Prognostic role of miR-9 expression in various human malignant neoplasms: a meta-analysis

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Abstract: Emerging evidence has shown that aberrant microRNA expression has the potential to be used for predicting survival and treatment response of malignant neoplasms. In recent years, the role of miR-9 had been investigated in various types of cancers, and it was found that the results were inconsistent and inconclusive. Hence, in this study, a meta-analysis was conducted to assess the prognostic value of miR-9 in various types of tumors. Eligible studies were identified through a systematic search in PubMed and EMBASE and then were assessed by further quality evaluation. Pooled hazard ratios (HRs) with 95% confidence intervals for overall survival (OS) were calculated to investigate the association between miR-9 expression and cancer prognosis. The pooled results of eight published studies showed that elevated miR-9 was a predictor of poor survival of various carcinomas, with pooled HR of 3.04 (95% confidence interval: 1.96–4.73) for OS. Subgroup analysis on the basis of tumor type, sample size, and HR estimate also showed that high levels of miR-9 were also significantly correlated with OS. In addition, when the subgroup analyses were grouped by follow-up time, it was found that the elevated expression of miR-9 was associated with a lower long-term survival when the follow-up time was >60 months, but there was no correlation between the outcomes and those patients whose follow-up time was <60 months. Funnel plots and Egger’s tests revealed that there was no obvious publication bias risk in the meta-analysis. In conclusion, our results demonstrated that higher expression level of miR-9 significantly predicted worse OS in various carcinomas and that miR-9 may act as a novel biomarker in the prognosis of malignant neoplasms.

Keywords: microRNA-9, meta-analysis, prognosis, overall survival, malignant neoplasms

Introduction

Malignant neoplasms had been found to be the main cause of death worldwide for a long time, and many research studies have been conducted to explore the molecular mechanism, cancer therapy, and prognosis. MicroRNAs (miRNAs), a class of small noncoding RNAs of ~20–25 nucleotides long, had been demonstrated to play vital roles in tumorigenesis and tumor progression.1 The majority of the effects of miRNAs was mediated through targeting different genes by regulating their expressions.2–4 Different expression levels of miRNAs were found in various malignant neoplasms, which were associated with the prognosis of various carcinomas. For instance, downregulation of miR-100 was correlated with poor prognosis in cervical cancer and hepatocellular carcinoma patients,5,6 and high expression of miR-21 predicted weak survival status in pancreatic cancer and colorectal cancer.7,8

miR-9, whose transcript was produced by three independent genes (miR-9-1, miR-9-2, and miR-9-3), was also related to oncogenesis.9 The expression level of miR-9 was different in various carcinomas, which was also connected to tumor prognosis.
Significant upregulation of miR-9 level was observed in osteosarcoma and hepatocellular carcinoma with poor prognosis.\textsuperscript{10,11} However, miR-9 was deregulated in colon cancer\textsuperscript{12} and nasopharyngeal carcinoma\textsuperscript{13} and may serve as prognostic marker. In addition, the expression of miR-9 was conflicting in some studies with the same cancer, such as breast cancer,\textsuperscript{14,15} gastric cancer,\textsuperscript{16,17} lung cancer,\textsuperscript{18,19} and acute myeloid leukemia,\textsuperscript{20,21} and the prognostic significance remained unclear. In a word, the results of miR-9 expression in different studies were inconsistent or even opposite, and the prognostic role of aberrantly expressed miR-9 remained to be elucidated in malignant neoplasms.

Thus, the results of the present studies were inconsistent, and it was unclear whether miR-9 acted as oncogene or tumor suppressor. Nevertheless, this contradictory phenomenon greatly aroused our interest, and we were eager to know the accurate role of miR-9 in patients with malignant neoplasms. Therefore, a meta-analysis (which identifies a common statistical measure to contrast and combine results from different studies) to clarify the overall role of miR-9 for the prognosis in multiple human tumors was conducted.

\textbf{Methods}

This meta-analysis was performed by following the guidelines of Preferred Reporting Items for Systematic Reviews and Meta-analysis criteria.\textsuperscript{22}

\textbf{Search strategy}

Online databases PubMed and EMBASE were systematically searched by two reviewers (Peng and Luo) independently, in order to identify relevant published studies (published from January 1, 1993 to May 13, 2015) that evaluate the prognostic value of miR-9 in various cancers. Titles, abstracts, and full text of the identified articles were independently assessed according to the inclusion and exclusion criteria. The final selected studies in the meta-analysis were researched by consensus, and the disagreements were resolved with a discussion by the third reviewer (Liu). The combination of keywords that was used are as follows: (microRNA-9, mirna-9, or mir-9) and (cancer, neoplasm, tumor, malignant, carcinoma, hematology*, leukemia, AML, ALL, lymphoma, or multiple myeloma) and (incidence, mortality, follow-up studies, prognosis*, predict*, course*, survival, hazard ratio, HR) (Table 1). We designed the strategy to be optimized for a sensitive and broad search. Meanwhile, the reference lists and conference abstracts were also searched to obtain additional eligible articles.

<table>
<thead>
<tr>
<th>Table 1</th>
<th>The strategies used for searching PubMed and EMBASE</th>
</tr>
</thead>
</table>

\textbf{Abbreviations:} miR-9, microRNA-9; AML, acute myelocytic leukemia; ALL, acute lymphoblastic leukemia; HR, hazard ratio.

\textbf{Inclusion criteria}

The inclusion criteria for the study are as follows: 1) studied miR-9 in any type of human malignant neoplasms, 2) expression of miR-9 was measured in human samples, 3) the correlation between miR-9 expression and survival outcome was investigated, 4) full-text articles in English, and 5) survival outcome was further explored considering hazard ratio (HR) with 95% confidence interval (95% CI) and HR with a \textit{P}-value.

\textbf{Exclusion criteria}

Articles were excluded on the basis of the following criteria: 1) case reports, laboratory articles, letters, reviews, and animal trials; 2) did not describe the detailed information of the survival outcome, such as HR, 95% CI, and \textit{P}-value; 3) no value of miR-9 expression level; 4) studies had overlapping or duplicate data – when multiple articles from the same author
or group reported on the same patient population, only the most recent or complete study was chosen; 5) articles concerning polymorphisms or methylation patterns of a miRNA and articles involving oncoviruses; and 6) articles focused on other miRNAs. If any doubt of suitability remained after abstract and full manuscript was examined, it was discussed by the authors and resolved by consensus.

Data extraction and quality assessment
Two reviewers (Peng and Luo) evaluated the methodological quality of potentially selected articles, regardless of the results. Extracted data were then crosschecked between the two reviewers to rule out any discrepancy. Data from all the eligible studies were extracted as follows: 1) basic characteristics of publications, including name of first author, year of publication, country of the study, types of diseases, number of samples, and types of samples; 2) age and sex; 3) the measurement method of miR-9 and the cutoff of miR-9 expression; 4) overall survival (OS), event-free survival or relapse-free survival, OS with HR of miR-9 expression as well as corresponding 95% CI and P-value. If both univariate analysis and multivariate analysis were reported to get the HR, and the results of multivariate analysis including HR and 95% CI should be preferably taken in meta-analysis because they could be more accurate; and 5) sufficient period of follow-up time. The quality of all including publications was systematically assessed.

Statistical analysis
The forest figure was carried out using the Review Manager software Version 5.2 (The Nordic Cochrane Center, The Cochrane Collaboration, Copenhagen, Denmark), and the statistical between-study heterogeneity was assessed by visual inspection of forest plots, performing the chi-square test (assessing the P-value), and calculating the $I^2$ statistic.23 The log HR and standard error were used for aggregation of the survival results in the forest plots. $F$ values range from 0% to 100% ($F=0\%–25\%$, low heterogeneity; $F=25\%–50\%$, moderate heterogeneity; $F=50\%–75\%$, large heterogeneity; $F=75\%–100\%$, extreme heterogeneity).23 If the P-value was <0.05 and/or $F$ exceeded 50%, indicating the presence of heterogeneity, then the random effects model was performed among the included studies, otherwise the fixed effects model was selected. An observed HR $>1$ indicated a worse prognosis in patients with miR-9 overexpression and HR $<1$ suggested a better prognosis. Secondly, publication bias was visually inspected by the STATA software Version 12.0 (Stata Corp LP, College Station, TX, USA) with the methods of Begg’s funnel plots (asymmetric funnel plot indicated possible risk of publication bias) and Egger’s test ($P<0.05$, publication bias was statistically significant).24 Funnel plot asymmetry on the natural logarithm scale of the HR was measured by a linear regression approach. All the $P$-values were two-sided.

Results
Literature selection and characteristics
A total of 285 studies for miR-9 associated with cancer prognosis were identified from a primary literature search in PubMed and EMBASE databases. About 131 citations were excluded from the analysis after the first screening based on the species, article types, and language. After manually screening the titles and abstracts, 125 records were excluded because they were either a duplicate or irrelevant to the current study. The remaining 29 publications were carefully reviewed and assessed, and eleven articles were further removed because they were unrelated to miR-9 expression levels or because of lack of survival statistics such as HR, 95% CI, and P-value. Finally, 18 studies, which investigated the potential relationship between miR-9 expression and patients’ survival or disease relapse in various malignant neoplasms, remained for detailed screening and data extraction (Figure 1). Clinical characteristics of these articles are summarized in Table 2.

In these 18 studies, a total of 3,935 patients from the US, France, People’s Republic of China, Germany, Brazil, the Netherlands, Spain, Japan, and Korea were diagnosed with various types of cancers, such as solid tumors (colorectal cancer, laryngeal squamous cell carcinomas, esophageal squamous cell carcinoma, non-small lung cancer, glioma, ovarian, osteosarcoma, adrenocortical cancer, hepatocellular carcinoma, bladder cancer, and breast cancer) and hematological malignant (leukemia). The majority of the studies examined the expression of miR-9 in cancerous tissue, yet five studies of leukemia targeted bone marrow as a source of interest, three detected the expression index from formalin-fixed paraffin-embedded samples, only one from peripheral blood. Quantitative real-time polymerase chain reaction was widely used in 16 studies, and miRNA assay was used in the other two studies. Notably, the cutoff values of miRNAs were different in each study, most with the median. Detailed screening revealed that six of 18 studies did not report multivariate analysis, two failed to provide HR value of multivariate analysis, one did not evaluate OS, and one did not report
95% CI. As a result, eight eligible studies were included in the meta-analysis to evaluate the prognostic role of miR-9 in malignant tumors (Table 3).

**Meta-analysis**

There was obvious between-study heterogeneity among those included studies \((P<0.05)\); hence, in order to make a conservative estimate, the random-effects model rather than a fixed-effects model was utilized to pool data. Figure 2 displays the forest plot of the analysis about miR-9 expression and OS in patients with various types of cancers, which included leukemia, glioma, laryngeal squamous cell carcinomas, osteosarcoma, esophageal squamous cell carcinoma, non-small lung cancer, and hepatocellular carcinoma. Extreme heterogeneity was observed when eight studies were pooled \((P=76.0\%, \; P=0.0001)\), indicating that the variation was due to heterogeneity rather than chance. When all the study populations were combined, dismal survival outcomes were observed with the overexpression of miR-9. The result showed that a higher expression level of miR-9 significantly predicted worse OS in various carcinomas, with the pooled HR of 3.04 (95% CI: 1.96–4.73, \(P<0.0001\); Figure 2).

The most possible sources of the heterogeneity were also analyzed by using different methods (Table 4). Subgroup analysis was carried out on the basis of the types of cancers, such as solid tumor and leukemia. First, as an obvious heterogeneity \((P<0.0001, \; I^2=82\%)\) existed in those research studies on OS of solid tumor patients, a random model was used to pool the HRs. The combined HR, 2.97 (95% CI: 1.76–5.00, \(P<0.0001\)), indicated that overexpressed miR-9 would potently predict unfavorable OS for patients with a solid tumor. Two research studies focused on the prognostic effect of miR-9 on the OS of leukemia patients, and a meta-analysis was conducted. A further analysis indicated that high expression of miR-9 in leukemia was significantly related to poor prognosis (pooled HR =2.87, 95% CI: 1.55–5.333; \(P=0.0008\)). Concerning sample sizes, miR-9 expression in small-sized studies \((n<100)\) was considered to be correlated with the outcome (combined HR =4.88, 95% CI: 3.40–6.99; \(P<0.00001\)), and the elevated expression in large-sized studies \((n\geq 100)\) also revealed a relation with the outcome of tumor patients (pooled HR =2.58, 95% CI: 1.63–4.08; \(P<0.0001\)), which suggested that the sample sizes did not significantly influence the predictive effect of miR-9. Seeing that the follow-up time of enrolled studies
### Table 2 Main characteristics of 18 studies after screening

<table>
<thead>
<tr>
<th>First author</th>
<th>Publication year</th>
<th>Country</th>
<th>Disease</th>
<th>Number</th>
<th>Sample (years)</th>
<th>Age (M/F)</th>
<th>MiR-9 assay</th>
<th>Cutoff value</th>
<th>Survival analysis</th>
<th>Multivariate analysis</th>
<th>Hazard ratio</th>
<th>Follow-up (months)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Xu et al&lt;sup&gt;23&lt;/sup&gt;</td>
<td>2014</td>
<td>People's Republic of China</td>
<td>Osteosarcoma</td>
<td>79</td>
<td>Tissue</td>
<td>NR</td>
<td>qRT-PCR</td>
<td>Median</td>
<td>OS</td>
<td>Reported</td>
<td>Reported</td>
<td>60</td>
</tr>
<tr>
<td>Cai and Cai&lt;sup&gt;11&lt;/sup&gt;</td>
<td>2014</td>
<td>People's Republic of China</td>
<td>HCC</td>
<td>200</td>
<td>Tissue</td>
<td>NR</td>
<td>qRT-PCR</td>
<td>Median</td>
<td>OS</td>
<td>Reported</td>
<td>Reported</td>
<td>60</td>
</tr>
<tr>
<td>Stattery et al&lt;sup&gt;25&lt;/sup&gt;</td>
<td>2015</td>
<td>USA</td>
<td>Colorectal cancer</td>
<td>1,141</td>
<td>FFPE</td>
<td>30–79</td>
<td>miRNA array</td>
<td>Interquartile</td>
<td>OS</td>
<td>NR</td>
<td>Reported</td>
<td>NR</td>
</tr>
<tr>
<td>Weidner et al&lt;sup&gt;18&lt;/sup&gt;</td>
<td>2014</td>
<td>Germany</td>
<td>AML</td>
<td>131</td>
<td>BM</td>
<td>22–75</td>
<td>qRT-PCR</td>
<td>Median</td>
<td>Relapse</td>
<td>NR</td>
<td>NR</td>
<td>48</td>
</tr>
<tr>
<td>Wu et al&lt;sup&gt;17&lt;/sup&gt;</td>
<td>2014</td>
<td>People's Republic of China</td>
<td>LSCC</td>
<td>103</td>
<td>Tissue</td>
<td>NR</td>
<td>qRT-PCR</td>
<td>Median</td>
<td>OS</td>
<td>Reported</td>
<td>Reported</td>
<td>&gt;24</td>
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<tr>
<td>Gwak et al&lt;sup&gt;18&lt;/sup&gt;</td>
<td>2014</td>
<td>Korea</td>
<td>Breast cancer</td>
<td>295</td>
<td>FFPE</td>
<td>26–87</td>
<td>qRT-PCR</td>
<td>Median</td>
<td>DFS</td>
<td>Reported</td>
<td>NR</td>
<td>2.4–127.2</td>
</tr>
<tr>
<td>Fei et al&lt;sup&gt;19&lt;/sup&gt;</td>
<td>2014</td>
<td>People's Republic of China</td>
<td>Osteosarcoma</td>
<td>178</td>
<td>PB</td>
<td>7–68</td>
<td>qRT-PCR</td>
<td>Median</td>
<td>OS</td>
<td>NR</td>
<td>NR</td>
<td>10–81</td>
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<tr>
<td>Xu et al&lt;sup&gt;30&lt;/sup&gt;</td>
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<td>People's Republic of China</td>
<td>NSCLC</td>
<td>116</td>
<td>Tissue</td>
<td>NR</td>
<td>qRT-PCR</td>
<td>Median</td>
<td>OS/PFS</td>
<td>Reported</td>
<td>Reported</td>
<td>20–48</td>
</tr>
<tr>
<td>Zhao et al&lt;sup&gt;31&lt;/sup&gt;</td>
<td>2014</td>
<td>Germany</td>
<td>HCC</td>
<td>91</td>
<td>Tissue</td>
<td>NR</td>
<td>qRT-PCR</td>
<td>Median</td>
<td>OS/DFS/RR</td>
<td>NR</td>
<td>NR</td>
<td>NR</td>
</tr>
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<td>Sugita et al&lt;sup&gt;22&lt;/sup&gt;</td>
<td>2014</td>
<td>Japan</td>
<td>ALL</td>
<td>55</td>
<td>BM</td>
<td>15–78</td>
<td>qRT-PCR</td>
<td>Median</td>
<td>OS/RFS</td>
<td>Reported</td>
<td>Reported</td>
<td>60</td>
</tr>
<tr>
<td>Wu et al&lt;sup&gt;13&lt;/sup&gt;</td>
<td>2013</td>
<td>People's Republic of China</td>
<td>Glioma</td>
<td>138</td>
<td>Tissue</td>
<td>38–46</td>
<td>qRT-PCR</td>
<td>Median</td>
<td>OS</td>
<td>Reported</td>
<td>Reported</td>
<td>60</td>
</tr>
<tr>
<td>Sun et al&lt;sup&gt;24&lt;/sup&gt;</td>
<td>2013</td>
<td>People's Republic of China</td>
<td>Ovarian</td>
<td>113</td>
<td>FFPE</td>
<td>50–median</td>
<td>qRT-PCR</td>
<td>Median</td>
<td>PFS</td>
<td>NR</td>
<td>NR</td>
<td>NR</td>
</tr>
<tr>
<td>Faria et al&lt;sup&gt;23&lt;/sup&gt;</td>
<td>2013</td>
<td>Brazil</td>
<td>ACC</td>
<td>30</td>
<td>Tissue</td>
<td>NR</td>
<td>qRT-PCR</td>
<td>NR</td>
<td>OS/RFS</td>
<td>N</td>
<td>NR</td>
<td>NR</td>
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<td>Pignot et al&lt;sup&gt;25&lt;/sup&gt;</td>
<td>2013</td>
<td>France</td>
<td>Bladder cancer</td>
<td>166</td>
<td>Tissue</td>
<td>31–91</td>
<td>qRT-PCR</td>
<td>Median</td>
<td>OS/RFS</td>
<td>Reported</td>
<td>Reported</td>
<td>2–100</td>
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<tr>
<td>Sun et al&lt;sup&gt;27&lt;/sup&gt;</td>
<td>2012</td>
<td>the Netherlands</td>
<td>AML</td>
<td>647</td>
<td>BM</td>
<td>NR</td>
<td>qRT-PCR</td>
<td>NR</td>
<td>OS/EFS/RFS</td>
<td>Reported</td>
<td>Reported</td>
<td>NR</td>
</tr>
<tr>
<td>Mald et al&lt;sup&gt;28&lt;/sup&gt;</td>
<td>2012</td>
<td>Japan</td>
<td>Leukemia</td>
<td>124</td>
<td>BM</td>
<td>20–85</td>
<td>qRT-PCR</td>
<td>NR</td>
<td>OS/RFS</td>
<td>Reported</td>
<td>Reported</td>
<td>17 (median)</td>
</tr>
<tr>
<td>Díaz-Beyá et al&lt;sup&gt;29&lt;/sup&gt;</td>
<td>2011</td>
<td>Spain</td>
<td>AML</td>
<td>85</td>
<td>BM</td>
<td>18–71</td>
<td>mRNA array</td>
<td>Median</td>
<td>S-year survival</td>
<td>Reported</td>
<td>Reported</td>
<td>NR</td>
</tr>
<tr>
<td>Song et al&lt;sup&gt;30&lt;/sup&gt;</td>
<td>2014</td>
<td>People's Republic of China</td>
<td>ESCC</td>
<td>243</td>
<td>Tissue</td>
<td>NR</td>
<td>qRT-PCR</td>
<td>Median</td>
<td>OS</td>
<td>Reported</td>
<td>Reported</td>
<td>60</td>
</tr>
</tbody>
</table>

**Note:** Studies that are in bold format were enrolled in the following meta-analysis.

**Abbreviations:** M, male; F, female; MiR-9, microRNA-9; NR, not reported; qRT-PCR, quantitative real-time polymerase chain reaction; mRNA, microRNA; OS, overall survival; FFPE, formalin-fixed paraffin-embedded; AML, acute myelocytic leukemia; BM, bone marrow; LSCC, laryngeal squamous cell carcinomas; PB, peripheral blood; NSCLC, non-small lung cancer; PFS, progression-free survival; HCC, hepatocellular carcinoma; DFS, death-free survival; RR, recurrence; ALL, acute lymphoblastic leukemia; RFS, relapse-free survival; ACC, adrenocortical cancer; EFS, event-free survival; ESCC, esophageal squamous cell carcinoma.
was not consistent, >60 months or <60 months, HRs were also pooled according to these two conditions. A fixed model was used to pool the HRs of research studies with patients whose follow-up time was >60 months (low heterogeneity, \( P=0.3 \) and \( I^2=18\% \)), and the combined HR was 3.97 (95\% CI: 3.12–5.07, \( P=0.00001 \)), which implied that high expression of \( \text{miR}-9 \) was associated with a lower long-term survival. Because a large heterogeneity (\( P=0.1 \) and \( I^2=64\% \)) existed between two research studies with patients whose follow-up time was <60 months, a random model was used to pool the HRs. However, \( \text{miR}-9 \) did not seem to play a predictive role of outcome (pooled HR = 1.96, 95\% CI: 0.96–4.02; \( P=0.06 \)) in this subgroup.

Publication bias

Begg’s plot and Egger’s test were used to assess the publication bias of the literatures. As shown in Figure 3, the Begg’s plot was almost symmetric, and the Egger’s regression intercept was 0.255. There was no evidence for significant publication bias in this meta-analysis.

Discussion

Currently, >2,000 miRNAs have been discovered in humans,\(^{31}\) and increasing evidence has indicated that numerous aberrant expression of miRNAs have been involved in many diseases.\(^{42}\) It is well known that >50\% of miRNAs were located in fragile sites or cancer-associated genomic region,\(^{43}\) and different expression levels of miRNAs had been found in various malignancy examination.\(^{44}\) Some high-expressed miRNAs acted as oncogenes by repressing tumor suppressors, and some downexpressed miRNAs acted as tumor suppressors by negatively regulating the oncogenes. They are therefore good candidates for using as diagnostic, prognostic, and predictive biomarkers.\(^{45-47}\)

\( \text{miR}-9 \) was initially found to be associated with neurogenesis.\(^{48}\) As its function and spectrum of action begin to be unraveled, \( \text{miR}-9 \) proves to be highly versatile, exerting various and sometimes opposite activities depending on the species and cellular context. Although most of the evidences indicate that \( \text{miR}-9 \) is upregulated in carcinomas and was related to cell proliferation, cell apoptosis, cell motility,
and tumor metastasis, conflicting findings exist. For instance, miR-9 was downregulated in ovarian cancer, and overexpression of miR-9 can suppress cellular proliferation and enhance apoptosis by downregulating nuclear factor κB1, testifying to the tumor suppressive role of miR-9. According to these, there was no accurate data to describe the role of miR-9 in carcinomas, and it was difficult to classify miR-9 as a tumor suppressor gene or an oncogene. But, miR-9 was still a good biomarker for evaluating the tumors prognosis. Thus, we conducted this meta-analysis to investigate the relationship between miR-9 expression and the survival in patients with cancers.

This systematic review with meta-analysis, representing a quantified synthesis of all published studies of miR-9, has found that high expression of miR-9 was significantly associated with poor survival in patients with various tumors. For OS, the pooled HR of higher miR-9 expression in tissues or bone marrow from patients with various tumors was 3.04 (95% CI: 1.96–4.73; \( P < 0.0001 \)). And subgroup analyses also showed interesting results. Elevated miR-9 expression was significantly related to a worse prognosis according to our study, based on 879 samples of solid tumor, which had an unfavorable role in leukemia patients (179 samples) as well. Furthermore, the result seemed to suggest that miR-9 was an ideal biomarker for poor outcome, not only in small-sized (50<n<100) research studies but also in larger (n>100) ones. In addition, in the subgroup analyses grouped by follow-up time, it was found that high expression of miR-9 was associated with a longer long-term survival when follow-up time was >60 months, but no correlation was found between the outcomes and those patients whose follow-up time was <60 months. This is the first meta-analysis to investigate the effectiveness of miR-9 in the prognosis for various types of tumors, and hence it substantially adds knowledge.

The findings of this review are based on a small sample size; hence, caution is required while interpreting the results. Although miR-9 has been widely investigated, unfortunately, only eight studies were eligible for pooled analysis, which might weaken the reliability of our results. Moreover, miR-9 expression level and prognosis were evaluated in various types of tumors, and only two studies were of the same type; hence, more well-designed clinical studies with a larger number of samples might be most effective. Besides, lack of abundant miR-9 expression data in a global population makes it difficult to set a standard value for the measurement of miR-9. Therefore, in the future research, it would be essential to include a larger number of samples to explore these questions in more depth, and there is a particular need for studies to assess the merits of miR-9 in all kinds of carcinomas.

Table 4 Meta-analysis of overall and subgroup analysis for miR-9 expression and OS in cancers

<table>
<thead>
<tr>
<th>Categories</th>
<th>Studies</th>
<th>Patients</th>
<th>HR (95% CI)</th>
<th>Model</th>
<th>Heterogeneity</th>
</tr>
</thead>
</table>
| OS               | 8       | 1,058    | 3.04 (1.96–4.73) | Random | 29.65
| Tumor type       |         |          |             |        |               |
| Solid tumor      | 6       | 879      | 2.97 (1.76–5.00) | Random | 27.79
| Leukemia         | 2       | 179      | 2.87 (1.55–5.33) | Fixed  | 1.85
| Sample size      |         |          |             |        |               |
| Smaller size (50<n<100) | 2   | 134      | 4.88 (3.40–6.99) | Fixed  | 0.27
| Larger size (n>100)  | 6       | 924      | 2.58 (1.63–4.08) | Random | 16.47
| Follow-up months |         |          |             |        |               |
| ≥60              | 6       | 839      | 3.97 (3.12–5.07) | Fixed  | 6.08
| <60              | 2       | 219      | 1.96 (0.96–4.02) | Random | 2.74

Abbreviations: miR-9, microRNA-9; OS, overall survival; HR, hazard ratio; CI, confidence interval.

![Begg's funnel plot with pseudo 95% confidence limits](image)

**Figure 3** Funnel plot for the publication bias.

**Abbreviations:** HR, hazard ratio; SE, standard error.
There were still several limitations in our meta-analysis. First, the results showed extreme heterogeneity between the studies of various types of cancers ($\chi^2=76.0\%$, $P=0.0001$), and subgroup analyses for OS were conducted according to the cancer subtype, the sample size, and the duration of follow-up. The subgroup analyses might explain a part of heterogeneity. Even so, more research studies for subgroup analyses are still needed to explore the source of identified heterogeneity. Second, although there was no significant evidence of publication bias in funnel plot of this meta-analysis, cautions should be taken because only studies published in English were selected, which could definitely cause language bias. And finally, the tendency for journals to publish positive results could also create certain bias.

Conclusion

Despite the aforementioned limitations, our results support that miR-9 has a prognostic role in various types of carcinomas and therefore might be useful therapeutic targets for the treatment of multiple tumors. Adequately, multicenter-designed prospective with a larger sample size would be of great value to confirm these findings in the future, and more clinical studies should be carried out to focus on the relationship between the expression of miR-9 and prognosis of other types of tumors.

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Disclosure

The authors report no conflicts of interest in this work.

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