Null Results in Brief

Common Genetic Variants in the MicroRNA Biogenesis Pathway Are Not Associated with Breast Cancer Risk in Asian Women

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Abstract

Background: Although the role of miRNA in cancer development and progression has been well established, the association between genetic variants in miRNA biogenesis pathway genes and breast cancer risk has been yet unclear.

Methods: We analyzed data from two genome-wide association studies conducted in East Asian women including 5,066 cases and 4,337 controls. Among the single-nucleotide polymorphisms (SNP), which were directly genotyped or imputed, we selected 237 SNPs in 32 genes involved in miRNA biogenesis pathway and its regulation.

Results: Although eight SNPs were nominally associated with breast cancer risk in combined samples (P < 0.05), none of them were significant after adjustment for multiple comparisons.

Conclusions: The common genetic variants in miRNA biogenesis pathway genes may not be associated with breast cancer risk.

Impact: This study suggests no association between the polymorphisms in miRNA biogenesis pathway genes and breast cancer risk. Studies with large sample size and more genetic variants should be warranted to adequately evaluate the potential association. Cancer Epidemiol Biomarkers Prev; 21(8); 1385–7. ©2012 AACR.

Introduction

MiRNAs are a major class of noncoding RNAs that posttranscriptionally modulate gene expression in a sequence specific manner. The role of miRNAs in human cancer pathogenesis has been well established by the identification of aberrant expression of miRNAs in many types of cancer (1). There is increasing evidence that the genetic variants in miRNA genes, in their biogenesis pathway genes and binding sites of target mRNA are associated with cancer risk and survival (2). However, the association between the polymorphisms of miRNA biogenesis pathway genes and breast cancer risk is uncertain. The previous study focusing on this pathway was conducted in small sample size and the coverage of genes of interests was limited (3). More recently, the results on the effects of genetic variants in miRNA biogenesis pathway genes were inconsistent even in the same cancer type (4). We comprehensively evaluated the common variants in miRNA biogenesis pathway genes by analyzing data from the 2 previous genome-wide association studies (GWAS) conducted in women of Asian ancestry consisted of 5,066 breast cancer cases and 4,337 controls.

Materials and Methods

Detailed methods for the Seoul Breast Cancer Study and the Shanghai Breast Cancer Study have been published elsewhere (5, 6) and described in brief in Supplementary Table S1 (3). This study included 5,066 histologically confirmed breast cancer cases and 4,337 controls [(2,190/2,052) Koreans and (2,876/2,285) Chinese]. The protocol was approved by the Institutional Review Board, and all participants provided written informed consent. The 35 genes (ADAR, ADARB1, DDX5, DDX17, DDX20, Dicer1, Dicer2, DROSHA, DGCR8, DICER1, DROSHA, EIF2C1, EIF2C2, GEMIN4, HNRNPA1, ILF2, ILF3, KHRSRP, LIN28A, RAN, SMAD1, SMAD2, SMAD3, SMAD4, SMAD5, SMAD6, SMAD7, SNIP1, SRRT, SRSF1, TARBP, TRIM32, TRIM71, XPO5, XRNR2, and ZCCHC11) were selected on the basis of their biologic role in miRNA biogenesis as determined by the combination of literature review (7) and the bioinformatics tool the Gene Ontology.
Table 1. Association between the SNPs with a \( P_{\text{meta}} < 0.050 \) in the genes of interests and breast cancer risk

<table>
<thead>
<tr>
<th>Gene</th>
<th>SNP Position</th>
<th>Genomic Location</th>
<th>Location from GRCh36/hg19</th>
<th>Genomic Location</th>
<th>Gene Function</th>
<th>Alleles</th>
<th>OR (95% CI)</th>
<th>( P_{\text{meta}} )</th>
<th>( P_{\text{meta}}^{\text{adj}} )</th>
<th>( P_{\text{het}} )</th>
</tr>
</thead>
<tbody>
<tr>
<td>DDX20</td>
<td>rs2802025</td>
<td>10p13.2/112104760</td>
<td>100 kb upstream of the largest cDNA</td>
<td>10p13.2/112104760</td>
<td>10p13.2/112104760</td>
<td>A/T</td>
<td>0.94 (0.81–1.09)</td>
<td>1.00</td>
<td>1.00</td>
<td>0.05</td>
</tr>
<tr>
<td></td>
<td>rs578126</td>
<td>1p13.2/112104760</td>
<td>100 kb upstream of the largest cDNA</td>
<td>1p13.2/112104760</td>
<td>1p13.2/112104760</td>
<td>T/A</td>
<td>0.48 (0.38–0.61)</td>
<td>1.00</td>
<td>1.00</td>
<td>0.02</td>
</tr>
<tr>
<td></td>
<td>rs6578126</td>
<td>8q24.3/141704788</td>
<td>100 kb upstream of the largest cDNA</td>
<td>8q24.3/141704788</td>
<td>8q24.3/141704788</td>
<td>A/G</td>
<td>0.96 (0.84–1.10)</td>
<td>1.00</td>
<td>1.00</td>
<td>0.04</td>
</tr>
<tr>
<td></td>
<td>rs7834784</td>
<td>8q24.3/141693661</td>
<td>100 kb upstream of the largest cDNA</td>
<td>8q24.3/141693661</td>
<td>8q24.3/141693661</td>
<td>C/T</td>
<td>0.82 (0.70–0.96)</td>
<td>1.00</td>
<td>1.00</td>
<td>0.07</td>
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<td>rs10848087</td>
<td>12q24.33/129405118</td>
<td>100 kb upstream of the largest cDNA</td>
<td>12q24.33/129405118</td>
<td>12q24.33/129405118</td>
<td>A/G</td>
<td>0.96 (0.85–1.10)</td>
<td>1.00</td>
<td>1.00</td>
<td>0.04</td>
</tr>
<tr>
<td></td>
<td>rs12432281</td>
<td>14q32.13/94674881</td>
<td>100 kb upstream of the largest cDNA</td>
<td>14q32.13/94674881</td>
<td>14q32.13/94674881</td>
<td>A/G</td>
<td>0.89 (0.79–1.03)</td>
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<td>0.03</td>
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<tr>
<td></td>
<td>rs1991401</td>
<td>20p11.22/21266977</td>
<td>100 kb upstream of the largest cDNA</td>
<td>20p11.22/21266977</td>
<td>20p11.22/21266977</td>
<td>A/C</td>
<td>0.91 (0.82–1.01)</td>
<td>1.00</td>
<td>1.00</td>
<td>0.01</td>
</tr>
</tbody>
</table>

Discussion

In this study, SNPs in miRNA biogenesis pathway genes were not associated with breast cancer risk. We could not exclude the possibility that the lack of association could come from the differences in subject characteristics, the interactions of environmental modifiers, and other uncontrolled bias between both studies. We also could not replicate the SNPs shown in previous report (3) although highly correlated proxies were included aside from SNPs in DDX20. Considering the sample size of the previous report, it could be a chance finding and at least need to be further investigated in other populations. The strengths of this study are its large sample size and comprehensive search of genes of interests and the high coverage of known SNPs. With the current sample size, for a SNP with MAF as 0.26 (average value of all tested SNPs), the minimum log-additive OR that we can detect at 99% power is 1.22, considering the Bonferroni-corrected significance level (\( P = 1E-04 \)). Future genomic scan including several kinds of structural variations, copy number variants, new variants identified by high-resolution sequencing with larger sample size, as well as subtype specific

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analysis, could elucidate further information on the potential association.

Disclosure of Potential Conflicts of Interest
No potential conflicts of interest were disclosed.

Authors' Contributions
Conception and design: H. Sung, S.K. Park, D. Kang
Development of methodology: H. Sung, D. Kang
Acquisition of data (provided animals, acquired and managed patients, provided facilities, etc.): H. Sung, K.-Y. Yoo, D.-Y. Noh, W. Zheng

Writing, review, and/or revision of the manuscript: H. Sung, B. Zhang, Y.-J. Choi, S.K. Park, D.-Y. Noh, D. Kang
Administrative, technical, or material support (i.e., reporting or organizing data, constructing databases): D.-Y. Noh, W. Zheng
Study supervision: D. Kang, W. Zheng

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