A MicroRNAExpression Signature for Cervical Cancer Prognosis

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Abstract

Invasive cervical cancer is a leading cause of cancer death in women worldwide, resulting in about 300,000 deaths each year. The clinical outcomes of cervical cancer vary significantly and are difficult to predict. Thus, a method to reliably predict disease outcome would be important for individualized therapy by identifying patients with high risk of treatment failures before therapy. In this study, we have identified a microRNA (miRNA)-based signature for the prediction of cervical cancer survival. miRNAs are a newly identified family of small noncoding RNAs that are extensively involved in human cancers. Using an established PCR-based miRNA assay to analyze 102 cervical cancer samples, we identified miR-200a and miR-9 as two miRNAs that could predict patient survival. A logistic regression model was developed based on these two miRNAs and the prognostic value of the model was subsequently validated with independent cervical cancers. Furthermore, functional studies were done to characterize the effect of miRNAs in cervical cancer cells. Our results suggest that both miR-200a and miR-9 could play important regulatory roles in cervical cancer control. In particular, miR-200a is likely to affect the metastatic potential of cervical cancer cells by coordinate suppression of multiple genes controlling cell motility. Cancer Res; 70(4); 1441–8. ©2010 AACR.

Introduction

It is estimated that there will be about 11,270 new cases of cervical cancer and that 4,070 women will die of this disease in the United States in 2009 (statistics provided by American Cancer Society). Worldwide, invasive cervical cancer is an even greater problem and is a leading cause of cancer death in women. Most cervical cancer patients receive standard radiotherapy and chemotherapy. However, clinical outcomes vary significantly and are difficult to predict. The lack of effective outcome prediction models makes it difficult to apply individualized treatment protocols to cervical cancer patients. A method to accurately predict disease outcome before standard therapy would be important for the early identification of patients with a high risk of treatment failures. For these high-risk patients, modified therapy, involving different radiation doses or adjuvant therapy, could potentially be applied to improve patient survival.

MicroRNAs (miRNA) are a family of small non-coding RNA molecules that downregulate the expression of their protein-coding gene targets (1). As of January 2010, 721 human miRNAs have been identified. Despite the relatively small number of miRNAs, both computational and experimental studies have shown that thousands of human protein-coding genes are collectively regulated by miRNAs (2–4). Thus, miRNAs are considered to be master regulators of many important biological processes such as cell growth, apoptosis, viral infection, and cancer development (1, 5–8). Genome-wide analyses indicate that about half of miRNA genes are located at fragile sites and genomic regions with frequently dysregulated expression in cancers (9, 10). Thus, one major mechanism that underlies the roles of miRNAs in cancer development could be deregulated miRNA expression as compared with normal cells.

miRNA expression signatures have been shown to be promising biomarkers for the classification or outcome prediction of a wide array of human cancers (reviewed in refs.11, 12). For example, a miRNA signature has been identified by expression profiling for the prediction of lung cancer outcome (13). However, to date, the prognostic value of miRNAs in cervical cancer has not been investigated. Recent studies indicate that multiple miRNAs have altered expression in human papillomavirus (HPV)–integrated cervical cancer cells compared...
with HPV-negative cervical cancer cells or normal cervical tissues (14, 15). In addition, altered miRNA expression profiles have also been reported in cervical carcinomas as compared with normal cervix (16–18).

Here, we present a miRNA-based prediction model to identify cervical cancer patients who are likely to fail radiation and chemotherapy. In addition, we also characterized the functions of two prognostic miRNAs in cervical cancer cells. Our functional studies on the involvement of miRNAs in cervical cancer could be a promising starting point for developing future miRNA-based cervical cancer therapy.

Materials and Methods

Patients and tumor RNA samples. One hundred two cervical carcinomas were included in this study, including 60 for training and 42 for testing the outcome prediction model, respectively. These cancer patients had been treated with standard chemoradiation at Washington University School of Medicine in St. Louis. The patient characteristics are summarized in Table 1. This study was approved by the Human Research Protection Office at the Washington University. For the 60 cervical cancers for model training, formalin-fixed paraffin-embedded (FFPE) tumor tissue biopsies were collected before radiotherapy. First, sections from the FFPE tumor blocks were stained with H&E to identify the tumor regions. Then, one 0.6-mm tissue core was obtained from the tumor region of each FFPE block. Total RNAs were extracted from these tissue cores for miRNA expression profiling. In this way, we were able to focus on tumor tissue analysis with minimal contamination from normal adjacent tissues. Total RNAs were isolated with miRNeasy FFPE Kit (QIAGEN) according to the manufacturer’s protocol.

The 42 independent cervical tumor samples for prediction model testing included 22 FFPE tumor samples and 20 snap-frozen tumor samples collected from 42 patients in the testing cohort. The testing FFPE samples were processed in the same way as the training FFPE samples described above. The frozen samples were prepared by snap-freezing fresh tumor samples in Tissue Tek optimum cutting temperature compound (EMS) before radiotherapy. Specimens were sectioned on a cryostat and stained with H&E for pathologic review. The percentage of tumor cells from each individual tumor sample was assessed by a single pathologist at Washington University specializing in gynecologic oncology. All 20 frozen tumor samples included in this study had at least 75% tumor content. Total RNA was extracted from each sample by the Tissue Core Procurement Facility at Washington University using the Trizol reagent (Invitrogen) according to the manufacturer’s protocol.

miRNA expression profiling with real-time reverse transcription-PCR. miRNA expression profiling of 96 cancer-related miRNAs was done using our recently developed assays, which are based on real-time reverse transcription-PCR (RT-PCR), for both the training and testing tumor samples (19). All the RT and PCR primers were synthesized by Integrated DNA Technologies. The detailed experimental procedure has been described previously (19). In brief, the RT reactions were done with the High Capacity cDNA Reverse Transcription Kit (Applied Biosystems). Each RT reaction included 150 ng RNA as the template and a pool of RT primers. Real-time PCR was done with Power SYBR Green PCR Master Mix (Applied Biosystems). Raw threshold cycle (Ct) values from real-time PCR were normalized using a quantile-based scaling method as described previously (19).

Survival analysis. Statistical data analyses were done with the R package4 and MATLAB. Univariate Cox proportional hazards regression analyses were done to evaluate the association of each miRNA to overall patient survival. The P values were calculated using the Wald test and then corrected by a permutation test as previously described (13). Multivariate Cox proportional hazards analyses were done to evaluate the independent prognostic value of the miRNA signature. The Kaplan-Meier estimator was used to evaluate the significance of the outcome prediction model that was based on miRNA expression signature. The P values of the model prediction in the Kaplan-Meier analysis were calculated with the log-rank test. Overall patient survival was used as the end point to evaluate cervical cancer outcome. Overall survival was defined as the time interval between the date of diagnosis and the date of patient death. Recurrence-free survival was defined as the time interval between the date of diagnosis and the date of first failure.

Cell culture and miRNA transfection. The human cervical cancer cell line HeLa (purchased from American Type Culture Collection) was used in all miRNA transfection experiments. HeLa cells were seeded 24 h before transfection. Transfection experiments were done with 60 nmol/L miRNA mimics (pre-miR-200a or pre-miR-9) from Ambion and with Lipofectamine 2000 from Invitrogen. Negative controls were included in each transfection experiment, including both the negative control miRNA (Ambion) and mock transfection (no RNA added). A parallel glyceraldehyde-3-phosphate dehydrogenase siRNA (Ambion) transfection experiment was done as a positive control to monitor transfection efficiency as determined by real-time RT-PCR. In addition, the ectopic expression of transfected miR-200a or miR-9 in HeLa cells was also confirmed directly by real-time RT-PCR. Total RNA was extracted from the cells using the mirVana RNA Isolation Kit (Ambion).

Microarrays. Microarrays were done using the Illumina BeadChip platform at the Washington University Genome Center. Total RNA quality was assessed with Agilent 2100 Bioanalyzer (Agilent Technologies) before the microarray experiments. Total RNA samples were first amplified with the MessageAmp TotalPrep Kit (Ambion). Amplified RNA samples were applied to HumanHT12 Expression BeadChip arrays according to Illumina standard protocol for hybridization and washing. Arrays were scanned on an Illumina BeadArray Reader, and images were quantitated by Illumina Beadscan and analyzed by the Beadstudio software. On-slide spot replicates were averaged and individual spot data were

4 http://www.r-project.org/
reported. Raw array data were normalized by the quantile normalization method. The microarray data were deposited in the National Center for Biotechnology Information (NCBI) Gene Expression Omnibus database (accession no. GSE18545).

Gene Ontology analysis. The Gene Ontology (GO) annotation database was downloaded.5 The gene IDs were mapped to GO annotations using the NCBI Gene database.6 Because the Gene IDs were mapped only to the lowest child level of GO categories, a recursive search was done to associate the Gene IDs to all parent GO categories based on the GO hierarchical structure. To reduce the redundancy in GO annotation, only GO functional categories with 5 to 300 expressed genes in HeLa cells, as determined by microarrays, were included for further analysis. The hypergeometric test was done to identify gene enrichment in the GO functional categories, using all 9,500 HeLa-expressing genes as the background.

miRNA target validation with real-time RT-PCR. Total RNA was reverse transcribed using the High Capacity RT kit (Applied Biosystems). All PCR primers for gene target candidates were retrieved from PrimerBank (20). Real-time PCR was done to validate the downregulation of candidate miRNA targets with our previously described protocol (20). Glyceraldehyde-3-phosphate dehydrogenase and β-actin were used as internal controls for expression data normalization. Potential target expression changes were determined by comparison with the negative control RNA experiment.

Transwell migration assay. HeLa cells were transfected with miRNA mimics, pre-miR-200a (Ambion), for 48 h, followed by resuspension and washing with PBS buffer. Fifty thousand cells in 100 μL serum-free medium were added to the upper chamber of each 8-μm Transwell (Costar). The lower chamber was filled with 600 μL of medium with 10% bovine serum. The cells were incubated for 6 h and then cells on top of the Transwell membrane were removed with a cotton-tipped swab. Migrated cells (through the membrane to the bottom) were fixed and stained with Hema-3 (Fisher Scientific) for counting. The percentage of migrated cells with overexpressed miR-200a was normalized to that of negative control cells with overexpressed negative control RNA.

Results

miRNA expression profiles were associated with cervical cancer survival. Sixty cervical tumors were analyzed as training samples to identify prognostic factors for outcome prediction. The characteristics of this patient cohort are summarized in Table 1. The prognostic values of multiple commonly used clinicopathologic features were analyzed with univariate Cox regression analysis. Only lymph node status was significantly associated with survival ($P = 0.03$), whereas other features, including tumor grade, stage, hemoglobin level at diagnosis, glucose uptake level at diagnosis, and patient age at diagnosis, were not (Table 2).

Next, we evaluated the prognostic value of miRNAs by expression profiling. Total RNA samples were isolated from 60 FFPE cervical tumor tissues. One RNA sample did not pass the quality control check and was excluded from further profiling analysis. The expression profiles of 96 cancer-related miRNAs across the remaining 59 cervical cancers were determined using our recently established real-time PCR-based miRNA assays (19). These 96 cancer-related miRNAs were selected based on bioinformatics analysis of public miRNA microarray data as well as mining of public literature. These

| Table 1. Characteristics of 102 cervical cancer patients
<table>
<thead>
<tr>
<th>Training cohort</th>
<th>Testing cohort</th>
</tr>
</thead>
<tbody>
<tr>
<td>($n = 60$)</td>
<td>($n = 42$)</td>
</tr>
<tr>
<td>Median age at diagnosis (y)</td>
<td>53</td>
</tr>
<tr>
<td>Tumor histology</td>
<td></td>
</tr>
<tr>
<td>Squamous</td>
<td>50</td>
</tr>
<tr>
<td>Adenocarcinoma</td>
<td>7</td>
</tr>
<tr>
<td>Clear cell</td>
<td>2</td>
</tr>
<tr>
<td>Undifferentiated</td>
<td>1</td>
</tr>
<tr>
<td>FIGO stage</td>
<td></td>
</tr>
<tr>
<td>I</td>
<td>17</td>
</tr>
<tr>
<td>II</td>
<td>22</td>
</tr>
<tr>
<td>III</td>
<td>18</td>
</tr>
<tr>
<td>IV</td>
<td>3</td>
</tr>
<tr>
<td>Histologic grade</td>
<td></td>
</tr>
<tr>
<td>Well</td>
<td>2</td>
</tr>
<tr>
<td>Moderate</td>
<td>29</td>
</tr>
<tr>
<td>Poorly</td>
<td>19</td>
</tr>
<tr>
<td>Undetermined</td>
<td>10</td>
</tr>
</tbody>
</table>


Table 2. Univariate Cox proportional hazards regression analysis of clinical parameters in relation to disease outcome

<table>
<thead>
<tr>
<th>Clinical variable</th>
<th>Overall survival</th>
</tr>
</thead>
<tbody>
<tr>
<td>Lymph node status</td>
<td>0.03</td>
</tr>
<tr>
<td>Histologic grade</td>
<td>0.09</td>
</tr>
<tr>
<td>Clinical stage</td>
<td>0.15</td>
</tr>
<tr>
<td>Hemoglobin level at diagnosis</td>
<td>0.19</td>
</tr>
<tr>
<td>Patient age at diagnosis</td>
<td>0.42</td>
</tr>
<tr>
<td>Glucose uptake level at diagnosis</td>
<td>0.65</td>
</tr>
</tbody>
</table>

NOTE: The numbers in the table represent $P$ values calculated with the Wald test.
selected miRNAs (listed in Supplementary Table S1) have been implicated in a variety of human cancers based on many previous studies and are not necessarily cervical cancer specific. The PCR-based profiling assays designed for these miRNAs have been extensively validated in our recent study (details available in ref. 19). The expression profiles of individual miRNAs were correlated to overall patient survival with univariate Cox proportional hazards regression analysis. \( P \) values were calculated with the Wald test and further corrected by a permutation test as previously described (13). Among all miRNAs included in the profiling experiment, five were significantly associated with cancer survival (miR-9, miR-21, miR-200a, miR-218, and miR-203 with corrected \( P = 0.02 \)-0.05). Among these five miRNAs, three have been reported to be differentially expressed (upregulation of miR-21 and downregulation of miR-203 and miR-218) in cervical cancers compared with normal cervix (15–17). None of these five miRNAs were significantly associated with the lymph node status as determined by the log-rank test.

**A miRNA-based model to predict cervical cancer survival.**

Given the significant association of miRNA expression profiles with patient survival, it is likely that a selected set of miRNAs could be used to build a predictive model for cervical cancer prognosis. To identify the most predictive miRNAs, we used the recursive feature elimination (RFE) technique to rank the relative importance of each miRNA in disease outcome classification. In this RFE analysis, a machine learning framework, support vector machine (SVM), was used to evaluate all the miRNAs collectively. The least important miRNA was first identified by the SVM and subsequently eliminated. The remaining miRNAs were then evaluated collectively again using the SVM framework to identify the next least important miRNA for elimination. The process was repeated with one miRNA eliminated from each cycle until only one miRNA was left. SVM-RFE is especially useful to determine the independent contribution of each miRNA for model performance. To reduce potential overtraining risk, 10-fold cross-validation was done during the miRNA selection process. The top-ranking miRNAs selected by SVM-RFE were miR-200a, miR-9, miR-10b, miR-183, miR-204, miR-24, miR-181a, miR-193b, miR-146b, and miR-10a (ranked 1 to 10 in order).

Among all the miRNAs that we analyzed, miR-200a and miR-9 were especially promising. Both miRNAs were significantly associated with disease outcome by univariate Cox regression analysis (corrected \( P \) values of 0.03 and 0.02, respectively) and had the highest rankings for disease outcome classification as revealed by SVM-RFE (ranked 1 and 2, respectively). Therefore, miR-200a and miR-9 were used to build a logistic regression model for outcome prediction as follows: \( S = 17.9 - 0.284 \times \log_{10}\text{miR-9} - 0.376 \times \log_{10}\text{miR-200a} \), where \( S \) represents the risk score for each patient and \( E_{\log_{10}\text{miR-9}} \) and \( E_{\log_{10}\text{miR-200a}} \) represent the normalized expression levels of miR-9 and miR-200a in each patient, respectively. In this prediction model, a high risk score (>0) predicts poor survival and a low risk score (<0) predicts good survival. Kaplan-Meier survival analysis indicated that our miRNA-based model was significantly predictive of overall patient survival for the 59 cervical cancers (Fig. 1A; \( P = 0.0003 \) with the log-rank test).

The majority of the cancers (45 of 59) were predicted to be of low risk, which was consistent with the fact that the majority of the patients (36 of 59) survived at the end of the study period. This miRNA signature was also significantly predictive of local-recurrence-free survival (\( P = 0.036 \) with the log-rank test). The model prediction was still statistically significant after controlling lymph node status, tumor stage, and patient age with multivariate Cox proportional hazards regression analysis, indicating its significant independent prognostic value from clinicopathologic features (Table 3, \( P = 0.001 \)).

![Figure 1. Kaplan-Meier analysis to evaluate the statistical power of a miRNA-based model on predicting cervical cancer survival. A risk score was assigned to each patient as calculated by the prediction model. Based on the risk score, the patients were classified into either the low-risk group (score <0) or the high-risk group (score >0). A, application of the model to 59 training tumor samples. The risk scores generated by the model were significantly predictive of overall patient survival (\( P = 0.0003 \) with the log-rank test). B, application of the model to 42 independent testing tumor samples. The risk scores generated by the model were significantly predictive of overall patient survival (\( P = 0.002 \) with the log-rank test).](image-url)
Model validation with independent cervical cancers.

The prediction model was further validated with 42 independent cervical cancer samples, including 22 FFPE samples and 20 frozen samples. First, the expression profiles of miR-200a and miR-9 in the 42 validation cervical cancers were determined using our recently established PCR-based assays (19). Then, a risk score was calculated for each of the 42 cancer patients by applying the miRNA expression values to the outcome prediction model. Based on the risk score, the patients were classified into either the high-risk group (score >0) or the low-risk group (score <0). Kaplan-Meier analysis indicated that these two patient groups had significantly different overall survival rates (Fig. 1B; P = 0.002 with the log-rank test). The model prediction was still significant when applied to the frozen and FFPE samples separately for predicting overall survival (P = 0.02 and P = 0.05 for 20 frozen testing samples and 22 FFPE testing samples, respectively, with the log-rank test). These two patient groups were also significantly different for recurrence-free survival (P = 0.002 with the log-rank test). Thus, our logistic regression model was predictive of patient survival when applied to 42 independent cervical cancers.

Functional characterizations of the prognostic miRNAs in cervical cancer cells. To characterize the global cellular functions of the prognostic miRNAs included in the outcome prediction model, miR-200a and miR-9 were individually transfected into cervical cancer HeLa cells, and microarrays were done to identify genes downregulated by miR-200a or miR-9 overexpression. Based on recent studies, the majority of miRNA targets are downregulated at both the mRNA and protein levels. The high-throughput nature of microarrays is ideal for systematic analysis of miRNA target regulation even though some miRNA targets are likely to be missed by microarrays. For the genes downregulated by miRNAs, GO enrichment analysis was done to evaluate the effects of miRNA overexpression on cervical cancer cell functions. The most significantly affected GO functional categories by miRNA overexpression are listed in Table 4. For miR-200a, the most affected functional category was "regulation of cell adhesion." In addition, the structure formation involved in morphogenesis was also significantly affected. These biological properties are known to be critical for the regulation of the metastatic potential of cancer cells to migrate to distant sites. Thus, miR-200a could potentially be involved in tumor control by regulating cancer cell metastasis. Similarly, the effects of miR-9 overexpression were also evaluated by GO analysis. Interestingly, most of the affected functional categories were related to tumor cell metabolism (Table 4). The maintenance of high metabolic rate is important for the rapid proliferation of cervical cancer cells (21). Thus, miR-9 could potentially be involved in tumor control by regulating tumor cell metabolism.

### Table 3. Multivariate Cox proportional hazards regression analysis to evaluate the independent prognostic value of miRNA signature and clinical parameters

<table>
<thead>
<tr>
<th>Parameters</th>
<th>Overall survival</th>
</tr>
</thead>
<tbody>
<tr>
<td>Lymph node status</td>
<td>0.02</td>
</tr>
<tr>
<td>Histologic grade</td>
<td>0.11</td>
</tr>
<tr>
<td>Clinical stage</td>
<td>0.78</td>
</tr>
<tr>
<td>Patient age at diagnosis</td>
<td>0.50</td>
</tr>
<tr>
<td>miRNA signature</td>
<td>0.001</td>
</tr>
</tbody>
</table>

NOTE: The numbers in the table represent P values calculated with the Wald test.

### Table 4. The most affected GO categories by miR-200a and miR-9 as revealed by microarrays

<table>
<thead>
<tr>
<th>GO ID</th>
<th>GO description</th>
<th>Enrichment P value</th>
</tr>
</thead>
<tbody>
<tr>
<td>GO:0030155</td>
<td>Regulation of cell adhesion</td>
<td>7.30e–05</td>
</tr>
<tr>
<td>GO:0060348</td>
<td>Bone development</td>
<td>1.70e–04</td>
</tr>
<tr>
<td>GO:0032940</td>
<td>Secretion by cell</td>
<td>1.80e–04</td>
</tr>
<tr>
<td>GO:0045646</td>
<td>Regulation of erythrocyte differentiation</td>
<td>2.70e–04</td>
</tr>
<tr>
<td>GO:0048646</td>
<td>Anatomic structure formation involved in morphogenesis</td>
<td>2.80e–04</td>
</tr>
<tr>
<td>GO:0009396</td>
<td>Folic acid and derivative biosynthetic process</td>
<td>2.50e–05</td>
</tr>
<tr>
<td>GO:0048514</td>
<td>Blood vessel morphogenesis</td>
<td>3.70e–04</td>
</tr>
<tr>
<td>GO:0006752</td>
<td>Group transfer coenzyme metabolic process</td>
<td>5.70e–04</td>
</tr>
<tr>
<td>GO:0016887</td>
<td>ATPase activity</td>
<td>7.10e–04</td>
</tr>
<tr>
<td>GO:0009064</td>
<td>Glutamine family amino acid metabolic process</td>
<td>1.10e–03</td>
</tr>
</tbody>
</table>

NOTE: P values were used to assess the enrichment of genes downregulated by miR-200a or miR-9, as revealed by microarrays, in each GO category. The P values were calculated with the hypergeometric test using all expressed genes in HeLa cells as background. The five most significantly affected GO categories by miR-200a or miR-9 are presented here.
Detailed target analysis was done to further characterize the functional involvement of the prognostic miRNAs in cervical cancer. Identification of miRNA gene targets is critical to understanding the direct regulatory roles of miRNAs in cervical cancer. We have recently developed a robust bioinformatics algorithm, MirTarget2, for miRNA target prediction (22). MirTarget2 has been shown to have superior performance over other existing algorithms by comparative analysis (22). In addition, we have also developed a new strategy to systematically identify miRNA targets by combining computational target prediction with microarray expression profiling (23). These methods were used in this study to identify genes targeted by miR-200a and miR-9. Predicted gene targets were retrieved from the miRDB database, which was developed based on the MirTarget2 algorithm (24). There were 9,500 genes with detectable expression in HeLa cells. Figure 2.

**A** miR-200a

All predicted targets

312 58 247

Downregulated genes

miR-9

All predicted targets

222 52 233

Downregulated genes

**B**

![Graph showing remaining gene expression](image)

**C**

![Bar chart showing migrated cells](image)
cells as determined by microarrays. Among these genes, 305
were downregulated by miR-200a overexpression and 370
were predicted to be miR-200a targets (Fig. 2A). In this
way, we identified 58 genes that were both predicted miR-
200a targets and downregulated by miR-200a as revealed
by microarrays. Thus, these genes are likely to be directly tar-
geted by miR-200a. Similarly, we also characterized the genes
downregulated by miR-9 overexpression (Fig. 2A). Among all
the genes expressed in HeLa cells, there were 274 predicted
miR-9 targets and 285 miR-9 downregulated genes. Altoget-
er, 52 genes were predicted to be both targeted by miR-9 tar-
gets and downregulated by miR-9 as revealed by microarrays.
Thus, these 52 genes represent likely direct miR-9 targets.

Based on the bioinformatics target analysis, we further
characterized the roles of miRNA-200a in cervical cancer pro-
gression. Real-time RT-PCR experiments were done to validate
the microarray results for miR-200a overexpression. Thirteen
candidate miR-200a targets, as identified by both microarrays
and computational target prediction, were selected for real-
time RT-PCR validation. These genes were selected for their
known involvement in carcinogenesis. Among these 13 genes,
9 showed downregulated expression by at least 40% as a result
of miR-200a overexpression in cervical cancer HeLa cells
(Fig. 2B; Table 5). Among these downregulated genes, several
are related to the metastatic potential of the tumor
cells, including ZEB1, ZEB2, TGFβ2, and EXOC5 (details avail-
able in Discussion). Thus, simultaneous repression of these
metastasis-related genes by miR-200a could be important
for controlling cervical cancer cell morphology and the ability
to migrate to distant sites. This hypothesis is also consistent
with the GO analysis results described earlier. To further test
the hypothesis, we overexpressed miR-200a in cervical cancer
HeLa cells. The effect of miR-200a overexpression on HeLa
cell motility was examined by transwell migration assays.
As shown in Fig. 2C, overexpression of miR-200a led to a
significant reduction (46%) of cervical cancer cell mobility.

Discussion

Although miRNA expression signatures have been applied
to the outcome prediction of multiple cancers such as lung
cancer and breast cancer, no study to date has been reported
for the application of miRNAs to cervical cancer prognosis.
One unique challenge in cervical cancer biomarker study is
the lack of large amounts of tumor tissues because most cerv-
ix biopsies are relatively small. In addition, most existing
cervical cancer tissues in hospitals are preserved using the
FFPE method, leading to severe degradation of the RNA in
tumor cells. These issues pose a significant challenge to miRNA
expression profiling analysis. To address this challenge, we
have recently developed a new PCR-based profiling method
for miRNA expression analysis, which has been shown to have
superior performance in detection sensitivity and specificity
compared with traditional profiling methods (19). This new
method has also been successfully applied to the profiling of
minute amounts of highly degraded clinical RNA samples (19).
In this study, this new method was applied for the miRNA pro-
file of FFPE cervical tumors, resulting in the identification
of a miRNA signature for predicting cervical cancer survival.
Furthermore, this prognostic miRNA signature was validated
by both independent FFPE and snap-frozen cervical cancer
samples. Interestingly, our new miRNA signature was success-
fully validated despite the difference in tissue preservation
method (FFPE versus snap-frozen), indicating that miRNAs
are robust biomarkers in cervical cancer. This miRNA signa-
ture has provided a new biomarker-based strategy for the iden-
tification of high-risk cervical cancer patients for potential
individualized therapy.

Our functional studies indicated that by targeting multiple
cancer-related genes, miR-200a likely acts as a master regu-
lator that is critical to cervical cancer control. In support of
this view, recent studies show that the miR-200 miRNA fam-
ily may inhibit the epithelial to mesenchymal transition
(viewed as an important initiating step for tumor metastasis)
by directly targeting E-cadherin transcriptional repressors
ZEB1 and ZEB2 (25–27). Interestingly, ZEB1 and ZEB2 were
also among the genes downregulated by miR-200a in our cer-
vical cancer study. Besides ZEB1 and ZEB2, we also identified
other miR-200a targets that are involved in metastasis. For
example, TGFβ2 (transforming growth factor β2) has been
shown to promote metastasis in multiple cancers (28, 29);
EXOC5 (exocyst complex component 5) is involved in the ac-
tin cytoskeletal remodeling machinery and is essential for the
biogenesis of epithelial cell surface polarity (30). Thus, our

<p>| Table 5. miR-200a gene targets validated by real-time RT-PCR |</p>
<table>
<thead>
<tr>
<th>Gene symbol</th>
<th>Accession no.</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>MYH10</td>
<td>NM_005964</td>
<td>Myosin, heavy chain 10, nonmuscle</td>
</tr>
<tr>
<td>ZEB1</td>
<td>NM_030751</td>
<td>Zinc finger E-box binding homeobox 1</td>
</tr>
<tr>
<td>DCP2</td>
<td>NM_152624</td>
<td>DCP2 decapping enzyme homolog (S. cerevisiae)</td>
</tr>
<tr>
<td>YWHAG</td>
<td>NM_012479</td>
<td>Tyrosine 3-monooxygenase, y polypeptide</td>
</tr>
<tr>
<td>KIDINS220</td>
<td>NM_020738</td>
<td>Kinase D–interacting substrate of 220 kDa</td>
</tr>
<tr>
<td>ZEB2</td>
<td>NM_014795</td>
<td>Zinc finger E-box binding homeobox 2</td>
</tr>
<tr>
<td>TGFβ2</td>
<td>NM_003238</td>
<td>Transforming growth factor, β2</td>
</tr>
<tr>
<td>RANBP5</td>
<td>NM_002271</td>
<td>Importin 5</td>
</tr>
<tr>
<td>EXOC5</td>
<td>NM_006544</td>
<td>Exocyst complex component 5</td>
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</table>
target analysis indicated that miR-200a can simultaneously target multiple genes that are important to the metastatic potential of cervical cancer cells. In this way, miR-200a could potentially act as a master suppressor for cervical cancer metastasis. Indeed, cervical cancer cell motility was significantly reduced when miR-200a was overexpressed (Fig. 2C). Thus, one potential tumor control strategy could be the manipulation of miR-200a expression. Recent studies indicate that the therapeutic delivery of miR-26a and miR-31 can suppress liver and breast cancers, respectively (31, 32). Similarly, based on our research, it is reasonable to expect that the therapeutic delivery of miR-200a could be a promising new treatment strategy for cervical cancer control.

Disclosures of Potential Conflicts of Interest

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