The predictive value of microRNAs for pathological response after neoadjuvant treatment in esophageal squamous cell carcinoma: a systematic review

Dong Lin, Xiaosang Chen, Lijie Tan

Department of Thoracic Surgery, Zhongshan Hospital of Fudan University, Shanghai, China

Abstract: Neoadjuvant treatment followed by esophagectomy has been the standard strategy for resectable locally advanced esophageal squamous cell carcinoma (ESCC). Pathological response after neoadjuvant treatment is of vital importance in the determination of long-term survival. Due to the involvement of microRNAs (miRNAs) in ESCC, some studies have proposed miRNA models to predict the pathological response. We aimed to summarize current studies on the predictive value of the miRNA models. We searched the relevant studies on PubMed, Web of Science and Cochrane Library up to February 14, 2020, using the following search term: (esophageal OR esophagus OR oesophageal OR oesophagus) AND (miR OR miRNA OR microRNA) AND (neoadjuvant OR preoperative OR induction). The initial search retrieved 206 studies. We briefly summarized the involvement of miRNAs in the origin, development and chemo- and radioresistance in ESCC. Then, 9 studies were enrolled in the systematic review. A great heterogeneity was observed across these studies. Of the 6 studies with diagnostic tests, the area under curve varied a lot. Although much evidence demonstrated the correlation between miRNAs and pathological response after in ESCC, the current studies has not established any promising models. A well-designed prospective study is essential to investigate the potential predictive models for pathological response after neoadjuvant treatment in ESCC.

Keywords: Esophageal squamous cell carcinoma (ESCC); microRNAs (miRNA); pathological response; predictive

Introduction

Esophageal cancer is one of the most common malignancies worldwide, which led to approximately 500,000 deaths in 2018 (1). Its two main histological subtypes, esophageal squamous cell carcinoma (ESCC) and esophageal adenocarcinoma (EAC), have significant differences in epidemiology, etiology, and treatment response (2). In East Asia and Africa, ESCC is the predominant subtype (3).

Patients with ESCC have poor overall survival, which is partly due to advanced stages at initial diagnosis (4), and the limited approaches for metastatic diseases (5,6). In recent years, neoadjuvant treatment, including neoadjuvant chemotherapy (nCT) or neoadjuvant chemoradiotherapy (nCRT), followed by esophagectomy, has been the standard strategy for resectable locally advanced esophageal cancer due to the survival benefit (7-9). Moreover, the pathological response after nCT or nCRT has been demonstrated to be independently associated with overall survival (10,11). Therefore, predicting pathological response is important.

To date, researchers have proposed models based on
medical images (12), inflammatory markers (13), and nutrient indices (14); however, no promising models have been established.

MicroRNAs (miRNAs), short nucleotide as 28–25 base pairs, are considered potential candidates for predicting pathological response. They post-transcriptionally regulate gene expression, including that of oncogenes and onco-suppressor genes, by complementary binding to 3′-untranslated regions of the target messenger RNA. Previously published studies have reported that miRNAs are involved in the origin and development, and the chemo- and radio-resistance of ESCC (15-20). In recent years, some studies have further explored whether miRNAs could effectively predict tumor response after nCT or nCRT in ESCC. However, variable miRNAs, together with different pathological response classifications, lead to complex outcomes that require further consideration.

In the present study, we briefly reviewed the involvement of miRNAs in the development and treatment resistance of ESCC. This systematic review aimed to analyze the predictive value of miRNAs in the pathological response of ESCC after nCT or nCRT. We present the following article in accordance with the PRISMA reporting checklist (available at http://dx.doi.org/10.21037/atm-20-3000) (21).

Methods

Search strategy

A literature search of PubMed, Web of Science, and Cochrane Library was conducted using the following search terms: (esophageal OR esophagus OR oesophageal OR oesophagus) AND (miR OR miRNA OR microRNA) AND (neoadjuvant OR preoperative OR induction). The search was restricted to English-language literature published from inception to February 14, 2020.

Inclusion and exclusion criteria

The inclusion criteria were as follows: (I) patients histologically diagnosed with esophageal cancer; (II) patients receiving nCT or nCRT followed by esophagectomy; and (III) studies on the association between miRNAs and pathological response to neoadjuvant treatment. The exclusion criteria were as follows: (I) published studies that were not original articles; (II) studies not on ESCC or miRNAs; and (III) studies not on pathological response. The reference lists of the original articles and literature reviews were also examined.

Data extraction

Data including first author, year of publication, sample size, neoadjuvant treatment, testing materials, pathological response classification, miRNA model, and statistical methods were extracted.

All procedures were independently double-checked by two investigators (D Lin and X Chen). Discrepancies were resolved through group discussions with all the authors.

Statistical analysis

It is well known that the part of Statistical Analysis is essential in original articles. However, this is a systematic review with no meta-analysis due to the heterogeneity across the enrolled studies. So, we think that the part of statistical analysis can be waived in our review article. We look forward to further communication at any time.

Results

Study characteristics

The initial search retrieved 206 studies. According to the inclusion and exclusion criteria, 197 studies were eliminated and 9 were finally selected for the review. The literature retrieval process is shown in Figure 1.

All 9 studies were published in the past decade (22-30). As summarized in Table 1, the 4 studies from Japan used nCT, while the other 5 studies, from China, Germany, and Canada, used nCRT. All chemotherapy regimens were platinum-based. The radiotherapy doses ranged from 30 to 60 Gy. Significant diversity was also observed in the testing materials, pathological response classifications, and the miRNA models. These findings indicated great heterogeneity among the studies, which eliminated the need for a quantitative analysis. The pathological response criteria are presented in Table S1.

Involvement of miRNAs in the origin and development of ESCC

In 2008, Guo et al. first reported the global microRNA expression profile of ESCC (31). They identified 46 miRNAs that were differentially expressed in malignant and adjacent normal tissue, of which 7 could distinguish between the
malignant and normal tissues. Moreover, they determined that miR-103/107 could be an independent prognostic marker. Kano et al. reported that the downregulation of miR-145, miR-133a, and miR-133b could lead to the activation of FSCN1, which promotes cell growth and invasion (32). Hamano et al. reported that miR-200c expression knockdown is associated with the increased expression of PPP2R1B, which might inhibit tumor invasiveness. Liu et al. revealed that ADAM9 is a key target of miR-126, and that the ectopic expression of miR-126 or silencing of ADAM9 reduces the proliferation and migration abilities of ESCC cells (22). Harada et al. stated that the complicated dysregulation of miRNAs could be responsible for the origin and development of ESCC (19).

**Involvement of miRNAs in treatment sensitivity or resistance of ESCC**

Chen et al. revealed that the combined downregulation of miR-133a and miR-133b enhances chemosensitivity to paclitaxel-based chemotherapy (33), and miR-141 was revealed to confer resistance to cisplatin in ESCC (34). Zang et al. revealed that miR-199a-3p regulates radioresistance by targeting the AK4 gene (35). Moreover, miR-96 promotes chemo- and radio-resistance in ESCC through the downregulation of RECK (36). Accumulating evidence has confirmed the associations between miRNAs and chemo- or radio-resistance, or chemo- or radio-sensitivity in ESCC. Vrana et al. stated that the role of miRNAs was interactive and complicated (20).

**Correlation between miRNAs and pathological response**

As mentioned above, the involvement of miRNAs in ESCC is an important precondition of potential predictive models. Recent studies have investigated whether single or panel miRNAs could effectively predict pathological response after nCT or nCRT in ESCC (25-30). As shown in Table 2, regarding the statistical methodology, 3 studies published from 2011–2013 that did not use diagnostic tests reported a correlation between miRNAs and pathological response. The other 6 studies, which were all published after 2013, used diagnostic tests, despite the absence of the STARD guidelines and external validation.

**Studies that did not use diagnostic tests**

In 2011, Hamano et al. reported that miR-200c was significantly correlated with pathological response (P=0.007) to nCT based on cisplatin, adriamycin and 5-FU (22).
In a study of pathological complete response (pCR) and non-pCR patients, Ko et al. found that 71 miRNAs were significantly different, and 5 miRNAs had greater than 2-fold differences (23). This study included 5 cases with ESCC and 20 with EAC. Odenthal et al. reported that the expression of miR-192 (P=0.005) and miR-194 (P=0.040) were significantly different between ESCC patients who showed minor and major response (24). Further, these studies found that the expression levels of specific miRNAs changed significantly before and after nCT or nCRT. These dynamic changes offered a possibility of early evaluation during neoadjuvant treatment. These studies revealed a significant correlation between miRNAs and pathological response.

Table 1 Summary of nine studies on the miRNAs and pathological response after neoadjuvant treatment in ESCC

<table>
<thead>
<tr>
<th>Authors (year)</th>
<th>Ref</th>
<th>Sample size</th>
<th>Neoadjuvant treatment</th>
<th>Testing materials</th>
<th>Pathological response classification (response criteria)</th>
<th>miRNA models</th>
</tr>
</thead>
<tbody>
<tr>
<td>Niwa et al. (2019)</td>
<td>(26)</td>
<td>92</td>
<td>nCT (multiple drugs based on platinum)</td>
<td>Pretreatment serum (microarray, qPCR)</td>
<td>Responders vs. non-responders (JES: Grade 2–3 vs. 0–1)</td>
<td>The panel of miR-23a-5p, 193b-5p and Ly; the panel of miR-193-5p and 873-3p; the panel of miR-23a-5p, 193-5p and 873-3p miR-194; miR-665; the panel of miR-194 and 665 miR-192b</td>
</tr>
<tr>
<td>Slotta-Huspenina et al. (2018)</td>
<td>(29)</td>
<td>84</td>
<td>nCRT (DDP/OXA, 5-Fu; 30–60 Gy)</td>
<td>Pretreatment biopsy, FFPE (microarray, qPCR)</td>
<td>Responders vs. non-responders (TRG Criteria: TGR 1a vs. 3)</td>
<td>miR-193a</td>
</tr>
<tr>
<td>Chan et al. (2018)</td>
<td>(30)</td>
<td>67</td>
<td>nCRT (DDP, 5-Fu; 40 Gy)</td>
<td>Pretreatment serum (microarray, qPCR)</td>
<td>Good vs. poor responders (0 vs. ≥50% viable tumor cells)</td>
<td>miR-21</td>
</tr>
<tr>
<td>Komatsu et al. (2016)</td>
<td>(28)</td>
<td>37</td>
<td>nCRT (DDP, 5-Fu)</td>
<td>Pretreatment plasma (microarray, qPCR)</td>
<td>Low vs. high response grade (JES: Grade 0–1a vs. 1b–3)</td>
<td>the panel of miR-145-5p, 152, 193b-3p and 376a-3p</td>
</tr>
<tr>
<td>Komatsu et al. (2016)</td>
<td>(27)</td>
<td>37</td>
<td>nCRT (DDP, 5-Fu)</td>
<td>Pretreatment plasma (microarray, qPCR)</td>
<td>Low vs. high response grade (JES: Grade 0–1a vs. 1b–3)</td>
<td>miR-21</td>
</tr>
<tr>
<td>Wen et al. (2016)</td>
<td>(25)</td>
<td>106</td>
<td>nCRT (DDP, NVB; 40 Gy)</td>
<td>Pretreatment biopsy (microarray, qPCR)</td>
<td>Responders vs. non-responders (≤50% vs. &gt;50% viable tumor cells)</td>
<td>NA (miR-192, 194 cluster)</td>
</tr>
<tr>
<td>Odenthal et al. (2013)</td>
<td>(24)</td>
<td>88</td>
<td>nCRT (DDP, 5-Fu; 40 Gy)</td>
<td>Pretreatment biopsy (microarray, qPCR)</td>
<td>Major vs. minor response (&lt;10% vs. ≥10% vital tumor cells)</td>
<td>NA (miR-296)</td>
</tr>
<tr>
<td>Ko et al. (2012)</td>
<td>(23)</td>
<td>25</td>
<td>nCRT (DDP, CPT-11;50.4 Gy)</td>
<td>Pretreatment biopsy, (microarray)</td>
<td>pCR vs. non-pCR</td>
<td>NA (miR-200c)</td>
</tr>
<tr>
<td>Hamano et al. (2011)</td>
<td>(22)</td>
<td>98</td>
<td>nCT (DDP, ADM, 5-Fu)</td>
<td>FFPE, fresh-frozen (microarray qPCR)</td>
<td>Responders vs. non-responders (JES: Grade 3 vs. 0–2)</td>
<td></td>
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</table>

Ref, reference; Ly, lymphatic invasion; DDP, cisplatin; 5-Fu, fluorouracil; NVB, vinorelbine; CPT-11, irinotecan; ADM, adriamycin; JES, Japan Esophageal Society; TRG, tumor regression grade.

In a study of pathological complete response (pCR) and non-pCR patients, Ko et al. found that 71 miRNAs were significantly different, and 5 miRNAs had greater than 2-fold differences (23). This study included 5 cases with ESCC and 20 with EAC. Odenthal et al. reported that the expression of miR-192 (P=0.005) and miR-194 (P=0.040) were significantly different between ESCC patients who showed minor and major response (24). Further, these studies found that the expression levels of specific miRNAs changed significantly before and after nCT or nCRT. These dynamic changes offered a possibility of early evaluation during neoadjuvant treatment. These studies revealed a significant correlation between miRNAs and pathological response.

Studies that used diagnostic tests

In 2016, Wen et al. identified 10 miRNAs with greater than 1.5-fold changes between pathological responders (<50% residual tumor) and non-responders (≥50% residual tumor), and established a combination of 4 miRNAs (miR-145-5p, miR-152, miR-193-3p, and miR-376a-3p) as a predictive model (25). The model provided a satisfactory predictive value for pathological response in an external validation cohort [area under the curve (AUC): 0.86, 95% confidence interval (CI): 0.77–0.96, P<0.001]. In this study, patients underwent homogeneous concurrent nCRT. But the underlying mechanism of these miRNAs was still unclear.
In recent years, circulating miRNAs have attracted significant attention due to their non-invasiveness and convenience. In 2019, Niwa et al. conducted serum-based miRNA signature research, which was carried out in accordance with the STARD guidelines (26). They identified 62 miRNAs in responders (grades 2–3) and non-responders (grade 0–1) after nCT. MiR-193b-5p, miR-873-3p, and miR-23a-5p, as well as microscopic lymphatic invasion, were included in the models. Consequently, receiver-operative characteristic (ROC) analysis confirmed that the combination of miR-193b-5p, miR-873-3p, and lymphatic invasion achieved the highest predictive value (AUC: 0.73, 95% CI: 0.60–0.86; no sensitivity, specificity, or accuracy data). However, the models did not show any independent prognostic value for long-term survival.

Komatsu et al. proposed miR-21 (27) and miR-23a (28) from pretreatment plasma as useful biomarkers for pathological response. However, these 2 miRNAs were found to have only low predictive value (AUC: 0.6794, sensitivity: 92.3%, specificity: 54.2%, and accuracy: 67.6%; AUC: 0.696, sensitivity: 79.2%, and specificity: 64.2%, respectively).

Slotta-Huspenina et al. identified 12 miRNAs from 15 responders [tumor regression grade (TRG) 1a] and 16 non-responders (TRG 3) after nCRT (29). ROC analysis confirmed the predictive value of miR-194* and miR-665, and their combination for pathological response (AUC: 0.811, 0.817, and 0.824, respectively) in the expanded 53 cases including 26 responders (TRG 1a) and 27 non-responders (TRG 3) after nCRT. Similarly, Chan et al. identified 3 miRNAs from 10 good responders (with no viable tumor cells) and 10 poor responders (≥50% viable tumor cells) after nCRT (30). The subsequent validation among 24 patients with good response (with no viable tumor cells) and 23 patients with poor response (≥50% viable tumor cells) revealed that miR-193b had a strong predictive power to discriminate between the patients (AUC: 0.8949, 95% CI: 0.7912–0.9987, \( P<0.0001 \)).

### Discussion

Pathological response is of importance for long-term survival after neoadjuvant treatment (10,11). Therefore, numerous efforts have been made to establish predictive models. In the past decade, miRNAs have been the focus of attention in cancer research. Vrana et al. analyzed the involvement of miRNAs in the origin and development of ESCC, and in the chemo- and radio-resistance of
ESCC (20). All of these formed one precondition for the hypothesis that miRNAs might be biomarkers for pathological response.

The aim of our review was to analyze studies on the predictive value of miRNAs for pathological response after nCT or nCRT in ESCC. After the selection and evaluation of articles, however, we observed great heterogeneity among the studies, and their methodologies and outcomes required further consideration.

Of the 6 studies that used diagnostic tests, 3 reported AUCs >0.80. Wen et al. proposed a predictive panel of miRNAs miR-145-5p, 152, 193b-3p, and 376a-3p in patients undergoing homogeneous nCRT (25). The effects of these miRNAs on tumor invasion varied. MiR-145-5p has been found to have an oncogenic function in esophageal cancer (37), while the overexpression of miR-152 sensitizes cisplatin-resistant ovarian cancer cells (38). Meanwhile, miR-193b-3p and 376a-3p have been shown to be tumor suppressors (39,40). In this study, however, Wen et al. did not investigate its prognostic value. In our opinion, complete or major pathological response is an indicator of long-term survival. Survival benefit, rather than pathological response, is the aim of any potential predictive model. An ideal model with the aims of predicting response and selecting patients should also have an independent association with survival benefit.

Apart from Wen et al.’s study, Slotta-Huspenina et al. (29) and Chan et al. (30) respectively reported models with high predictive values. However, in these latter 2 studies, we observed that the miRNA candidates were identified from 2 extreme pathological response classifications: TRG1a and TRG3 in Slotta-Huspenina et al.’s study, and no viable tumor cells versus ≥50% viable tumor cells in Chan et al.’s study. The spectrum bias would overestimate the predictive power (41). Moreover, the models were validated among patients with extreme pathological response classifications. The models offer limited value for decision-making in the clinical setting. Therefore, future well-designed studies that adhere to the standard guidelines of diagnostic tests are essential (42).

All 9 studies used pretreatment specimens as the testing materials. The studies in the early period had found the dynamics of miRNAs before and after nCT or nCRT. The possibility of early evaluation during neoadjuvant treatment could be an important direction. Four studies used serum or plasma specimens as the testing materials. Circulating miRNAs could serve as sensitive and informative biomarkers for certain diseases (43). However, inconsistencies between miRNAs in serum and miRNAs in tumor tissues have been reported (44). The use of miRNA panels, with or without clinicopathological factors, was also observed to have increased in recent years. The combination of miRNAs and other potential biomarkers, such as medical images, inflammatory markers, and nutrient indices, deserves further investigation.

Our systematic review has several limitations. First, the retrospective nature of the enrolled studies led to inherent selection bias. Second, only studies published in English were enrolled, leading to publication bias. Third, heterogeneity existed in treatment regimens, response classifications, and miRNA panels across the enrolled studies. Although previous studies have comprehensively analyzed the involvement of miRNAs in ESCC treatment resistance (20), the present review concentrated on the predictive value of miRNAs in pathological response after nCT or nCRT in ESCC. Despite the limited number of enrolled studies, our review uncovered some issues and proposed our opinions, and these would be helpful to further studies.

Conclusions

More and more evidence has demonstrated the correlation between miRNAs and pathological response after nCT and nCRT in ESCC. However, the current studies had not established any promising model. A well-designed prospective study is essential to investigate the potential models for pathological response after neoadjuvant treatment in ESCC.

Acknowledgments

We thank Dr. Jiaying Deng (Fudan University Shanghai Cancer Center) for his contribution to the search strategy. We thank Xuejuan Jin (Zhongshan Hospital of Fudan University) for her contribution to the statistical interpretation in this article. We acknowledge R. Scott and J. Reynolds from AME Editing Service for their help in language editing.

Funding: This study was supported by the Fund of Zhongshan Hospital of Fudan University (No. 2019ZSFZ16, No. 2016ZSLC15). The funding had no impact on study design, data collection, data interpretation or manuscript writing.
Footnote

Reporting Checklist: The authors have completed the PRISMA reporting checklist. Available at http://dx.doi.org/10.21037/atm-20-3000

Conflicts of Interest: All authors have completed the ICMJE uniform disclosure form (available at http://dx.doi.org/10.21037/atm-20-3000). The authors have no conflicts of interest to declare.

Ethical Statement: The authors are accountable for all aspects of the work in ensuring that questions related to the accuracy or integrity of any part of the work are appropriately investigated and resolved. The data used in this study are from the database, so ethical approval and informed consent of the patient are not required.

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References

19. Harada K, Baba Y, Ishimoto T, et al. The role of...


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<tr>
<th>Japan Esophageal Society (JES criteria)</th>
<th>Grade 0: No recognizable cytological or histological therapeutic effect</th>
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<tr>
<td></td>
<td>Grade 1: Apparently viable cancer cells (including cells having eosinophilic cytoplasm with vacuolation and swollen nuclei) account for 1/3 or more of tumor tissue, but there is some evidence of degeneration of cancer tissue or cells</td>
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<td></td>
<td>1a: Viable cancer cells accounting for 2/3 or more tumor tissue</td>
</tr>
<tr>
<td></td>
<td>1b: Viable cancer cells accounting for 1/3 or more, but less than 2/3, of tumor tissue</td>
</tr>
<tr>
<td></td>
<td>Grade 2: Viable cancer cells account for less than 1/3 of tumor tissue, while other cancer cells are severely degenerated or necrotic</td>
</tr>
<tr>
<td></td>
<td>Grade 3: No viable cancer cells are evident</td>
</tr>
<tr>
<td>Tumor regression grades (TRG criteria)</td>
<td>TRG 1a: No residual tumor/tumor bed</td>
</tr>
<tr>
<td></td>
<td>TRG 1b: &lt;10% residual tumor/tumor bed</td>
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<tr>
<td></td>
<td>TRG 2: 10–50% residual tumor/tumor bed</td>
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<td>TRG 3: &gt;50% residual tumor/tumor bed</td>
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