Prognostic Role of MicroRNA-21 in Non-small Cell Lung Cancer: a Meta-analysis

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Abstract

**Introduction**: Many studies have reported that microRNA-21 (miR-21) might predict the survival outcome in non-small cell lung cancers (NSCLCs) but the opposite opinion has also been expressed. The aim of this study was to summarize the evidence for a prognostic role of miR-21. **Materials and Methods**: All the eligible studies were searched by Medline and EMBASE and patients’ clinical characteristics and survival outcome were extracted. Then a meta-analysis was performed to clarify the prognostic role of the miR-21 expression in different subgroups. **Results**: A total of 8 eligible articles were yielded covering survival outcomes or clinical characteristics. The combined hazard ratio (HR) and 95% confidence interval (95% CI) for overall survival (OS) was 2.19 [0.76, 6.30], while the combined HR (95% CI) of Asian group for OS had a significant result, 5.49 [2.46, 12.27]. The combined HR (95% CI) for recurrence free survival or disease free survival (RFS/DFS) was 2.31 [1.52, 3.49]. Odds ratios (ORs) showed that the miR-21 expression was associated with lymph node status and histological type. **Conclusion**: miR-21 expression could predict the prognostic outcome of NSCLC in Asians, despite some deficiencies in the study data.

**Keywords**: MicroRNA-21 - lung cancer - prognosis - survival outcome - meta-analysis

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Introduction

Lung cancer is the most common cause of cancer mortality in the world. Approximately 1.6 million new cases of lung cancer will be diagnosed and 1.4 million deaths will occur from lung cancer during 2008. Among all cases suffered lung cancer, non-small-cell lung cancer (NSCLC) approximately accounts for 80% (Ramalingam et al., 1998; Jemal et al., 2011).

MicroRNAs (miRNAs) are endogenous, small non-coding and have a length of 18-25 nucleotides RNAs. These miRNAs could identify post transcriptional gene regulators that paired to complementary sequences in the 3’ untranslated region (3’ UTR) of target mRNAs, leading to mRNA degradation or translational repression (Bartel 2004; Bartel and Chen 2004).

Many studies have reported that over expression of microRNA-21 (miR-21) play important roles in increasing cell proliferation, migration, invasion and survival (Lu et al., 2008; Yang et al., 2011). Relatively speaking suppression or knock-down of miR-21 could induce apoptosis and repress cell proliferation and invasion (Zhang et al., 2010). The miR-21 was also found to be elevated in many cancers such as lymphoma, prostate cancer, colorectal cancer and breast cancer (Lawrie et al., 2007; Siva et al., 2009; Qian et al., 2009; Nielsen et al., 2011). However, the expression of miR-21 in NSCLC and the prognostic significance remains unclear.

The aim of this study is to comprehensively and quantitatively summarize the evidence for the use of miR-21 to predict the clinical results of NSCLC patients. And we also want to evaluate the overall risk of elevated miR-21 for survival in patients with NSCLC.

Materials and Methods

Medline and EMBASE were searched for the last time on Apr 10, 2012. The search strategy included the following keywords variably combined by “microRNA-21”, “miR-21”, “lung cancer” and “NSCLC”.

Study inclusion/exclusion criteria

Studies were considered eligible if they met all of the following inclusion criteria, (i) discussed patients with NSCLC (ii) measured the miR-21 expression in tumor and serum; (iii) investigated the survival outcome or the correlation between miR-21 expression and the clinical variables. Studies were excluded based on any of the following reasons, (i) were review articles, laboratory articles or letters (ii), described the survival outcome of other tumors or other markers, (iii) lacked key information for calculation with methods developed by Parmar, Williamson, and Tierney (Parmar et al., 1998; Williamson et al., 2002; Tierney et al., 2007), (iv) the articles from one
author and the studies brought into the repeated samples from the same patients.

Data Extraction

Eligible articles were reviewed independently by two investigators (Ma XL and Liu Lei). Disagreements were resolved by consensus. Multivariate Cox hazard regression analysis reported in the article was included in our analysis; if these data were not available, we extracted univariate Cox hazard regression analysis or log-rank p value and Kaplan–Meier survival curves of survival outcomes instead. Above primary information had been extracted by two investigators (Ma XL and Liu XX) independently. Additional data were extracted from the studies included first author, publication year, study size, patients age and sexuality, smoker or not, TNM stage, lymph status, histological classification, methods to detect miR-21, positive miR-21 definition, the attitude conclusion and other clinical characteristics.

Statistical Methods

All these HRs and 95% confidence interval (CI) were calculated following Tierney’s method and the logHR and SE (logHR) (SE) were used for aggregation of the survival results, but these statistical variables were not given directly in most studies. We calculated the necessary statistics on the basis of available numerical data with methods developed by Parmar, Williamson, and Tierney. Calculation was accomplished by the software designed by Matthew Sydes and Jayne Tierney with these methods (Medical Research Council Clinical Trials Unit, London, UK) (Tierney et al., 2007).

We also examine the correlation between miR-21 expression and the clinical variables including TNM stage, lymph node status, histological type, sexuality and smoking status. According to clinical characteristics, Stage I and Stage II were combined and Stage III and Stage IV were combined. Odds ratio (OR) was used as the measure index to describe the correlation (CORNFIELD 1951).

Forrest plots were used to estimate the effect of miR-21 expression on survival outcome and the correlation between miR-21 expression and the clinical variables. Heterogeneity was defined as p < 0.10 or I² > 50%. When homogeneity was fine, we assumed a fixed effect model and used for secondary analysis. If not, a random effect model was used (Higgins et al., 2003). An observed HR > 1 indicated worse outcome for the positive group relative to the negative group and would be considered statistically significant if the 95% CI did not overlap 1. The Begg’s rank correlation also was applied to assess the potential publication bias, p < 0.05 was considered that there was no potential publication bias (Begg, 1994). All above calculations were performed using RevMan 5.1 (Cochrane collaboration, Oxford, UK). Publication biases were evaluated using the Begg’s funnel plot by STATA 11.0 (STATA Corporation, College Station, TX).

Results

Eligible Studies

The initial search returned 42 studies in PubMed and EMBASE. Following review of these abstracts, 13 potentially relevant studies were identified as eligible for full-text review. 5 studies were excluded, because these studies were short of the necessary data for calculation. One article from Saito M (Saito et al., 2011) gave the CSS for Maryland/Norway cohort, and the recurrence free survival (RFS) for Japan cohort. Because there was only one study for CSS, we just used the RFS for Japan cohort in our meta-analysis. We combined the results disease free survival (DFS) and RFS together as RFS/DFS. There were 3 articles from Gao W, one article used RFS to describe the survival outcome (Gao et al., 2012), while another two used OS (Gao et al., 2010, 2011). We exclude one article for overall survival (OS) in the meta-analysis, because Gao W referred in the article

Table 1. Clinical Characteristics of Included Studies

<table>
<thead>
<tr>
<th>author</th>
<th>Population</th>
<th>N</th>
<th>Positive</th>
<th>Sampling</th>
<th>sex</th>
<th>smoker</th>
<th>TNM stage</th>
<th>LNM</th>
<th>histological method</th>
<th>cut-off</th>
<th>Survival</th>
<th>Multivariate</th>
<th>conclusion</th>
</tr>
</thead>
<tbody>
<tr>
<td>Markou A 2008</td>
<td>Greece</td>
<td>48</td>
<td>25</td>
<td>tumor</td>
<td>—</td>
<td>44</td>
<td>I/II32</td>
<td>25</td>
<td>ADC 25</td>
<td>qRT-PCR</td>
<td>OS, DFS</td>
<td>No</td>
<td>Positive</td>
</tr>
<tr>
<td>Voortman J 2010</td>
<td>France</td>
<td>631</td>
<td>316</td>
<td>tumor</td>
<td>—</td>
<td>—</td>
<td>I/II39</td>
<td>76</td>
<td>ADC 218</td>
<td>qRT-PCR</td>
<td>median</td>
<td>OS Yes</td>
<td>Negative</td>
</tr>
<tr>
<td>Saito M 2011</td>
<td>USA</td>
<td>126</td>
<td>62</td>
<td>tumor</td>
<td>—</td>
<td>109</td>
<td>I/II8</td>
<td>—</td>
<td>all ADC</td>
<td>qRT-PCR</td>
<td>USA 2.11</td>
<td>CSS No</td>
<td></td>
</tr>
<tr>
<td></td>
<td>Norway</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td>I/II27</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Gao W 2010</td>
<td>China</td>
<td>47</td>
<td>—</td>
<td>tumor</td>
<td>—</td>
<td>31</td>
<td>I/II22</td>
<td>22</td>
<td>ADC 21</td>
<td>qRT-PCR</td>
<td>1.4</td>
<td>OS Yes</td>
<td>Positive</td>
</tr>
<tr>
<td>Gao W 2012</td>
<td>China</td>
<td>58</td>
<td>29</td>
<td>tumor</td>
<td>—</td>
<td>32</td>
<td>I/II16</td>
<td>32</td>
<td>ADC 33</td>
<td>qRT-PCR</td>
<td>1.5</td>
<td>DFS Yes</td>
<td>Positive</td>
</tr>
<tr>
<td>Gao W 2010</td>
<td>China</td>
<td>30</td>
<td>15</td>
<td>tumor</td>
<td>—</td>
<td>25</td>
<td>I/II17</td>
<td>11</td>
<td>—</td>
<td>qRT-PCR</td>
<td>1.47</td>
<td>OS Yes</td>
<td>Positive</td>
</tr>
<tr>
<td>Liu XG 2011</td>
<td>China</td>
<td>70</td>
<td>48</td>
<td>tumor</td>
<td>—</td>
<td>56</td>
<td>I/II13</td>
<td>32</td>
<td>ADC 34</td>
<td>qRT-PCR</td>
<td>2</td>
<td>OS No</td>
<td>Negative</td>
</tr>
<tr>
<td>Wang ZX 2011</td>
<td>China</td>
<td>88</td>
<td>49</td>
<td>tumor</td>
<td>—</td>
<td>46</td>
<td>I/II47</td>
<td>35</td>
<td>ADC 37</td>
<td>qRT-PCR</td>
<td>5</td>
<td>OS Yes</td>
<td>Positive</td>
</tr>
</tbody>
</table>

ADC, adenocarcinoma; AQC, squamous cell carcinoma; LNM, lymph node metastasis; CSS, cancer-specific mortality; DFS, disease-free interval; OS, overall survival; RFS, relapse free survival; qRT-PCR, Quantitative reverse transcriptase PCR
that they used the repeated data have been defined and described previously (Gao et al., 2011). Liu XG’s study (Liu et al., 2011) gave the HRs and CI both in the tumor and serum, we used the correspond data in different nation, we found that the combined HR of Asian studies was 2.31 [1.52, 3.49] (n=297, F=0%, P=0.56). The pooled HR for serum miR-21 was 2.08 [1.55, 2.80] (n=158, F=13%, P=0.28) (Liu et al., 2011; Wang et al., 2011). All the above meta-analysis used the fixed effect model except the HR for OS (Table 2, Figure 2).

**Subgroup analysis**

When we grouped the meta-analysis by the patients’ ethnicity, we found that the combined HR of Asian studies (Gao et al., 2011; Liu et al., 2011) was 5.49 [2.46, 12.27] (n=128, F=0%, P=0.59), while the combined HR of other yielded non-Asian studies (Markou et al., 2008; Voortman et al., 2010) was 1.25 [0.48, 3.25] (n=679, F=86%, P=0.007) (Table 2). We also tried to use the other grouping term to examine the prognostic role of miR-21 such as histological type, TNM stage, and lymph status. No result could give clinical significance.

**Correlation between miR-21 expression and clinical characteristics**

The studies which referred the correlation between miR-21 expression and some clinical characteristics (TNM stage, lymph metastasis, sex, histological type and smoking status) have been pooled to calculate

### Table 2. Meta-analyses of miR-21 Expression to Predict the Survival Outcome

<table>
<thead>
<tr>
<th>Survival outcome</th>
<th>Study n.</th>
<th>Patient n.</th>
<th>Model</th>
<th>HR(95% CI)</th>
<th>P value</th>
<th>Heterogeneity (I^2, p)</th>
<th>Conclusion</th>
</tr>
</thead>
<tbody>
<tr>
<td>miR-21 total</td>
<td>OS</td>
<td>4</td>
<td>796</td>
<td>2.19 [0.76, 6.30]</td>
<td>0.15</td>
<td>88% &lt; 0.0001</td>
<td>negative</td>
</tr>
<tr>
<td></td>
<td>RFS/DFS</td>
<td>3</td>
<td>297</td>
<td>2.31 [1.52, 3.49]</td>
<td>&lt;0.0001</td>
<td>0% 0.56</td>
<td>positive</td>
</tr>
<tr>
<td>miR-21 Asian</td>
<td>OS</td>
<td>2</td>
<td>117</td>
<td>5.49 [2.46, 12.27]</td>
<td>&lt;0.0001</td>
<td>0% 0.59</td>
<td>positive</td>
</tr>
<tr>
<td>miR-21 non Asian</td>
<td>OS</td>
<td>2</td>
<td>679</td>
<td>0.89 [0.72, 1.10]</td>
<td>0.27</td>
<td>86% 0.007</td>
<td>negative</td>
</tr>
<tr>
<td>Serum Asian</td>
<td>OS</td>
<td>2</td>
<td>158</td>
<td>2.08 [1.55, 2.80]</td>
<td>&lt;0.00001</td>
<td>13% 0.28</td>
<td>positive</td>
</tr>
</tbody>
</table>

### Table 3. Meta-analyses of miR-21 Expression Classified by Clinical Characteristics

<table>
<thead>
<tr>
<th>Analysis</th>
<th>Study n.</th>
<th>Patient n.</th>
<th>Model</th>
<th>OR(95% CI)</th>
<th>p value</th>
<th>Heterogeneity Conclusion</th>
</tr>
</thead>
<tbody>
<tr>
<td>Serum Asian OS</td>
<td>2</td>
<td>158</td>
<td>Random</td>
<td>1.19 [0.55, 2.58]</td>
<td>&lt;0.00001</td>
<td>13%, 0.28 positive</td>
</tr>
<tr>
<td>miR-21 non Asian OS</td>
<td>2</td>
<td>679</td>
<td>Random</td>
<td>0.89 [0.72, 1.10]</td>
<td>0.27</td>
<td>86% 0.007 negative</td>
</tr>
<tr>
<td>miR-21 Asian OS</td>
<td>2</td>
<td>117</td>
<td>Fixed</td>
<td>5.49 [2.46, 12.27]</td>
<td>&lt;0.0001</td>
<td>0% 0.59 positive</td>
</tr>
<tr>
<td>RFS/DFS</td>
<td>3</td>
<td>297</td>
<td>Fixed</td>
<td>2.31 [1.52, 3.49]</td>
<td>&lt;0.0001</td>
<td>0% 0.56 positive</td>
</tr>
</tbody>
</table>

**Figure 1. Selection of Studies**

**Figure 2. Estimated Hazard Ratios (HRs) Summary**

(A) overall survival with miR-21 expression in tumor tissue, (B) disease free survival or recurrence free survival with miR-21 expression in tumor tissue, and (C) overall survival with miR-21 expression in serum

was 2.31 [1.52, 3.49] (n=297, F=0%, P=0.56). The pooled HR for serum miR-21 was 2.08 [1.55, 2.80] (n=158, F=13%, P=0.28) (Liu et al., 2011; Wang et al., 2011). All the above meta-analysis used the fixed effect model except the HR for OS (Table 2, Figure 2).

**Correlation between miR-21 expression and survival outcome (OS and RFS/DFS)**

**Overall Analyses**

The meta-analysis of all studies for OS showed no significant prognostic effect on miR-21 detected in tumor samples. The combined HR (95% CI) of 4 studies (Markou et al., 2008; Gao et al., 2010; Voortman et al., 2010; Liu et al., 2011) for OS was 2.19 [0.76, 6.30] (n=796, F=88%, P<0.0001), and the HR (95% CI) of 3 studies (Markou et al., 2008; Saito et al., 2011; Gao et al., 2012) for RFS/DFS. When we grouped the meta-analysis by the patients’ ethnicity, we found that the combined HR of Asian studies (Gao et al., 2011; Liu et al., 2011) was 5.49 [2.46, 12.27] (n=128, F=0%, P=0.59), while the combined HR of other yielded non-Asian studies (Markou et al., 2008; Voortman et al., 2010) was 1.25 [0.48, 3.25] (n=679, F=86%, P=0.007) (Table 2). We also tried to use the other grouping term to examine the prognostic role of miR-21 such as histological type, TNM stage, and lymph status. No result could give clinical significance.

**Correlation between miR-21 expression and clinical characteristics**

The studies which referred the correlation between miR-21 expression and some clinical characteristics (TNM stage, lymph metastasis, sex, histological type and smoking status) have been pooled to calculate
Figure 3. Estimated Odds Ratios (ORs) Summary for Correlation of (A) miR-21 expression and lymph node status, (B) miR-21 expression and histological differentiation

The ORs. In our study we did not find miR-21 expression had significant correlation with the TNM stage (Markou et al., 2008; Voortman et al., 2010; Jamal et al., 2011; Wang et al., 2011; Gao et al., 2012), sexuallity (Gao et al., 2011, 2012; Wang et al., 2011) and smoking status (Markou et al., 2008; Gao et al., 2011; Wang et al., 2011) in the eligible studies. The ORs and the corresponding CIs were 1.19 [0.55, 2.58], 1.09 [0.59, 2.02] and 0.79 [0.38, 1.62], respectively. Meanwhile, the correlation results for lymph metastasis (Markou et al., 2008; Voortman et al., 2010; Gao et al., 2011, 2012; Wang et al., 2011) and histological type (Markou et al., 2008; Voortman et al., 2010; Wang et al., 2011; Gao et al., 2012) were evidently significant (Figure 3). The ORs and long-rank p-value of studies for lymph metastasis and histological type were 1.80 [1.24, 2.60], p=0.004 and 0.60 [0.44, 0.81], p=0.0008, respectively. All these results could be reviewed in Table 3.

Assessment of publication bias
Begg’s test was used to examine publication bias. No significant publication biases were found in results of meta-analyses of miR-21 prediction value for OS both using tumor and serum samples (P=0.497 and P=0.317 respectively). There was also no publish bias in the studies for RFS/DFS (P=0.602) (Figure 4).

Discussion
As we know, it was the first time that a comprehensive and detailed meta-analysis revealed the prognostic role of tumor and serum miR-21 for NSCLC. The prognostic role of miR-21 expression was still a great puzzle according to the evidence-based medicine in our study.

The prognostic values of miR-21 have been proven in the recent meta-analysis in head and neck squamous cell carcinoma (HNSCC) and carcinomas in digestion system. Our result of HR for OS was 2.19 [0.76, 6.30]. The interval of HR overlapped 1, it showed that the miR-21 expression had no prognostic significance on NSCLC. The subgroup analysis showed that the HR for Asian group was 5.49 [2.46, 12.27], it suggested that the miR-21 expression played significant prognostic role on NSCLC. Meanwhile, the combined HR for non-Asian group was 1.25 [0.48, 3.25], it suggested that the miR-21 was no find the effect to predict survival outcome in non-Asian group.

The HR for RFS/DFS to predict the survival outcome was statistically significant. As referred in Hayes (Hayes et al., 2001), a prognostic factor with RR>2 is considered as useful practical value. All the meta-analysis except the pooled result for OS had a well result. It may suggest that detected miR-21 expression in tumor tissue (B) disease free survival or recurrence free survival with miR-21 expression in tumor tissue, and (C) overall survival with miR-21 expression in serum

In the correlation study of miR-21 expression with patients’ clinical characteristics, TNM stage, sexuallity and smoking status showed complete no correlation with miR-21 expression while ORs for lymph metastasis and histological type were significant (Figure 3). The ORs and long-rank p-value of lymph metastasis and histological type were 1.80 [1.24, 2.60], p=0.004 and 0.60 [0.44, 0.81], p=0.0008, respectively. All these results could be reviewed in Table 3.

Corresponding Meta-analysis in Figure 2. Orderly, they are Funnel plots of publication bias for meta-analysis of hazard ratios (HRs) for (A) overall survival with miR-21 expression in tumor tissue (B) disease free survival or recurrence free survival with miR-21 expression in tumor tissue, and (C) overall survival with miR-21 expression in serum

The HR for RFS/DFS to predict the survival outcome was statistically significant. As referred in Hayes (Hayes et al., 2001), a prognostic factor with RR>2 is considered as useful practical value. All the meta-analysis except the pooled result for OS had a well result. It may suggest that detected miR-21 expression in tumor tissue (B) disease free survival or recurrence free survival with miR-21 expression in tumor tissue, and (C) overall survival with miR-21 expression in serum

In the correlation study of miR-21 expression with patients’ clinical characteristics, TNM stage, sexuallity and smoking status showed complete no correlation with miR-21 expression while ORs for lymph metastasis and histological type were significant. The miR-21 have been proven to regulates the metastatic behavior in both mouse and human by activating many signal ways (Gao et al., 2011, 2012; Wang et al., 2011). This puzzle could be solved when much more studies were conducted to confirm clinical value of the miR-21 expression. And the prognostic role of miR-21 for Asian group could be confirmed by adequately multi-center designed prospective studies in Asian country in future. We could also find the serum miR-21 could play prognostic role on NSCLC (HR 2.08[1.55, 2.80]). This result indicated that serum miR-21 could be a diagnostic tool to detect the NSCLC. Some clinical studies and review have been proven the application of the microRNA (Liang 2008; de Planell-Saguer M and Rodicio, 2011; Wei et al., 2011).
method, and histological classification. These entire attempts could not eliminate the heterogeneity. The heterogeneity came from the Voortman J’s study. This study had a opposite survival outcome. When we removed this study, the adjusted HR was 3.37 [1.60, 7.13] (I² = 39%, P=0.19). It suggested that the miR-21 expression could predict prognostic outcome in lung cancer.

In another article, we found that the software we used before, designed by Matthew Sydes and Jayne Tierney retained only percentile when calculated the logHR and SE. To eliminate this bias, we designed a new software following Tierney’s method by Lei Deng. The publication biases were additional problem for the meta-analysis. Fortunately, the Begg’s test showed no significant publication bias in this study (p>0.05).

In conclusion, the meta-analysis suggested that it was still a puzzle whether the miR-21 expression could predict the poor prognosis. Meanwhile our meta-analysis showed that serum miR-21 expression had a prognostic role on NSCLC. The miR-21 expression might have some correlation with the metastasis behavior in the NSCLC, though the p-value were on borderline. Future adequately multi-center designed prospective with larger sample size were of great value to confirm these findings.

Acknowledgements

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References

