SOX1 and PAX1 Are Hypermethylated in Cervical Adenocarcinoma and Associated with Better Prognosis

Zitong Zhao, Xiaoye Zhang, Xueheng Zhao, Jingting Cai, Na-Yi Yuan Wu, and Jing Wang

Hunan Cancer Hospital, The Affiliated Cancer Hospital of Xiangya School of Medicine, Central South University, China

Correspondence should be addressed to Na-Yi Yuan Wu; wunayiyuan@163.com and Jing Wang; wangjing0081@hnca.org.cn

Zitong Zhao and Xiaoye Zhang contributed equally to this work.

Received 15 July 2020; Revised 24 November 2020; Accepted 27 November 2020; Published 8 December 2020

Background. The increased risk and poor survival outcome of cervical adenocarcinoma (CAC) demand for effective early diagnostic biomarkers that can predict the disease progression and outcome. The purpose of this study was to investigate the value of methylation status of SOX1 and PAX1 in the detection and prognosis of CAC. Methods. We performed a quantitative methylation-specific polymerase chain reaction in 205 cervical paraffin-embedded specimens (175 CACs, 30 noncancer cervical tissues). Overall and progression-free survival (OS and PFS, respectively) rates were calculated and compared using the Kaplan-Meier method. The prognostic value of SOX1m and PAX1m on CAC patients was assessed by the Cox regression model. A mathematical formula combining SOX1m, PAX1m, and age was constructed for survival prediction. Results. The methylation status of SOX1 and PAX1 was higher in CAC tissues than in noncancer cervical tissues. In addition, SOX1m-positive CAC patients showed a higher 5-year OS rate than SOX1m-negative patients. In CAC patients with smaller tumor size (<4 cm), the PAX1m-positive group showed a higher 5-year PFS rate than the PAX1m-negative group. In the algorithm combining SOX1m, PAX1m, and age, the low-risk group showed a better 5-year OS and PFS rate than the high-risk group. Conclusion. SOX1 and PAX1 methylation levels are higher in CAC than in normal cervical tissues and are potential biomarkers for monitoring CAC prognosis.

1. Introduction

Cervical cancer is the second commonest tumor in women worldwide [1]. Moreover, it is a major cause of cancer-related death among women in developing countries [2]. Cervical adenocarcinoma (CAC) ranks second after cervical squamous cell carcinoma (SCC) as the most common pathological type. Although the use of human papillomavirus (HPV) vaccines and effective Pap smear screening have significantly decreased the incidence rate of cervical carcinoma in most regions, the percentage of CAC has been increasing, especially in younger women, accounting for 20-25% of all cervical carcinoma in some developed countries [2, 3]. Moreover, the high propensity of CAC for ovarian metastases always leads to fertility destruction in young women [4–10]. Several studies have shown that at the same stage, CAC has a worse prognosis than SCC, mainly because of its higher rate of metastase [6] and lower sensitivity to radiotherapy and chemotherapy [11]. The increased frequency and poor survival outcome raise the need for useful biomarkers that can predict the progression and prognosis of CAC.

Epigenetic alterations include heritable DNA methylation and histone protein modifications that do not affect the DNA transcriptional sequence [12–15]. DNA methylation is an epigenetic alteration, which always occurs in the early stage of carcinogenesis, leading to lessen even lost expression of the methylated gene [16]. Expression of SOX1 correlated with early embryogenesis, central nervous system development, and neural stem cell maintenance [17]. Nonetheless, hypermethylation in the promoter region and/or somatic mutations in the so-called tumor suppressor genes might cause silencing or inhibition of SOX1, which in turn...
may result in cancer cell proliferation and migration and finally progression of cervical carcinogenesis [18]. Hypermethylated SOX1 (SOX1\textsuperscript{m}) has been associated with several cancer types, including hepatocellular cancer, lung cancer, urothelial bladder cancer, endometrial cancer, and SCC [19–22]. PAX1 expression is correlated with embryogenesis, particularly with the development of the thymus, parathyroid glands, and skeleton [23–25]. Hypermethylated PAX1 (PAX1\textsuperscript{m}) has been found in ovarian cancer, oral cancer, and SCC [26–29]. Our previous study confirmed SOX1 and PAX1 methylation as promising screening biomarkers in cervical neoplasia, mainly in high-grade squamous intraepithelial lesions and SCC, because of its remarkable discriminating ability between normal tissues and high-grade cervical lesions [30–33]. However, CAC and SCC are different with respect to tumor development, progression, and molecular pathology. It remains unknown whether the methylation status of SOX1 and PAX1 is different between CAC and SCC. In addition, the methylation level and prognostic value of SOX1 and PAX1 for CAC are unclear. In this study, we investigated the methylation levels of SOX1 and PAX1 differ in CAC and evaluated the potential value of SOX1 and PAX1 gene methylation for prognosis in CAC.

2. Methods

2.1. Patients and Tissue Specimens. A total of 205 cervical paraffin-embedded specimens between 2013 and 2015 were collected from the Hunan Cancer Hospital, the Affiliated Cancer Hospital of Xiangya School of Medicine, Central South University, including 30 noncancer cervical samples and 175 adenocarcinoma samples (Table 1). The patients’ demographic and clinicopathological data, including clinical stage (FIGO Committee on Gynecologic Oncology, 2009), tumor size, depth of invasion, histologic tumor grade, lymph node metastasis, and treatment modality, were recorded. The study protocols were agreed by the Hunan Cancer Hospital ethics committee (project number: 2015[01]) and the Chinese Clinical Trial Registry (registration number: ChiCTR180018931).

2.2. DNA Preparation, Bisulfite Conversion, and Quantitative Methylation-Specific Polymerase Chain Reaction (qMSP). An ISO17025-certified laboratory (iStat Biomedical Co., Ltd., New Taipei City, Taiwan) carried out total methylation tests. They first defaraffinized paraffin-embedded cervical tissues and then extracted genomic DNA (gDNA) samples and bisulfite converted by using an Epigen\textsuperscript{m} nucleic acid extraction kit and an Epigene\textsuperscript{m} bisulfite conversion kit (iStat Biomedical Co., Ltd., New Taipei City, Taiwan). Quantitative methylation-specific PCR (qMSP) was then used for analyzing the methylation level of SOX1 and PAX1 by the TaqMan Probe system in a Light Cycler LC480 system (Roche Applied Science, Penzberg, Germany). Our previous study described specific primers and probes for qMSP [31, 34, 35]. The registered A375 and CaSki two cancer cell lines were treated as methylation and nonmethylation controls to ensure the quality of the bisulfite conversion and qMSP processes. The DNA methylation level was assessed as the methylation index (M-index) using the formula [36]: 

\[
\text{M-index} = \frac{2^{(C_{\text{SOX1}} - C_{\text{PAX1}})}}{C_{\text{SOX1}}} - 1 
\]

where \(C_{\text{SOX1}}\) and \(C_{\text{PAX1}}\) are the \(Cp\) values for SOX1 and PAX1, respectively.

2.3. Statistical Analyses. The cut-off values for SOX1\textsuperscript{m} and PAX1\textsuperscript{m} were generated from 205 clinical samples (175 CACs and 30 noncancer cervical tissues). Receiver operating characteristic (ROC) curves were performed, and the area under the ROC curve (AUC) was calculated for the detection of the CAC.

All statistical analyses were performed using GraphPad Prism\textsuperscript{®} 7.00 (GraphPad, La Jolla, CA, USA) and SPSS Statistics 24 (SPSS, Inc., Chicago, IL, USA). The correlation between SOX1\textsuperscript{m} or PAX1\textsuperscript{m} and each clinicopathological characteristic of the CAC patients was evaluated by the Mann-Whitney and Dunnett’s tests. Kaplan-Meier method was used to describe the progression-free survival and overall survival (PFS and OS). The PFS was judged from the date of the first relapse at any site or death including all causes, and OS was calculated from treatment to death covering any cause. Hazard ratio (HRs) was calculated with multivariate Cox regression analysis.

2.4. A Mathematical Algorithm Combining SOX1\textsuperscript{m}, PAX1\textsuperscript{m}, and Age for CAC Prognosis Prediction. To investigate the effectiveness of the combination of the methylation statuses of these two genes and the clinicopathological factors to
predict the clinical outcome, we constructed a mathematical formula for survival prediction. Each patient was assigned with a risk score in accordance with a linear combination of the expression level of the two genes. The risk score was calculated as follows:

$$
\text{risk score} = \frac{1}{2} W_1 \times SOX_1 + \frac{1}{2} W_2 \times PAX_1 + \frac{1}{2} W_3 \times \text{age}.
$$

The weight factors ($W_1$–$W_3$) were generated from the regression coefficients derived from the aforementioned univariate Cox regression analysis (Lossos et al., 2004). We divided patients into low-risk and high-risk groups according to the median risk score as the cut-off point. The OS and PFS were then estimated by the Kaplan-Meier method.

3. Results

3.1. SOX1 and PAX1 Are Hypermethylated in CAC Tissues than in Noncancer Cervical Tissues. Among our 205 cervical specimens, 30 were noncancer cervical samples and 175 were adenocarcinoma samples (Table 1). The mean M-index for SOX1 ($476.80 \pm 92.47$) and 0.48 ± 0.29, respectively, $p < 0.05$)
and PAX1 (515.70 ± 56.30 and 28.19 ± 9.19, respectively, p = 0.05) was significantly higher in CAC tissues than in noncancer tissues (Figure 1(a)). By ROC analysis, the positive cut-off value for SOX1m was ΔCp ≤ 11, with a high AUC level of 88.42%, a sensitivity of 87.22%, and specificity of 56.67%. The positive cut-off value for PAX1m was ΔCp ≤ 9, with a high AUC level of 70.80%, sensitivity of 44.30%, and specificity of 100% (Figure 1(b)), which suggested that SOX1m and PAX1m may be detection biomarkers for CAC.

The SOX1 and PAX1 methylation statuses showed no significant difference based on age, FIGO stage, tumor size, depth of invasion, lymph node metastasis, and histologic grade in CAC patients (Table 2).

### 3.2. Hypermethylated SOX1 and PAX1 Are Associated with Better Survival in CAC Patients

Further studies were conducted to investigate whether the methylation of SOX1 and PAX1 was correlated with the prognosis in CAC patients. The SOX1m-positive group showed a higher 5-year OS rate of 93.35% than the SOX1m-negative group, which showed a 5-year OS rate of 68.29% (p = 0.048) (Figure 2(a)). While no remarkable finding was obtained in the analysis of the 5-year PFS rate. For PAX1, there was no evident difference in 5-year OS rate or 5-year PFS rate between these two groups (data not shown). However, in CAC patients with smaller tumor size (<4 cm), the PAX1m-positive group had a higher 5-year PFS rate than the PAX1m-negative group (100% vs. 82.4%, p = 0.044) (Figure 2(b)).

### 3.3. Algorithm Combining SOX1m, PAX1m, and Age for Prognosis of CAC Patients

We established an algorithm for quantifying age, SOX1m, and PAX1m as a prognostic factor to calculate the recurrence risk and outcome of patients with CAC. The final algorithm for OS was as follows: risk score = −1.109 × SOX1m + −0.849 × PAX1m + 0.399 × age. The final algorithm for PFS was as follows: risk score = −0.586 × SOX1m + −0.553 × PAX1m + 0.674 × age. The algorithm divided patients into low-risk and high-risk groups. However, the low-risk group showed a better 5-year OS rate (95.89% vs. 81.47%, p = 0.019) (Figure 3(a)) and a much better 5-year PFS rate (90.58% vs. 72.50%, p = 0.006) than the high-risk group (Figure 3(b)).

### 4. Discussion

It is well known that the prognosis of CAC is worse than cervical SCC, even for early-stage patients, especially in developing countries [37]. Gene methylation is an epigenetic modification, which has tumor-suppressive or tumorigenic two opposite effects, possibly playing key roles in carcinogenesis and cancer progression. Before this study, the methylation status and prognostic value of SOX1m and PAX1m for CAC were unclear. In this study, we observed higher methylation levels of SOX1 and PAX1 in CAC than in noncancer cervical tissues. For the detection of CAC, SOX1m showed 87.22% sensitivity and 56.67% specificity, while PAX1m showed 44.30% sensitivity and 100% specificity. Moreover, several studies have demonstrated that PAX1 methylation increases following increased disease grade: PAX1 methylation in SCC > high-grade squamous intraepithelial lesion (HSIL) > low-grade squamous intraepithelial lesion (LSIL) > normal tissue [38, 39]. These suggest that hypermethylation of SOX1 and PAX1 might play an important role in the diagnosis and cancer progression of CAC.

The current study also showed, for the first time, that CAC patients who are SOX1m-positive show a better

### Table 2: Association between SOX1m or PAX1m and clinicopathological characteristics in 175 CAC patients.

<table>
<thead>
<tr>
<th>Variable</th>
<th>Number of patients (n = 175)</th>
<th>Positive SOX1m Negative</th>
<th>p value</th>
<th>Positive PAX1m Negative</th>
<th>p value</th>
</tr>
</thead>
<tbody>
<tr>
<td>Age (years)</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>&lt;50</td>
<td>96 (54.86%)</td>
<td>83</td>
<td>13</td>
<td>28</td>
<td>68</td>
</tr>
<tr>
<td>≥50</td>
<td>79 (45.14%)</td>
<td>70</td>
<td>9</td>
<td></td>
<td></td>
</tr>
<tr>
<td>FIGO stage</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>&lt;IB</td>
<td>127 (71.57%)</td>
<td>112</td>
<td>15</td>
<td>36</td>
<td>91</td>
</tr>
<tr>
<td>≥IB</td>
<td>48 (27.43%)</td>
<td>41</td>
<td>6</td>
<td>14</td>
<td>33</td>
</tr>
<tr>
<td>Tumor size</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>&lt;4</td>
<td>101 (57.71%)</td>
<td>89</td>
<td>12</td>
<td>27</td>
<td>74</td>
</tr>
<tr>
<td>≥4</td>
<td>72 (41.14%)</td>
<td>62</td>
<td>10</td>
<td>23</td>
<td>49</td>
</tr>
<tr>
<td>Deep of invasion</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>&lt;1/2</td>
<td>74 (42.29%)</td>
<td>64</td>
<td>10</td>
<td>21</td>
<td>53</td>
</tr>
<tr>
<td>≥1/2</td>
<td>90 (51.43%)</td>
<td>78</td>
<td>12</td>
<td>24</td>
<td>66</td>
</tr>
<tr>
<td>LNM</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>No</td>
<td>126 (72%)</td>
<td>111</td>
<td>15</td>
<td>37</td>
<td>89</td>
</tr>
<tr>
<td>Yes</td>
<td>41 (23.43%)</td>
<td>34</td>
<td>7</td>
<td>8</td>
<td>33</td>
</tr>
<tr>
<td>Histologic grade</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Well/moderate</td>
<td>119 (68%)</td>
<td>104</td>
<td>15</td>
<td>33</td>
<td>86</td>
</tr>
<tr>
<td>Poor</td>
<td>45 (25.71%)</td>
<td>38</td>
<td>7</td>
<td>17</td>
<td>28</td>
</tr>
</tbody>
</table>
prognosis, suggesting that SOX1 gene methylation has the potential to predict the 5-year OS. In CAC patients with small tumor size (<4 cm), PAX1\textsuperscript{m}-positive patients showed a longer 5-year PFS, suggesting that PAX1 gene methylation might be useful for monitoring the 5-year progression in CAC patients with small tumor size. This study, meanwhile,
has several limitations. First, our patients all came from a single medical center and the sample size was comparatively small. Second, the detailed molecular relationship between SOX1m and PAX1m in CAC has not been explored, which deserves further investigation.

Despite the poor prognosis of CAC, there is still no valid prognostic risk model. By far, age is a strong risk factor for cancer [40, 41]. The current paper showed corresponding directed changes in DNA methylation with age, which is characterized by hypermethylation of targets of polycomb group proteins (PCGTS) that are crucial in embryonic stem cell lineage differentiation [42]. In the algorithm combining SOX1m, PAX1m, and age, the low-risk group, composed of high methylation level of SOX1 and PAX1 and younger age, showed a significantly higher 5-year OS rate and 5-year PFS rate than the high-risk group. These results suggested that the algorithm has the potential for a 5-year CAC prognosis.

In our previous study, negative gene methylation correlated with high protein expression, which increased the resistance of cervical cancer cells to radiation and chemotherapy. In further studies, it will be essential to analyze the correlation between SOX1 and PAX1 methylation status and sensitivity of the cervical cancer cell to radiotherapy and chemotherapy.

In conclusion, this study suggests that SOX1 and PAX1 methylation levels are higher in CAC than in cervical SCC, and SOX1m and PAX1m are potential biomarkers for monitoring CAC prognosis.

Abbreviations
CAC: Cervical adenocarcinoma
SCC: Cervical squamous cell carcinoma
SOX1m: Methylation status of SOX1
PAX1m: Methylation status of PAX1
FIGO: International Federation of Gynecology and Obstetrics
PFS: Progression-free survival
OS: Overall survival.

Data Availability
The data used to support the findings of this study are included in the article.

Ethical Approval
This project was licensed by the Hunan Cancer Hospital ethics committee (project number: 2015[01]) and the Chinese Clinical Trial Registry (registration number: ChiCTR1800018931).

Conflicts of Interest
The authors declare that they have no competing interests.

Authors’ Contributions
J Wang, NY Wu, and ZT Zhao did the concept and design; ZT Zhao did the literature search; NY Wu and ZT Zhao did the clinical studies; XH Zhao, ZT Zhao, and NY Wu did the data acquisition; ZT Zhao and NY Wu did the data analysis; ZT Zhao and NY Wu did the statistical analysis; ZT Zhao, XY Zhang and NY Wu did the manuscript preparation; all authors did the manuscript editing and manuscript review. Zitong Zhao and Xiaoye Zhang contributed equally to this work.

Acknowledgments
The authors would like to thank all members of the Jing Wang laboratory, Istat Biomedical Co., Ltd., and Hunan Hongya Gene Technology Co., Ltd. This work was supported by the Clinical Research Center in Gynecologic Cancer, Hunan Cancer Hospital, National Natural Science Foundation of China (82003050 and 81972836), Natural Science Foundation of Hunan Province (2020JJ5338 and 2020JJ8020), the Foundation from Social development science and technology division (2018SK2121, qk2004138, and qk1801104), Scientific research project of Hunan Health Commission (20201487), and Hunan Provincial Health Commission (20201487).

References


