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DNA Methylation in Breast Tumor from High-risk Women in the Breast Cancer Family Registry

HUI-CHEN WU[1], MELISSA C. SOUTHEY[2], HANINA HIBSHOOSH[3], REGINA M. SANTELLA[1,4] and MARY BETH TERRY[4,5]

[1]*Department of Environmental Health Sciences, Mailman School of Public Health of Columbia University, New York, NY, U.S.A.;*
[2]*Department of Pathology, The University of Melbourne, Melbourne, Victoria, Australia;*
[3]*Department of Pathology and Cell Biology, College of Physicians & Surgeons of Columbia University, New York, NY, U.S.A.;*
[4]*Herbert Irving Comprehensive Cancer Center, Columbia University Medical Center, New York, NY, U.S.A.;*
[5]*Department of Epidemiology, Mailman School of Public Health of Columbia University, New York, NY, U.S.A.*

Abstract. *To examine DNA methylation profiles in breast tumors of women with a strong breast cancer family history, we measured methylation by bisulfite sequencing in 40 genes in 40 breast tumor tissues from women in the Breast Cancer Family Registry. We selected candidate genes from analysis of the Cancer Genome Atlas project (TCGA) breast data. Compared to TCGA breast cancer, BCFR cases are younger and more likely to be ER-negative. Overall, we found that many of the methylation differences between BCFR tumor and normal adjacent tissues were smaller than that in TCGA samples. We found only 32% of tested genes were hypermethylated in BCFR; the largest difference was 36.1% for SEPW1, and the smallest difference was 10% for RYR2. These data suggest the importance of examining breast cancer cases including familial cases enriched with early-onset cancers to identify methylation markers that can be examined in blood as biomarkers for early detection.*

Studies examining the associations between whole-genome DNA methylation and breast cancer classification found that there were distinct methylation patterns by hormone receptor status (1, 2) and by *BRCA* mutation state (3). In addition, DNA methylation profiles can also identify a cluster of breast cancers that are not classified by current expression subtypes (4). Only few studies have examined breast tumor tissues on DNA methylation in selected genes in familial breast cancer (5-7). Examining methylation in the promoter region of 10 selected genes in both inherited and non-inherited breast cancer, Esteller *et al*. (5) suggested that hereditary breast cancers have methylation levels similar to that of sporadic tumors in these genes. However, another study reported that the median cumulative methylation index calculated as the sum of the percentage methylation for 11 genes was significantly lower in *BRCA1*-related breast cancers than in sporadic breast cancers (6).

Recent data from The Cancer Genome Atlas (TCGA) has dramatically expanded the number of genes identified as aberrantly methylated in breast cancer (8). The aim of the current study was to examine the methylation values in selected genes that are highly methylated in TCGA breast tumor tissues in breast cancer tissues from high-risk women. By analyzing data of Illumina HumanMethylation450 array in breast cancer in TCGA Network, we first selected 40 genes that are hypermethylated in breast tumor than adjacent non-tumor tissues. We then compared DNA methylation levels of these 40 genes using high throughput targeted bisulfite sequencing in 40 breast tumor and non-tumor tissue pairs from high-risk women from the New York site of the Breast Cancer Family Registry (BCFR). We also examined the relationship of methylation in each loci with estrogen receptor (ER) status and age at cancer diagnosis.

Materials and Methods

Study participants. We selected breast cancer cases from families participating in the New York site of the BCFR (9, 10). We recruited high risk breast and/or ovarian cancer families from clinical and community settings within the Metropolitan New York area who

Correspondence to: Dr. Hui-Chen Wu, Department of Environmental Health Sciences, Mailman School of Public Health of Columbia University 650 West 168th St., 1608, New York, NY 10032, U.S.A. Tel: +1 2123058158, e-mail: hw2057@columbia.edu

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Table I. *Clinical characteristics of breast cancer patients in the Breast Cancer Family Registry (BCRF) and The Cancer Genome Atlas (TCGA).*

	BCFR	TCGA
Age at diagnosis (Mean, SD), years	46.4 (11.4)	57.2 (15.4)
Race, %		
White	77.5	93.3
Hispanics	7.5	0.0
Black	5.0	4.4
Others	10.0	2.3
Menopausal status, %		
Pre	37.5	26.7
Post	50.0	54.4
Indeterminate/others	12.5	18.9
ER Status, %		
Negative	47.5	16.7
Positive	52.5	71.1
Unknown	0.0	12.2

were eligible to participate if they met one of the following criteria: i) have a female relative with breast or ovarian cancer diagnosed before age 45 years, ii) have a female relative with both breast and ovarian cancer regardless of age at diagnosis, iii) have two or more relatives with breast or ovarian cancer diagnosed after age 45 years, iv) be a male with breast cancer diagnosed at any age, or v) have a family member with a known *BRCA* mutation. The study was approved by Columbia University's Institutional Review Board; written informed consent was obtained from all subjects, and strict quality controls and safeguards were used to protect confidentiality. For DNA methylation analysis, we analyzed 40 formaldehyde-fixed paraffin embedded (FFPE) breast tumors and adjacent non-tumor tissues from breast cancer cases who have family history of breast cancer, including 19 ER-negative and 21 ER-positive tumors.

DNA extraction and bisulfite treatment. With the H&E-stained slide used as a guide, the pathologist (Dr. Hibshoosh) circled the region of breast carcinoma on the corresponding unstained slide for macrodissection. Non-tumor tissue from outside the circled area was also removed. Tissues were de-paraffinized before DNA extraction. We used two 10-μm sections per case to extracted DNA by a standard phenol-chloroform protocol. Aliquots of DNA (1 μg) were bisulfite-treated with Epitect kit (Qiagen) as per the manufacturer's instructions. The DNA was resuspended in 20 μL of distilled water and stored at –20˚C until use.

TCGA data analysis for selection of genes. To identify breast-specific DNA methylation markers, we downloaded Illumina Infinium HumanMethylation450 data (Level 3 data) for tumor tissues and adjacent non-tumor tissues and clinical annotation tables for 96 breast invasive carcinomas from TCGA data portal (https://tcga-data.nci.nih.gov/tcga/tcgaHome2.jsp) (5/20/2014). We used paired sample t-test with Bonferroni's correction for multiple testing to identify CpG sites that were differentially methylated between tumor and adjacent tissues. A statistically significant difference was defined as sites with a Bonferroni-corrected *p*-value <0.0005; a total of 84,584 CpG sites were identified. We then selected candidate genes (Table I) based on the criteria for selecting driver methylation changes (11) from TCGA breast cancer data; they are: 1) effect size, with >20% higher methylation in tumor tissues, 3) genomic location, with CpG sites located in the CpG Island, 4) excluding any CpG sites with SNPs on the array probe. Among those 5,762 CpG sites, we selected the top 40 CpG sites with largest difference in methylation. The difference in beta value between tumor and adjacent nontumor tissues in these CpG sites range from 0.40 to 0.54.

Table II. *Distribution of DNA methylation levels in 40 loci in breast tumor and adjacent non- tumor tissues from the New York site of Breast Cancer Family Registry by bisulfite sequencing and in The Cancer Genome Atlas by Illumina 450k array.*

Gene	Breast tumor Mean (SD), %	Non-tumor breast Mean (SD), %	Difference	*p*-Value	TCGA 450K data Difference, beta
SEPW1	74.7 (22.6)	38.6 (30.4)	36.1	<0.0001	0.45
PCDHGA4	46.0 (34.7)	17.9 (15.4)	28.1	0.02	0.45
CCDC36	42.7 (30.7)	16.2 (10.6)	26.5	0.03	0.48
C1orf14	55.7 (24.6)	29.3 (25.6)	26.4	0.01	0.45
RPTOR	53.2 (29.2)	28.9 (26.9)	24.3	0.01	0.46
C1orf114	54.6 (33.4)	31.0 (31.5)	23.7	0.03	0.47
ZNF454	32.9 (29.2)	10.1 (12.5)	22.8	<0.001	0.44
DBX1	27.4 (26.3)	9.7 (5.2)	17.7	0.06	0.43
USP44	40.1 (28.7)	22.4 (23.1)	17.7	0.04	0.54
CSMD3	29.1 (20.8)	12.1 (9.6)	17.0	0.01	0.46
MACF1	62.5 (15.9)	46.0 (20.7)	16.5	0.06	0.45
FOXA2	40.4 (23.1)	24.0 (17.3)	16.4	0.08	0.43
SCRT2	44.2 (31.7)	28.6 (29.1)	15.6	0.23	0.44
OTX2OS1	36.7 (31.0)	22.7 (18.7)	14.0	0.08	0.54
C12orf68	46.6 (30.1)	32.9 (28.7)	13.7	0.05	0.45
CPXM1	27.6 (31.6)	14.7 (24.9)	12.8	0.08	0.46
ZNF177	25.7 (27.6)	13.2 (11.5)	12.6	0.06	0.43
PRKAR1B	61.1 (20.2)	48.6 (25.8)	12.5	0.04	0.45
TBR1	30.4 (32.2)	18.3 (9.7)	12.1	0.30	0.45
TNR	57.1 (32.3)	45.2 (35.2)	12.0	0.16	0.43
SLC7A14	32.9 (18.4)	21.0 (19.1)	11.9	<0.001	0.46
SOX2OT	32.1 (28.0)	20.6 (21.0)	11.5	0.03	0.46
GRM1	34.8 (24.8)	23.7 (20.6)	11.1	0.09	0.40
RYR2	24.0 (15.6)	14.0 (13.8)	10.0	0.01	0.48
PTPRN	30.8 (25.1)	21.6 (30.7)	9.2	0.43	0.48
PAX6	22.0 (22.8)	14.5 (14.3)	7.5	0.10	0.47
C1orf94	34.5 (23.0)	27.2 (21.1)	7.3	0.31	0.43
SST	27.8 (24.9)	20.8 (21.5)	7.0	0.27	0.42
TLX1	23.1 (28.8)	16.5 (22.3)	6.6	0.18	0.48
H2AFY	28.6 (21.3)	23.5 (20.7)	5.1	0.44	0.48
GPRC5B	9.3 (15.8)	5.4 (13.2)	3.9	0.31	0.46
ALX1	42.4 (28.5)	39.3 (27.6)	3.1	0.67	0.41
GAL3ST3	23.6 (20.6)	22.3 (24.9)	1.3	0.84	0.46
VAX1	14.1 (15.5)	13.1 (15.5)	1.0	0.76	0.44
GRASP	39.7 (36.9)	39.7 (30.0)	1.0	0.95	0.49
TTBK1	17.4 (13.5)	18.5 (21.8)	–1.0	0.84	0.49
TULP1	31.3 (18.3)	32.6 (20.1)	–1.3	0.72	0.50
FEZF2	25.2 (25.3)	26.9 (18.7)	–1.7	0.82	0.43
L1TD1	42.7 (27.7)	45.3 (26.0)	–2.6	0.82	0.42
KLHDC7B	56.7 (31.9)	60.1 (29.7)	–3.4	0.72	0.41

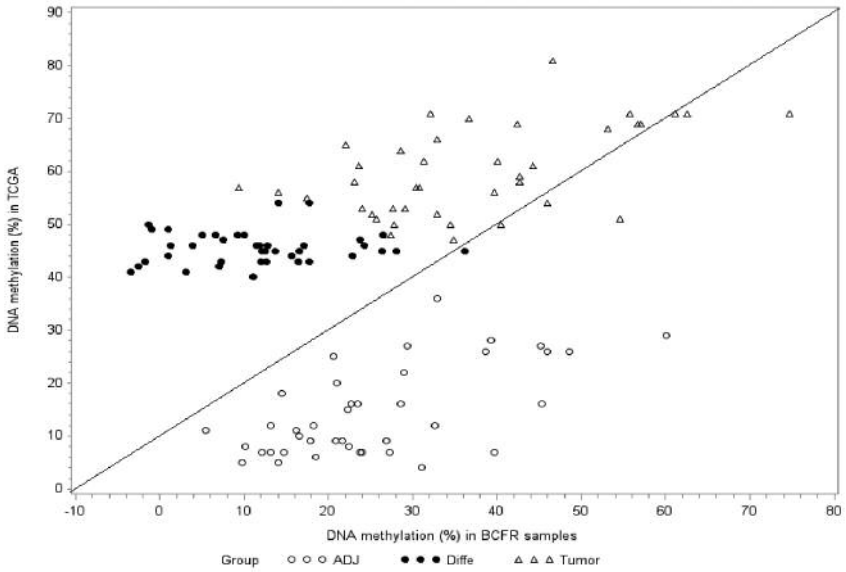

Figure 1. *DNA Methylation in tumor and adjacent tissues and the difference in DNA methylation between tumor and adjacent tissues by samples from the New York site of the BCFR and from The Cancer Genome Atlas.*

Bisulfite DNA sequencing for measuring DNA methylation in candidate genes. DNA methylation was measured using an Illumina MiSEQ instrument as per the manufacturer's instructions. We designed 40 pairs of oligonucleotide primers to cover the target CpG site region using MethPrimer with default parameters (12). The number of CpG sites per amplicon ranges from 4 to 34. We trimmed the Fastq files generated by sequencing (http://www.bioinformatics.babraham.ac.uk/projects/trim_galore/) for both adapters and for a quality cut off of 30 using trimmed galore. Sequencing alignment and methylation calls was done *via* Bismark (13) and bowtie2 (14) and the methylation status and methylation level of each analyzed CpG-sites were then determined. The methylation level for each gene was assigned by averaging the methylation level of all CpG sites in the gene for each sample. Primers are available on requesting from the authors.

Statistical methods. We used paired-*t*-test to determine the differences in methylation between breast tumor and adjacent nontumor tissues of BCFR samples. We used Wilcoxon Rank Sum test to examine methylation by ER status (positive *vs*. negative) and age at cancer diagnosis (<50 *vs*. ≥50 years of age) among tumor tissues. We used SAS software 9.3 (SAS Institute, Cary, NC, USA) for the analyses.

Results

Table I presents the distributions of selected characteristics in BCFR cases and TCGA breast cancer cases. BCFR breast cases were younger than TCGA cases. The mean age of breast cancer diagnosis was 46.4±11.4 for BCFR cases and 57.2±15.4 for TCGA cases. Sixty-five percent of BCFR breast cases were diagnosed with breast cancer before the age of 50, while only 33% of TCGA breast cases were early onset cases. Most breast cancer cases (71%) in TCGA were ER positive and 53% cases in the BCFR were ER positive.

The overall methylation levels for each locus in tumor and adjacent tissues in BCFR tissue samples and corresponding methylation difference in TCGA breast and adjacent non-tumor tissues are given in Table II. Overall, the methylation levels for most of genes were higher in tumor samples than in adjacent tissues in BCFR tissue samples. Seven genes (*SEPW1, PCDHGA4, CCDC36, C1orf14, RPTOR, C1orf114*, and *ZNF454*) had methylation levels in tumors at least 20% higher than in adjacent tissues. The largest difference was 36.1% for *SEPW1*. A total of 13 genes (*SEPW1* (74.4 *vs*. 38.6%), *PCDHGA4* (46.0 *vs*. 17.9 %), *CCDC36* (42.7 *vs*. 16.2%), *C1orf14* (55.7 *vs*. 29.3%), *RPTOR* (53.2 *vs*. 28.9%), *C1orf114* (54.6 *vs*. 31.0%), *ZNF454* (32.9 *vs*. 10.1%), *USP44* (40.1 *vs*. 22.4%), *CSMD3* (29.1 *vs*. 12.1%), *PRKAR1B* (61.1 *vs*. 48.6%), *SLC7A14* (32.9 *vs*. 21.0%), *SOX2OT* (32.1 *vs*. 20.6%) and *RYR2* (24.0 *vs*. 14.0%)) showed significantly higher methylation in breast tumor compared to adjacent non-tumor tissues. Although the technologies for DNA methylation measurement are different between our and TCGA, the methylation levels in TCGA breast tumor were higher than that in BCFR tumor samples, while the methylation levels in TCGA adjacent samples were lower than that in BCFR adjacent samples (Figure 1).

We also examined the methylation of these genes by ER status and age at cancer diagnosis in BCFR samples and TCGA breast tumor data. In TCGA breast tumor, methylation

Table III. *Distribution of DNA methylation levels by estrogen receptor (ER) status (A) and by age at breast cancer diagnosis (B) in breast tumors from the New York site of the BCFR by bisulfite sequencing and from The Cancer Genome Atlas Illumina 450k array.*

Gene	BCFR			TCGA		
	ER Positive Mean (SD),%	ER Negative Mean (SD),%	*p*-Value	ER Positive Mean (SD), Beta	ER Negative Mean (SD), Beta	*p*-Value
C1orf14	58.5 (27.7)	52.0 (24.3)	0.54	0.74 (0.22)	0.56 (0.38)	0.01
ZNF454	37.8 (33.7)	23.4 (27.0)	0.28	0.57 (0.25)	0.37 (0.29)	0.01
GRM1	40.1 (30.6)	39.6 (26.8)	0.96	0.39 (0.25)	0.68 (0.16)	<0.0001
GPRC5B	13.9 (21.0)	7.3 (15.2)	0.31	0.62 (0.26)	0.32 (0.30)	0.0002
VAX1	13.8 (14.6)	15.0 (15.8)	0.82	0.53 (0.17)	0.64 (0.12)	0.03
TULP1	33.6 (16.6)	29.3 (27.5)	0.65	0.59 (0.24)	0.76 (0.15)	0.01
L1TD1	55.6 (28.0)	33.5 (27.2)	0.08	0.55 (0.21)	0.68 (0.14)	0.03
KLHDC7B	61.9 (33.6)	61.4 (30.1)	0.97	0.73 (0.20)	0.59 (0.30)	0.03
	<50 yrs of age	>50 yrs of age		<50 yrs of age	>50 yrs of age	
RPTOR	46.0 (28.1)	63.7 (27.5)	0.09	0.59 (0.24)	0.72 (0.15)	0.0002
TBR1	37.8 (37.6)	14.0 (10.3)	0.41	0.47 (0.27)	0.62 (0.28)	0.02
TTBK1	21.7 (17.8)	21.0 (23.1)	0.92	0.40 (0.33)	0.64 (0.33)	0.002

in *C1orf14, ZNF454, GPRC5B* and *KLHDC7B* were higher, while methylation in *GRM1, VAX1, TULP1*, and *L1TD1* were lower in ER positive than ER negative (Table III). The methylation levels in 3 genes were higher in older cases of TCGA samples (Table III). We did not observe any different by ER status or age in BCFR tumor samples.

Discussion

In this study, we examined DNA methylation profiles in breast tumor tissues from women at high risk. Among 40 tested genes that are hypermethylated in TCGA breast tumor tissues, we found that only 13 of them were highly methylated in our sample of high-risk women. Consistent with the TCGA breast data, methylation levels in *SEPW1, PCDHGA4, CCDC36, C1orf14, RPTOR, C1orf114, ZNF454, USP44, CSMD3, PRKAR1B, SLC7A14, SOX2OT* and *RYR2* were significantly higher in the breast tumor than in adjacent histologically normal tissues. The difference in methylation between tumor and adjacent tissues ranged from 10.0% for *RYR2* to 36.1% for *SEPW1*. Compared to data from TCGA breast tissues that are from mainly sporadic breast cancer cases, the methylation levels were lower in our BCFR tumor samples, however, the levels were higher in our adjacent samples then in TCGA adjacent tissues.

Differences in the technologies for DNA methylation measurement between our study (bisulfite sequencing) and TCGA (Illumina arrays) cannot explain the observation of smaller differences in DNA methylation between breast tumor and adjacent non-tumor tissues in our study than in TCGA data, as we compared methylation difference between tumor and non-tumor tissues within the same platform. The TCGA was not enriched for women at very high risk (*e.g.*, strong family history of breast cancer) and young cancer cases (33% in TCGA *vs*. 65% in BCFR samples). Clinical observations and molecular studies suggest biology of early-onset breast cancer is different from that of late-onset cancer (15). In contrast to later-onset cancer, early-onset breast cancer is enriched with ER-negative tumor (16). We did not see any methylation difference by ER status, but we found that methylation status of 11 genes differed by either ER status or age of cancer diagnosis in TCGA samples. As we only examined a small fraction (<1%) of hypermethylated genes in TCGA breast data, to better characterize DNA methylation profiles in familial breast cancer, studies examining a large-scale of DNA methylation profiles in breast tumor tissues with detail family history of breast cancer are needed.

Examining epigenome-wide DNA methylation profiles in breast tumors, several studies have identified a number of alternately methylated genes including *SEPW1, PCDHGA4, CCDC36, C1orf14, RPTOR, C1orf114, ZNF454, USP44, CSMD3, PRKAR1B, SLC7A14, SOX2OT*, and *RYR2* (8, 17). Comparing DNA methylation profiles between healthy breast tissue and ductal carcinoma in situ using HumanMethylation450 microarrays, Fleischer *et al*. (17) found a total 16,949 CpGs were differentially methylated, representing 5,659 genes including *SEPW1, PCDHGA4, CCDC36, C1orf114, CSMD3, SLC7A14, RYR2*, and *RPTOR*, suggesting hypermethylation of these selected genes occurs early in breast cancer development including familial breast cancer. Hypermethylation in the promoter regions of key genes might allow for clonal selection and growth of tumor cells (18).

Using whole-exome sequencing in breast tumor tissue, mutations in *RYR2, C1orf14, SLC7A14*, and *RPTOR* have been identified (8, 19-21). The observation of hypermethylation of these genes in breast cancer suggests that epigenetic silencing *via* methylation is another important mechanism for inactivating these genes in breast cancer tumorigenesis. Genome-wide DNA methylation studies have supported the correlation of CpG island DNA hypermethylation and gene expression (4, 22-24). Using MEXPRESS (25) (http://mexpress.be/) to visualize and examine DNA methylation and expression data from data in TCGA breast tumor, methylation was significantly associated with gene expression in *SEPW11* (person correlation coefficient r=–0.11), *PCDHGA4* (r=–0.21), *CCDC36* (r=0.42), *RPTOR* (r=0.24), *ZNF454* (r=–0.60), *USP44* (r=0.63), *CSMD3* (r=0.01), *PRKAR1B* (r=0.39), *SLC7A14* (r=–0.32), and *RYR2* (r=–0.19). Further studies are need to better understand the role of DNA methylation alterations in these genes involved in breast tumorigenesis.

In summary, we found that the genes we selected from TCGA breast data, because they were dysregulated in DNA methylation were not all dysregulated in breast tumor tissues from women with a strong breast cancer family history. As accumulating data suggest the importance of DNA methylation alternations for cancer risk, a more comprehensive set of breast cancer cases including familial cases enriched with early-onset cancers need to be studied in order to identify methylation changes in genes that can be examined in the peripheral blood as biomarkers for early detection.

Conflicts of Interest

There is no conflict for all authors.

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