Genetic Variants in the Promoter Region of miR-10b and the Risk of Breast Cancer

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Received 1 March 2017; Accepted 14 May 2017; Published 12 June 2017

A cademic Editor: Hushan Yang

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Variants in microRNA genes may affect their expression by interfering with the microRNA maturation process and may substantially contribute to the risk of breast cancer. Recent studies have identified miR-10b as an interesting candidate because of its close association with the metastatic behavior of breast cancer. However, the roles of miR-10b-related single nucleotide polymorphisms in breast cancer susceptibility remain unclear. This case-control study evaluated the associations between variants in the upstream transcription regulation region of miR-10b and the risk of breast cancer among Chinese women. Seven potentially functional SNPs were investigated using genotyping assays. The potential biological functions of the identified positive SNPs were further evaluated using in silico databases. We found that rs4078756, which was located at the promoter region of miR-10b, was significantly associated with breast cancer risk (rs4078756 AG/GG versus AA, adjusted odds ratio: 1.17, 95% confidence interval: 1.02–1.35). The other six single nucleotide polymorphisms exhibited negative associations. Based on the in silico prediction, rs4078756 potentially regulated miR-10b expression through promoter activation or repression. These findings indicate that a potentially functional SNP (rs4078756) in the promoter region of miR-10b may contribute to breast cancer susceptibility among Chinese women.

1. Introduction

Breast cancer is the most common malignancy among women, with an estimated 1.7 million cases diagnosed worldwide in 2012 [1]. In China, breast cancer is the most common cancer among women and is the sixth most common cause of death among Chinese women [2]. The precise mechanisms underlying breast cancer have not been fully explored, although several strong genetic and environmental risk factors for breast cancer have been identified and have been addressed in public awareness campaigns and clinical monitoring strategies [3, 4].

Recent research has revealed that microRNAs (miRNAs) participate in human carcinogenesis as either tumor suppressors or oncogenes, and the disruption of specific miRNA expression levels and functions might play a key role in the genesis of diverse cancer types [5–7]. Abnormal expressions of many miRNAs, including miR-34a, miR-210, miR-567, and miR-10b, were also associated with breast cancer tumorigenesis or progression [8–11]. As a key molecule in the development of breast cancer, miR-10b was first identified as being downregulated in primary breast tumors, compared to normal breast samples [11]. However, Ma et al. reported conflicting findings in 2007, as they observed that miR-10b was upregulated in metastatic breast cancer [12]. Subsequent studies have revealed that overexpression of miR-10b triggered migration and invasion processes in various cancer cell lines, as well as distant metastasis in xenotransplantation models [12–18]. Furthermore, miR-10b exerted its oncogenic...
effects by directly targeting various tumor-associated genes, such as HOXD10, TBX5, KLF4, and PTEN, in breast cancer, pancreatic cancer, glioblastoma, and bladder cancer [12–19]. These findings indicate that miR-10b plays a central role in cancer metastasis and may be used as a biomarker for breast cancer carcinogenesis.

A growing number of studies have revealed that single nucleotide polymorphisms (SNPs) in miRNA genes may interfere with the miRNA transcription or maturation processes and are associated with susceptibility to cancer development [20–26]. For example, rs16159732 in the miR-6826 primary sequence was associated with breast cancer among women of African ancestry [22]. In addition, rs164913 in the miR-196a2 precursor sequence may affect the miRNA-196a2 maturation process and is associated with the risk of breast cancer among Chinese and American women [23–25]. Furthermore, rs2682818 in the stem-loop sequence of the miR-618 precursor may alter the secondary stem-loop structure and is associated with an increased breast cancer risk in a South American population [26]. However, we are not aware of any studies regarding the role of miR-10b SNPs in breast cancer risk. Nevertheless, given the important biological functions of miR-10b in breast cancer, polymorphisms in the miR-10b gene could potentially confer a risk of disease. Therefore, the present study used a case-control design to evaluate 7 potentially functional SNPs in the upstream transcription regulation region of the miR-10b gene. All candidate SNPs had a minor allele frequency (MAF) of ≥0.05 among Han Chinese women. We hope that the results can provide useful insights for breast cancer prevention and personalized treatment.

2. Materials and Methods

2.1. Study Population. This case-control study’s protocol was approved by the Institutional Review Board of Nanjing Medical University. A total of 1,064 breast cancer cases and 1,073 cancer-free controls were included in this study, which has been described previously [27]. Briefly, the patients were recruited between January 2004 and April 2010 at the First Affiliated Hospital of Nanjing Medical University, Gulou Hospital, and Cancer Hospital of Jiangsu Province (Nanjing, China). The diagnosis of breast cancer was confirmed using pathological examination. Patients with a history of cancer, radiotherapy, or chemotherapy were excluded. Cancer-free controls were randomly selected from a pool of individuals who voluntarily participated in a community-based screening program that was performed in Jiangsu Province during the same time period. The controls had no self-reported history of cancer and were frequency-matched with the cases according to age and residential area. All subjects were genetically unrelated Han Chinese women. Approximately 95% of the eligible population provided written informed consent for participation. Each participant completed an interview using a structured questionnaire to collect information regarding the demographic characteristics, menstrual history, reproductive history, and environmental exposure history. Information regarding the estrogen receptor (ER) and progesterone receptor (PR) statuses of breast cancer cases was extracted from their medical records. After each interview, a 5 mL venous blood sample was collected from each participant.

2.2. SNP Selection and Genotyping Assays. The miR-10b gene is located at 2q31.1, which is in an intergenic region between HOXD4 and HOXD8 genes. Its promoter has recently been identified in human mammary cells and is located approximately 12 kb upstream of precursor miR-10b (pre-miR-10b) [28]. We searched the International HapMap Project (http://www.hapmap.org), dbSNP (http://www.ncbi.nlm.nih.gov/projects/SNP/), SNAP (http://archive.broad-institute.org/mpg/snap/), and UCSC (http://genome.ucsc.edu/) databases for SNPs that were located between the promoter and pre-miR-10b. The linkage disequilibrium (LD) value ($r^2 < 0.8$) and MAF value ($≥0.05$) in the Chinese Han population were also applied to select candidate SNPs. We ultimately identified nine SNPs (rs3731795, rs79025511, rs4078756, rs1348807, rs1018827, rs6736786, rs10196832, rs4972806, and rs1867863) in the upstream region of pre-miR-10b, although we omitted rs3731795 and rs79025511 because of their high LD with rs4078756 ($r^2 > 0.8$) to optimize the assay. Thus, seven SNPs in the miR-10b transcript were genotyped for the present case-control study (Table 1).

The seven SNPs were genotyped using the Illumina Infinium® HumanExome BeadChip platform (Illumina, USA) and 2,137 DNA samples, which have been reported in the previous study [27]. Genotype calling was performed using Illumina’s GenTrain clustering algorithm (version 1.0) in GenomeStudio (V2011.1). The genotyping call rates for all SNPs were >97% among the 1,064 breast cancer cases and the 1,073 controls. Genotyping was performed without knowledge of the individual’s case or control status, and approximately equal numbers of case and control samples were tested during each assay, with two blank controls.

2.3. Statistical Analyses. Differences in demographic characteristics, selected variables, and genotype frequencies were compared between the cases and controls. These differences were evaluated using Student’s t-test (equal variance assumed) for continuous variables and the $\chi^2$ test for categorical variables. The Hardy-Weinberg equilibrium was tested using the goodness-of-fit $\chi^2$ test to compare the observed and expected genotype frequencies among the control subjects.

Associations between the genotypes and breast cancer risk were estimated using logistic regression analyses adjusted for age, age at menarche, and menopausal status. The effects were reported as odds ratios (ORs) and 95% confidence intervals (CIs). All statistical analyses were performed using SAS software (version 9.1.3; SAS Institute, Cary, NC, USA). P values of ≤0.05 were considered statistically significant.

3. Results

3.1. Associations between the Selected SNPs and Breast Cancer Risk. The included individuals’ basic characteristics are presented in Supplementary Table 1 in Supplementary Material available online at https://doi.org/10.1155/2017/2352874. After
| SNP       | Chr | Position      | Location                      | Alleles | Cases<sup>b</sup> N = 1,064 | Controls<sup>b</sup> N = 1,073 | Call rate (%) | MAF<sup>c</sup> (case/control) | HWE<sup>d</sup> | OR (95% CI)<sup>e</sup> | P value<sup>e</sup> |
|-----------|-----|---------------|-------------------------------|---------|-----------------------------|-----------------------------|---------------|-------------------------------|----------------|-----------------|----------------|
| rs4078756 | 2q31.1 | 177,004,115 | 11 kb upstream of pre-mir-10b | A/G     | 540/436/84                  | 582/425/66                  | 97.80         | 0.285/0.260                    | 0.341          | 1.17 (1.02–1.35) | 0.027          |
| rs1348807 | 2q31.1 | 177,005,757 | 9.3 kb upstream of pre-mir-10b | A/G     | 403/499/156                 | 391/507/171                 | 97.52         | 0.383/0.398                    | 0.750          | 0.91 (0.80–1.03) | 0.148          |
| rs3018827 | 2q31.1 | 177,007,664 | 7.5 kb upstream of pre-mir-10b | A/G     | 514/448/99                  | 502/471/99                  | 97.85         | 0.304/0.312                    | 0.477          | 0.92 (0.80–1.05) | 0.210          |
| rs6736786 | 2q31.1 | 177,008,914 | 6 kb upstream of pre-mir-10b  | A/G     | 419/495/148                 | 446/495/132                 | 97.89         | 0.372/0.354                    | 0.79           | 1.13 (0.99–1.29) | 0.066          |
| rs80196832 | 2q31.1 | 177,011,655 | 3.5 kb upstream of pre-mir-10b | A/G     | 936/127/1                   | 920/143/7                   | 97.89         | 0.061/0.073                    | 0.502          | 0.87 (0.68–1.12) | 0.281          |
| rs4972806 | 2q31.1 | 177,012,578 | 2.5 kb upstream of pre-mir-10b | A/G     | 352/512/197                 | 361/529/183                 | 97.85         | 0.427/0.417                    | 0.706          | 1.03 (0.91–1.17) | 0.643          |
| rs1867863 | 2q31.1 | 177,014,970 | 161 bp upstream of pre-mir-10b | A/C     | 434/488/140                 | 403/519/151                 | 97.89         | 0.362/0.383                    | 0.477          | 0.90 (0.79–1.02) | 0.105          |

<sup>a</sup>Major/minor allele; <sup>b</sup>major homozygote/heterozygote/rare homozygote between cases and controls; <sup>c</sup>minor allele frequency (MAF); <sup>d</sup>P values for the Hardy-Weinberg equilibrium (HWE) test; <sup>e</sup>logistic regression analysis with adjustment for age, age at menarche, and menopausal status in the additive model; Chr: chromosome, OR: odds ratio, CI: confidence interval.
Table 2: Associations between rs4078756 in the promoter region of miR-10b and breast cancer risk.

| Characteristics | Cases | Controls | OR (95% CI) | P   | pb |
|----------------|-------|----------|-------------|-----|----|
|                | AA (%)| AG (%)   | GG (%)      | AA | AG | GG (%) |              |
| Age            |       |          |             |     |    |        |              |
| <51 years      | 312 (53.0) | 242 (41.1) | 35 (5.9) | 289 (53.3) | 226 (41.7) | 27 (5.0) | 1.05 (0.86–1.28) | 0.648 | 0.111 |
| ≥51 years      | 228 (48.4) | 194 (41.2) | 49 (10.4) | 293 (55.2) | 199 (37.5) | 39 (7.3) | 1.32 (1.08–1.61) | 0.007 |       |
| Menopausal status |   |          |             |     |    |        |              |
| Premenopausal  | 266 (51.9) | 211 (41.1) | 36 (7.0) | 267 (53.0) | 212 (42.1) | 25 (5.0) | 1.15 (0.93–1.42) | 0.197 | 0.540 |
| Postmenopausal | 217 (48.2) | 194 (43.1) | 39 (8.7) | 286 (54.5) | 201 (38.3) | 38 (7.2) | 1.26 (1.03–1.54) | 0.028 |       |
| Age at menarche |       |          |             |     |    |        |              |
| <16 years      | 320 (53.5) | 236 (39.5) | 42 (7.0) | 217 (52.8) | 172 (41.9) | 22 (5.4) | 1.03 (0.84–1.26) | 0.799 | 0.115 |
| ≥16 years      | 211 (47.5) | 192 (43.2) | 41 (9.2) | 363 (55.0) | 253 (38.3) | 44 (6.7) | 1.29 (1.06–1.56) | 0.010 |       |
| Age at first live birth |       |          |             |     |    |        |              |
| <24 years      | 119 (49.6) | 104 (43.3) | 17 (7.1) | 204 (55.0) | 140 (37.7) | 27 (7.3) | 1.18 (0.90–1.53) | 0.229 | 0.831 |
| ≥24 years      | 392 (52.0) | 301 (39.9) | 61 (8.1) | 358 (53.4) | 276 (41.1) | 37 (5.5) | 1.14 (0.96–1.36) | 0.141 |       |
| ER status      |       |          |             |     |    |        |              |
| Positive       | 237 (48.6) | 211 (43.2) | 40 (8.2) | 237 (52.8) | 172 (41.9) | 22 (5.4) | 1.27 (1.07–1.52) | 0.008 | 0.713 |
| Negative       | 194 (51.5) | 146 (38.7) | 37 (9.8) | 193 (54.5) | 170 (45.5) | 21 (5.5) | 1.21 (1.0–1.46) | 0.055 |       |
| PR status      |       |          |             |     |    |        |              |
| Positive       | 237 (46.9) | 223 (44.2) | 45 (8.9) | 237 (52.8) | 172 (41.9) | 22 (5.4) | 1.34 (1.12–1.60) | 0.001 | 0.204 |
| Negative       | 192 (53.3) | 136 (37.8) | 32 (8.9) | 193 (54.5) | 170 (45.5) | 21 (5.5) | 1.13 (0.93–1.37) | 0.235 |       |

a Per-allele odds ratio (OR) and 95% confidence interval (CI) adjusted for age, age at menarche, and menopausal status where appropriate; b P value for the heterogeneity test; ER: estrogen receptor; PR: progesterone receptor.

Frequency matching, the cases and controls had comparable ages (P > 0.05). Compared to the controls, patients with breast cancer had significantly earlier menarche and later first live births (P < 0.0001). Among the 1,064 breast cancer cases, 490 cases (46.05%) were ER-positive and 506 cases (47.56%) were PR-positive.

The loci information and association results for the seven SNPs are described in Table 1. The multivariate logistic regression models revealed that rs4078756 was significantly associated with breast cancer risk (rs4078756 AG/GG versus AA, adjusted OR: 1.17, 95% CI: 1.02–1.35). The remaining six SNP were not significantly associated with breast cancer risk (Table 1).

We also performed stratification analysis of the associations between rs4078756 and breast cancer risk according to age, age at menarche, age at first live birth, and menopausal status. As shown in Table 2, the breast cancer risk associated with variant AG/GG genotypes (versus the AA genotype) was significantly higher among older women (adjusted OR: 1.32; 95% CI: 1.08–1.61), postmenopausal women (adjusted OR: 1.26; 95% CI: 1.03–1.54), women with later menarche (adjusted OR: 1.29; 95% CI: 1.06–1.56), ER-positive women (adjusted OR: 1.27; 95% CI: 1.07–1.52), and PR-positive women (adjusted OR: 1.34; 95% CI: 1.12–1.60). No heterogeneity was detected for each paired comparison (P > 0.05).

3.2. Bioinformatics Analysis of the Potentially Biological Functions of rs4078756.

The potential biological functions of rs4078756 were evaluated using bioinformatics analysis with HaploRegV4.1 and the UCSC database. As shown in Table 3, rs3731795 and rs79025511 exhibited strong linkage with rs4078756 (r² > 0.8) in Chinese and Japanese population and were strongly modified by histone H3K27Ac, which might lead to aberrant transcription of miR-10b (Figure 1). Based on the JASPAR database for predicting transcription factor binding, we found that the G allele of rs3731795 might increase the binding of transcription factors, such as TCF3, TFAP2A, and TCF4, to the promoter of miR-10b, compared to the C allele (Table 4).

4. Discussion

The present study investigated the associations between breast cancer and seven potentially functional SNPs that were located in the upstream transcription regulation region of the miR-10b gene. The results indicate that an A-to-G base change at rs4078756 increased the risk of breast cancer among a group of Han Chinese women. To the best of our knowledge, this is the first study to evaluate the associations between breast cancer susceptibility and genetic variations in the potential regulatory region of miR-10b.

Previous research has indicated that miR-10b appears to play a key role in breast cancer invasion and metastasis. Ma et al. reported that miR-10b was highly expressed in clinical samples of metastatic breast cancer, and the ectopic upregulation of miR-10b in nonmetastatic breast cancer cells initiated invasion and metastasis [12]. Moreover, miR-10b silencing inhibits breast cancer metastasis in a mouse mammary tumor model [12, 13]. Additional studies have suggested that miR-10b regulates invasion and metastasis in breast cancer by suppressing the translation of a targeting gene (HOXD10) [12]. In this context, HOXD10 is an mRNA
Table 3: Annotation of variants with strong linkage disequilibrium with the SNP rs4078756 in HaploRegV4.1.

| Chr | Pos (hg19) | LD  | Variant | Ref | Alt | ASN freq | Promoter histonemarks | DNAse | Proteins bound | Motifs changed |
|-----|------------|-----|---------|-----|-----|----------|----------------------|-------|----------------|----------------|
| 2   | 177000616  | 1.00| rs1348808| T   | C   | 0.23     | 15 tissues           | 12 tissues | CTBP2          | Ets, LF-A1, NF-E2 |
| 2   | 177001145  | 1.00| rs76652183| G   | T   | 0.23     | 19 tissues           | 18 tissues | 5 bound proteins | EBF            |
| 2   | 177001378  | 1.00| rs3731795 | A   | G   | 0.27     | 19 tissues           | 7 tissues  | CTCF, p300      |                |
| 2   | 177001962  | 0.96| rs79025511| C   | T   | 0.23     | 19 tissues           | 32 tissues | 5 bound proteins | 4 altered motifs|
| 2   | 177004689  | 0.92| rs79120932| G   | T   | 0.23     | 19 tissues           | 32 tissues | 5 bound proteins | 4 altered motifs|
| 2   | 177005519  | 1.00| rs67435554| G   | T   | 0.23     | 12 tissues           | 19 tissues | Pax-5           |                |
| 2   | 177007102  | 1.00| rs76652183| G   | T   | 0.23     | 12 tissues           | 19 tissues | 32 tissues       | 5 bound proteins|
| 2   | 177007527  | 1.00| rs76363873| A   | G   | 0.23     |                    |          | IPSC            | GATA, MZF1::1–4 |
| 2   | 177008484  | 1.00| rs79440139| T   | A   | 0.23     |                    |          | 6 altered motifs |

Chr: chromosome, Pos: position, LD: linkage disequilibrium in CHB + JPT population, Ref: reference, Alt: alternative, freq: frequency, MUS: musculus, and IPSC: induced pluripotent stem cell.

Encoding a transcriptional repressor that inhibits the expression of several genes that are involved in cell migration and extracellular matrix remodeling, such as RhoC, uPAR, α3 integrin, and MT1-MMP [12]. Furthermore, miR-10b could target the syndecan-1 gene and promote breast cancer cell motility and invasiveness through a Rho-GTPase-dependent and E-cadherin-dependent mechanism [29]. Another study revealed that miR-10b promotes cell proliferation, migration, and invasion by inhibiting the expression of the TRX5 transcription factor, which led to repression of the DYRK1A and PTEN tumor suppressor genes [19]. In addition, miR-10b could respond to vascular endothelial growth factor stimulation and was expressed at high levels in the human high-grade breast tumor vasculature, which suggested that vascular expression of miR-10b might reflect the metastatic progression of breast cancer [30].

Similar to other protein-coding genes, the miR-10b gene has its own promoter. The putative promoter of human miR-10b was initially characterized by Zhou et al., who found that it spanned between −111 bp and −460 bp upstream of pre-miR-10b [31]. Ma et al. also found that the Twist transcription factor could activate transcription of the miR-10b gene by binding to an E-box sequence that is proximal to its putative promoter [12]. Vrba et al. subsequently performed H3K4me3 chromatin immunoprecipitation assays using human mammary cells and redefined the promoter region of miR-10b as being located approximately 12 kb upstream of pre-miR-10b [28]. Several researchers have also suggested that SNPs in the
evaluations are warranted to confirm these findings. Studies with the technically diverse population and functional Han Chinese women. Larger well-designed epidemiological confirmation using biological assays in future studies.

speculations are based on computer simulations and require depending on the specific interacting protein. However, these

ingeneregulationthroughpromoteractivationorrepression, the G allele of rs3731795 might increase the binding of tran-

peak of the H3k27me3 histone mark in seven cell lines, and this mark is often found near active regulatory elements. In addition, according to JASPAR database, we observed that the G allele of rs3731795 might increase the binding of transcription factors, such as TCF3, TFAP2A, and TCF4, to the promoter region of miR-10b. These transcription factors are involved in gene regulation through promoter activation or repression, depending on the specific interacting protein. However, these speculations are based on computer simulations and require confirmation using biological assays in future studies.

In conclusion, the present results suggest that rs4078756 in the promoter region of the miR-10b gene is associated with a significantly increased risk of breast cancer among Han Chinese women. Larger well-designed epidemiological studies with ethnically diverse populations and functional evaluations are warranted to confirm these findings.

**Conflicts of Interest**

The authors declare that there are no conflicts of interest.

**Acknowledgments**

The authors thank the study participants and research staff for their contributions. Funding was provided by the Natural Science Foundation of Jiangsu Province (BK20151553), the Natural Science Foundation for Outstanding Youth of Jiangsu Province (BK20160095), the National Natural Science Foundation of China (81521004, 81230067), the Priority Academic Program for the Development of Jiangsu Higher Education Institutions (Public Health and Preventive Medicine), and the Top-notch Academic Programs Project of Jiangsu Higher Education Institutions (PPZY2015A067).

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