

Joint effects of WT1, CA10 methylation in peripheral blood leukocyte and dietary zinc on breast cancer risk: a case-control study

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Research article

Keywords: breast cancer, CA10, WT1, DNA methylation, leukocytes, zinc

Posted Date: May 27th, 2020

DOI: <https://doi.org/10.21203/rs.3.rs-27678/v1>

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Version of Record: A version of this preprint was published on July 31st, 2020. See the published version at <https://doi.org/10.1186/s12885-020-07183-8>.

Abstract

Background

Studies have shown that abnormal changes of specific-gene DNA methylation in leukocytes may be associated with elevated risk of cancer. However, associations between the methylation of zinc-related genes, *WT1* and *CA10*, and breast cancer risk, and interactions between *WT1*, *CA10* methylation and dietary zinc intake on breast cancer risk remain unknown.

Methods

The methylation of *WT1*, *CA10* was analyzed by methylation-sensitive high-resolution-melting (MS-HRM) in a case-control study with female subjects (N = 959). Logistic regression was used to analyze the associations and propensity score (PS) method was used to adjust confounders.

Results

The results showed that *WT1* hypermethylation was associated with an increased risk of breast cancer with an odds ratio (OR) of 3.069 [95% confidence interval (CI): 1.669–5.643, $P < 0.001$]. Subgroup analyses showed that *WT1* hypermethylation was specifically associated with an elevated risk of Luminal A subtype (OR = 2.620, 95%CI: 1.107–6.200, $P = 0.029$) and Luminal B subtype (OR = 3.231, 95%CI: 1.339–7.796, $P = 0.009$). *CA10* hypermethylation was associated with an increased risk of Luminal B subtype (OR = 1.798, 95%CI: 1.085–2.982, $P = 0.023$). Furthermore, the joint effects of methylation of *WT1*, *CA10* and lower dietary zinc intake were associated a strongly elevated risk of breast cancer with ORs of 11.220 (95%CI: 4.057–31.032, $P < 0.001$) and 4.145 (95%CI: 2.717–6.324, $P < 0.001$), respectively.

Conclusion

The study suggested the hypermethylation of *WT1* methylation in leukocytes was significantly associated with an increased risk of breast cancer. Notably, the joint effects of *WT1*, *CA10* methylation and lower dietary zinc intake might significantly associate with breast cancer risk.

Introduction

Breast cancer is one of the most common malignancies in women worldwide [1] and presents with different molecular subtypes, including luminal A, luminal B, HER2-enriched, and basal-like that also called triple negative [2]. As a major type of epigenetic modification, DNA methylation involves in regulating cellular processes, including chromosomal instability [3] and gene expression. Hypermethylation of CpG regions in specific genes contribute to neoplastic formation through the transcriptional silencing of tumor suppressor genes. Aberrant patterns of specific gene methylation can help identifying differences in breast cancer subtypes [2], and showing promise for utilizing in large-scale epidemiological studies. It is suggested that leukocyte DNA methylation, as simple non-invasive blood markers [4, 5], could serve as a surrogate of systematic methylation activity, which offered great potential for predicting the increasing breast cancer risk [6].

Wilm's Tumor gene (*WT1*) is tumor suppressor gene which involved in human cell growth and differentiation. *WT1* have been reported significantly different methylated in the tissues of hepatocellular carcinoma [7], lung cancer [8] and breast cancer [9]. *WT1* aberrant methylation may lead to the reduction or absence of expression of *WT1*, which results in the overexpression of the insulin-like growth factor I receptor (IGF 1R) and insulin-like growth factor II (IGF II), therefore promotes breast cancer process [10–12]. *CA10* is a member of the carbonic anhydrase family, which is a large family of zinc-containing metalloenzymes that catalyze the reversible hydration of carbon dioxide and the dehydration of carbonic acid [13]. Ivanov et al. suggested that induction or enhancement of carbonic anhydrase expression may contribute to the tumor microenvironment by maintaining extracellular acidic pH and helping cancer cells grow and metastasize [14]. Studies have found the abnormal expression of carbonic anhydrase family by aberrant methylation was related with gastric cancer and metastasis of ovary tumors [15, 16]. Furthermore, Wojdacz et al. reported that both *WT1* and *CA10* hypermethylation were significantly different between breast cancer tumor tissues and non-malignant tissues [17]. However, the methylation of these two genes in leukocyte DNA affects breast cancer susceptibility remains unclear.

In recent years, nutri-epigenetics, the influence of dietary components on the epigenome, has emerged as an exciting new field [18]. While earlier studies have shown that high dietary zinc intake could decrease cancer risk [19, 20], the association of zinc intake and breast cancer risk remained controversial [21, 22]. Zinc deficiency may influence the function of zinc related genes, including changes the expression of *WT1* in zinc deficiency animal model [23], and decreases blood carbonic anhydrase activity in males in a double-blind, randomized crossover study [24]. Hu et al. discovered that zinc deficiency increased *BDNF* methylation level in *in vitro* experiment [25]. However, studies have yet examined the associations between dietary intake of zinc and zinc related genes, *WT1* and *CA10*, genes methylation in white blood cells with breast cancer risk.

In this study, we explored the associations between the methylation of *WT1*, *CA10* in peripheral blood leukocyte DNA and breast cancer risk. We further used a dataset of nested case-control cohort within the EPIC-Italy cohort study as external data to validate the association between gene methylation and breast cancer risk. We also investigated the associations between the methylation of two genes and the risk of different molecular types of breast

cancer. Furthermore, we examined the interaction and combination effects between methylation of the genes with dietary zinc intake on the risk of breast cancer.

Materials And Methods

Study subjects

We investigated the relationship between *WT1*, *CA10* methylation and breast cancer risk using a case-control study. All included breast cancer patients were newly diagnosed female and were recruited from the Tumor Hospital of Harbin Medical University from 2010 to 2014. Controls were recruited from patients admitted to the Orthopedic and Ophthalmology Department of the Second Affiliated Hospital of Harbin Medical University and volunteers from the Xiangfang community of Harbin within the same period. All controls were also female. In addition, all control participants were asked about their disease history in the questionnaire and the ones with any cancer history were excluded from our final subjects. Finally, 402 female breast cancer cases and 557 female controls were included in our study. Informed written consent was provided by all the subjects, and 5 mL blood samples were collected and then stored at -80°C . This study was approved by the Human Research and Ethics Committee of Harbin Medical University.

Data collection

All subjects were interviewed face-to-face by trained investigators with normalized questioning methods. The questionnaire was adopted from the study of Shu et al. [26], which included demographic information (age, ethnicity, and others); daily dietary intake (vegetables, fruits, beverages, and snacks); behaviors (smoking, drinking, physical activity and work activity); female-specific questions involving menstruation status, breast disease history (lobular hyperplasia, cyst, and others); gynecologic surgery history (hysterectomy, ovariectomy) and family history of cancer and breast cancer. The questions involved in dietary and behavioral were about the participants' daily routine of one year prior to the interview. The daily dietary intake information were collected with Food Frequency Questionnaire contained 9 major food groups, which represented approximately 77 food items including Chinese staple foods, vegetables, fruits, dairy products, soybean products, meat products, egg, sea-food and fungus. The zinc intake derived from nutrient supplement was also included. The content of zinc in different foods were derived and calculated based on country specific food composition, Chinese Food Composition Table [27].

The study was validated with GEO-GSE51032 (IPEC-Italy cohort) dataset with nested case control study design to analyze the association between the methylation of *CA10*, *WT1* and breast cancer risk in female. The blood samples were also collected and other anthropometric measurements were taken. The detailed criteria for sample selection and the methods were reported by Riboli et al. [28]. We extracted all 232 female breast cancer cases and all 340 female controls from this nested case-control study and located the methylation probes from Illumina 450 K array. The annotated CG sites covered by our MS-HRM sequence were illustrated in Fig. 1.

DNA extraction and bisulfite conversion

DNA was extracted from peripheral blood samples using a commercial DNA extraction kit (QIAamp DNA Blood Mini Kit, Hilden, Germany). The concentration and the purity of DNA were detected by Nanodrop 2000 Spectrophotometer (Thermo Scientific). Genomic DNA was bisulfite-modified with an EpiTect Bisulfite Kit (Qiagen, Hilden, Germany). Bisulfite DNA was normalized at a concentration of 20 ng/mL and was stored at -20°C for the following experiment. DNA extraction and DNA sodium bisulfite modification were performed according to the manufacturer's instructions.

Gene methylation status analysis

We adopted methylation-sensitive high-resolution melting analysis (MS-HRM) to evaluate the methylation of *WT1* and *CA10* with the LightCycler 480 system (Roche Applied Science, Mannheim, Germany) equipped with Gene Scanning software (version 2.0). The primers were adopted from a published article [17]. We used universal methylated and unmethylated DNA standards (ZYMO, USA) and mixed them at different ratios to create standards with a 0.5%, 1%, 2%, and 5% methylation levels of *WT1* and *CA10*, respectively (Fig. 2). PCR amplification and MS-HRM were optimized and performed. The conditions, reaction mixture and primer sequences used in the MS-HRM experiments are listed in Table S1-2. Each standard reaction was performed in duplicate in each run. Each plate included duplicate water blanks as negative controls. We also repeated some samples in different runs to exam the consistency of the experiment. There was a significant agreement of these samples in different runs in detection of the methylation and unmethylation status of *WT1* and *CA10*, with kappa value of 1.000 ($P=0.001$) and 0.936 ($P=0.001$), respectively (Table S3).

Definition of different molecular subtypes of breast cancer

Four subtypes of breast cancer were defined as luminal A, luminal B, HER-2 enriched and triple negative breast cancer (TNBC) by immunohistochemical analysis based on previously validated clinicopathological criteria [29].

Statistical analysis

For the distribution of basic demographic characteristics, continuous variables such as age were analyzed by two-sample t-tests, and categorical variables were analyzed by chi-square (χ^2) tests. For missing values in the environmental factors, we applied multiple imputation to generate possible values. To measure the association between methylation of *WT1*, *CA10* and breast cancer risk and different molecular types breast cancer, we used univariate and multivariate unconditional logistic regression analyses to estimate the crude and adjusted odds ratios (ORs) and 95% confidence

intervals (95%CI). For our case-control study, we used 0% methylation as cutoff for both *WT1* and *CA10*. We used ROC curves to calculate the cut-off value of β for validation dataset. Interactions or combination effects between zinc intake and methylation of genes on breast cancer risk were analyzed by multivariate logistic regression and crossover analysis. We also applied propensity score (PS) method to adjust covariates (involving all environmental factors in the questionnaire), in which the study outcome served as the dependent variable and PS served as the confounding variable. Kappa values were calculated to analyze the consistency between same samples in different runs. All two-sided *P* values < 0.05 were considered statistically significant. Data were analyzed by using the software SPSS v.24.0 (SPSS Inc., Chicago, IL, USA).

Results

Characteristics of the cases and controls

This study included 402 female cases with a mean age of 51.75 ± 9.39 and 557 female controls with a mean age of 51.85 ± 10.31 . Other demographic information of the cases and controls is listed in Table 1.

Table 1
Demographic characteristics of breast cancer patients and controls.

Characteristics		No. of Controls(%)	No. of Cases (%)	<i>P</i> Value
Age	Mean \pm Std	51.85 \pm 10.31	51.75 \pm 9.39	
	< 40	82(14.7)	41(10.2)	0.024
	40-	333(59.8)	274(68.2)	
	\geq 60	142(25.5)	87(21.6)	
BMI	\leq 18.5	35(6.3)	14(3.5)	0.115
	18.5-	274(49.2)	211(52.5)	
	\geq 24.0	248(44.5)	177(44.0)	
Urban and Rural Status	Rural	236(42.4)	232(57.7)	< 0.001
	Urban	321(57.6)	170(42.3)	
Education Level	Primary School or Below	162(29.1)	98(24.4)	0.270
	Middle School	175(31.4)	135(33.6)	
	Senior School and Higher	220(39.5)	169(42.0)	
Occupation Type	White Collar	273(49.0)	233(58.2)	0.007
	Blue Collar	284(51.0)	169(41.8)	
Ethnicity	Han	529(95.0)	386(96.0)	0.273
	Other	28(5.0)	16(4.0)	

Associations between *WT1*, *CA10* methylation and breast cancer risk

WT1 methylation was associated with breast cancer risk both in multivariate and PS adjusted methods with ORs of 2.420 (95%CI: 1.449–4.040, *P*< 0.001) and 3.069 (95%CI: 1.669–5.643, *P*< 0.001), respectively. *CA10* methylation was statistically significant associated with breast cancer in multivariate adjustment with an OR of 1.531 (95%CI: 1.144–2.051, *P*= 0.004), but only marginally associated with breast cancer with an OR of 1.354 (95%CI: 0.967–1.896, *P*= 0.078) after the adjustment of PS (Table 2).

Table 2
The associations between gene methylation and risk of breast cancer and different molecular types of breast cancer.

	Molecular types ^a	No. of Unmethylation(%)	No. of Methylation(%)	Crude OR (95% CI)	P Value	OR _{adjusted} ^b (95% CI)	P Value	OR _{adjusted} ^c (95% CI)	P Value
<i>WT1</i>	Control	65(11.7)	492(88.3)	1		1		1	
	Luminal A	9(6.4)	132(93.6)	1.990(0.937–4.226)	0.073	2.605(1.183–5.736)	0.018	2.620 (1.107–6.200)	0.029
	Luminal B	8(6.0)	125 (94.0)	2.121(1.504–2.990)	0.066	2.491(1.126–5.507)	0.024	3.231(1.339–7.796)	0.009
	HER-2 Enriched	5(8.9)	51(91.1)	1.341(0.514–3.499)	0.549	1.910(0.688–5.303)	0.214	1.913(0.664–5.512)	0.230
	TNBC	1(2.9)	33(27.1)	4.338(0.582–32.331)	0.152	5.627(0.726–43.626)	0.098	6.044(0.763–47.897)	0.088
	All cases	26(6.5)	376 (93.5)	1.921(1.178–3.132)	0.009	2.420(1.449–4.040)	0.001	3.069(1.669–5.643)	< 0.001
<i>CA10</i>	Control	209 (37.5)	348(62.5)	1		1		1	
	Luminal A	40(28.4)	101(71.6)	1.506(1.004–2.259)	0.048	1.598(1.042–2.451)	0.032	1.505(0.939–2.410)	0.089
	Luminal B	34(25.6)	99(74.4)	1.787(1.165–2.742)	0.008	2.043(1.301–3.211)	0.002	1.798(1.085–2.982)	0.023
	HER-2 Enriched	18(32.1)	38(67.9)	1.270(0.706–2.286)	0.425	1.424(0.762–2.662)	0.268	1.366(0.708–2.634)	0.353
	TNBC	14(41.1)	20(58.8)	0.860(0.425–1.740)	0.674	0.939(0.450–1.955)	0.865	1.006 (0.461–2.198)	0.988
	All cases	119 (29.6)	283(70.4)	1.427(1.084–1.878)	0.011	1.531(1.144–2.051)	0.004	1.354(0.967–1.896)	0.078
^a The result excluded 38 breast cancer patients with incomplete immunohistochemical records.									
^b Adjusted for age, BMI, ethnicity, urban and rural status and family history of breast cancer and cancer.									
^c Adjusted by propensity score(potential confounder included age, BMI, urban and rural status, ethnicity, education level, mammography, gynecologic surgery, breast disease history, menstrual cycle, menopause, reproduction, abortion, breast feeding, oral contraceptive, female hormone intake, fruit intake, vegetable intake, tomato intake, broccoli intake, bean products, pungent food, pork, beef and lamb consumption, chicken consumption, sea-fish, egg, diary, fungus, pickles, alcohol consumption, tea consumption, cigarette, physical activity, occupation type, family history of breast cancer and cancer).									

In the subgroup analyses, after the adjustment of PS, *WT1* methylation was associated with breast cancer risk in both younger (< 60-years-old) and older (\geq 60-years-old) group, with ORs of 2.640 (95%CI: 1.311–5.316, $P=0.007$) and 4.720 (95%CI: 1.312–16.974, $P=0.007$), respectively. *CA10* methylation was associated with breast cancer risk in younger age group (< 60-years-old) before the adjustment of PS, with OR of 1.556 (95%CI: 1.145–2.114, $P=0.005$); However, the association was not statistically significant after PS adjustment (Table 3).

Table 3
The subgroup analysis of the associations between methylation of genes and the risk of breast cancer based on different age.

			Crude OR (95% CI)	P Value	OR _{adjusted} ^a (95% CI)	P Value
<i>WT1</i>	≤60	Unmethylation	1		1	
		Methylation	1.639 (0.945–2.843)	0.079	2.640 (1.311–5.316)	0.007
	≥ 60	Unmethylation	1		1	
		Methylation	3.155(1.048–9.495)	0.041	4.720 (1.312–16.974)	0.018
<i>CA10</i>	≤60	Unmethylation	1		1	
		Methylation	1.556 (1.145–2114)	0.05	1.327 (0.900-1.956)	0.153
	≥ 60	Unmethylation	1		1	
		Methylation	1.201 (0.608–2.372)	0.598	1.527 (0.692–3.371)	0.295

^a Adjusted by propensity score.

Associations between methylation of WT1, CA10 and risk of different molecular types of breast cancer

WT1 methylation was significantly associated with the risk of Luminal A subtype of breast cancer with multivariate adjusted OR of 2.605 (95%CI: 1.183-5.736, $P=0.018$), and PS adjusted OR of 2.620 (95%CI: 1.107-6.200, $P=0.029$). *WT1* methylation was also significantly associated with the risk of Luminal B subtype breast cancer with ORs of 2.491 (95%CI: 1.126-5.507, $P=0.024$) and 3.231 (95%CI: 1.339-7.796, $P=0.009$) after multivariate and PS adjustment. However, *WT1* methylation was not significantly associated with the risk of HER-2 enriched and TNBC subtypes (Table 2).

The associations between *CA10* methylation and the risk of Luminal B subtype breast cancer with multivariate adjusted and PS adjusted ORs were 2.043 (95%CI: 1.301-3.211, $P=0.003$) and 1.798 (95%CI: 1.085-2.982, $P=0.023$), respectively. However, *CA10* methylation had no significant associations with the risk of Luminal A, HER-2 enriched and TNBC subtypes after the adjustment of PS.

Association between WT1, CA10 methylation and breast cancer risk in GEO dataset

GSE51032 dataset is a nested case control study included 233 female breast cancer cases and 340 female cancer-free controls. After the data extraction from 450K array, we found two CG locus each in our targeted *WT1* and *CA10* sequences (Fig. 1). ROC curves were used to calculate the cut-off values of β , which were 0.057 and 0.226 for average β of probes in *WT1* and *CA10*. The average methylation level of Cg14657517 and Cg19074340, which located within the *WT1* targeted sequence, was associated with breast cancer with OR of 1.879 (95%CI: 1.247–2.830, $P=0.03$). However, the average methylation level of Cg14054928 and Cg20405017, which located within the targeted sequence of *CA10*, was not statistically significant associated breast cancer risk (OR = 0.759, 95%CI: 0.543–1.061, $P=0.107$) (Table 4).

Table 4
The association between gene average CpG sites methylation and risk of female breast cancer in GEO51032.

		Hypomethylation(%)	Hypermethylation (%)	Crude OR (95% CI)	P Value
<i>WT1</i>					
	Control	285(83.8)	55(16.2)	1	
	Case	171(73.4)	62(26.6)	1.879(1.247–2.830)	0.03
<i>CA10</i>					
	Control	146(42.9)	194(57.1)	1	
	Case	116(49.8)	117(50.2)	0.759(0.543–1.061)	0.107

Associations of zinc intake and its interaction with methylation of WT1, CA10 on the risk of breast cancer

Low zinc intake (< 41.81 mg/week) was significantly associated with breast cancer risk with an adjusted OR of 2.321 (95%CI: 1.747–3.083, $P < 0.001$) (Table S4). No significant interactions between total zinc intake and *WT1*, *CA10* methylations on breast cancer risk were observed. The combination effects of lower level of total zinc intake and *WT1*, *CA10* methylation on breast cancer risk were strongly significant, with ORs of 11.220 (95%CI: 4.057–31.032, $P < 0.001$) and 4.145 (95%CI: 2.717–6.324, $P < 0.001$), respectively (Table 5).

Table 5
The interaction between gene methylations and total zinc intake on the risk of breast cancer.

		Total Zinc Intake(mg/week)		Interaction	<i>P</i>
		≥ 41.81	< 41.81		
		OR _{Reg} adjusted [†] (95% CI)		OR _I adjusted [†] (95% CI)	
<i>WT1</i>	Unmethylation	1	5.227(1.516–18.029)	1	
	Methylation	3.985(1.406–11.298)	11.220(4.057–31.032)	0.539(0.147–1.974)	0.346
<i>CA10</i>	Unmethylation	1	2.969(1.825–4.829)	1	
	Methylation	1.488(0.961–2.305)	4.145(2.717–6.324)	0.938(0.519–1.695)	0.833

† Adjusted for age, BMI, ethnicity, urban and rural status and family history of breast cancer and cancer.

Discussion

This is the first case-control study to investigate the associations between the methylation of *WT1*, *CA10* in leukocyte DNA and breast cancer risk, and the risk of different molecular types of breast cancer in a Chinese female population. After PS adjustment, we found that methylation of *WT1* was significantly elevated breast cancer risk by 2.069-fold, *CA10* methylation was marginally associated with breast cancer risk with OR of 1.354. Women with *WT1* methylation presented a 1.620 higher risk of Luminal A and 2.231 higher risk of Luminal B subtype of breast cancer than those without methylation. *CA10* methylation was significantly associated with the risk of Luminal B subtype with OR of 1.798. We further used GEO-GSE51032, a nested case control study with clear temporal relationship between methylation changes and breast cancer, as an external dataset to validate our retrospective study's results. The nested case control study's results showed a lower but still significant association between *WT1* methylation and breast cancer risk, but the association between *CA10* methylation and breast cancer risk was not statistically significant. Furthermore, we found that low level of dietary zinc intake combined with *WT1*, *CA10* methylation was strongly associated with breast cancer risk.

Breast cancer is a heterogeneous disease with different molecular subtypes, which may present different genetic and epigenetic susceptibilities. Previous studies predominantly focused on the aberrant methylation in tissue samples and its association with the risk of different molecular types of breast cancer [30, 31], few studies have focused on the gene-specific methylation in leukocyte DNA. The methylation alternation in leukocyte DNA presented a response of the hematopoietic system [32]. Leukocyte DNA methylation could represent germline methylation, which can be applied to analyze the association with cancer risk [33]. It was further reported that *BRCA1* hypermethylation in peripheral blood DNA was associated with TNBC with an OR of 5.0 [34]. Our study indicated that, after adjustment of PS, *WT1* methylation was associated with the risk of Luminal A and Luminal B subtype of breast cancer with ORs of 2.620 and 3.231, and *CA10* methylation was significantly associated with Luminal B subtype of breast cancer with OR of 1.798.

WT1 is a zinc finger transcription factor located on 11p13, which was first identified as a tumor suppressor gene. *WT1* exon displayed significantly increased methylation in cancer tissue compared to nonmalignant breast tissue [17]. *WT1* methylation in the promoter and first exon region was associated with silencing *WT1* mRNA expression in MCF-7 and MDA-MB-231 breast cancer cells [9]. Our investigated sequence was 160 bp downstream of the Laux et al. sequence position. Here, we reported the methylation of the CpG island in the first exon of *WT1* in blood leukocyte DNA, which contains 11 CpGs in CpG island. Furthermore, we used external data of IPEC- Italy (GEO-GSE51032) with nested case control study design and found the significant association between *WT1* methylation and breast cancer risk, with two CpG probes inside our sequence, with OR of 1.879.

Previous study has shown *CA10* could undergo methylation during breast carcinogenesis in tumor tissue [17]. *CA10* was reported to be hypermethylated among a panel of genes in urine, which may contribute to highly accurate early detection of bladder cancer [35]. Our study suggested that *CA10* methylation in leukocyte DNA was marginally associated with an elevated breast cancer risk after the adjustment of PS. The amplified sequence contained 7 CpGs and located at the second exon of *CA10*. The external validation dataset of GEO-GSE51032 only included 2 CpG probes and did not observe statistically significant association between *CA10* hypermethylation and breast cancer risk.

To further investigate the functional relevance of the observed associations, it would be important to test whether methylation in the CpGs associated with the alteration of the expression of *WT1* and *CA10*. Therefore, we investigated the correlations between methylation probes and expression using TCGA (<http://cancergenome.nih.gov/>) and Mexpress (<https://mexpress.be/>) The result showed that *WT1* hypermethylation was negatively correlated with its expression (Cg14657517, $r = -0.204$, $P < 0.001$; Cg19074340, $r = -0.201$, $P < 0.001$), and *CA10* hypermethylation was negatively related to its mRNA expression as well (Cg14054928, $r = -0.182$, $P < 0.001$; Cg20405017, $r = -0.162$, $P < 0.001$). Although discounted by different sample-derived DNA, the significant negative correlations between *WT1*, *CA10* methylation and gene expression were consistent with our study and indicated promising potential in breast cancer risk assessment.

Recently, more researchers have focused on nutri-epigenetics, which refers to the study of nutrient with any genetic or epigenetic interaction that leads to phenotypic changes [36]. Zinc is a trace mineral that is vital for numerous cellular processes and may play an important role in cancer etiology [37]. Zinc is also an essential component of DNA-binding proteins with zinc fingers, such as *WT1* [23], and carbonic anhydrase function might be influenced by the concentration of erythrocyte Zn [38]. Studies on dietary zinc intake showed that high zinc intake could reduce the risk of various cancers [20, 39, 40], including breast cancer [40]. Previous studies also reported that zinc deficiency in dietary might be associated with increasing level of specific gene methylation [25, 41]. In this study, we first investigated if dietary zinc intake interacted with DNA methylation to affect the risk of breast cancer. Although we did not observe statistically significant interactions between lower dietary zinc intake and *WT1*, *CA10* methylation on breast cancer risk, we did find that lower zinc intake combined with methylation of *WT1*, *CA10* significantly increased the breast cancer risk by 10.220-fold and 3.145-fold, respectively.

Our previous study have tested the accuracy of MS-HRM by detecting the *WT1* methylation level with both MS-HRM and pyrosequencing, and the results were highly correlated between these two methods [42]. However, the methylation level of leukocyte DNA is relatively low and the limitation of pyrosequencing is 2%. As a reliable and high sensitive technique, MS-HRM can assess the methylation level of targeted CpGs as low as 0.1% [43]. The high consistency of our test for different runs which making the non-misclassification of methylation level between case and control and the probability of higher sensitivity of MS-HRM comparing pyrosequencing can make our study result more conserved [44].

Limitations should be taken into consideration before drawing a conclusion: first, as in all retrospective analyses, our study may have some recall bias when collecting information on environmental factors including the intake of zinc. Second, the sample size of our study is not large enough for subgroup analysis, including the subgroup analyses of low frequency environmental factors, like smoking behavior, therefore their associations with DNA methylation of *WT1*, *CA10* could not be analyzed.

In summary, our study suggested that methylation of *WT1* and *CA10* in blood leukocytes may associate with the risk of breast cancer. There were also associations between *WT1* methylation and risk of Luminal subtypes of breast cancer, *CA10* methylation and risk of Luminal B subtype of breast cancer. Lower level of dietary zinc intake combined with methylation of *WT1*, *CA10* may be associated with breast cancer risk.

Abbreviations

WT1: Wilm's Tumor 1; *CA10*:Carbonic Anhydrase 10; MS-HRM:Methylation-Sensitive High-Resolution Melting; TNBC:Triple Negative Breast Cancer; CIs:Confidence Intervals; OR:Odds Ratio; ER:Estrogen Receptor; PR:Progesterone Receptor; HER-2:Human Epidermal growth factor Receptor-2; BMI:Body Mass Index

Declarations

Ethics approval and consent to participate

Not applicable

Consent for publication

Not applicable

Availability of data and materials

The datasets used and/or analysed during the current study are available from the corresponding author on reasonable request

Competing interests

The authors declare that they have no competing interests

Funding

This study was supported by the National Natural Science Foundation of China (Yashuang Zhao, grant no. 81172743)

Authors' contributions

GA and GS have been involved in drafting the manuscript. LY and ZH performed subsequent data analysis. WX, ZL and above researchers together completed experiment part of this research. Dr. ZY and Dr. PD revised the manuscript for important intellectual content.

Acknowledgements

The authors thank all the patients and healthy volunteers for providing blood samples and all the research staff for their contributions to this project.

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Figures

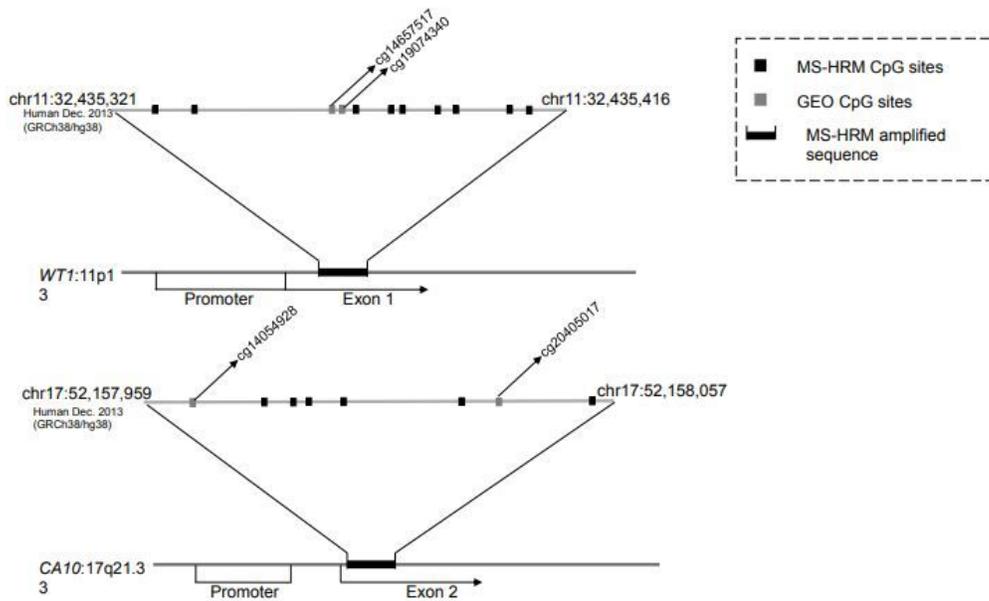


Figure 1

MS-HRM amplified sequence of WT1 and CA10 and the validated Cg sites in GSE51032

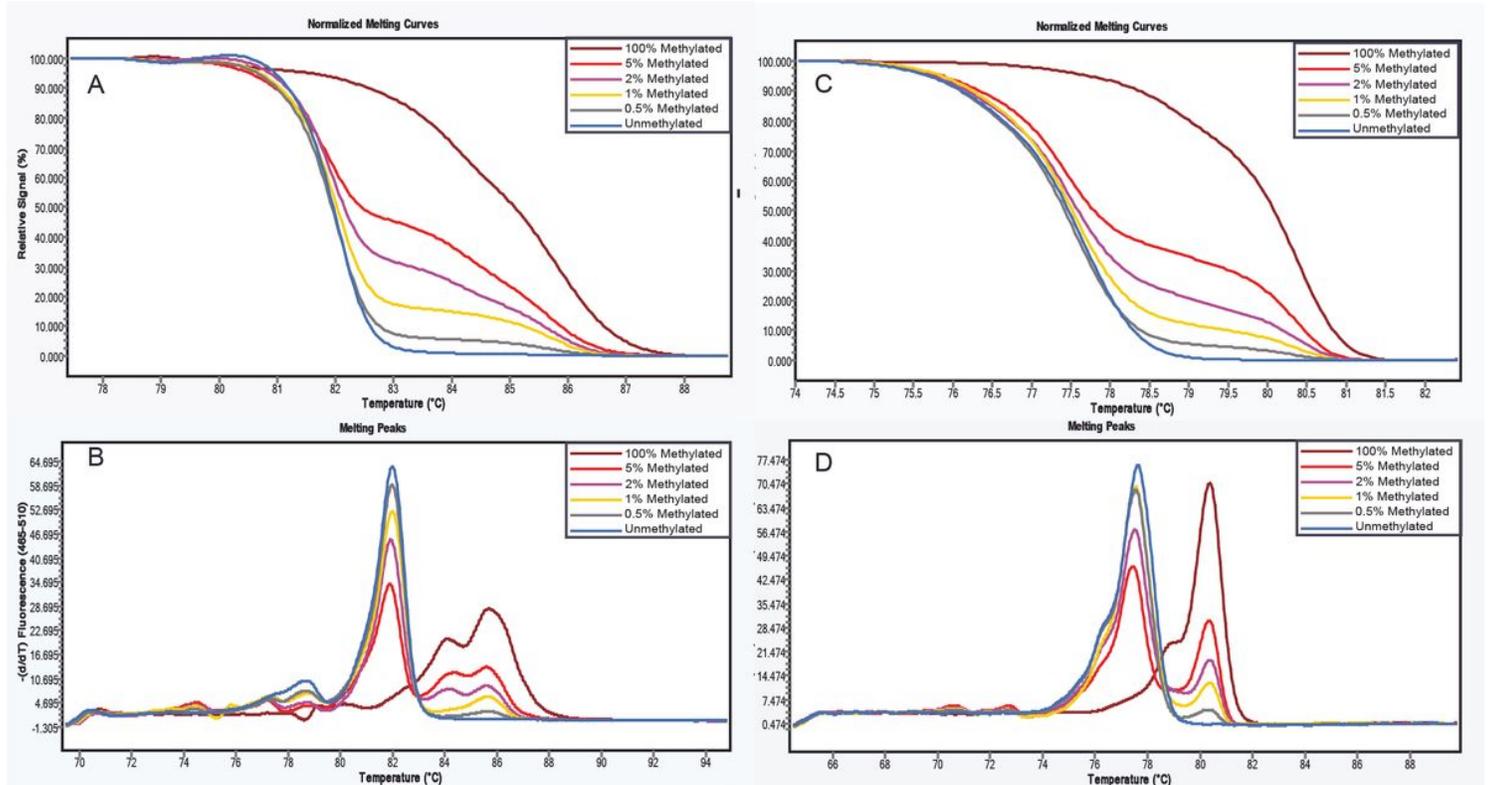


Figure 2

The MS-HRM based method for WT1 and CA10 methylation detection. The figures showed normalized melting curves and melting peaks for standards methylation level and of WT1(A)(B) and CA10(C)(D).The methylation status of the standards were 0%, 0.5%, 1%, 2%, 5%, 100%, respectively

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