Clinically Relevant microRNAs in Ovarian Cancer

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Abstract

microRNAs (miRNAs/miRs) belong to a class of small noncoding RNAs that can negatively regulate messenger RNA (mRNA) expression of target genes. miRNAs are involved in multiple aspects of ovarian cancer cell dysfunction and the phenotype of ovarian cancer cells can be modified by targeting miRNA expression. miRNA profiling has detected a number of candidate miRNAs with the potential to regulate many important biologic functions in ovarian cancer, but their role still needs to be clarified, given the remarkable heterogeneity among ovarian cancers and the context-dependent role of miRNAs. This review summarizes the data collected from The Cancer Genome Atlas (TCGA) and several other genome-wide projects to identify dysregulated miRNAs in ovarian cancers. Copy number variations (CNVs), epigenetic alterations, and oncogenic mutations are also discussed that affect miRNA levels in ovarian disease. Emphasis is given to the role of particular miRNAs in altering expression of genes in human ovarian cancers with the potential to provide diagnostic, prognostic, and therapeutic targets. Particular attention has been given to TP53, BRCA1/2, CA125 (MUC16), HE4 (WFDC2), and imprinted genes such as ARHI (DIRAS3). A better understanding of the abnormalities in miRNA expression and downstream transcriptional and biologic consequences will provide leads for more effective biomarkers and translational approaches in the management of ovarian cancer. Mol Cancer Res; 13(3); 393–401. © 2014 AACR

Introduction

In the United States, ovarian cancer is the most lethal gynecologic malignancy in women with 22,240 estimated new cases and 14,030 estimated deaths in 2013 (1). With advances in diagnosis and treatment, 5-year survival rate has improved significantly over the last three decades, but the overall cure rate remains at 30% (2). Poor outcomes relate to late diagnosis and persistence of dormant, drug-resistant cancer cells (2). If we are to improve clinical outcomes, we must take advantage of contemporary technologies to identify the molecular alterations that occur in ovarian cancer and to define the heterogeneity that is observed within and between cancers from different patients. Having identified these changes, we can better develop strategies for earlier diagnosis or more effective therapy.

miRNAs (miRNAs) are small noncoding RNAs of 19–25 nucleotides that can modulate gene expression by hybridizing to complementary target messenger RNAs (mRNA), resulting in either mRNA degradation or direct inhibition of translation.

miRNA can also activate gene expression by interacting with complementary regions found in the promoter and coding region, as well as the 3′-untranslated region (UTR) of mRNA targets (3). Expressed miRNAs provide a novel layer of regulation for human gene expression and play important roles in diverse biologic processes (4) including carcinogenesis (5). Alterations in miRNAs have been detected in human ovarian cancers (6). The Cancer Genome Atlas (TCGA) project has recently published an integrated analysis of nearly 500 high-grade serous ovarian cancers that clearly documents multiple changes in miRNA levels (7). In this review, we focus on changes in miRNA expression in ovarian cancers and their potential application for earlier detection, more accurate prognostication, and more effective treatment of the disease. Several miRNAs are predicted to regulate a number of clinically relevant genes in ovarian cancer such as MUC16 (CA125), WFDC2 (HE4), and several imprinted tumor-suppressor genes such as DIRAS3 (ARHI) that are downregulated in ovarian cancer.

Dysregulation of miRNAs has been detected by miRNA profiling of ovarian cancers

Several studies have compared expression of miRNAs in ovarian cancers to whole normal ovaries, primary ovarian surface epithelial (OSE) cells, and immortalized OSE (IOSE; refs. 8–11). Among these reports, 310 dysregulated miRNAs in ovarian cancers have been reported. Of these 310 miRNAs, 34 miRNAs were found to be consistently dysregulated in ovarian cancers from at least three independent studies (Tables 1 and 2; refs. 8, 9, 12–15). Several miRNAs that regulate growth in other cancer types are downregulated in ovarian cancers (Tables 1 and 2), including let-7a/b/d/f, miR-31, miR-34abc, miR-125b, and miR-127. Other oncogenic miRNAs, such as miR-20a, miR-23a/b, and miR-200b/c, are upregulated in ovarian cancers (Tables 1 and 2).
High-grade serous ovarian cancers exhibit distinctive changes in miRNA expression

Ovarian cancers are remarkably heterogeneous at the cellular and molecular level and can be divided into type I low-grade and type II high-grade cancers based on histologic appearance and molecular profile. More than 70% of ovarian cancer related deaths occur in patients with advanced stage, high-grade serous ovarian cancer (7). High-grade cancers are characterized by multiple copy number abnormalities, TP53 mutation, and epigenetic changes. When alterations in BRCA1 and BRCA2 occur, they are most frequently associated with high-grade serous ovarian cancers.

Table 1. Consistently deregulated miRNAs in ovarian cancers

<table>
<thead>
<tr>
<th>miRNAs</th>
<th>Alteration Counterpart</th>
<th>Effect</th>
<th>Mechanism</th>
<th>Targets</th>
<th>Associated references</th>
</tr>
</thead>
<tbody>
<tr>
<td>Let-7a/b/d/f</td>
<td>Downregulated HOSE, IOSE, ovary, fallopian tube from fimbriated end</td>
<td>Tumor suppressor</td>
<td>Promoter methylation, CNVs</td>
<td>KLK10, HMG2</td>
<td>11, 12, 17, 18, 21, 43, 63, 64</td>
</tr>
<tr>
<td>miR-22</td>
<td>HOSE</td>
<td>Tumor suppressor</td>
<td>CNVs, Promoter methylation, CNVs and p53 mutation</td>
<td>ARRB1, CLIP2, EVI1, FRAT2, EDC3</td>
<td>9-11, 18, 21</td>
</tr>
<tr>
<td>miR-31</td>
<td>HOSE</td>
<td>Tumor suppressor</td>
<td>CNVs, Promoter methylation, CNVs and p53 mutation</td>
<td>EZF2, STK40, CEBPA, MET, CDK4</td>
<td>10, 11</td>
</tr>
<tr>
<td>miR-34a/b/c</td>
<td>HOSE, IOSE, ovary, fallopian tube from fimbriated end</td>
<td>Tumor suppressor</td>
<td>Related to drug-resistant promoter methylation</td>
<td>BCL5, VEGF, HIF-1a, HER2</td>
<td>11, 15, 17, 18, 42, 43, 63, 65</td>
</tr>
<tr>
<td>miR-125b</td>
<td>HOSE, IOSE, ovary, fallopian tube from fimbriated end</td>
<td>Putative tumor suppressor</td>
<td>Imprinting, CNVs, promoter methylation</td>
<td>9, 11, 18, 21</td>
<td></td>
</tr>
<tr>
<td>miR-127-3p</td>
<td>HOSE, NOSE, ovary, serum</td>
<td>Related to drug-resistant promoter methylation</td>
<td>10, 11, 17, 21</td>
<td></td>
<td></td>
</tr>
<tr>
<td>miR-152</td>
<td>HOSE, IOSE, fallopian tube from fimbriated end</td>
<td>Putative tumor suppressor</td>
<td>Promoter methylation</td>
<td>21, 64</td>
<td></td>
</tr>
<tr>
<td>miR-155</td>
<td>HOSE, IOSE, fallopian tube from fimbriated end</td>
<td>Putative tumor suppressor</td>
<td>CNVs, promoter methylation</td>
<td>11, 18</td>
<td></td>
</tr>
<tr>
<td>miR-18a-3p</td>
<td>HOSE, ovary, blood</td>
<td>CNVs, promoter methylation</td>
<td>9-11</td>
<td></td>
<td></td>
</tr>
<tr>
<td>miR-18b</td>
<td>HOSE</td>
<td>CNVs, promoter methylation</td>
<td>9-11</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

Mining the TCGA data, Miles and colleagues (16) identified 17 miRNAs that were dysregulated in high-grade serous cancers when compared with normal ovarian samples, including eight upregulated miRNAs (miR-183-3p, miR-15b-3p, miR-135b, miR-590-5p, miR-18a, miR-16, miR-96, and miR-18b) and nine downregulated miRNAs (miR-140-3p, miR-145-3p, miR-143-5p, miR-34b-5p, miR-145, miR-139-5p, miR-34c-3p, miR-133a, and miR-34c-5p). In other reports that compared miRNA expression in ovarian cancers and normal ovarian tissues (17–19), five miRNAs were downregulated (miR-140-3p, miR-143-5p, miR-34b-5p, miR-34c-3p, and miR-145) and three were upregulated (miR-96, miR-15b, and miR-16) and these were among the top 10 miRNAs.

Table 2. Consistently deregulated miRNAs in ovarian cancers

<table>
<thead>
<tr>
<th>miRNAs</th>
<th>Alteration Counterpart</th>
<th>Effect</th>
<th>Mechanism</th>
<th>Targets</th>
<th>Associated references</th>
</tr>
</thead>
<tbody>
<tr>
<td>miR-15a/16</td>
<td>Upregulated HOSE, fallopian tube from fimbriated end</td>
<td>Oncogenic miRNA</td>
<td>Promoter methylation</td>
<td>Bmi-1</td>
<td>8-11, 14, 17, 42, 43</td>
</tr>
<tr>
<td>miR-20a</td>
<td>HOSE</td>
<td>Oncogenic miRNA</td>
<td>CNVs promoter methylation</td>
<td>APP</td>
<td>9, 10, 17, 43, 67</td>
</tr>
<tr>
<td>miR-23a/b</td>
<td>HOSE, fallopian tube from fimbriated end</td>
<td>Oncogenic miRNA</td>
<td>CNVs promoter methylation</td>
<td>AVEN, GALNT1</td>
<td>8, 42, 43</td>
</tr>
<tr>
<td>miR-30a/b/c</td>
<td>HOSE, IOSE, fallopian tube from fimbriated end</td>
<td>Related to drug-resistant promoter methylation</td>
<td>9-11, 17, 18, 42</td>
<td></td>
<td></td>
</tr>
<tr>
<td>miR-92</td>
<td>HOSE</td>
<td>Putative oncogenic miRNA</td>
<td>11-17, 18, 42</td>
<td></td>
<td></td>
</tr>
<tr>
<td>miR-93</td>
<td>HOSE</td>
<td>Putative oncogenic miRNA</td>
<td>11, 17, 42</td>
<td></td>
<td></td>
</tr>
<tr>
<td>miR-106a</td>
<td>HOSE</td>
<td>Putative oncogenic miRNA</td>
<td>11, 17, 42</td>
<td></td>
<td></td>
</tr>
<tr>
<td>miR-146b</td>
<td>HOSE, fallopian tube from fimbriated end</td>
<td>Putative oncogenic miRNA</td>
<td>17, 64</td>
<td></td>
<td></td>
</tr>
<tr>
<td>miR-182</td>
<td>HOSE, IOSE, fallopian tube from fimbriated end</td>
<td>Putative oncogenic miRNA</td>
<td>8, 9, 17, 21, 28, 69</td>
<td></td>
<td></td>
</tr>
<tr>
<td>miR-200</td>
<td>HOSE</td>
<td>Oncogenic miRNA (67)</td>
<td>CNVs promoter methylation</td>
<td>ZEB, c-Myc, TUBBIII, FNI, NTRK2, QKI</td>
<td>8, 11, 13, 17, 18, 43, 63, 68</td>
</tr>
<tr>
<td>miR-203</td>
<td>HOSE</td>
<td>Oncogenic miRNA</td>
<td>CNVs promoter methylation</td>
<td>ZEB, c-Myc, TUBBIII, FNI, NTRK2, QKI</td>
<td>10, 11, 17, 18</td>
</tr>
<tr>
<td>miR-205</td>
<td>HOSE</td>
<td>Putative oncogenic miRNA</td>
<td>11, 17, 42</td>
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<tr>
<td>miR-223</td>
<td>HOSE</td>
<td>Putative oncogenic miRNA</td>
<td>10, 11, 42</td>
<td></td>
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</table>
from TCGA data listed in Tables 1 and 2. These miRs could well contribute the pathogenesis of high-grade serous ovarian cancers, but their dysregulation needs to be confirmed in larger datasets and their functional roles need to be elucidated. Use of whole normal ovaries as a control in profiling is problematic. As epithelial cells comprise the majority of cells within a cancer but only a small subpopulation among cells within the normal ovary, apparent differences in miRNA expression could reflect differences in miRNA profiles between normal epithelial cells, granulosa-theca cells, and germ cells. Epithelial cells that cover the ovary or that line the fallopian tube would provide more relevant as a control.

Copy number alterations regulate miRNAs

One of the characteristics of ovarian cancer is genomic instability (7). Chromosomal abnormalities are common in high-grade serous ovarian cancers, as are alterations in DNA copy number (8). Overall, about 50% of miRNAs are found at fragile sites of chromosomes, as well as at the minimal regions of deletion, amplification, or common chromosome breakpoints associated with different cancers (20). Chromosome abnormalities that involve miRNAs are not random events (4). Alterations of DNA copy number could account for much of the miRNA dysregulation in ovarian cancers (21). Through a high-resolution array-based genomic hybridization study of 227 human cancer samples, Zhang and colleagues (22) found that certain genomic loci containing miRNA genes were frequently altered in human ovarian cancers, breast cancers, and melanomas. There were 26 miRNAs consistently associated with copy number gains and 15 miRNAs consistently associated with copy number losses in all three-cancer types (22). Downregulation of eight potential tumor-suppressor miRs (miR-337, mir-376a, mir-376b, miR-432, miR-368, miR-495, miR-377, and miR-410) mapped to a deletion in chromosome 14 (Dlk1-Gtl2 domain) and correlated with poor survival in epithelial ovarian cancer (23). Furthermore, the positive correlation between copy number and dysregulation of five miRNAs has been repeatedly confirmed by a number of studies involving miR-31 in 9p21; miR-93 in 7q22.1; miR-182 in 7q32.2, and miR-200b/429 in 1p36 (Fig. 1; refs. 10, 21, 22, 24).

In the TCGA data, several miRNAs are located in amplified or deleted genomic regions (25). Downregulation of let-7b is related to recurrent hemizygous genomic loss (86% of samples) and homozygous deletion (7% of samples), miR-31 is another frequently deleted miRNA. In contrast, miR-30 family members, located at two different focally amplified loci (8q24 and 1p34), are the most frequently amplified miRNAs, and copy number correlates with the expression of mature miRNA (25). Creighton and colleagues (25) computed the correlation between miRNA and its host gene expression and indicated that miRNA-host gene pairs tended to be highly correlated with each other, with 52% of the miRNA-host gene pairs showing significant positive correlation. Cyclin E1 (CCNE1), Notch3, HBXAP/Rsf-1, AKT2, and PIK3CA are among the most frequently amplified genes in high-grade serous ovarian cancer (26). No known miRNA is found within 2 Mb downstream of CCNE1, HBXAP/Rsf-1, or PIK3CA. Downstream of Notch3, however, miR-23a (19p13, negative strand, −13947483:−13947389) has been shown to be consistently upregulated in ovarian cancers in different studies (11). miR-641 (19q13.2, negative strand, −40788533:−40788510) is located near the amplicon that contains AKT2, but miR-641 is not overexpressed in high-grade serous ovarian cancers.

Epigenetic alterations regulate miRNAs

In addition to copy number changes, Iorio and colleagues (18) found that miR-21, miR-203, and miR-205 were overexpressed in ovarian cancers and that levels could be further increased in the ovarian cancer cell line OVCAR3 by incubation with the demethylating agent 5-aza-2-deoxycytidine (5-AZA), suggesting that these miRNAs might be regulated by methylation. Zhang and colleagues (21) treated five ovarian cancer cell lines with 5-AZA and a histone deacetylase inhibitor 4-phenylbutyric acid and found that 16 of 44 (36.4%) miRNAs downregulated in advanced-stage ovarian cancer could be restored using these drugs. Recently, the hypermethylation of tumor-suppressor mir-34a and mir-34b/c has also been confirmed in patients with ovarian cancer with decreased mir-34 (19, 24). Thus, epigenetic alteration is also an important mechanism for miRNA dysregulation.

TP53 regulates miRNAs

TP53 mutation is found in at least 96% of high-grade serous ovarian cancers and can regulate miRNAs. As the miR-34 family is upregulated by wild-type TP53, expression of miRNA 34a was decreased in 100% and 34b and 34c in 72% of cancers with TP53 mutation (17). In addition to genomic deletion, TP53 mutation may also be responsible for the underexpression of mir-31 (10).

miRNAs can downregulate BRCA1 and BRCA2 expression

Approximately 15% of patients with ovarian cancer have a strong family history associated with germline mutations of
BRCA1, BRCA2, mismatch repair genes or, on rare occasions, TP53 (27). Although mutations of BRCA1 and BRCA2 can affect gene expression profiles, at least one study found that a fraction of high-grade serous ovarian cancers exhibited BRCA1/2-associated abnormalities in the absence of mutation (17). miRNAs can downregulate wild-type BRCA1 expression. A G to C polymorphism (rs2910164) in the miR-146a precursor leads to mismatch in its stem region. This variant allele can increase miR-146a expression as well as the binding capacity between miR-146a and the 3’-UTR of BRCA1. Thus, miR-146a can bind to the 3’-UTRs of BRCA1 and BRCA2 miRNAs and potentially modulate their expression. The rs2910164 polymorphism of miR-146a may affect the age of cancer onset. Patients who had at least one miR-146a variant allele were diagnosed at a younger age than women without a variant allele (28).

Low-grade serous ovarian cancers exhibit distinctive changes in miRNA expression

Only 10% of ovarian cancers are low grade. Clinically, these cancers grow slowly and present in early stage, but are not as responsive as high-grade cancers to platinum- and taxane-based therapy (29). More than half of low-grade serous ovarian cancers are responsive as high-grade cancers to platinum- and taxane-based therapy (29). Although miRNAs differ in expression between low-grade and high-grade serous ovarian cancers (17). By analyzing the miRNA profiles of the NCI-60 panel of 60 human cancer cell lines, Patnaik and colleagues (30) found that mutation of BRAF and PTEN affects miRNA expression, but mutation of KRAS did not. Among the miRNAs related with mutant BRAF, four miRNAs (miR-509-3p, miR-30d, miR-30b-3p, miR-30b) have been reported to be upregulated in low-grade serous ovarian cancers, when compared with normal fallopian tube (17). The BRAFV600E mutation can increase MAPK signaling, lead to higher levels of mature miRNAs, and enhance miRNA processing in undifferentiated pleomorphic sarcoma (31), but its role in low-grade serous cancer still needs to be explored. PTEN mutation is responsible for downregulation of miR-29b and miR-769-3p in cancer cell lines, PIK3CA mutation has not yet been linked to any change in miRNA expression. Dysregulation of miRNAs and predicted targets tend to be anticorrelated in ovarian cancer gene expression

The function of miRNAs is determined by the genes and signaling pathways regulated by each miRNA. Having assembled the published transcriptome profiling data in ovarian cancer, we have integrated the results from both miRNA and transcriptome profiling to identify genes that are regulated by miRNAs. A number of differentially expressed genes in ovarian cancers have been reported (32). Approximately 200 miRNAs were anticorrelated with the 186 most differentially expressed genes using the miRNA algorithm Targetscan (http://www.targetscan.org/ Release 5.1 April 2009; Supplementary Tables S1 and S2). Among these 186 genes, 10 differentially expressed genes have been reported in at least two independent studies (33, 34). These 10 gene changes are thought to associate with ovarian cancers and are summarized in Table 3 along with their potential regulating miRNAs. Three pairs of miRNA/mRNA association are of particular interest: (i) downregulation of tumor suppressor gene ID4 and miR-203 upregulation in ovarian cancers; (ii) BCAT1 upregulation and downregulation of let-7, miR-125b & miR-155; and (iii) SERPINE1 upregulation and miR-152 downregulation (Fig. 2). ID4 has a regulatory loop with another tumor suppressor BRCA1, which enables appropriate normal cycling during cell division. There is a modestly correlated downregulation between BRCA1 and ID4 (35). The BRCA1–ID4 regulatory loop might be disrupted in many breast and ovarian cancers (35). Upregulation of miR-203 may be responsible for this disruption. Because downregulation of ID4 has been indicated as a potential biomarker of recurrence in breast cancer (35), both ID4 and miR-203 might serve as disease biomarkers in ovarian cancers as well.

BCAT1 is a direct target of c-myc, which is important in oncogenesis and amplified in a fraction of ovarian cancers (37). The let-7 family also performs a tumor-suppressor role in many cancer types including ovarian cancers. miR-125b is a putative tumor suppressor in ovarian cancers and can suppress cancer proliferation by targeting BCL3 (15). Although miR-155 levels are increased in B-cell lymphoma (38), miR-155 has been consistently downregulated in ovarian cancers with a potential

Table 3. Ten consistently deregulated genes and their regulating miRNAs in ovarian cancers

<table>
<thead>
<tr>
<th>Genes</th>
<th>Gene ID</th>
<th>Alteration</th>
<th>Description</th>
<th>Effect</th>
<th>Regulating miRNAs</th>
<th>Associated references</th>
</tr>
</thead>
<tbody>
<tr>
<td>CLU</td>
<td>191</td>
<td></td>
<td>Clustering</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>ID4</td>
<td>3400</td>
<td>Down</td>
<td>Inhibitor of DNA binding 4, dominant negative helix-loop-helix protein</td>
<td></td>
<td>miR-203</td>
<td></td>
</tr>
<tr>
<td>BCA1</td>
<td>586</td>
<td></td>
<td>Branched chain amino-acid transaminase 1, cytosolic</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>FNI</td>
<td>2355</td>
<td></td>
<td>Fibronectin 1</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>MAL</td>
<td>418</td>
<td></td>
<td>Mal, T-cell differentiation protein</td>
<td></td>
<td></td>
<td></td>
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<tr>
<td>SERPINE1</td>
<td>5054</td>
<td>up</td>
<td>Serpin peptidase inhibitor, clade E (neixin, plasminogen activator inhibitor type 1), member 1</td>
<td></td>
<td>miR-152</td>
<td></td>
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<tr>
<td>SERPINE5</td>
<td>5104</td>
<td></td>
<td>Serpin peptidase inhibitor, clade A (α-1 antiproteinase, antitrypsin), member 5</td>
<td></td>
<td></td>
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<tr>
<td>SOX7</td>
<td>64321</td>
<td></td>
<td>SRY (sex determining region Y)-box 17</td>
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<tr>
<td>TOP2A</td>
<td>7952</td>
<td></td>
<td>Topoisomerase (DNA) II α 170 kDa</td>
<td></td>
<td></td>
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</tr>
<tr>
<td>THBS2</td>
<td>7058</td>
<td></td>
<td>Thrombospondin 2</td>
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</tbody>
</table>
miRNAs regulate ovarian cancer-associated imprinted genes

Genomic imprinting represents another level of regulation in gene expression in which one allele of each autosomal gene pair is preferentially silenced depending upon its parent-of-origin, leaving only a single functional allele. Disruption of imprinted gene expression is linked to the initiation of malignancy (40). Of the candidate imprinted genes identified to date, four tumor-suppressor genes, including ARHI (DIRAS3), LOT1 (also known as PLAGL1/ZAC1), PEG3, and NDN, are consistently downregulated in ovarian cancers (2, 41). A TargetScan algorithm predicted that there are 53 miRNAs with poorly conserved binding sites in the 3'-UTR of ARHI, two conserved sites in PEG3, 15 conserved sites in PLAGL1, and four conserved sites in NDN. As shown in Fig. 3, ARHI-targeting miR-203 and miR-194, PLAGL1-targeting miR-15a/16 and miR-23a/b, and NDN-targeting miR-200b/c/429 have been reported to be overexpressed in ovarian cancers (9–11, 17, 18, 42, 43). Among these miRNAs, miR-194 and miR-23a/b are overexpressed in a number of human cancers (44, 45). NDN-targeting miR-200b/c/429 is associated with decreased progression-free survival and overall survival in patients with ovarian cancer (43). ARHI-targeting miR-203 and PLAGL1-targeting miR-15a/16 have been reported as putative tumor suppressors in other cancer types (46). miR-221 and 222 are also predicted to target ARHI and their negative regulation effects on ARHI gene has been confirmed in prostate cancer cells (47). However, dysregulation of miR-221 and 222 in ovarian cancers has not been observed in all studies (8, 10, 11, 18, 21, 42, 43). In addition, ARHI-targeting miR-371 and miR-181b/c are reported to be overexpressed in chemoresistant biopsies and cell lines (48). miRNA can be imprinted in normal physiologic development and in oncogenesis (49).
miRNAs may serve as biomarkers and also regulate levels of protein biomarkers

Detection of altered levels of miRNA dysregulation in blood, serum, and tumor-derived exosomes of patients with cancer might provide biomarkers for early detection (50). Among the consistently dysregulated miRNAs in ovarian cancers listed in Tables 1 and 2, two downregulated miRNAs, let-7 family and miR-155, and five upregulated miRNAs, miR-15/16 cluster, miR-20a, miR-92, miR-203, and miR-205 are found in the peripheral circulation of patients with ovarian cancers and represent promising biomarkers for early diagnosis (50). The miR-15/16 cluster, miR-20a, and miR-205 were also identified as the top 10 upregulated miRNAs in the TCGA dataset (Tables 1 and 2; ref. 7).

CA125, also known as MUC16, is a well-characterized biomarker that is used to monitor the progression and regression of epithelial ovarian cancer (51). The complete sequence of the cDNA-encoding MUC16 has been determined (52). On the basis of our in silico analysis of the TCGA database and literature reports, a number of miRNAs could potentially regulate the MUC16 gene (Table 4). Several miRNAs in this list have already been shown to be low in cancers. For example, miR-9 and miR-584 are downregulated in ovarian cancers when compared with normal ovary (18, 42, 53). miR-124 and miR-637 were also downregulated in ovarian cancer cell lines compared with IOSE (18, 21). If miRNAs in Table 4 are true regulators of CA125, downregulation of these miRNAs could be one of mechanisms that lead to abnormal CA125 levels in ovarian cancers and could be potential biomarkers along with CA125 for patients with ovarian cancers.

In addition, the Notch 3 amplification is located upstream of the HE4 gene on Chromosome 19, in high-grade serous ovarian cancer (26). In addition to miR-23a mentioned above, several miRNAs, including miR-27a (−13947324: −13947241), miR-24-2 (−13947183:−13947089), miR-199a-1 (−10928182:−10928090), and miR-1181 (−10514225:−10514121) map between Notch 3 and the CA125 (MUC16) gene (Fig. 3). miR-1181 increased serially in blood samples from patients diagnosed with relapsed ovarian cancers (22 serous and 2 endometrioid) when compared with age- and sex-matched volunteers without a history of cancer. So far, there is no report that links these miRNAs with CA125 levels.

Human epididymis secretory protein 4 (HE4) is a member of a family of whey acidic four-disulphide core proteins (WFCD2) that are secreted at high levels by normal endometrium and by endometrial and epithelial ovarian cancers. HE4 overexpression in ovarian cancers has been confirmed through microarray studies (54). Gene therapy targeting the promoter of HE4 can reduce the xenograft growth, block primary and metastatic tumors, and prolong life span of mice with ovarian cancer (55). The HE4 ELISA assay has been shown to have a potential advantage over the CA125 assay in that it is less frequently positive in premenopausal women with nonmalignant gynecologic conditions (56). HE4 protein can also provide a useful biomarker in a small fraction of ovarian cancers that have little or no CA125 expression (57). A predictive model—ROMA (Risk of Ovarian Malignancy Algorithm)—uses the combination of HE4 and CA125 to triage patients with pelvic masses to gynecologic oncologists (58). The HE4 gene is located at 20q12-q13.2 without any known miRNAs that map within or near this region. After analysis with the TargetScan algorithm, seven miRNA binding sites were found in the 3'-UTR of the HE4 gene. Among these miRNAs, miR-140-5p and miR-409-5p are downregulated in ovarian cancers (Fig. 3; refs. 9, 11). These two miRNAs that regulate the HE4 gene might serve as candidate miRNA biomarkers for detecting or monitoring ovarian cancers.

miRNAs might serve as potential prognostic biomarkers

On the basis of currently available data, some miRNAs have the potential to be prognostic biomarkers for ovarian cancer. Overexpression of miR-200 family members and miR-519a, underexpression of let-7 family members and miR-153 have been linked to a poor prognosis of patients with ovarian cancers (42, 43, 59). Underexpression of a tumor-suppressor miR-9 in recurrent ovarian cancers is reported as a signature for recurrence (42). Low expression of miR-31 in ovarian cancers could also be an indicator for earlier disease recurrence and metastasis. Upregulation of miR-15a, miR-21, and miR-92 has been reported to signal recurrent disease. Let-7 family members have also served as prognostic biomarkers in ovarian cancer (43). Downregulation of miR-34a/b/c, miR-449b, miR-503, and miR-507 has been observed in late-stage and high-grade ovarian cancers (17, 21, 24). However, at the present time, the mechanism that underlies the change in the expression of miRNA in ovarian cancer recurrence and metastasis remains elusive.

miRNAs can provide predictive biomarkers for response or lack of response to treatment

miRNAs have been implicated in the initiation, progression, metastasis, and chemoresistance of cancers at different sites. In theory, targeting miRNAs could provide a therapeutic strategy. Transfection of paclitaxel-resistant A2780 ovarian cancer cells with miR-27a inhibitors has been reported to reduce the expression of MDR1 mRNA and P-gp protein, to increase HIPK2 protein expression, and to enhance paclitaxel sensitivity (60). Exogenous expression of miR-31 has been shown to inhibit proliferation and induce significant p53-independent apoptosis in ovarian cancers (10). Considering that virtually all high-grade serous ovarian cancers exhibit p53 deficiency, miR-31-based therapy might be particularly effective in this subset of ovarian cancers (10).
miR-152 and miR-185 can increase cisplatin sensitivity ovarian cancer in vitro and in vivo by targeting DNMT1 (61).

miRNAs could provide targets for therapy

miRNA mimics, adenosine-associated vectors that express miRNAs, miRNA masks, and miRNA sponges are being developed to modulate the gain or loss of miRNA function (62). Many miRNA targets have been identified. Among the most consistently deregulated miRNAs in ovarian cancers are listed in Tables 1 and 2 and in Figs. 2 and 3. Targeting miR-203 may restore both the BRCA1–ID4 regulatory loop and expression of ARHI in ovarian cancers. Delivery of let-7, miR-125b, miR-155, and miR-152 might suppress tumorigenesis and metastasis by targeting BCAT1 and SERPINE1 (Tables 1 and 2 and Fig. 2). In addition, about 50 dysregulated miRNAs have been linked to chemoresistance or chemosensitivity to taxanes or platinum compounds (48). Overexpression of miR-27a and miR-514 and downregulation of let-7e have been related to development of resistance to taxanes and/or platinum. miR-214 expression can induce platinum resistance by affecting PTEN function (63). Conversely, the upregulation of miR-378 and miR-625 has correlated with sensitivity to platinum-based therapy.

Conclusions

Epithelial ovarian cancers are remarkably heterogeneous and this heterogeneity is reflected in dysregulation of multiple miRNAs. Different miRNA profiles are observed in high-grade and in low-grade cancers. miRNAs can be regulated by abnormalities in DNA copy number, methylation, histone acetylation, and mutation in TP53. In turn, miRNAs can regulate BRCA1, BRCA2, and imprinted tumor-suppressor genes such as ARHI (DRAS3). Loss of certain miRNAs may upregulate ovarian cancer biomarkers such as CA125 (MUC16) and HE4 (WFCD2). Altered levels of miRNAs may also serve as potential biomarkers for detecting, monitoring, estimating resectability, determining prognosis, and predicting response to conventional therapy. As methods are developed to manipulate miRNAs in the clinic certain miRs may also serve as targets for therapy.

Disclosure of Potential Conflicts of Interest

No potential conflicts of interest were disclosed.

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