated from cancer specimens, and used to transfect 3T3 cells to obtain transformed cell foci. It should be noted, however, that, since expression of any genes in these experiments are driven by their own promoters/enhancers, oncogenes in PDC can exert their effects in 3T3 cells only when the promoter/enhancer regions of such genes are active in fibroblasts, which is not always guaranteed.

To ensure the sufficient expression of cDNAs in 3T3 cells, their transcription should be regulated by an exogenous promoter fragment. We have therefore constructed a retroviral cDNA expression library from a PDC cell line, MiaPaCa-2, which was used to infect 3T3 cells. In the preparation of cDNA library, we further took advantage of the SMART polymerase chain reaction (PCR) system (Clontech, Palo Alto, CA), which preferentially amplifies full-length cDNAs. A focus formation assay with the library resulted in an identification of a transforming *ARAF1* gene.

2. Materials and methods

2.1. Cells and culture

MiaPaCa-2, Capan-2, PANC-1, 3T3, and BOSC23 [11] cell lines were obtained from American Type Culture Collection, and maintained in Dulbecco's modified Eagle medium/F12 (DMEM/F12; Invitrogen, Carlsbad, CA) containing 10% fetal bovine serum (Invitrogen) and 2 mM L-glutamine.

The fresh clinical specimens were obtained from patients who gave informed consent, and the study was approved by the institutional review board of Jichi Medical School. Cells were collected from the pancreatic juice by centrifugation, labeled with anti-MUC1 antibody [12] (Novocastra Laboratories, Newcastle upon Tyne, UK), and subjected to chromatography on a miniMACS magnetic cell separation column (Miltenyi Biotec, Auburn, CA) [13]. The purity of the resultant MUC1⁺ cell fraction was confirmed by staining with Wright Giemsa solutions and microscopy examination for each case (data not shown).

2.2. Retrovirus library construction

Total RNA was extracted from MiaPaCa-2 cells by an RNeasy Mini column with RNase-free DNase (Qiagen,

Valencia, CA), and the first strand cDNA was synthesized by PowerScript reverse transcriptase (Clontech) with SMART IIA oligonucleotide and CDS primer IIA (both from Clontech). The cDNAs were then amplified for 12 cycles with 5' PCR primer IIA according to the instruction of the SMART PCR cDNA synthesis kit (Clontech) except a substitution of LA Taq polymerase (Takara Bio, Shiga, Japan) for Advantage 2 DNA polymerase provided with the kit. Resultant cDNAs were treated with proteinase K, blunt-ended by T4 DNA polymerase, and ligated to the BstXI-adaptor (Invitrogen). Unbound adaptors were removed through the cDNA size fractionation column (Invitrogen), and the cDNAs were finally ligated to the pMXS retroviral plasmid (a kind gift of Dr. T. Kitamura at Institute of Medical Science, University of Tokyo) [14] digested with BstXI. The pMXS-cDNA plasmids were introduced into ElectroMax DH10B cells (Invitrogen) with electroporation.

2.3. Focus formation assay

Generation of recombinant retroviral library and focus formation assay was conducted as described previously [15]. Briefly, BOSC23 cells were transfected with Lipfectamin reagent (Invitrogen) and 2 µg of retroviral plasmid together with 0.5 µg of pGP plasmid 0.5 µg of pE-eco plasmid (both from Takara Bio). Two days after the transfection, polybrene (Sigma, St. Louis, MI) was added to the culture supernatant at a concentration of 4 µg/ml, and the supernatant was subsequently used to infect 3T3 cells for 48 h. For the focus formation assay, the culture medium of 3T3 cells was then changed to DMEM-high glucose (Invitrogen) supplemented with 5% calf serum and 2 mM L-glutamine. Transformed foci were picked up after 3 weeks of culture. Genomic DNA was extracted from each transformed focus, and was subjected to PCR with 5' PCR primer IIA (Clontech) and LA Taq polymerase for 50 cycles of 98 °C for 20 s and 68 °C for 6 min. Amplified genome fragments were purified for nucleotide sequencing. For tumorigenicity assay in nude mice, transformed 3T3 cells were injected into each shoulder of nu/nu Balb-c mice (6 weeks old). Tumour formation was assessed after 4 weeks.

2.4. "Real-time" RT-PCR

Portions of oligo(dT)-primed cDNA were subjected to PCR with a QuantiTect SYBR Green PCR Kit (Qiagen). The amplification protocol was comprised of incubations at 94 °C for 15 s, 57 °C for 30 s, and 72 °C for 60 s. Incorporation of the SYBR Green dye into PCR products was monitored in real time with an ABI PRISM 7900HT sequence detection system (PE Applied Biosystems, Foster City, CA), thereby allowing determination of the threshold cycle (C_T) at which exponential amplification of products

begins. The C_T values for cDNAs corresponding to the β -actin gene (*ACTB*) and to the *ARAF1* gene were used to calculate the abundance of the latter mRNA relative to that of the former. The oligonucleotide primers for PCR were as follows: 5'-CCATCATGAAGTGTGACGTGG-3' and 5'-GTCCGCCTAGAAGCATTTGCG-3' for *ACTB*, and 5'-ACTACCTCCATGCCAAGAACATCA-3' and 5'-GACGTCTGACTGGAAGCTGTAGGG-3' for *ARAF1*.

3. Results

3.1. Screening with focus formation assay

From mRNA of MiaPaCa-2 cells, full-length cDNAs were selectively amplified and ligated to a retroviral vector pMXS. We could obtain a total of 2.1×10^6 colony forming units (cfu) of independent plasmid clones. Thirty clones were randomly selected from the library, and examined for the incorporated cDNAs. Twenty-seven (90%) out of the 30 clones contained inserts with an average length of 2.05 kbp.

By introducing the plasmid DNA into a packaging cell line, we generated a recombinant ecotropic retrovirus library that was subsequently used to infect mouse 3T3 fibroblasts. Infection experiments were repeated for a total of 6 times. After 3 weeks of culture, 30 transformed foci were observed (Fig. 1(b)). No foci could be found among the cells infected with an empty virus (Fig. 1(a)), while numerous foci were easily identified

in the cells infected with a virus expressing v-Ras oncoprotein (Fig. 1(c)).

Each focus was isolated, expanded independently, and was subject to the extraction of genomic DNA. We then tried to recover retroviral inserts from the genomic DNA by PCR amplification with the primer used originally to amplify the cDNAs in the construction of the library. In most cases, two to three DNA fragments were recovered from each genome (Fig. 2(a)), implying a multiple retroviral infection on the recipient 3T3 cells.

We obtained a total of 56 cDNA fragments by PCR, all of which were subjected to nucleotide sequencing from both ends. Screening of the cDNA sequences against human genome sequence database assembled as of July 2003 by the Genome Bioinformatics Group of the University of California at Santa Cruz (<http://genome.ucsc.edu>) revealed that the 56 fragments correspond to 13 independent genes, eleven of which could be matched at >95% identity to the human genome sequence (Table 1). Among the 11 genes, 7 of them were known genes while the rest 4 were unknown. Each cDNA clone was ligated to pMXS in both directions, and a recombinant retrovirus was generated from each resultant plasmid. Transforming ability of the cDNAs was thus confirmed by a focus formation assay with the recombinant virus.

Focus formation assays were conducted for the 26 independent viruses (all 13 independent genes for both directions), and one of them, expressing ARAF1 protein (GenBank accession number, NM_001654), gave transformed foci in repeated experiments. ARAF1 belongs to

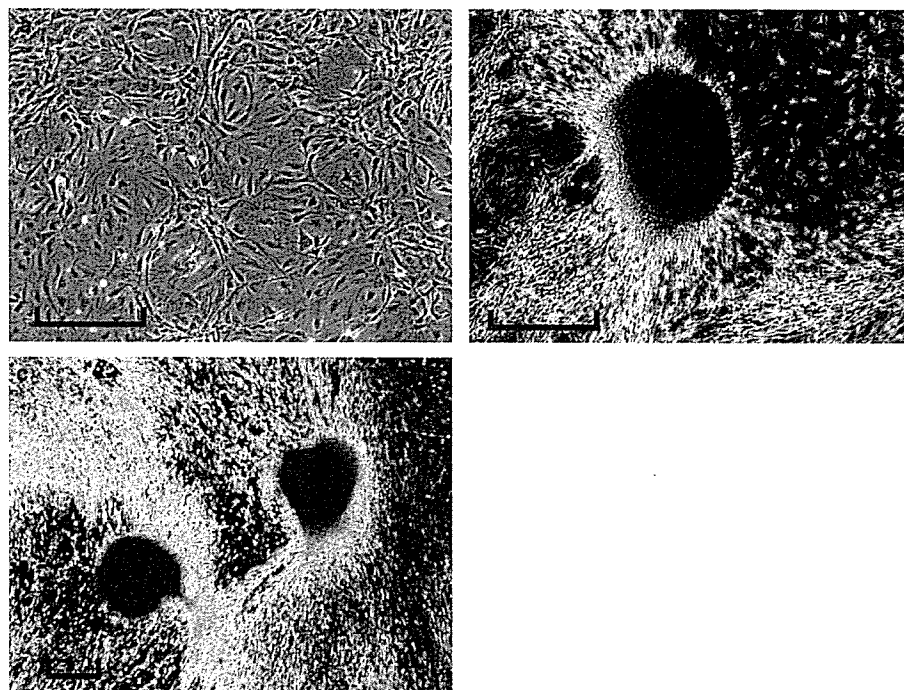


Fig. 1. Focus formation assay with retroviral library. Mouse 3T3 cells were infected with (a) an empty virus, (b) retroviruses from the MiaPaCa-2 library, or (c) a retrovirus expressing v-Ras as a positive control. Pictures were taken after 3 weeks of culture. Scale bar, 100 μ m.

Table 1
cDNAs isolated from 3T3 transformants

Clone #	Gene symbol	GenBank number	Covering full ORF
1	Unknown	AK026325	ND
2	No homologues sequences	ND	ND
3	Unknown	AF318370	Yes
4	PITPNM1	NM_004910	No
5	Unknown	BC022099	Yes
6	DECR2	NM_020664	Yes
7	ARAF1	NM_001654	Yes
8	BCLG	NM_138724	No
9	No homologues sequences	ND	ND
10	Unknown	AL607122	ND
11	JAG1	NM_000214	Yes
12	MRPL43	NM_176792	Yes
13	PLOD3	NM_001084	No

ORF, open reading frame; ND, not determined.

the RAF family of serine/threonine kinases, and phosphorylates MEK1 [16]. It had not been known whether an overexpression of wild ARAF1 protein has a transforming activity.

3.2. ARAF1 as an oncogene

We thus determined the whole nucleotide sequence of our ARAF1 cDNA (cDNA clone ID #7). The sequence is 2441 bp, and contains an open reading frame (spanning nucleotide position 126–1943) encoding a protein of 606 amino acids, which is identical to ARAF1 (Fig. 2(b)). Within the protein-coding region, there is only one nucleotide mutation compared to the published ARAF1 cDNA sequence; a “T” at nucleotide position 1550 in the reported sequence (NM_001654) is replaced with a “C” in our sequence. The codon sequence “TTG” at the amino acid position 450 of ARAF1 is thus changed to “CTG” in our cDNA. However, both codons encode the same leucine residue, and thus the mutation does not affect the protein sequence.

To confirm that mere overexpression of wild ARAF1 protein has a transforming activity, we repeated the focus formation assay with the retrovirus generated from our ARAF1 cDNA. As shown in Fig. 2(c), the recombinant virus reproducibly induced transformed foci (30–50 foci per microgram of the input plasmid) in the recipient 3T3 cells. The transforming ability of ARAF1 was also tested by the tumorigenicity assay with athymic nude mice. The 3T3 cells infected with the empty virus or retrovirus expressing ARAF1 or v-Ras were inoculated subcutaneously into nude mice. As shown in Fig. 2(d), tumour formation was observed in all mice for the latter 2 cases, arguing that ARAF1 has oncogenic potential.

3.3. Expression of ARAF1 in PDC

We finally measured the expression level of ARAF1 mRNA in PDC by the quantitative real-time reverse

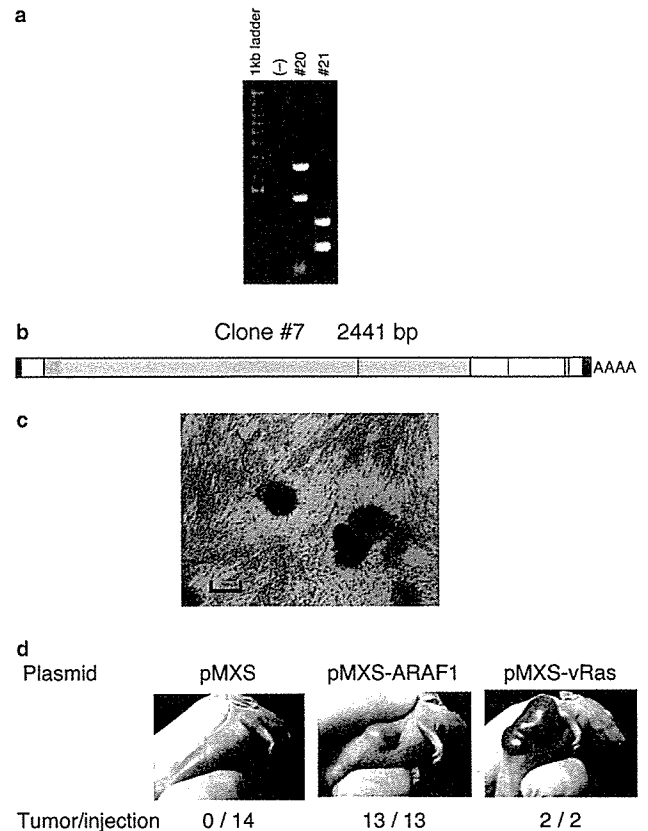


Fig. 2. Identification of the transforming ARAF1 gene. (a) Genomic DNAs isolated from the transformed foci (cell clone ID #20 and #21) were subjected to PCR. A PCR without DNA template was also conducted as a negative control (-). DNA size markers (1 kb DNA ladder; Invitrogen) are electrophoresed at the left. (b) A 3T3 clone yielded a PCR product of 2441 bp long (cDNA clone ID #7). The cDNA has a protein-coding region (gray) for 606 amino acids that was identical to human ARAF1 protein. Nucleotides that did not match the published ARAF1 cDNA are indicated by red lines. (c) Our ARAF1 cDNA was ligated to pMXS, and used to generate recombinant virus. Infection with the virus induced multiple transformed foci in 3T3 cells. Scale bar, 100 μ m. (d) 3T3 cells (5×10^5) were cultured for two days with retrovirus made from pMXS, pMXS-ARAF1 or pMXS-vRas plasmid, and were injected subcutaneously into nu/nu mice. Tumour formation was examined after 4 weeks.

transcription (RT)-PCR method. As shown in Fig. 3, all 3 PDC cell lines express similar amounts of ARAF1 mRNA. In addition, we quantified ARAF1 mRNA in human clinical specimens. Pancreatic juice from patients with PDC contains cancer cells (transformed ductal cells) in addition to normal ductal cells and blood cells. The former two fractions were purified, by an affinity column for MUC1 surface protein [12], from pancreatic juice of PDC patients ($n = 14$). Such purified fractions should be highly enriched for PDC cells [13]. Similar MUC1-positive fractions were also purified from the pancreatic juice of healthy individuals ($n = 7$). Quantification of ARAF1 mRNA revealed that its mRNA level was highly elevated in six out of the 14 patient, but not in the specimens from healthy individuals. These data

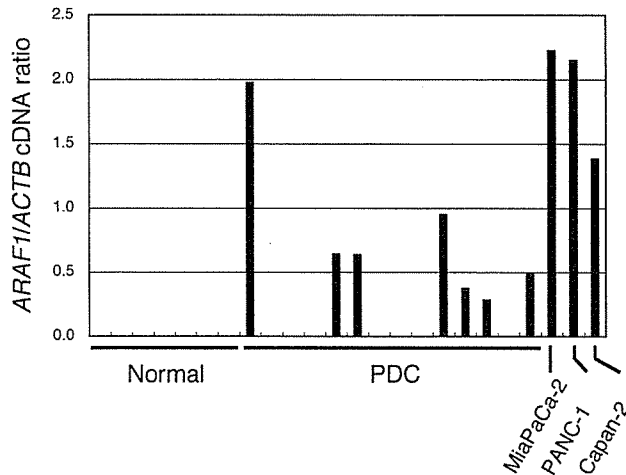


Fig. 3. Quantification of *ARAF1* mRNA. Complementary DNA was prepared from PDC cell lines (MiaPaCa-2, PANC-1 and Capan-2) or MUC1⁺ ductal cell preparations purified from healthy individuals (Normal) or patients with PDC, and were then subjected to real-time RT-PCR analysis with primers specific for the *ARAF1* or *ACTB* genes. The ratio of the abundance of *ARAF1* mRNA to that of *ACTB* mRNA was calculated as 2^n , where n is the C_T value for *ACTB* cDNA minus the C_T value for *ARAF1* cDNA.

indicate that the transcription of *ARAF1* is selectively activated in PDC cells.

4. Discussion

In this manuscript, we have constructed a retroviral cDNA expression library of PDC. Since 90% (27/30) of the viral plasmids carried cDNA inserts and since the overall clone number was >2 millions, our library should cover nearly all transcriptome in MiaPaCa-2 cells.

RAF family is composed of RAF1, ARAF1 and BRAF in humans. All these serine/threonine kinases are believed to act downstream of RAS-family proteins, and to phosphorylate and regulate downstream MAP kinase kinases (MAPKKs). Many studies have revealed transforming potentials of RAF family proteins. RAF was originally identified as a cellular homologue of viral oncoprotein, v-Raf [17]. Deletion of amino-terminal regions unmasks the transforming ability of RAF1 [18] and ARAF1 [19]. On the other hand, somatic point mutations have been found in the *BRAF* gene among clinical specimens of colorectal carcinoma [20]. Such mutations were shown to induce transforming activity in BRAF protein. In contrast to *BRAF*, somatic point mutations are rarely found in *ARAF1* gene [21].

Overexpression of wild forms of RAF1 or BRAF failed to exert a transforming activity [18,20]. Although deletion/truncation of amino terminal regions of ARAF1 induced transformed foci in 3T3 fibroblasts [22] and abrogated cytokine-dependency in hematopoietic cells [19], it has not been tested whether wild ARAF1 protein has transforming potential. In this

manuscript, however, it was unexpectedly revealed that a long terminal repeat-driven expression of ARAF1 induces transformed foci in 3T3 cells, which subsequently generated tumours in immunocompromised mice. Therefore, it has been unveiled here that an overexpression of wild ARAF1 is directly linked with cellular transformation process.

These data also indicate the importance of measuring protein/mRNA amounts of ARAF1 in various human cancers. In this context, it was interesting to find a high expression of *ARAF1* mRNA in fresh clinical specimens of PDC. Our findings shed new light on the understanding of RAF family kinases, and open up the possibility that ARAF is involved in carcinogenesis in human cancers through a previously unexpected mechanism.

Conflict of interest statement

None declared.

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Research Article

Regulation of *Amh* during sex determination in chickens: *Sox* gene expression in male and female gonads

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Abstract. During mammalian sexual development, the SOX9 transcription factor up-regulates expression of the gene encoding anti-Müllerian hormone (AMH), but in chickens, *Sox9* gene expression reportedly occurs after the onset of *Amh* expression. Here, we examined expression of the related gene *Sox8* in chicken embryonic gonads during the sex-determining period. We found that *cSox8* is expressed at similar levels in both sexes at embryonic day 6 and 7, and only at the anterior tip of the

gonad, suggesting that SOX8 is not responsible for the sex-specific increase in *cAmh* gene expression at these stages. We also found that several other chicken *Sox* genes (*cSox3*, *cSox4* and *cSox11*) are expressed in embryonic gonads, but at similar levels in both sexes. Our data suggest that the molecular mechanisms involved in the regulation of *Amh* genes of mouse and chicken are not conserved, despite similar patterns of *Amh* expression in both species.

Key words. Sex determination; *Amh*; chicken; testis.

Even though molecular mechanisms of patterning and morphogenesis are surprisingly well conserved during metazoan evolution, mechanisms governing sex determination and gonadal development are diverse, even among vertebrates. In mammals, the heterogametic pairing of sex chromosomes (XY) results in male development. The mouse and human sex-determining gene, *Sry/SRY* (sex-determining region on Y chromosome), has been identified [1, 2] and is known to cause the bipotential gonad to differentiate into a testis [3]. However, *Sry* is not a conserved sex-determining gene as it exists only in mammals [4–7]. In contrast to mammals, in birds males are homogametic (ZZ) and females are heterogametic for the sex chromosomes (ZW). Whether avian sex is

determined by a master female-determining gene on the W chromosome or by Z chromosome gene dosage is still unclear [8].

There are reports for the mouse that several genes are expressed predominantly in the developing testis but not in the ovary and, therefore, are likely to be important for male sex determination and differentiation. Some of these genes, such as *Amh* (anti-Müllerian hormone) and *Sox9* [9–12] are expressed similarly in mouse and chicken gonads, suggesting that there could be some degree of similarity between the molecular pathways and sexual development in chicken and mouse. However, some differences are evident. For example, *Sfl* (steroidogenic factor 1) and *Gata4* are predominantly expressed in the male gonad in mice [13, 14], while in chicken expression levels of both genes are similar between male and female gonads [12, 15].

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