Prognostic significance of CDH13 hypermethylation and mRNA in NSCLC

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Abstract: Aberrant methylation of CpG dinucleotides is a commonly observed epigenetic modification in human cancer. Thus, detection of aberrant gene promoter methylation as a tool for diagnosis of tumors or as a prognostic marker has been widely described for many types of cancers, including nonsmall cell lung cancer (NSCLC). Emerging evidence indicates that CDH13 is a candidate tumor suppressor in several types of human tumors, including NSCLC. However, the correlation between CDH13 hypermethylation and clinicopathological characteristics of NSCLC remains unclear. In the current study, we conducted a systematic review and meta-analysis to quantitatively evaluate the effects of CDH13 hypermethylation on the incidence of NSCLC and clinicopathological characteristics. Final analysis of 803 NSCLC patients from eleven eligible studies was performed. CDH13 hypermethylation was observed to be significantly higher in NSCLC than in normal lung tissue, with the pooled odds ratio (OR) from seven studies including 448 NSCLC and 345 normal lung tissue (OR, 7.85; 95% confidence interval, 5.12–12.03; P<0.00001). CDH13 hypermethylation was also associated with pathological types. The pooled OR was obtained from four studies, including 111 squamous cell carcinoma and 106 adenocarcinoma (OR, 0.35; 95% confidence interval, 0.19–0.66; P=0.001), which indicated that CDH13 hypermethylation plays a more important role in the pathogenesis of adenocarcinoma. NSCLC with CDH13 hypermethylation was found more frequently in poorly differentiated NSCLC patients. NSCLC patients with CDH13 hypermethylation had a lower survival rate than those without CDH13 hypermethylation. In addition, CDH13 mRNA high expression was found to correlate with better overall survival for all NSCLC patients followed for 20 years (hazard ratio, 0.81; P=0.0056). Interestingly, CDH13 mRNA overexpression was found to correlate with better overall survival only in adenocarcinoma patients (hazard ratio, 0.42; P=9.6e−09), not in squamous cell carcinoma patients (hazard ratio, 0.93; P=0.59). The results of this meta-analysis suggest that CDH13 hypermethylation is associated with an increased risk and worse survival in NSCLC. CDH13 hypermethylation and mRNA expression play an important role in carcinogenesis, progression, and development, as well as clinical outcomes.

Keywords: prognosis, methylation, lung cancer, tumor suppressor gene, meta-analysis, odds ratio, hazard ratio

Introduction

Epigenetic modification of gene expression plays an important role in carcinogenesis. Aberrant methylation of CpG dinucleotides is a commonly observed epigenetic modification in human cancer.¹⁻³ Loss of function in cancer suppressor genes may hinder cancer cell growth inhibition, which leads to malignant transcription and translation during replication of DNA. Thus, analysis of specific gene promoter methylation as a
tool for diagnosis of tumors and its use as a prognostic marker have been widely used for many different cancers, including nonsmall cell lung cancer (NSCLC). A number of genes including the cyclin-dependent kinase inhibitor (p16), the tumor suppressor gene cystic fibrosis transmembrane conductance regulator, the DNA repair gene MGMT, Ras association domain family protein 1A, and Kelch-like ECH-associating protein 1, and so on are demonstratively methylated across NSCLC.  

Cadherins, which function as membrane receptors mediating outside-in signals, activating small GTPases and the β-catenin/Wnt pathway, and resulting in dynamic cytoskeleton reorganization and changes in the phenotype, are important determinants of tumor progression, serving as suppressors of invasion and metastasis in many contexts. Although signaling partners and adapter proteins for CDH13 remain to be elucidated, it is well known that CDH13 is involved in low-density lipoproteins, hormone-like effects on Ca\(^{2+}\)-mobilization and increased cell migration, phenotype changes, insulin-dependent signaling, eNOS activation, and angiogenesis.

Its precise function has been intensively studied in several tumors, with upregulation of inducing cell cycle arrest, apoptosis, and inhibition of angiogenesis. Lack of protein expression of CDH13 by promoter methylation (hypermethylation) and/or gene deletion has been found to play an important role in lung alveolar differentiation regulation and epithelial tumorigenesis. However, its roles in NSCLC and clinical significance have not been thoroughly investigated. In this study, we review and update the published clinical investigations regarding the effect of CDH13 on patients with NSCLC.

Material and methods

Search strategy and selection criteria

We searched PubMed, Embase and ISI Web of Knowledge to identify studies from May 1, 1998, to March 1, 2014, using the search terms “lung,” “cancer or tumor or neoplasm or carcinoma,” “methylation,” and “CDH13 or H-cadherin or T-cadherin or cadherin 13.” We also manually searched the reference lists of the retrieved articles and reviews for additional articles.

Although our search did not have language limits initially, for the full-text reading and final evaluation, we only performed a review of the studies published in the English language. After exclusion of irrelevant and/or redundant publications from the different databases, the remaining papers were evaluated in the full-text version for inclusion and exclusion criteria, and for relevant articles in the reference lists. All searched data were retrieved. Authors’ bibliographies and references from selected studies were also searched for other relevant studies. The most complete study was chosen to avoid duplication if the same patient populations were reported in several publications.

The criteria that an eligible study had to meet were as follows: CDH13 hypermethylation evaluated in the primary NSCLC tissues, studies revealed the relationship between CDH13 hypermethylation and NSCLC clinico pathological parameters and prognosis, CDH13 hypermethylation examined by polymerase chain reaction, and studies provided sufficient information to estimate hazard ratio (HR) about overall survival (OS) and 95% confidence intervals (CIs). The exclusion criteria included the following: letters, reviews, case reports, conference abstracts, editorials, and expert opinion; all publications regarding in vitro/ex vivo studies, cell lines, and human xenografts were also excluded.

Data extraction and methodological assessment

Two authors (RX, CY) independently reviewed and extracted data from eligible studies. Disagreements were resolved by discussion and consensus. Two authors (FZ, DL) reviewed all of the articles that fit inclusion and exclusion criteria. The following information was recorded for each study: first author name, year of publication, sample source, number of cases, clinico pathological parameters, cancer tumor node metastasis stage, methylation detection method, methylation rate and/or expression, and follow-up. Data for study characteristics and clinical responses were summarized and turned into a table. The heterogeneity of the investigation was evaluated to determine whether the data of the various studies could be analyzed for a meta-analysis.

For the methodological evaluation of the studies, three investigators (DL, CY, and FZ) read through the publications independently and assessed and scored them according to Reporting Recommendations for Tumor Marker Prognostic Studies guidelines and the European Lung Cancer Working Party quality scale. The three readers provided the quality scores, compared them, and then reached a consensus value for each item.

Patient survival analysis

An online database was used to assess relevance of CDH13 mRNA expression to relapse-free survival. The database

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was established using gene expression data and survival information from 1,405 NSCLC patients downloaded from Gene Expression Omnibus. Briefly, CDH13 was entered into the database (http://kmplot.com/analysis/index.php?p=service&cancer=lung) to obtain Kaplan-Meier survival plots in which the number at risk is indicated below the main plot. HR and 95% CIs and logrank $P$ were calculated and displayed on the Web page.

Statistical analysis
Analysis was conducted using the STATA 12.0 (Statat Corporation) and Review Manager 5.2 (Cochrane Collaboration). The pooled frequency of CDH13 hypermethylation and 95% CIs were estimated. The frequency of CDH13 hypermethylation was compared in different tumor characteristics. Heterogeneity among studies was evaluated with Cochran’s Q test and the $I^2$ statistic. When heterogeneity was not an issue ($I^2$ values $\leq 50\%$), a fixed-effect model was used to calculate parameters. If there was substantial heterogeneity ($I^2$ values $\geq 50\%$), a random-effects model was used to pool data and to attempt to identify potential sources of heterogeneity based on subgroup analyses. The pooled OR was estimated for the association between CDH13 hypermethylation and clinicopathological features. $P$-values two-tailed less than 0.05 were considered statistically significant.

Publication bias was assessed by using a method reported by Egger and colleagues. We also explored reasons for statistical heterogeneity using meta-regression, subgroup analysis, and sensitivity analysis. The analysis of meta-regression and publication bias was performed by using STATA version 10.0.

Results
Identification of relevant studies
Forty-five publications were identified by the search method, as described earlier. Thirty-four of those were excluded because they were laboratory studies, nonoriginal articles (reviews), or studies irrelevant to the current analysis. Eventually, there were eleven studies included in final meta-analysis, as shown in Figure 1.

Study characteristics
Eleven studies published from 2001 to 2012 were eligible for meta-analysis. A total of 803 NSCLC patients from China, Japan, South Korea, Italy, Serbia, and the United States were enrolled. There were five studies from Western countries, in which CDH13 hypermethylation rates were from 15.6%–65.6%, with an average of 44.0%. There were six studies from Asian countries, in which CDH13 hypermethylation rates were from 26.7%–53.6%, with an average of 39.3%. There are no big differences in CDH13

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Figure 1 Flow chart of study selection.
hypermethylation rates between Western and Asian patients. Their basic characteristics are summarized in Table 1.

The correlation of \textit{CDH13} hypermethylation with clinicopathological features

The inactivation of \textit{CDH13} through hypermethylation in NSCLC

The loss of \textit{CDH13} mRNA and/or protein expression was strongly correlated with the promoter hypermethylation in several types of cancer including NSCLC.\textsuperscript{25,26,35–43} \textit{CDH13} hypermethylation was significantly higher in NSCLC than normal lung tissue. The pooled OR from seven studies including 448 NSCLCs and 345 normal lung tissues is shown in Figure 2 (OR, 7.85; 95% CI, 5.12–12.03; \(P<0.00001\)), indicating that \textit{CDH13} inactivation through hypermethylation plays an important role in the carcinogenesis of NSCLC.

Relationship between the frequency of \textit{CDH13} hypermethylation and pathological types

Histology was associated with \textit{CDH13} hypermethylation, which was observed more frequently in patients with adenocarcinoma.\textsuperscript{44} The pooled OR from 4 studies, including 111 of squamous cell carcinoma and 106 of adenocarcinoma, is shown in Figure 3 (OR, 0.35; 95% CI, 0.19–0.66; \(P=0.001\)), indicating that \textit{CDH13} hypermethylation plays more important role in the pathogenesis of adenocarcinoma.

The role of \textit{CDH13} hypermethylation in NSCLC progression

We analyzed 363 NSCLC patients pooled from 4 studies to assess whether the aberrant \textit{CDH13} hypermethylation

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**Table 1 Basic characteristics of the included studies**

<table>
<thead>
<tr>
<th>Study</th>
<th>Country</th>
<th>Patients</th>
<th>Methods</th>
<th>Primary aim</th>
<th>Methylation site</th>
<th>CDH13 expression</th>
</tr>
</thead>
<tbody>
<tr>
<td>Kontic et al\textsuperscript{44}</td>
<td>Serbia</td>
<td>65</td>
<td>MSP</td>
<td>Determine the frequency of \textit{CDH13} hypermethylation in NSCLC</td>
<td>Promoter, CpG islands</td>
<td>–</td>
</tr>
<tr>
<td>Zhang et al\textsuperscript{45}</td>
<td>People’s Republic of China</td>
<td>78</td>
<td>MSP</td>
<td>Determine the methylation status of multiple genes in NSCLC</td>
<td>Promoter, CpG islands</td>
<td>–</td>
</tr>
<tr>
<td>Kubo et al\textsuperscript{46}</td>
<td>Japan</td>
<td>100</td>
<td>MSP</td>
<td>Determine the methylation status of five tumor suppressor in NSCLC</td>
<td>Promoter, CpG islands</td>
<td>–</td>
</tr>
<tr>
<td>Feng et al\textsuperscript{47}</td>
<td>United States</td>
<td>49</td>
<td>DNA methylation (MethyLight analysis)</td>
<td>Determine the clinical significance of seven tumor suppressors in NSCLC</td>
<td>Promoter, CpG islands</td>
<td>–</td>
</tr>
<tr>
<td>Brock et al\textsuperscript{48}</td>
<td>United States</td>
<td>79</td>
<td>MSP</td>
<td>Determine the association between gene methylation and recurrence in NSCLC</td>
<td>Promoter, CpG islands</td>
<td>–</td>
</tr>
<tr>
<td>Wang et al\textsuperscript{49}</td>
<td>People’s Republic of China</td>
<td>28</td>
<td>DNA microarray-coupled polymerase chain reaction</td>
<td>Determine 15 genes’ methylation status in NSCLC</td>
<td>Promoter, CpG islands</td>
<td>–</td>
</tr>
<tr>
<td>Kim et al\textsuperscript{50}</td>
<td>South Korea</td>
<td>88</td>
<td>MSP</td>
<td>Determine the role of \textit{CDH13} in pathogenesis of NSCLC</td>
<td>Promoter, CpG islands</td>
<td>–</td>
</tr>
<tr>
<td>Hsu et al\textsuperscript{51}</td>
<td>People’s Republic of China</td>
<td>63</td>
<td>MSP</td>
<td>Determine methylation patterns of six tumor suppressor gene in NSCLC</td>
<td>Promoter, CpG islands</td>
<td>–</td>
</tr>
<tr>
<td>Suzuki et al\textsuperscript{52}</td>
<td>Japan</td>
<td>150</td>
<td>MSP</td>
<td>The methylation profile of nine genes for NSCLC were analyzed and correlated with clinical data</td>
<td>Promoter, CpG islands</td>
<td>–</td>
</tr>
<tr>
<td>Ulivi et al\textsuperscript{53}</td>
<td>Italy</td>
<td>61</td>
<td>MSP</td>
<td>Detection of promoter methylation of p16\textsuperscript{INK4A} and \textit{CDH13} genes in NSCLC</td>
<td>Promoter, CpG islands</td>
<td>–</td>
</tr>
<tr>
<td>Toyooka et al\textsuperscript{54}</td>
<td>United States</td>
<td>42</td>
<td>MSP</td>
<td>Analyze DNA methylation status of \textit{CDH13} gene in NSCLC patients</td>
<td>Promoter, CpG islands</td>
<td>–</td>
</tr>
</tbody>
</table>

**Abbreviations:** NSCLC, nonsmall cell lung cancer; MSP, methylation-specific polymerase chain reaction.
in NSCLC was associated with advanced stage. As shown in Figure 4, aberrant CDH13 hypermethylation was not significantly higher in advanced NSCLC (stage III and IV) than in early-stage NSCLC (stage I and II; OR, 0.93; 95% CI, 0.57–1.53; P=0.79). However, as shown in Figure 5, aberrant CDH13 hypermethylation was significantly higher in poorly differentiated NSCLC than in moderately and highly differentiated NSCLC (OR, 3.61; 95% CI, 1.76–7.39; P=0.0004). These results suggest that CDH13 hypermethylation may play an important role in NSCLC progression and development.

**CDH13 hypermethylation as a prognostic factor for NSCLC**

There were four studies that estimated the relationship between CDH13 hypermethylation and OS in NSCLC. The pooled HR for OS showed that CDH13 hypermethylation was associated with worse survival in NSCLC patients, as shown in Figure 6 (HR, 3.21; 95% CI, 1.41–7.31; P=0.005).

**Sensitivity analyses and publication bias**

A sensitivity analysis, in which one study was removed at a time, was conducted to assess the result stability. The pooled ORs and HRs were not significantly changed, indicating the stability of our analyses. The funnel plots were largely symmetric (Figure 7), suggesting there were no publication biases in the meta-analysis of CDH13 hypermethylation and clinicopathological features.

**Effect of CDH13 mRNA expression on prognosis of NSCLC**

The clinical relevance of CDH13 was further corroborated in a patient survival analysis, using an online database containing...
Table 1

<table>
<thead>
<tr>
<th>Study or subgroup</th>
<th>Events Total</th>
<th>Odds ratio M–H, fixed, 95% CI</th>
<th>Weight</th>
</tr>
</thead>
<tbody>
<tr>
<td>Poorly differentiated</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Kontic et al44</td>
<td>10 37</td>
<td>16 51</td>
<td>30.1% 0.81 (0.32, 2.07)</td>
</tr>
<tr>
<td>Kubo et al56</td>
<td>3 23</td>
<td>7 41</td>
<td>13.4% 0.73 (0.17, 3.14)</td>
</tr>
<tr>
<td>Suzuki et al68</td>
<td>29 99</td>
<td>11 51</td>
<td>31.5% 1.51 (0.68, 3.34)</td>
</tr>
<tr>
<td>Ulivi et al60</td>
<td>9 17</td>
<td>31 44</td>
<td>24.9% 0.47 (0.15, 1.49)</td>
</tr>
<tr>
<td>Total (95% CI)</td>
<td>176 187</td>
<td>100.0%</td>
<td>0.93 (0.57, 1.53)</td>
</tr>
</tbody>
</table>

Heterogeneity: $\chi^2=2.44, df=2 (P=0.30); I^2=18\%$
Test for overall effect: $Z=3.51 (P=0.0004)$

Figure 5 Aberrant CDH13 hypermethylation was significantly higher in poorly differentiated nonsmall cell lung cancer than that in moderately and highly differentiated nonsmall cell lung cancer.

Notes: Odds ratio, 3.61; 95% CI, 1.76–7.39; $P=0.0004$.
Abbreviations: CI, confidence interval; M–H, Mantel–Haenszel.
<table>
<thead>
<tr>
<th>Study or subgroup</th>
<th>Log (Hazard ratio)</th>
<th>SE</th>
<th>Weight IV, random, 95% CI</th>
<th>Hazard ratio IV, random, 95% CI</th>
</tr>
</thead>
<tbody>
<tr>
<td>Brock et al²³</td>
<td>2.054</td>
<td>0.563</td>
<td>23.8%</td>
<td>7.80 (2.59, 23.51)</td>
</tr>
<tr>
<td>Kim et al²⁴</td>
<td>0.238</td>
<td>0.471</td>
<td>27.3%</td>
<td>1.27 (0.50, 3.19)</td>
</tr>
<tr>
<td>Suzuki et al²⁵</td>
<td>1.649</td>
<td>0.519</td>
<td>25.4%</td>
<td>5.20 (1.88, 14.39)</td>
</tr>
<tr>
<td>Zhang et al²⁴</td>
<td>0.827</td>
<td>0.57</td>
<td>23.5%</td>
<td>2.29 (0.75, 6.99)</td>
</tr>
<tr>
<td><strong>Total (95% CI)</strong></td>
<td></td>
<td></td>
<td></td>
<td>3.21 (1.41, 7.31)</td>
</tr>
</tbody>
</table>

Heterogeneity: $\chi^2 = 7.56$, df = 3 ($P = 0.06$); $I^2 = 60\%$

Test for overall effect: $Z = 2.78$ ($P = 0.005$)

Figure 6 The four studies included investigated the relationship between overall survival and $CDH13$ hypermethylation.

Notes: The pooled hazard ratio for overall survival showed that $CDH13$ hypermethylation was associated with worse survival in nonsmall cell lung cancer. Hazard ratio, 3.21; 95% CI, 1.41–7.31; $P = 0.005$.

Abbreviations: SE, standard error; CI, confidence interval.

significantly higher in advanced NSCLC (stage III and IV) than in early-staged NSCLC (stage I and II). However, aberrant $CDH13$ hypermethylation was significantly higher in poorly differentiated NSCLC than in moderately and highly differentiated NSCLC. In addition, NSCLC patients with $CDH13$ hypermethylation had a lower survival rate than those without $CDH13$ hypermethylation. The results from the current study demonstrated that the hypermethylation rate of the $CDH13$ gene promoter in NSCLC was significantly higher than that in the normal lung tissues, indicating that $CDH13$ promoter hypermethylation was common in NSCLC. Because changes in $CDH13$ promoter hypermethylation are reversible, drug treatment through demethylation may be useful to delay carcinogenesis and progression and improve prognosis.

Figure 7 The funnel plots were largely symmetric, suggesting there were no publication biases in the meta-analysis of $CDH13$ hypermethylation and clinicopathological features.

Notes: (A) The funnel plot from seven studies comparing nonsmall cell lung cancer and normal lung tissue. (B) The funnel plot from four studies comparing $CDH13$ hypermethylation between squamous cell carcinoma and adenocarcinoma. (C) The funnel plot from four studies in determining $CDH13$ hypermethylation in differently staged nonsmall cell lung cancer. (D) The funnel plot from three studies determining $CDH13$ hypermethylation in different differentiated nonsmall cell lung cancer. (E) The funnel plot from four studies determining the relationship between $CDH13$ hypermethylation and overall survival in nonsmall cell lung cancer.

Abbreviations: OR, odds ratio; SE, standard error.
This approach may bring new direction and hope for cancer treatment through gene-targeted therapy.

Epigenetic alterations, particularly aberrant DNA methylation, one of the best-characterized epigenetic modifications, contribute to tumor initiation and progression. CDH13 is thought to affect cellular function and behavior largely through its signaling properties. CDH13 reexpression in most cancer cell lines inhibits cell proliferation and invasiveness, increases susceptibility to apoptosis, and reduces tumor growth in vivo models. Therefore, CDH13 can be considered a tumor suppressor, and its inactivation could contribute to tumor progression and poor prognosis. Although only four studies evaluated the relationship between overall survival and CDH13 hypermethylation in NSCLC, they showed very similar results.

According to this meta-analysis, we may consider that hypermethylation is associated with an increased risk and worse survival in NSCLC. Further large-scale studies, especially multicenter and well-matched cohort research, will provide more insight into the role of CDH13 in the prognosis and clinical implementation of NSCLC patients.

Disclosure
The authors report no conflicts of interest in this work.

References